Enrichment and Identification of Methylation at the Proteome Level

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ABSTRACT

Methylation is a post-translational modification which occurs on lysine and arginine residues. Methylation is difficult to detect due to its low abundance and lack of charge. Our laboratory previously developed a novel enrichment approach, ProMENADe, for lysine and arginine methylation in the human embryonic kidney (HEK) 293T cell line which is coupled with mass spectrometry.

Simplifying a lysate with subcellular fractionation prior to enrichment increased the identification of methylation sites by 39.5% while using multiple proteases for digestion increased identification by 27%. Combining these methods yielded a 47.2% increase. Analysis at the 1% methylation level FDR filtered for C-terminal methylation identified 169 sites and further analysis revealed 74 of these sites overlap with the PhosphoSite database. This ProMENADe enrichment strategy yielded 95 novel methylation sites to the field and can be a key tool in the field of methylation allowing for the enrichment and identification of methylated proteins.

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STATEMENT OF CONTRIBUTION

All experiments were conducted by Alexandra Star (AS). Experimental design was conducted by Daniel Figeys (DF), Janice Mayne (JM) and Zhibin Ning (ZN) and AS. Data analysis was conducted by AS with the advice and mentoring of ZN.

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ABBREVIATIONS

ACN: acetonitrile
ADAM10: a disintegrin and metalloproteinase domain-containing protein 10
ADMA: asymmetric di-methylation of arginine
ADP: adenosine diphosphate
ANOVA : analysis of variance
Blimp1: PR domain zinc-finger protein
BRG1: Brahma-related gene1, also known as transcription activator BRG1 or ATP-dependent helicase SMARCA4
CA150: coactivator 150 kDa
CARM1: coactivator-associated arginine methyltransferase
CBP: CREB-binding protein
CDK: cyclin-dependent kinase
Clr4: Histone lysine-N-methyltransferase, histone H3 lysine-9 specific
COMPASS: Complex of Proteins Associated with Set1
CREB: cAMP response element-binding protein
DAVID: The Database for Annotation, Visualization and Integrated Discovery
DDAH: dimethylarginine dimethylaminohydralase
DMEM: Dulbecco's Modified Eagle's Medium
DNA: deoxyribonucleic acid
DNMT: DNA methyltransferase
DOT1L: DOT1-like histone H3K79 methyltransferase
DTT: dithiothreitol
E2F: transcription factor E2F
E2F1: transcription factor E2F1
EEF1A1: elongation factor 1 A 1
EHMT1: histone-lysine-N-methyltransferase EHMT1, also known as GLP1
EHMT2: histone-lysine-N-methyltransferase EHMT2, also known as G9a
ERα: estrogen receptor alpha
ESCC: esophageal squamous cell carcinoma
EZ/E(z): enhancer of zeste
FA: formic acid
FBS: fetal bovine serum
FDR: false discovery rate
G9a: see EHMT2
GLP1: see EHMT1
GO: Gene Ontology
GRAVY: grand average of hydropathy
H3K4: histone H3 at lysine 4
H3K9: histone H3 at lysine 9

H3K36: histone H3 lysine 36
H3K79: histone H3 lysine 79
H3R8: histone H3 at arginine 8
H4R3: histone H4 at arginine 3
HBHA: heparin-binding hemagglutinin
hBRM: human Brahma protein
HCD: high energy C-trap dissociation
HCT116: human colon colorectal cell line
HCl: hydrochloric acid
HEK: human embryonic kidney
HeLaS3: a human cervix adenocarcinoma cell line
HILIC: hydrophilic interaction liquid chromatography
HP1: heterochromatin protein 1
HP1β: heterochromatin protein 1 β
HPLC: high performance liquid chromatography
HRP: horseradish peroxidase
IAA: iodoacetamide
KMTs: lysine methyltransferases
L3MBTL1: lethal (3) malignant brain tumour like protein 1
LBP: lipopolysaccharide binding protein
LC: liquid chromatography
3XMBT: 3 malignant brain tumour repeats
MDA: malondialdehyde
MEFs: mouse embryonic fibroblasts
MMA: mono-methylation on arginine
mmu: milli mass unit
mRNA: messenger RNA
MS: mass spectrometry
MYND: Myeloid, Nervy, and DEAF-1
MYPT1: myosin phosphatase target subunit 1
m/z: mass to charge ratio
NaOH: sodium hydroxide
NFκB: nuclear factor kappa B
NO: nitric oxide
NOS: nitric oxide synthase
OmpB: outer membrane protein B
OPA: ortho-phthaldialdehyde
p21 : cyclin-dependent kinase inhibitor
p53: tumour protein p53
p300: histone acetyltransferase p300
PaxDb: Protein Abundance Across Organisms Database

PBS: phosphate buffered saline
pI: isoelectric points
ppm: parts per million
pRb: tumour suppressor retinoblastoma protein
PRMTs: protein arginine methyltransferases
ProMENADe: Protein Methylation Enrichment by Neutralizing Amine through Derivatization
PTM: post translational modification
REAP: Rapid Efficient and Practical
RelA: REL-associated protein, nuclear factor kappa B p65 subunit
RIZ: retinoblastoma-interacting zinc-finger
RNA: ribonucleic acid
SAH: S-adenosyl-L-homocysteine
SAM: S-adenosyl-L-methionine
SAP49: RNA binding protein SAP49
SCX: strong cation exchange
SDMA: symmetric di-methylation of arginine
SDS: sodium dodecyl sulphate
SET: Suppressor of variegation 3-9, Enhancer of zeste, and Trithorax
SET1A/B: SET-domain protein 1 A/B
SET7/9: SET-domain protein 7/9
SILAC: stable isotope labeling by amino acids in cell culture
siRNA: small interfering RNA
SMA: spinal muscular atrophy
SMN: survival of motor neuron
SMYD: SET and MYND domain-containing protein
Snail: zinc-finger protein SNAI1
snRNA: small nuclear ribonucleic acid
snRNP: small nuclear ribonucleic protein
SRC3: steroid-receptor coactivator-3
STAT3: signal transducer and activator of transcription 3
SUV39: suppressor of variegation 3-9
Suv39h1: human homolog of SUV39
SUV4-20: suppressor of variegation 4-20
Swi6: chromatin-associated protein Swi6
TAF10: TBP-associated factor TAF10
TBP: TATA-box binding protein
TBST: tris-buffered saline and tween
THW loop: threonine-histidine/tryptophan loop
TiPP: 1,1,3,3-tetraisopropoxypropane
Trx: trithorax

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1. INTRODUCTION

I. Proteomics and Post-Translational Modifications

Proteomics studies the protein profile expressed and modified by cells and tissues [1]. The term was coined by Marc Wilkins in 1994 following the rise of other high throughput methodologies used for genomics. The study of proteins builds upon genomic data by allowing for the determination of the protein abundance, interactions, and modifications in cellular pathways under different conditions like disease states, over time, or upon drug treatment or mutation, in order to infer protein function. Uhlen *et al*. (2015) recently reported a genome-wide analysis of the ribonucleic acid (RNA) and proteins expressed in multiple tissue and organ samples in human [2]. This is the most comprehensive study of the human proteome to date and is a promising resource for the field of proteomics.

Post-translational modifications (PTMs) add a further level of complexity by modifying protein structure and function. According to UniProt, more than 200 PTMs have been characterized to date. These modifications include both proteolytic cleavage events and the covalent addition of a modifying group after protein synthesis. Proteolytic cleavage events include the removal of the N-terminal methionine on a protein, the removal of a signal peptide to target the protein to an organelle or for secretion, and the conversion of an inactive protein to an active one. For example, the C-terminal fragment of neuroligin-1 is cleaved by ɣ-secretase to release its intracellular domain. Inhibition of this cleavage results in the inhibition of neuroligin-1 shedding and accumulation of the full-length protein while overexpression of a disintegrin and metalloproteinase domain-containing protein 10 (ADAM10), the ɣ-secretase responsible for cleavage, increased the production of secreted

neuroligin-1. The protein level of neuroligin-1 is required for the formation of the dendritic spine and is thus regulated by the processing of neuroligin-1 [3].

Covalent modifications change the size, and charge of a protein resulting in a change of activity and function. They can help in recruiting to and concealing the active sites and motifs for protein-protein interactions [4]. These modifications occur at the C- and N-termini of the protein and also occur at the amino acid side chains. The nucleophilic side chains on amino acid groups are the ones most likely to have a modification: the hydroxyl groups on serine, threonine and tyrosine, the amine groups on lysine, arginine, and histidine, the thiolate anion on cysteine and the carboxyl groups of aspartate and glutamate.

The study of PTMs has increased in importance over the years as there is a desire to know more about how PTMs affect and regulate protein-protein interactions, biological functions, and other PTMs [5-8]. The study of PTMs can be challenging due to the transience of PTMs in signal transduction pathways, the introduction of experimentally-induced PTMs, as well as enriching for the low-abundant modified peptides as PTMs are of sub-stoichiometric abundance. Our laboratory focuses on method development to study PTMs such as glycosylation and phosphorylation [9-11]. These method development strategies are now being applied to perform a large-scale study of protein methylation.

II. Protein Methylation

Methylation was first discovered in the flagella protein of *Salmonella typhimurium* by Ambler and Rees in 1959 [12] and is one of the most prevalent PTMs [13]. It occurs in all three domains of life: eukaryotes, bacteria and archaea [14-17] and occurs on both nuclear and cytosolic proteins [18]. Methyl groups are transferred from S-adenosyl-L-methionine

(SAM) to deoxyribonucleic acid (DNA) [19-21], RNA [22, 23] and proteins [24-26] releasing S-adenosyl-L-homocysteine (SAH). These reactions are catalyzed by enzymes called methyltransferases. The methyl groups are added in a sequential order by the methyltransferases.

Protein methylation predominantly occurs on arginine [25] and lysine residues [27-32] but can also occur on other amino acid side chains such as cysteine [33], histidine [26], glutamate [34], aspartate [34], glutamine [35] and protein N- [36, 37] and C-termini [38, 39].

i. Arginine Methylation

Arginine residues can be mono-, or di-methylated at one or both of their amino groups. Three different types of methylation on arginine can occur in eukaryotes: mono-methylation (MMA), asymmetric di-methylation (ADMA), and symmetric di-methylation (SDMA) of the omega amino group [40] (Figure 1A). Asymmetric di-methylation refers to the addition of two methyl groups to one amino group in the arginine's guanidine group while symmetric di-methylation refers to the addition of one methyl group to each amino group of arginine's guanidine group. Mono-methylation at the delta amino group is rare and has only been reported in *Saccharomyces cerevisiae* [41].

The enzymes that catalyze methylation on arginine residues are the protein arginine methyltransferases (PRMTs) [40]. These methyltransferases have four conserved motifs: motif I, post-I, II, and III and the threonine-histidine/tryptophan (THW) loop [42]. The THW loop and I and post-I motifs make up the SAM-binding pocket [43, 44].

There are eleven known PRMTs in human and only four in *Saccharomyces cerevisiae* [45]. There are four types of PRMTs: Types I, II, III, and IV. Type I catalyze

formation of MMA and ADMA [46, 47], Type II catalyze formation of MMA and SDMA [48, 49], Type III PRMTs only catalyze MMA [50, 51] and Type IV mono-methylates the delta nitrogen in *Saccharomyces cerevisiae* [41]. Arginine methylation tends to occur on the following motifs: RGG repeats, RGX, RXG, GXXRXG, GXXR and WXXR motifs [17].

ii. Lysine Methylation

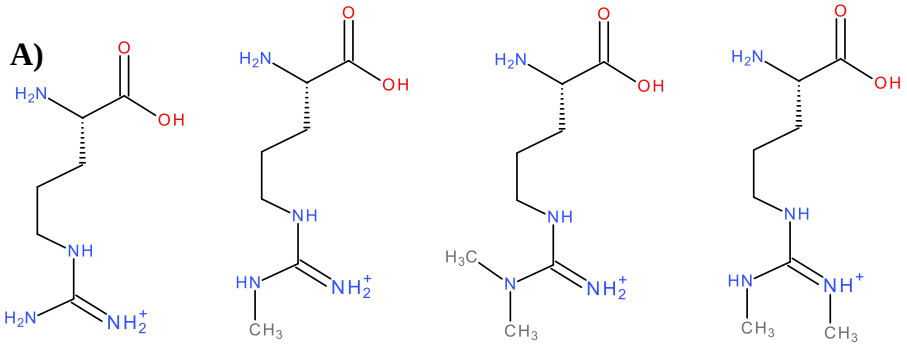
Lysine residues can have one, two or three methyl groups added at their epsilon (ε) amino group (Figure 1B). The transfer of a methyl group(s) to lysine from SAM is catalyzed by lysine methyltransferases (KMTs) by an S_N2 nucleophilic attack (Figure 1C). There are two classes of lysine methyltransferases which use SAM as a methyl donor: the SET domain KMTs and the seven-beta-strand methyltransferases [52]. The seven-beta-strand methyltransferases methylate several different types of residues while the SET domain KMTs are lysine-specific superfamily consisting of about 56 members.

The SET domain is a 130 amino acid long sequence named after the three *Drosophila melanogaster* proteins where it was first found to be conserved: suppressor of variegation 3-9 (Su(var)3-9) [53], the polycomb-group chromatin regulator enhancer of zeste (E(z)) [54], and the trithorax-group chromatin regulator trithorax (Trx) [55]. The SET protein KMTs can be organized into seven main families: suppressor of variegation 3-9 (SUV39), SET1, SET2, enhancer of zeste (EZ), retinoblastoma protein-interacting zinc finger (RIZ), SET and MYND (Myeloid, Nervy, and DEAF-1) domain-containing protein (SMYD), and suppressor of variegation 4-20 (SUV4-20) [56].

The SET domain is composed of three regions folded into a β-sheet which surround a "knot-like" structure. This structure forms the active site with the motifs GxG, YxG,

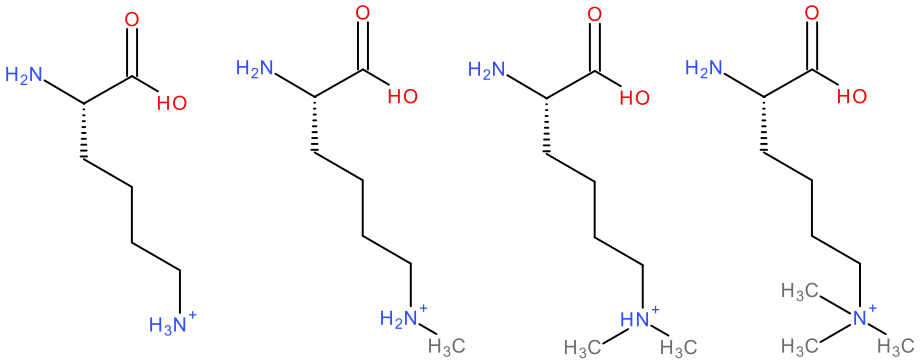
Figure 1: Structures of methylated lysine and arginine, and proposed mechanism of methyl transfer from S-adenosyl-L-methionine (SAM) to the epsilon amino group of lysine. A) Diagram of methylation on the amino groups of arginine. Arginine can be mono-methylated and di-methylated both symmetrically and asymmetrically. B) Lysine can be mono-, di-, and tri-methylated at its epsilon amino group. C) The transfer of the methyl group from SAM to the epsilon amino group of lysine by S_N2 nucleophilic attack on the SAM methyl group.

A)



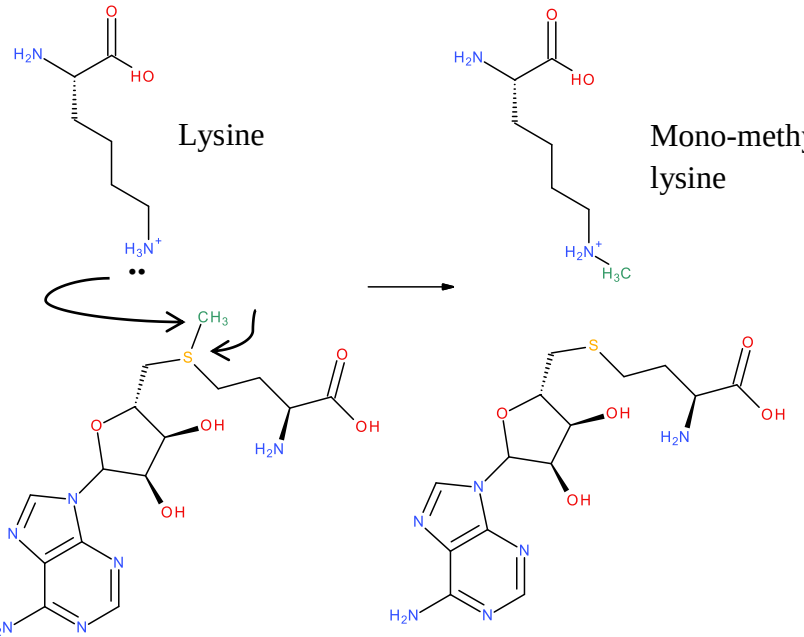
Arginine | Mono-methyl arginine | Asymmetrical dimethyl arginine | Symmetrical dimethyl arginine

B)



Lysine | Mono-methyl lysine | Di-methyl lysine | Tri-methyl lysine

C)



S-adenosyl-L-methionine | S-adenosyl-L-homocysteine

NHS/CxxPN, and ELxF/YDY next to where the methyl donor binds [56-58]. The SET domain is surrounded by the preSET (N-SET) and the postSET (C-SET) domains. The function of the preSET is to maintain the structural stability by interacting with the SET domain while an aromatic residue in the postSET domain aids in making the hydrophobic channel implicated in determining the multiplicity of methylation in the active site [57, 59, 60]. These sequences are not conserved between KMTs. Lastly, there is an inserted region called i-SET which is responsible for interaction with the lysine substrate [57, 61-64].

III. Biological Roles of Protein Methylation

i. Protein Methylation in Transcriptional Regulation

Along with acetylation, phosphorylation, ubiquitination and adenosine diphosphate (ADP)-ribosylation, methylation is involved in the modification of histone tails to regulate the access of transcriptional machinery to genes thus controling the expression of those genes. Lysine methylation is well characterized for its occurrence on histone proteins where it is associated with either the transcriptionally silent chromatin regions like heterochromatin [65-68], or with the active regions like in euchromatin [69-71]. Methylation on histone H3 at lysines 4, 36, or 79 are all found in active genes while methylation on histone H3 at lysine 9 or 27 or on histone H4 at lysine 20 are found at silenced genes.

An example at silenced genes is the methylation of histone H3 at lysine 9 (H3K9) which has been linked to formation of heterochromatin and to gene silencing. The Suv39h1/HP1 (heterochromatin protein 1) and the Histone-N-methyltransferase Clr4/ chromatin associated protein Swi6 systems are associated with transcriptionally inactive regions in mammals [68] [72]. H3K9 methylation is also involved in gene repression in

euchromatin where the Suv39h1/ HP1 complex is recruited by tumour suppressor retinoblastoma protein (pRb) to repress transcription of its target genes in euchromatin [73, 74].

On the other hand, the tri-methylation of histone H3 at lysine 4 (H3K4) is found at active promoter regions in many active genes [69]. The methyltransferase SET1A/B and its complex, COMPASS, establish this methylation mark and its interaction with chromatin and components of the transcriptional machinery [75]. This modification is additionally implicated in controlling transcription by mediating interactions with RNA polymerase proteins, being a binding site for chromatin-modifying enzymes and remodelling complexes, and recruit histone-modifying proteins as reviewed by Wozniak and Strahl (2014) [76].

Apart from chromatin modification, methylation is also implicated in regulation of transcription factors [64, 77-82], coactivators [83], and corepressors [84-86] and reviewed by Bedford and Clarke (2009) for arginine methylation [40]. For example SET7/9, a lysine methyltransferase, methylates TATA-box binding protein (TBP)-associated factor (TAF10). This increases the affinity of TAF10 to RNA polymerase II which aids in forming the pre-initiation complex for gene transcription [64, 77]. SET7/9 also represses transcription through the methylation of K873 of pRB which promotes its association with HP1. This association represses its gene targets and further differentiation [78]. Additionally, the methylation of K810 of pRB blocks interaction and phosphorylation by cyclin-dependent kinase (CDK) [79].

Another transcription factor, the tumour suppressor p53, is responsible for trigerring apoptosis. This is regulated by lysine methylation. The lysine methyltransferase SET7/9

monomethylates p53 at lysine 372 [80]. This mark promotes stability of p53 in the nucleus allowing for the expression of its target p21 and DNA-damage induced apoptosis. This methyl mark stimulates the acetylation of p53 by p300/CREB binding protein (CBP) [81]. Another lysine methyltransferase SMYD2 monomethylates p53 at lysine 370 which represses its ability to bind its target genes, thus preventing its apoptotic function [82]. Methylation at K372 by SET7/9 decreases the ablity of SMYD2 to bind p53 and methylate at K370 which demonstrates regulation between these PTMs [82].

PRMTs methylate and regulate the histone acetyltransferases p300, CBP, and steroid-receptor coactivator-3 (SRC3) to indirectly control the active transcription of genes [87]. The p300-CBP coactivator family increases gene expression by loosening chromatin at the gene promoter and recruiting transcriptional machinery to the promoter as reviewed by Goodman and Smolik [83]. Meanwhile PRMT5 is implicated in transcriptional repression due to its interaction with the repressor complexes Brahma-related gene1 (BRG1) and human Brahma protein (hBRM) [84], Blimp1 [85] and Snail [86]. These interactions with transcription factors, transcriptional coactivators and transcriptional corepressors affect the regulation of gene expression.

ii. Methylation in mRNA splicing

Methylation has been found to be implicated in messenger RNA (mRNA) splicing through modification of splicing proteins. The arginine methyltransferases PRMT5 and PRMT7 are responsible for symmetric di-methylation of Sm proteins. This modification is required for snRNP biogenesis [88]. During small nuclear ribonucleic protein (snRNP) biogenesis the survival of motor neuron (SMN) complex assembles Sm proteins and snRNAs. SMN has a higher affinity for symmetrically di-methylated Sm proteins compared to their

unmodified or asymmetrically di-methylated counterparts [89, 90]. Removal of PRMT5 or PRMT7 expression with small interfering RNA (siRNA) interferes with the interaction of SMN and the Sm proteins. Additionally, treatment of the cells with an inhibitor of methylation also disrupted snRNP assembly [88].

The coactivator-associated arginine methyltransferase (CARM1) has also been implicated in regulating alternative splicing [91]. The splicing factors CA150, SAP49, SmB, and U1C have been identified as substrates for CARM1 methylation. The methylation of CA150 has been shown to be a binding motif for the survival of motor neuron (SMN) Tudor domain [91].

iii. Effect of Methylation on Protein Stability

Methylation increases the stability of a protein by decreasing its susceptibility to proteases [92], increasing protein heat tolerance [93], and by preventing other PTMs like ubiquitination [17]. Pang *et al*., (2010) observed that 43% of their lysine methylation sites identified overlapped with ubiquitination sites which raises the possibility that methylation increases stability by competing with ubiquitination [17].

For example, the methylation of tumour protein p53 and estrogen receptor alpha (ERα) by the lysine methyltransferase SET7/9 is a stabilizing modification by preventing their degradation and thus allowing recruitment to their target genes [80, 94]. However, in the case of transcription factor E2F1 the outcome of methylation is reversed. Methylation of K185 was found to inhibit its acetylation and phosphorylation yet stimulate the ubiquitination and subsequent degradation of E2F1, thus inhibiting its pro-apoptotic function [95]. Similar to E2F1, the methylation of DNA methyltransferase (DNMT), signal transducer

and activator of transcription 3 (STAT3) and RelA subunit of nuclear factor NFκB negatively regulates their stability [95-100].

IV. Protein Methylation in Disease

i. Cancer

As mentioned above, the pro-apoptic function of tumour suppressor p53 is regulated by lysine methylation. The lysine methyltransferase SET7/9 mono-methylates p53 at lysine 372 thus promoting its stability and inducing apoptosis [80]. Methylation by SMYD2 at lysine 370 represses the ability of p53 to bind its target genes, thus preventing its apoptotic function allowing for tumour cell propagation [82]. SMYD2 also methylates retinoblastoma protein 1 (Rb1) at K810 which enhances phosphorylation of pRb, promoting cell cycle progression and cell proliferation. This is reported to occur through E2F transcriptional activity [101]. Methylation on pRb at K860 by SMYD2 stimulates binding to lethal (3) malignant brain tumour-like protein (L3MBTL1) to induce cell cycle arrest. Contradicting this evidence, methylation at K810 by SET7/9 occurs after DNA damage and has been found to lead to cell cycle arrest. SET7/9 also methylates at K873 leading to recruitment of HP1B to pRb target genes which also triggers cell cycle arrest [78, 79, 102].

The overexpression of the lysine methyltransferase SMYD2 is seen in various cancerous cell lines [82, 101] as well as in esophageal squamous cell carcinoma (ESCC) [103], gastric cancer [104], and bladder cancer [101]. In ESCC cell lines, it has been observed that both p53 expression and mutation is not correlated with SMYD2 expression. Also, in primary tumour cells with SMYD2 over-expression only 48.4% of cases had mutated p53 [103] . This leads to the belief that there are other unknown SMYD2 targets in these cancers demonstrating the importance in discovering methyltransferase substrates.

The overexpression of a SMYD2 family member, SMYD3, is found in breast carcinoma and its expression level correlates with tumour proliferation [105-107]. Euchromatic histone-lysine N-methyltransferase 2 (EHMT2), also known as G9a, overexpression is present in hepatocellular carcinoma [108] and it correlates with lung [109] and prostate [110] tumour invasiveness. These methyltransferases are being used as cancer biomarkers and inhibitors of these methyltransferases are being explored for cancer treatment [111-113].

An increase of PRMT1 expression has been observed in cancer. The histone H4 arginine 3 target for ADMA by PRMT1 is associated with transcription activation and this methylation status correlate with the tumour grade in prostate cancer [114]. The methyltransferase PRMT5 is a transcriptional repressor which has oncogenic properties because it is responsible for the repression of tumour suppressor genes [115].

PRMT6 is another methyltransferase found to be overexpressed in bladder and lung cancer [116]. In tumours with high levels of the methyltransferase PRMT6, the p53 pathway is hypothesized to be epigenetically silenced due to the senescence of mouse embryonic fibroblasts (MEFs) from Prmt6-/- knockout mice where the senescence phenotype was found due to the release of p53 and p21 repression [117].

ii. Embryo Development

Both arginine and lysine methyltransferases have been implicated during embryonic development. For example, the lysine methyltransferase SMYD1 is expressed in the developing heart and muscle of zebrafish [118], mouse [119] and human [120]. It is implicated in myogenic cell [120] and cardiomyocyte [119] differentiation and could be a regulator of myogenesis [120]. A knockout of SMYD1 results in improper heart

morphogenesis [119]. The expression of its close homologs, SMYD2 and SMYD3, is also required in development; the knockdown of the *smyd2a* gene in zebrafish results in defects in tail formation as well as severe delays in development [121] while the knockdown of SMYD3 in zebrafish embryos resulted in pericardial edema, trunk defects and abnormal looping of the heart tube [122]. SMYD3 is also implicated in regulating the atrophy of skeletal muscle partly by regulating the transcription of myostatin [123].

Arginine methyltransferases are also implicated in embryo development. Arginine methyltransferase PRMT5 is expressed in both male and female germ cells and the deletion of PRMT5 resulted in the loss of germ cells in adult mice [124]. Additionally, knockdown of PRMT8 in zebrafish demonstrated defects at gastrulation as well as a short body axis, curled tail and malformed brain and eyes. Catalytically inactive PRMT8 could not rescue the knockdown which shows the importance of the methyltransferase activity of PRMT8 in development [125].

iii. Methylation in Vaccination

Methylation may also play a role in vaccination as vaccination for *Rickettsia typhi* is aimed at targeting outer membrane protein B (OmpB). OmpB is found to be hyper-methylated around the N-terminus in infectious strains for *Rickettsia typhi* while OmpB is hypo-methylated in attenuated strains. Chao *et al.* found that the serological reactivity of an OmpB fragment can be increased upon chemical methylation of the lysine residues. A methylated form of OmpB may be a more serologically active vaccine [126, 127].

Mycobacterium tuberculosis proteins heparin-binding haemagglutinin (HBHA) and lipopolysaccharide binding protein (LBP) are heavily methylated and are implicated in

adhesion to host cells [128-132]. Vaccination efforts against *Mycobacterium tuberculosis* can potentially be increased by making a vaccine against the methylated form of HBHA [133].

iv. Cardiovascular Disease

Methylation is also implicated in cardiovascular disease as ADMA and MMA inhibit the activity of nitric oxide synthase (NOS) which leads to atherosclerosis [134]. These ADMA and MMA residues are made by proteolysis of methylated proteins *in vivo* which is a process catalyzed by dimethylarginine dimethylaminohydralase (DDAH) enzymes. The maintenance of a pool of ADMA and MMA residues is important for maintaining nitric oxide (NO) signalling which regulates blood pressure. It has been hypothesized and DDAH and PRMTs observed that *Ddah1* knockout mice accumulate ADMA and have reduced NO signalling resulting in an elevated blood pressure [135].

v. Spinal Muscular Atrophy

Spinal muscular strophy (SMA) is a disease resulting from mutations and deletions within the *SMN1* gene and is inherited in an autosomal recessive fashion [136, 137]. It results in the expression of a truncated SMN isoform. Truncated SMN protein affects motor neuron axonal guidance.

SMN is also responsible for assembling ribonucleoproteins (RNPs) and snRNPs by assembling spliceosome proteins onto their snRNAs. This process requires arginine methylation [138]. The SMN Tudor domain associates with methylated proteins of PRMT5 and CARM1 substrates [91] and these methylated residues are missing in the cells of SMA patients [139]. Point mutations on the SMN Tudor domain have been observed in SMA patients which demonstrates the requirement for a functional Tudor domain as well as demonstrating the link of SMN function in SMA [140].

With the vast complications arising from the expression of methyltransferases and their catalytic activity in gene expression, development and cancer, researchers have set out many strategies to uncover methyltransferase targets and to identify methylated proteins.

V. Current Approaches to Studying Methylation

i. Low-Throughput Targeted Approaches

The study of methylation remains a challenge due to the small size and lack of charge difference associated with the addition of a methyl group. In the beginning, methylation was confirmed using targeted approaches such as Edman amino acid sequencing [141-143], *in vitro* radioactive labelling assays [144, 145] and immunoblotting [14]. The shortcoming with these approaches is that, although they can confirm that there is methylation on a target protein, they cannot confirm location of methylation without further experiments, are not high-throughput and these methods have a low dynamic range for detection.

ii. High-Throughput Enrichment-Based Screening

With the advancement of mass spectrometry (MS), high-throughput studies of PTMs have become more common. Mass spectrometry is sensitive enough to detect the small size difference associated with mono-methylation and tandem MS/MS allows for the identification of the site which is methylated. However, another hurdle remains, that being the low abundance of lysine methylation making it more difficult to detect as mass spectrometry is more likely to identify high abundance peptides. To overcome this most methods currently focus on enriching methylated proteins/peptides prior to mass spectrometry analysis [146].

iii. Methyl-Lysine Binding Domains to Enrich for Methylated Proteins

One enrichment strategy is affinity enrichment using a methyl-lysine binding domain to enrich for methylated proteins [147]. In this approach the chromodomain of HP1β (heterochromatin protein 1) is used to bind and enrich methylated proteins. This method found 29 new methylated proteins with 40 sites of di- and tri-methylation on lysine in a human embryonic kidney (HEK) 293T lysate all associated to HP1β [147]. Similarly, another study made a methyl-lysine binding domain using 3 malignant brain tumour repeats (3XMBT) of the L3MBTL1 protein [28, 32]. They found 102 methylated peptides in a HEK293T nucleoplasmic extract. The drawbacks of this approach are that it theoretically only binds lysine methylation sites, and these sites must mimic the three dimensional conformation of the targets of the binding domain.

iv. Pan-Methyl Antibodies to Enrich for Methylated Peptides

Another affinity enrichment method uses pan-specific anti-mono-, di- and tri polyclonal antibodies which recognize methyl groups and are not limited to a particular amino acid sequence. Boisvert *et al*. (2013) used antibodies specific for asymmetric and symmetric arginine methylation to enrich their protein population prior to mass spectrometry to identify over 200 methylated proteins [148]. Another group used pan-methyl arginine antibodies coupled with hydrophilic interaction liquid chromatography (HILIC) prior to their mass spectrometry for further peptide separation to yield 249 arginine methylation sites [149].

Guo *et al.* (2013) used pan-methyl antibodies for mono-, di, and tri-methylation on lysine and mono-and di-methylation on arginine has yielded 160 distinct lysine methylation sites and over 1000 arginine sites in HCT116 cells a human colon colorectal cell line [150].

Similarly, another study by Cao *et al.* (2013) used pan-specific antibodies along with subcellular fractionation in HeLaS3 cells (a human cervix adenocarcinoma cell line) to yield enriched cytosolic and nuclear fractions to obtain 522 lysine methylation sites [27]. Bremang *et al.* (2013) used subcellular fractionation and 11 different pan-methyl antibodies to enrich for both lysine and arginine non-histone protein methylations in HeLaS3 cells. They identified 501 methylation events on 397 distinct lysine and arginine methylation sites [151].

v. Derivatization Coupled with Affinity Enrichment

Wu *et al.* (2015) has identified 446 mono-methylation sites on lysine in HeLa cells by chemical derivatization of mono-methylated lysine residues at the ε-amino group with propionyl anhydride. Affinity enrichment was then performed with an antibody raised to recognize the propionyl methyl-lysine [152]. These approaches are expensive due to the manufacturing costs of antibodies. Additionally antibodies suffer from a high variability between batches and low reproducibility.

vi. Click Chemistry to Determine Methyltransferase Targets

There are also chemical methods to enrich for methylated peptides. Click chemistry approaches have been used to modify SAM with a bioorthogonally-reactive chemical group that is transferred in place of a methyl group. These chemical groups have affinity tags added to them which allows for enrichment by immunoprecipitation [153]. One group conjugated biotin to the SAM and proceeded to immunoprecipitate methylated substrates with streptavidin agarose and were able to find 64 potential substrates of the methyltransferase histone-lysine N-methyltransferase EHMT1, also known as GLP1, and 82 potential substrates for G9a [154]. A drawback of the chemical enrichment method is that some KMTs will not accept modified SAM as a cofactor. Secondly, the methyltransferase can be

modified to accommodate the modified-SAM, however, this can allow one to question the validity of the targets.

vii. Predictive Modeling of Methylation Sites

Lastly, there are prediction-based methods to discover lysine methylation. This method is based on determining potential substrates of KMTs by using their methylation consensus motif to examine for methylation on a peptide library consisting of these sequences with systematically mutated residues. This approach has been used for G9a [155], SETD6 [31], SET7/9 [60, 156], SET8 [157] and SMYD2 [158]. The drawbacks with predictive modeling are the requirement of a secondary method to verify the findings as well as the requirement for well-developed motifs.

With these limitations in mind we developed a cost-effective novel and alternative approach to enrich for methylated peptides. Coupled with more stringent analysis for methylation, this approach could yield more biological methylation sites.

VI. Novel Approach to Enrich for Methylated Peptides

Our laboratory developed a novel approach for a negative selection methylation enrichment strategy performed at the peptide level where unmethylated lysine and arginine residues are modified to remove the charge at their amino groups. This method is termed Protein Methylation Enrichment by Neutralizing Amine through Derivatization (ProMENADe) (Figure 2). The ProMENADe method involves removing the charge on unmodified lysine and arginine residues with a derivatization reaction, making it unbiased in its selection of methylated substrates.

First, arginine residues on the peptide are reacted with malondialdehyde (MDA) in strongly acidic conditions to change arginine's guanidine group to 2-pyrimidine (Figure 2A). This reaction was first performed by King [159] and was first used for proteomics by Foettinger *et al.* [160]. This reaction lowers the pKa of the arginine residue to 3.6 allowing for its charge to be neutralized at a basic pH [160]. In this novel approach, 1,1,3,3-tetraisopropoxypropane (TiPP) was synthesized used in place of MDA along with 12 molar hydrochloric acid (12 M HCl) to form MDA *in situ*. The synthesis of TiPP could have some traces of methanol remaining. This can lead to esterification on the carboxy terminus of the peptides as well as on aspartic acid and glutamic acid residues (Figure 2B). Esterification on the peptide C-terminus can mimic methylation on lysine and arginine in tryptic peptides, and thus will be false positive results in methylation identifications.

This reaction was followed by neutralizing the charge on the epsilon primary amine of lysine and peptide N-terminals with ortho-phthaldialdehyde (OPA). Due to steric hindrance, methylated lysine residues cannot react with OPA which allows for the methylated lysines to remain positively charged (Figure 2C).

Following these modifications, strong cation exchange (SCX) chromatography is used to select for the charged, and thus methylated peptides (Figure 2D). Methylated peptides can be identified using liquid chromatography (LC)-MS/MS after enrichment. Using this method, 793 methylated peptides were identified from HEK293T cell lysates with a methylation false discovery rate (FDR) of 1% where 585 of these sites were for lysine methylation (Ning *et al*., manuscript in preparation).

The data will be analyzed at three levels of stringency: the 1% peptide FDR, 1% methylation FDR and the 1% methylation FDR filtered for methylation at peptide C-terminal. This analysis stringency increases our confidence in identified sites for protein methylation while most published data, including the studies discussed above use the 1% peptide FDR cut-off. The ProMENADe method is a good alternative to current methodology in the field as it finds a comparable number of sites using more stringent analysis. Secondly, the chemicals to perform the derivatization are cost effective and easy to synthesize. This method however, does have false-positive identifications of C-terminal methylation due to esterification of the peptide C-termini, aspartic acid and glutamic acid residues. We negate this shortcoming however through removal of all identified C-terminal methylation sites.

VII. Rationale

To date, relatively few methylation targets have been identified due to the limitations of the current technologies. Our novel enrichment method, ProMENADe was developed to enrich for methylated peptides within a given biological sample followed by identification of the proteins and their site(s) of methylation by LC-MS/MS analysis (Ning *et al*., manuscript in preparation). This technology has been employed to identify novel methylation sites in proteins expressed in HEK293T cells.

The number of methylation sites identified using ProMENADe can be further increased by simplifying the protein mixture as MS has a bias toward identifying highly abundant peptides. Using subcellular fractionation the cellular protein can be split into two more simple fractions: the cytosol and the nucleus for further methylation enrichment. Additionally, the number of methylation sites identified can be further increased upon using multiple proteases for digestion. Using proteases with different amino acid specificities

creates a more diverse pool of peptides which increases the chances of identifying methylation sites where tryptic peptides would not have suitable for MS. Combining these two techniques, the number of methylation events identified in HEK293T cells can be increased.

VIII. Statement of Hypothesis and Objectives

i. Hypothesis

With an optimized ProMENADe protocol, we can increase the number and confidence of methylation sites identified.

ii. Objectives

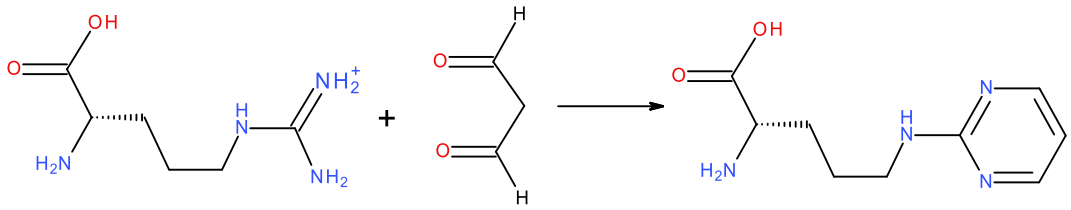
#1. To prove the ProMENADe enrichment reaction works in biological samples and to determine the ideal amount of protein starting material.

#2. To increase the number of identified methylation sites by simplifying the protein mixture for mass spectrometry using subcellular fractionation and to increase the number of identified methylation sites by increasing sequence coverage in biological samples using multi-protease digestion.

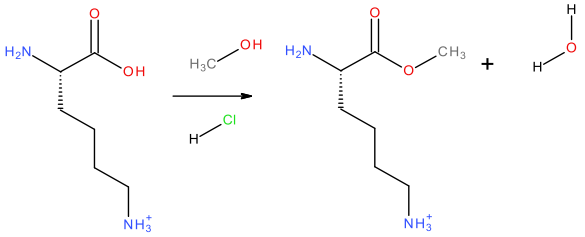
#3. To validate *in vivo* identified methylation sites by heavy labeling proteins using heavy methionine stable isotope labeling by amino acids in cell culture (SILAC).

Figure 2: Strategy for ProMENADe methylation enrichment. A) Arginine residues are reacted with malondialdehyde (MDA) in acidic conditions to change arginine's guanidine group to 2-pyrimidine. B) Esterification by-product reaction that can occur on peptide C-termini. C) Derivatization of unmodified lysine and peptide N-termini with ortho-phthaldialdehyde (OPA). D) The ProMENADe Workflow. Protein is tryptically digested overnight. The unmodified arginines are neutralized by reaction with MDA. OPA is subsequently added to react with the unmodified lysines and free peptide N-termini, thus neutralizing them. The peptides are then separated by strong cation exchange (SCX). The more highly charged, thus methylated, peptides should interact strongly with the SCX column resulting in their elution at a higher pH relative to their non-methylated counterparts.

A)

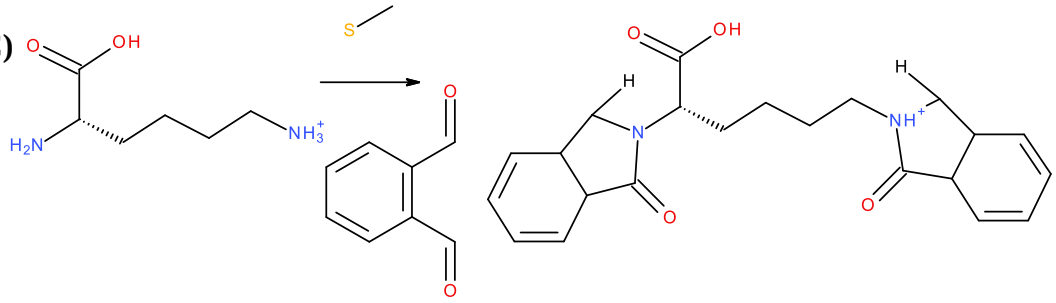


B)



R

C)



D)

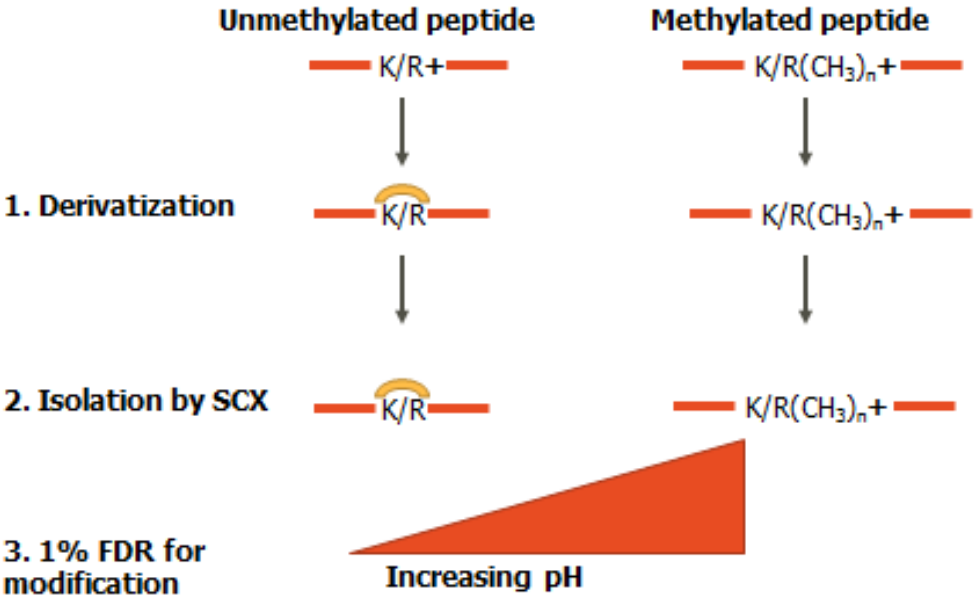

Unmethylated peptide
Methylated peptide
K/R+
K/R(CH3)n+
1. Derivatization
K/R
K/R(CH3)n+
2. Isolation by SCX
K/R
K/R(CH3)n+
3. 1% FDR for modification
Increasing pH

Table 1: Comparison of approaches to study methylation. Examination of the advantages, and disadvantages of using Edman amino acid sequencing, radio-active labelling assays, immunoblotting, enrichment with methyl-lysine binding domains, enrichment with pan-methyl antibodies, Click chemistry, predictive modeling, and enrichment with ProMENADe to study methylation.

Approach	Advantages	Disadvantages
Edman amino acid sequencing	• Identifies site of methylation	• Low-throughput
Radio-active labelling assays	• Determination of methyltransferase substrates	• Low-throughput • Further experiments required to identify site of methylation • Low dynamic range for detection
Immunoblotting	• Determination of methyltransferase substrates • Identifies site of methylation with site-specific antibody	• Low-throughput • With pan-methyl antibody further experiments required to identify site of methylation • Low dynamic range for detection • Low reproducibility in antibodies between batches
Methyl-lysine binding domain enrichment with MS	• High-throughput • Information on sites which can be bound by the domain • Identifies site of methylation	• Only detects methylation sites in the conformation of the domain
Pan-methyl antibody enrichment with MS	• High-throughput • Pan-specificity allows for non-sequence specific bias • Identifies site of methylation	• Low reproducibility in antibodies between batches • Pan-specific for lysine methylation have been found to be nonspecific
Click Chemistry	• High-throughput • Determination of methyltransferase substrates	• Further experiments required to identify site of methylation • Not all methyltransferases will use modified SAM • Have to modify methyltransferases to use modified SAM
Predictive Modeling	• High-throughput • Provides motif information for the methyltransferase • Predicts site of methylation	• Requires another method to validate *in vivo* or *in vitro* • Not all motifs are well defined
ProMENADe with MS	• High-throughput • Identifies site of methylation	• Esterification at peptide C-terminal leading to false methyl identifications • Peptides are chemically modified • Reproducibility untested

2. MATERIALS AND METHODS

I. Cell Culture

HEK293T cells (obtained from ATCC) were maintained at 37°C, 5% carbon dioxide, in Dulbecco's Modified Eagle's Medium (DMEM; 4.5 g/L D-glucose, L-glutamine; Gibco, Invitrogen, Burlington, ON, CAN) supplemented with 10% (v/v) qualified fetal bovine serum (FBS; Gibco , Invitrogen), gentamycin (0.028 g/L; Gibco , Invitrogen) and Plasmocin prophylactic (5 mg/L; InvivoGen, San Diego, CA, USA). Cells were grown to 90% confluence prior to harvest or subcellular fractionation in 100 mm dishes (BD Falcon, Ultident; Montreal, QC, CAN).

II. Heavy-Methionine Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC)

HEK293T cells were maintained at 37°C, 5% carbon dioxide, in the "light" Dulbecco's Modified Eagle's Medium (DMEM; 4.5 g/L D-glucose, L-glutamine; Gibco, Invitrogen, Burlington, ON, CAN) supplemented with 10% (v/v) qualified fetal bovine serum (FBS; Gibco, Invitrogen), gentamycin (0.28 g/L; Gibco, Invitrogen) and Plasmocin prophylactic (5 mg/L; InvivoGen, San Diego, CA, USA) alongside cells grown in "heavy" customized DMEM without L-Arginine, L-Lysine, or L-Methionine (Athena ES, Baltimore, MD, USA) supplemented with 84 mg/mL L-Arginine, 146 mg/mL L-Lysine, and 30 mg/mL [$^{13}CD_3$] L-Methionine (labeled amino acids from Sigma-Aldrich, Oakville, ON, CAN) supplemented with 10% (v/v) dialyzed FBS (Gibco, Invitrogen), gentamycin (0.028 g/L; Gibco , Invitrogen) and Plasmocin prophylactic (5 mg/L; InvivoGen, San Diego, CA, USA). Cells were maintained in culture for >7 doubling times to allow for complete incorporation

of the isotope-labeled methionine. Heavy methionine was >95% incorporated in cellular proteins.

III. Cell Lysis

The HEK293T cells were lysed using 1X RIPA (25 mM Tris·HCl pH 7.6, 150 mM NaCl, 1% (v/v) NP-40, 1% (w/v) sodium deoxycholate (EMD), 0.1% (w/v) sodium dodecyl sulphate (SDS; Sigma-Aldrich) with protease inhibitors (Roche; Indianapolis, IN, USA). The samples were sonicated using a Sonic Dismembrator (Fisher Scientific; Pittsburgh, PA, USA) for 15 seconds of pulse on with 10 seconds of pulse off break at 25% amplitude repeated four times per sample for a total of 1 minute of sonicating pulses. After sonication samples were centrifuged at 12 000 × g for 10 minutes at 4°C using the refrigerated Centrifuge 5430 R (Eppendorf; Mississauga, ON, CAN). The supernatants were collected and stored at -80ºC.

IV. Subcellular Fractionation

Rapid Efficient and Practical (REAP) subcellular fractionation was performed according to the protocol of Suzuki *et al.* [161]. HEK293T cells were cultured in 100 mm dishes (BD falcon) until 90% confluent. Cells were washed twice with ice-cold phosphate buffered saline (PBS, pH 7.4; Gibco, Invitrogen), harvested with a plastic cell scraper into 1 mL ice-cold PBS in a 1.7 mL microcentrifuge tube (Axygen, Corning Incorporated; Corning, NY, USA) on ice. The samples were spun for 10 seconds in a Galaxy Mini table top centrifuge at 2000 × g (VWR International; Mississauga, ON, CAN). The supernatant was removed and the cell pellet was lysed in 900 µL of ice-cold 0.1% (v/v) NP-40 (Fluka Analytical, Sigma-Aldrich; Oakville, ON, CAN) in PBS and pipetted up and down five times. 300 µL of this lysate was removed as the "starting material" and kept on ice until sonication.

The remaining 600 µL was centrifuged for 10 seconds at 2000 × g and the supernatant was removed as the "cytosolic fraction". This supernatant fraction was further purified by an additional 10 second quick spin at 2000 × g, and keeping the supernatant. Meanwhile, the pellet was washed with 1 mL 0.1% (v/v) NP40 in PBS and spun for 10 seconds at 2000 × g. The supernatant was removed and the "nuclear fraction" was resuspended in 300 µL of 0.1% (v/v) NP40 in PBS. Alongside this preparation, one 100 mm dish of HEK293T cells was lysed in 900 µL of ice-cold 0.1% (v/v) NP40 in PBS and pipetted up and down five times. This larger lysate was called "whole cell lysate" and was used for method comparison for unique sites identified.

All of the samples were sonicated as in section III. The samples were then centrifuged at 12 000 × g for 10 minutes at 4°C, supernatants removed, and samples stored at -80ºC.

V. Immunoblotting

The total protein for each fraction/sample was quantified by performing a Bradford assay (Bio-Rad Protein Assay Kit, Bio-Rad; Mississauga, ON, CAN). 20 µg of protein per sample in 1X NuPAGE® LDS Sample Buffer with Reducing Agent (Novex, Invitrogen) was loaded on a 1.5 mm X 10 well NuPAGE 4-12% Bis-Tris gradient gel (Novex, Invitrogen) alongside 10 µL of Precision Plus Protein Standards (Bio-Rad). The gel was run at 120V for two hours (Power Pac 300 Bio-Rad) and then electroblotted onto nitrocellulose membrane for 90 minutes at 30V. The membrane was stained with Ponceau S (Sigma-Aldrich) for 5 minutes, destained with water and then blocked in 5% (w/v) skim milk powder (US Biological, EMD Chemicals; Etobicoke, ON, CAN) in tris-buffered saline and tween 20 (TBST; 50 mM Tris, Calbiochem, EMD Millipore; 150 mM NaCl, Calbiochem, EMD

Millipore; 0.05% (v/v) Tween 20; Sigma-Aldrich, pH 7.6) for one hour at room temperature. Commercial primary antibodies for mouse anti-human actin (1 part in 5000; Cedarlane; Burlington, ON, CAN), rabbit anti-human lamin A/C (1 part in 1000; Cell Signaling Technology; Danvers, MA, USA), calnexin (1 part in 2500, Sigma-Aldrich), elongation factor-1 (eEF1A1) (1 part in 1000; Abcam; Toronto, ON, CAN), and histone H3 (1 part in 10 000, Abcam) were used. Secondary antibodies were used at 1 part in 5000 for lamin A/C immunoblots and 1 part in 10 000 for the other immunoblots (GE Healthcare, Amersham; Little Chalfont, UK). Chemiluminescence with Western Lightning Plus-ECL (Perkin Elmer Inc.; Waltham, MA, USA) was used for horseradish peroxidase (HRP) substrate detection on Progene film (Ultident).

VI. Proteomics Sample Preparation

i. Protein Precipitation

Proteins were precipitated in five volumes of ice-cold acetone at -20°C overnight. The next day the protein was centrifuged at 12 000 rpm with the Centrifuge 5430 R (Eppendorf) at 4°C and washed with ice-cold acetone twice more to remove SDS and protease inhibitor. The protein was then resuspended in 8M urea (Sigma-Aldrich) in 50 mM ammonium bicarbonate at pH 8.5 (Multipharm, EMD). In SILAC experiment, "heavy" and "light" protein was mixed in a 1:1 ratio.

ii. In-solution Protein Digestion

The total protein for post-acetone precipitation was quantified by performing a Bradford assay (Bio-Rad Protein Assay Kit). 500 μg of protein was used for each sample. The protein was reduced with dithiothreitol (DTT; Sigma-Aldrich) at a final concentration of 10 mM and incubated at 56°C for 30 minutes at 700 rpm in a Thermomixer (Eppendorf). The

protein was then alkylated with iodoacetamide (IAA; Sigma-Aldrich) at a final concentration of 20 mM and incubated for 40 minutes in the dark at room temperature. The sample was diluted six times in 50 mM ammonium bicarbonate pH 8.5 to dilute the urea. For protein digestion trypsin (Worthington; Lakewood, NJ, USA), chymotrypsin (Worthington), or Glu-C (Roche) was added at a ratio of 1 µg for 20 µg of total protein and incubated overnight for 16-20 hours at 37°C in a Thermomixer at 700 rpm.

Protein digestion was confirmed with gel electrophoresis and protein staining. 20 µg of protein of sample pre- and post-digestion was mixed with 1X NuPAGE® LDS Sample Buffer with Reducing Agent (Novex, Invitrogen) and was loaded on a 1.5 mm X 10 well NuPAGE 4-12% Bis-Tris gradient gel (Novex, Invitrogen) alongside 10 µL of Precision Plus Protein Standards (Bio-Rad). The gel was run at 120V for two hours (Power Pac 300 Bio-Rad). The gel was fixed is 50:50 of 50% methanol to 50% acetic acid and left for 30 minutes. The gel was subsequently immersed in Colloidal Blue Staining Solution (Invitrogen) and incubated at room temperature overnight rotating at 62 rpm. The following day the gel was destained in water with rotation at 62 rpm until minimal background staining was achieved.

iii. Peptide Desalting

Following protein digestion the sample was acidified to a pH of 3-4 with 5% (v/v) formic acid (FA; Sigma-Aldrich). A tC18 Sep-Pak Vac 1cc 50 mg cartridge (Waters; Mississauga, ON, CAN) was activated with 2 mL of 100% acetonitrile (ACN; J.T. Baker, Avantor; Center Valley, PA, USA) followed by equilibration with 2 mL 0.1% (v/v) formic acid. The peptides were added to the column and the column was washed twice with 1 mL of 0.1% (v/v) formic acid. The peptides were eluted with 1 mL of 80% (v/v) acetonitrile in 0.1% (v/v) formic acid and dried down in a SpeedVac (Thermo Scientific).

iv. Synthesis of 1,1,3,3-tetraisopropoxypropane (TiPP)

5.5 g of Amberlite IR-120 resin (Fluka Analytical, 06428-1KG, CAS: 39389-20-3) was weighed out and added to a large Erlenmeyer flask where it was washed with 2-propanol (Fisher Scientific, CAS: 67-63-0) until it runs clear. 182 mL of 2-propanol was then added to the resin followed by 4.95 mL of 1,1,3,3-tetramethoxypropane (Sigma Aldrich, 108383-500mL, CAS: 102-52-3). The reaction was left to stir for 2 hours at room temperature. The liquid was then transferred to a round bottom flask where it was separated using a rotary evaporator. The round bottom flask was half submerged in the water bath and was heated to 30-37°C and slowly rotated. The sample was left on the rotary evaporator for 30 minutes to evaporate. Another 182 mL of 2-propanol was added to the resin. The evaporation step was repeated once again. This was repeated a total of four times. The product was centrifuged at 1000 × g for 5 minutes to remove the glass bead debris. The TiPP supernatant was removed and stored at -80°C.

v. Preparation of Phthaldialdehyde (OPA) Reagent

50 mg of phthaldialdehyde (OPA, Sigma-Aldrich) was weighed out and resuspended in 1000 µL of 100% ethanol (Commercial alcohols; Brampton, ON, CAN). 50 µL of Sβ-2-mercaptoethanol (Calbiochem, 6010) was added followed by 9000 µL of 50 mM sodium bicarbonate, pH 10.5 (EMD Millipore). The OPA product was stored in the dark at 4°C until its use, but always within two hours.

vi. ProMENADe Enrichment Reaction

15 µL TiPP was added to the 500 µg peptide mixture followed by 100 µL 12 M hydrochloric acid (HCl; EMD) and reacted for one hour in the dark at room temperature. After the reaction it was diluted in water to ten times the volume. Two millilitres of 100%

acetonitrile was added to a HyperSep Strong Cation Exchange (SCX) 50 mg Column (Thermo Scientific) for activation. This column was equilibrated with 2 mL of 0.1% (v/v) formic acid and the sample was loaded. The sample was washed twice with 1 mL of 80% acetonitrile in 0.1% (v/v) formic acid to remove polymer by-products. The sample was eluted with 50 mM sodium carbonate pH 10.5 (BioShop; Burlington, ON, CAN) followed by 50 mM sodium hydroxide (NaOH; EMD Millipore) until eluent reaches a pH of 12. 450 µL of the 10X OPA reagent was added and reacted with the peptides for one hour at room temperature in the dark. The reaction was quenched by 5% (v/v) formic acid to obtain a pH of 3. The volume was diluted twice with water to lower the salt concentration. An SCX column was once again prepared as above and the sample was loaded onto it. The sample was washed twice with 1 mL of 80% (v/v) acetonitrile in 0.1% (v/v) formic acid once again and eluted sequentially off the column with 1 mL of 20 mM Britton-Robinson buffer (20 mM acetic acid, 20 mM phosphoric acid, and 20 mM boric acid) adjusted to pH 6, 8, 10, 11 and 12 with NaOH. These samples were then desalted and peptides were dried down as described above in section VI subsection iii.

VII. LC-MS/MS Measurement

The samples were resuspended in 0.1% (v/v) formic acid prior to loading onto mass spectrometer. The MS analysis platform had an Eskigent Nano 2D+ HPLC system (Agilent Technologies, Santa Clara, CA, USA) coupled with a Q-Exactive mass spectrometer (ThermoFisher Scientific, San Jose, CA, USA). This system contains a nano-electrospray interface operated in positive ion mode. The mobile phase consisted of 0.1% (v/v) formic acid in water as buffer A and 0.1% (v/v) formic acid in acetonitrile as buffer B. The separation of peptides was done on a 75 µm X 150 mm analytical column packed in-house

with reverse phase Magic C18A results (1.9μm; 100-Å pore size; Dr. Maisch GmbH, Ammerbuch, DEU). 4 μL was loaded onto the column using 98% buffer A and at a flow rate of 300 nL/min for 20 min. A gradient from 10% to 50% buffer B was used in 120 min at a flow rate of 300 nL/min. The MS method consisted of a MS scan from 350 to 1700 m/z followed by 12 data-dependent MS/MS HCD scans of the most intense ions with dynamic exclusion repeat count of 2 and a repeat duration of 90 seconds. The resolution of the MS was 75000 defined at m/z 200. To improve the mass accuracy the measurements were performed with internal recalibration at 445.1205[162]. The charge state rejection function was enabled with single and "unassigned" charge states rejected. The data was recorded with Xcalbibur (ThermoFisher Scientific).

VIII. Mascot Database Search

The database search was done by Mascot 2.3 [163]. Using the formatting tool in Proteomics Tool Suite 3.0.5 [164] the .raw files were converted into mascot generic format (.mgf) for the Mascot database search. The .mgf files were searched against the Uniprot fasta database (July 2013 version) including commonly observed contaminants. The fixed modifications parameter was set to cysteine carbamidomethylation (+57.021463) and the variable modifications were set as: methionine oxidation (+15.994915), protein N-terminal acetylation (+42.010565), MDA modification on arginine (+36.000000), OPA modification of peptide N-terminal and lysine (+116.026215), mono- (+14.015650) and di-methylation (+28.031300) on lysine and arginine, and tri-methylation (+42.046950) of lysine. Enzyme specificity was set to trypsin, chymotrypsin, or V8DE depending on the sample being analyzed. Two missed cleavages were allowed. The precursor ion mass tolerances were +/- 10 ppm and the MS/MS tolerances were 20 milli mass units (mmu) for HCD spectra on

Mascot. For samples with heavy methionine labeling, the methylation modifications were as follows: mono-methylation (+18.015650), di-methylation (+36.031300) on lysine and arginine, and tri-methylation (+54.046950) of lysine.

IX. Data Analysis

i. Proteomics Tool Suite

The .dat files generated by Mascot were parsed and filtered by BuildSummary in Proteomics Tool Suite [164]. The false discovery rate (FDR) for modified peptides, peptides and protein were all set to 1%, a precursor ion tolerance of 10 ppm and a minimum length of 6 amino acids were used for peptide filtration. An in-house Perl script was used to do the unique peptides assignment as well as extract the methylated peptides. Another in-house Perl script was used to do the 1% FDR filtration on methylated peptides. From this dataset the C-terminal methylation sites were removed for more stringent analysis.

ii. Statistical Analysis

The number of methylated peptides identified for data analysis between two samples was an average of three experimental repeats. The two-tailed student t-test was applied for statistical analysis to determine differences between datasets at $p<0.05$.

The number of methylated peptides identified for data analysis between greater than two samples was an average of three experimental repeats. One-way analysis of variance (ANOVA) $p<0.05$ was applied for statistical analysis to determine a trend in the data. Post-hoc t-test analysis was performed with a Bonferroni correction to determine significance of the data $p<0.01$.

iii. Gene Ontology Analysis

The gene names of the identified methylated proteins were extracted and imported into the Gene Ontology (GO) tool in the Database for Annotation, Visualization and Integrated Discovery v6.7 (DAVID). The background consisted of the gene names of all identified proteins from the dataset, and was also uploaded. The biological processes and cellular components results were obtained. The p-values were adjusted with a Benjamini-Hochberg false discovery rate using a cut-off rate of 0.05.

iv. SILAC Incorporation Calculation

To calculate SILAC incorporation, a 25 mm flask of 80% confluent "heavy" cells was collected and processed as described above in section VI and VII. The .raw files were searched in MaxQuant version 1.2.2.5 and all contaminants were removed. In the result file, all "0"s in the column of "Intensity Light" were replaced by "1". Incorporation was calculated using the formula 1-(1/(H/L)) using values in columns titled "Intensity H" and "Intensity L" and was displayed in a new column. The number of peptides that end with R and K with the calculation results of 95% or more were counted as "Labeled R" and "Labeled K". The number of peptides that were terminated with R were termed "Total R" and the number of peptides that were terminated with K were termed "Total K". The incorporation percentages were then calculated as the ratios of "Labeled R/Total R" and "Labeled K/Total K".

v. Protein Abundance Across Organisms Database (PaxDb) Analysis

The integrated dataset of the weighted average of all "H. sapiens WHOLE_ORGANISM" datasets with interaction consistency score of 14.85 and coverage of 87 was used for this analysis. This dataset contained 20 457 proteins with abundance

calculations in parts per million (ppm). The percentage of proteins in each abundance range (0-0.01 ppm, 0.01-0.1 ppm, 0.1-1 ppm, 1-10 ppm, 10-100 ppm, 100-1000 ppm and 1000+ ppm) was plotted on a line graph and had a normal curve of expression around the protein abundance of 0.1 to 1 ppm. Our methylated protein hits were then identified by the gene names of the methylated proteins. These proteins were then mapped to the abundance values from the "H. sapiens WHOLE_ORGANISM" dataset and plotted alongside the dataset on the line graph.

3. RESULTS

I. Optimization of the ProMENADe Protocol in Biological Samples

i. Determination of Optimal Amount of Protein Starting Material

The first step was to determine the optimal amount of protein starting material for the reaction to yield the highest number of methylated peptides. This is a measurement of the scalability of the method. First, HEK293T cells were lysed in 1X RIPA buffer and the total protein sample was precipitated with ice-cold acetone overnight. The protein was washed as described in the Materials and Methods Section VI. The protein was re-solubilized in 8M urea in 50 mM ammonium bicarbonate, pH 8.5, and aliquoted based on amount of starting material, ranging from 0.2 mg to 10 mg of protein. The protein was reduced, alkylated, tryptically digested and enriched for methylated peptides using ProMENADe. The amount of reagent for the enrichment reaction was scaled per mg of starting material. The samples were then analyzed by mass spectrometry and the peptides identified using Mascot version 2.3. The experiment was repeated three times. The total number of identified methylated peptides was identified per amount of protein starting material.

When analysis was performed using a 1% FDR at the peptide level, 2 mg and 0.5 mg of protein starting material yielded the most methylated peptides at an average of 712 methylated peptides and 617 methylated peptides respectively (Figure 3A). Using a 1% FDR at the methylation level, once again 2 mg and 0.5 mg of protein starting material yielded the most methylated peptides at an average of 192 and 165 methylated peptides respectively (Figure 3B). Once the data was filtered for methylation at peptide C-terminus, 5 mg, 2 mg

and 0.5 mg starting material yielded the most methylated peptides at an average of 158, 142 and 127 respectively (Figure 3C).

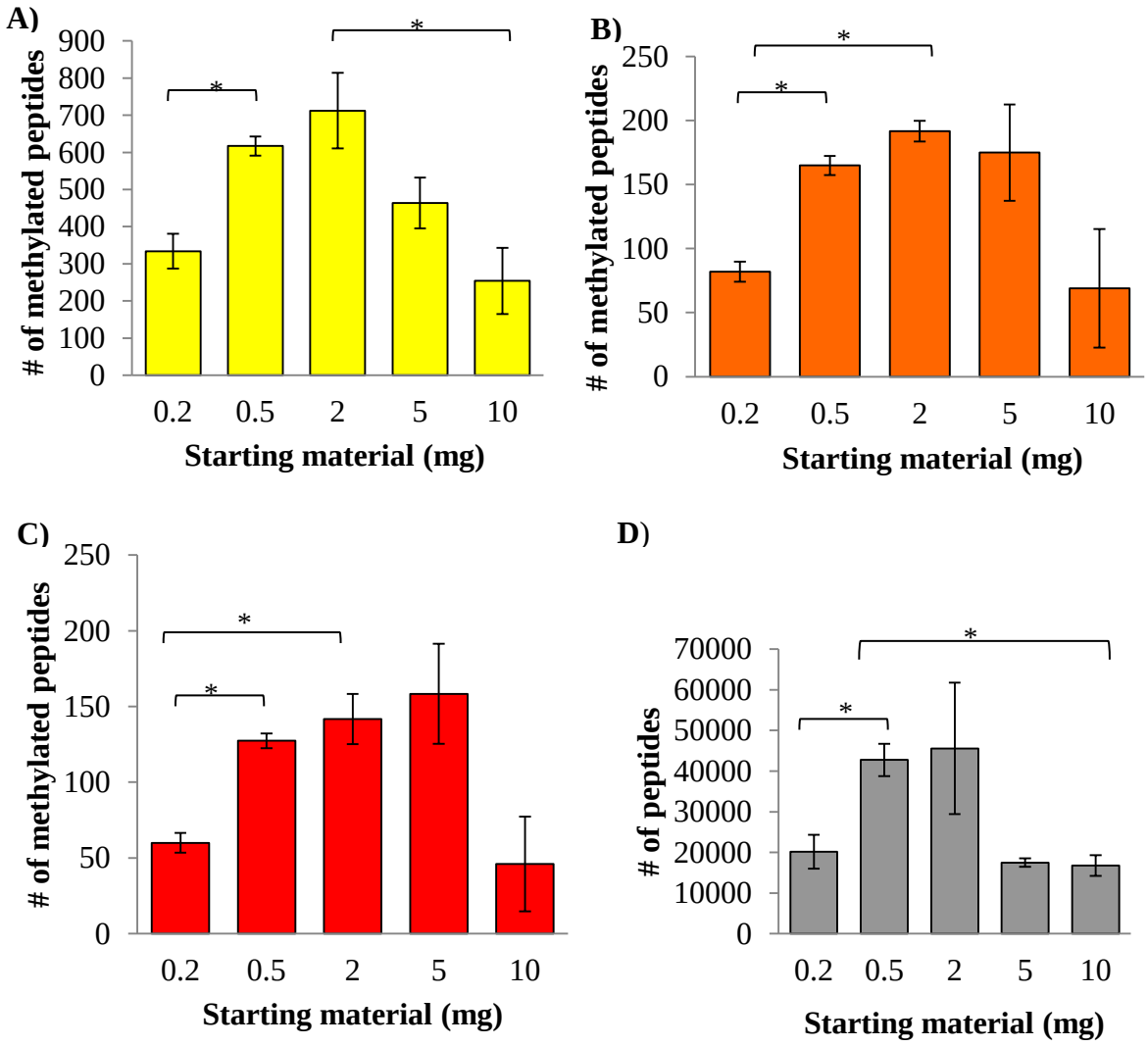
The average number of peptides identified in each mass spectrometry run peaked at just over 40,000 peptides in the 0.5 mg and 2 mg samples (Figure 3D). At 5 mg and 10 mg of starting material the number of peptides identified decreased to less than 20,000 peptides which was equivalent to having used 0.2 mg of starting material (Figure 3D).

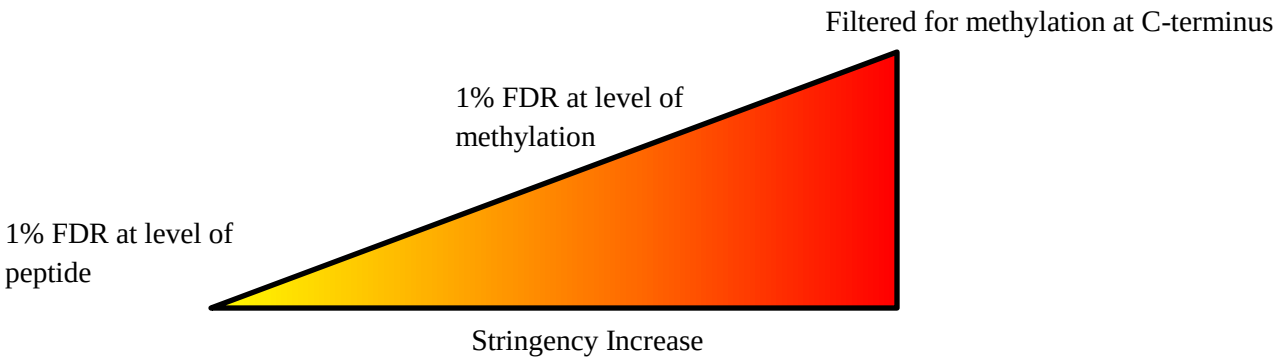
In order to examine the depth of the enrichment, the unique number of methylation sites was examined. This number indicates the amount of starting material required to get the largest number of non-overlapping sites. When analysis was performed using a 1% FDR at the peptide level, 2 mg and 0.5 mg of protein starting material yielded the most sites at an average of 152 methylation sites and 134 methylation sites respectively (Figure 4A). Using a 1% FDR at the methylation level, 2 mg of starting material identified 53 sites while 0.5 mg identified 44 sites, which is not a significant difference (Figure 4B). Once the C-terminal sites were removed, there is not a significant difference based on amount of starting material (Figure 4C).

ii. Discussion of Optimal Amount of Protein Starting Material

The data was analyzed from two angles: the total number of methylated peptides identified, as well as the number of unique methylated peptides identified. The total number of methylated peptides identified speaks to the overall scalability of the method for enriching the methylated peptide population whereas the number of unique methylated peptides identified speaks to the depth of identification at varying amounts of starting material.

Figure 3: The average number of methylated peptides identified with differing amounts of starting material. HEK293T cells were lysed and proteins isolated as per Materials and Methods. The protein was aliquoted based on amount of starting material ranging from 0.2 mg to 10 mg of protein. The proteins were reduced, alkylated, tryptically digested and enriched for methylated peptides using ProMENADe. The amount of reagent for the enrichment reaction was scaled per mg of starting material. The samples were then analyzed by mass spectrometry and the peptides identified using Mascot version 2.3. A) The average number methylated peptides identified at 0.2, 0.5, 2, 5 and 10 mg with a 1% FDR on the peptide level. B) The average number of methylated peptides identified at 0.2, 0.5, 2, 5 and 10 mg with a 1% FDR on the methylation level. C) The average number methylated peptides identified at 0.2, 0.5, 2, 5 and 10 mg with a 1% FDR on the methylation level filtered for methylation at C-terminus. D) The average number of peptides identified with the enrichment protocol. ANOVA test $p<0.05$. Post-hoc t-test analysis with Bonferroni correction $*p<0.01$.


A)
# of methylated peptides
900
800
700
600
500
400
300
200
100
0
0.2
0.5
2
5
10
Starting material (mg)
*
*
B)
# of methylated peptides
250
200
150
100
50
0
0.2
0.5
2
5
10
Starting material (mg)
*
*
C)
# of methylated peptides
250
200
150
100
50
0
0.2
0.5
2
5
10
Starting material (mg)
*
*
D)
# of peptides
70000
60000
50000
40000
30000
20000
10000
0
0.2
0.5
2
5
10
Starting material (mg)
*
*


Filtered for methylation at C-terminus
1% FDR at level of methylation
1% FDR at level of peptide
Stringency Increase

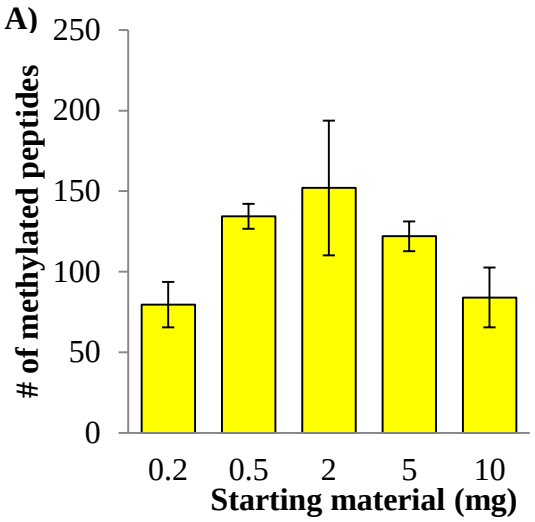
Using 0.5 mg of starting material yielded significantly more methylated peptides than 0.2 mg of starting material while the use of 2 mg of starting material did not yield significantly more sites than 0.5 mg of starting material (Figure 3 A, B, C). This indicates that 0.5 mg of starting material yielded the most methylated peptides for the least amount of starting material. Therefore, moving forward in experiments it was decided that the use of 0.5 mg of starting material would give the optimal amount of total methylation for the least amount of protein starting material.

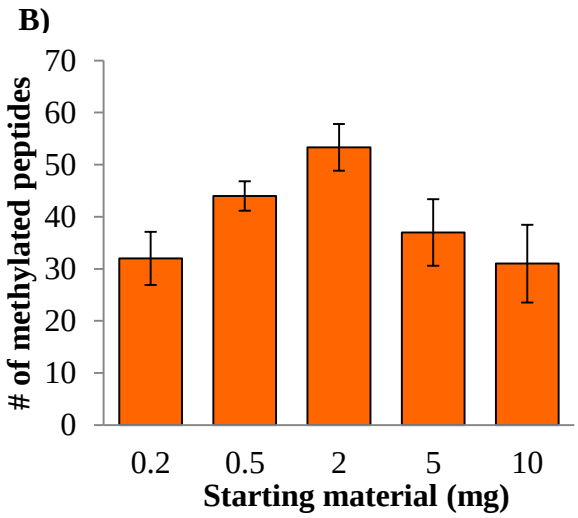
Additionally, the use of 10 mg of protein starting material yielded less methylated peptides than the use of 0.2 mg (Figure 3 A, B, C). This was unexpected as 10 mg is 50X more starting material than 0.2 mg, so the amount of peptides identified per sample was examined (Figure 3D). The use of both 5 mg and 10 mg of protein starting material yielded around 20, 000 peptides which resembled 0.2 mg of starting material. This could be the result of saturation of the SCX chromatography column prior to MS/MS analysis yielding less peptides and thus methylated peptides to be identified.

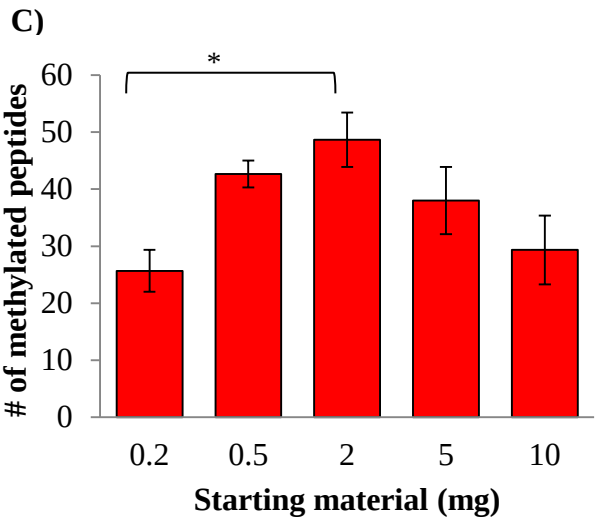
iii. ProMENADe Reaction Identifies More Confident Methylation Sites

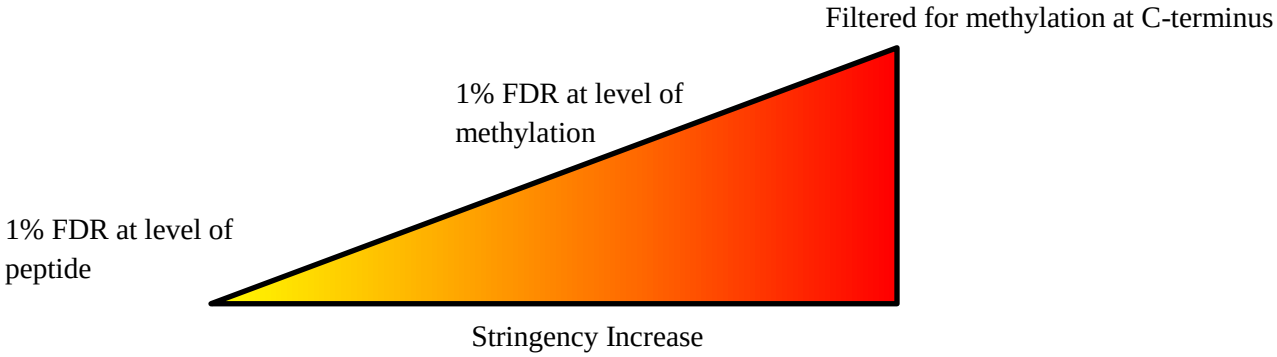
As this methodology was novel, the amount of enrichment in an HEK293T cell lysate had yet to be tested. The HEK293T cells were lysed in 1X RIPA buffer and proteins were precipitated overnight with acetone at -20°C, reduced with dithiothreitol (DTT), and alkylated with iodoacetamide (IAA), and tryptically digested over night as described in the Materials and Methods Sections III and VI . Three samples of 0.5 mg whole cell lysate underwent the ProMENADe reaction in parallel with three samples of 0.5 mg of whole cell lysate which did not undergo the ProMENADe reaction, which were the non-enriched

Figure 4: The number of unique methylated peptides identified with differing amounts of starting material. HEK293T cells were lysed and proteins isolated as per materials and methods. The protein was aliquoted based on amount of starting material ranging from 0.2 mg to 10 mg of protein. The protein was aliquoted based on amount of starting material ranging from 0.2 mg to 10 mg of protein. The proteins were reduced, alkylated, tryptically digested and enriched for methylated peptides using ProMENADe. The amount of reagent for the enrichment reaction was scaled per mg of starting material. The samples were then analyzed by mass spectrometry and the peptides identified using Mascot version 2.3. A) The number of unique methylated peptides identified at 0.2, 0.5, 2, 5 and 10 mg with a 1% FDR on the peptide level. B) The number of unique methylated peptides identified at 0.2, 0.5, 2, 5 and 10 mg with a 1% FDR on the methylation level. C) The number of unique methylated peptides identified at 0.2, 0.5, 2, 5 and 10 mg with a 1% FDR on the methylation level with all C-terminal methylated peptides removed for potential esterification false positives. ANOVA test $p<0.05$. Post-hoc t-test analysis with Bonferroni correction $*p<0.01$.


A)
# of methylated peptides
250
200
150
100
50
0
0.2
0.5
2
5
10
Starting material (mg)


B)
# of methylated peptides
70
60
50
40
30
20
10
0
0.2
0.5
2
5
10
Starting material (mg)


C)
*
# of methylated peptides
60
50
40
30
20
10
0
0.2
0.5
2
5
10
Starting material (mg)


Filtered for methylation at C-terminus
1% FDR at level of methylation
1% FDR at level of peptide
Stringency Increase

controls, and were analyzed by mass spectrometry. The peptides were identified using Mascot version 2.3.

The sample without the enrichment reaction had an average of 680 methylated peptides identified at a peptide FDR of 1%, an average of 49 methylated peptides identified at a methylation FDR of 1%, and an average of 22 methylated peptides identified at a methylation FDR of 1% followed by removal of methylation events on the C-terminal (Figure 5A). These sites were removed as they could have been false-positive identifications. It is reported that trypsin's efficiency is decreased when cleaving mono-methylated lysine and that cleavage does not occur with di- and tri- methylated lysine [92], therefore it would be unlikely for tryptic cleavage to occur on a methylated lysine or arginine. Secondly, the identifications on the C-terminal can be the result of esterification caused by the ProMENADe reaction (Figure 2B).

The enriched sample had an average of 363 methylated peptides identified at a peptide FDR of 1%, an average of 158 methylated peptides identified at a methylation FDR of 1%, and an average of 123 methylated peptides identified upon removal of methylation events on the C-terminal (Figure 5A). The sample without the enrichment reaction had significantly more methylated peptides identified than the ProMENADe enriched sample at the 1% FDR at the peptide level ($p<0.05$). The ProMENADe enrichment reaction showed a significant increase in the number of confidently identified methylation sites, at an FDR of 1% at the methylation level ($p<0.05$), over a sample without the enrichment reaction and at an FDR of 1% at the methylation level with C-terminal sites removed ($p<0.05$) (Figure 5B).

In order to examine the characteristics of the methylated peptides identified in the ProMENADe-enriched and non-enriched samples, the genes of the identified methylated proteins from the 1% FDR at the level of methylation filtered for C-terminal methylation were extracted and imported into the Gene Ontology (GO) tool in the Database for Annotation, Visualization and Integrated Discovery v6.7 (DAVID). The background, which consisted of the gene names of all identified proteins from the dataset, was also uploaded. For the ProMENADe-enriched samples, the biological processes of: RNA processing and splicing, mRNA processing, metabolic process, and nuclear splicing via spliceosome, negative regulation of gene expression and chromatin assembly or disassembly were significantly enriched while the non-enriched samples were enriched for the biological process of RNA processing (Figure 6A).

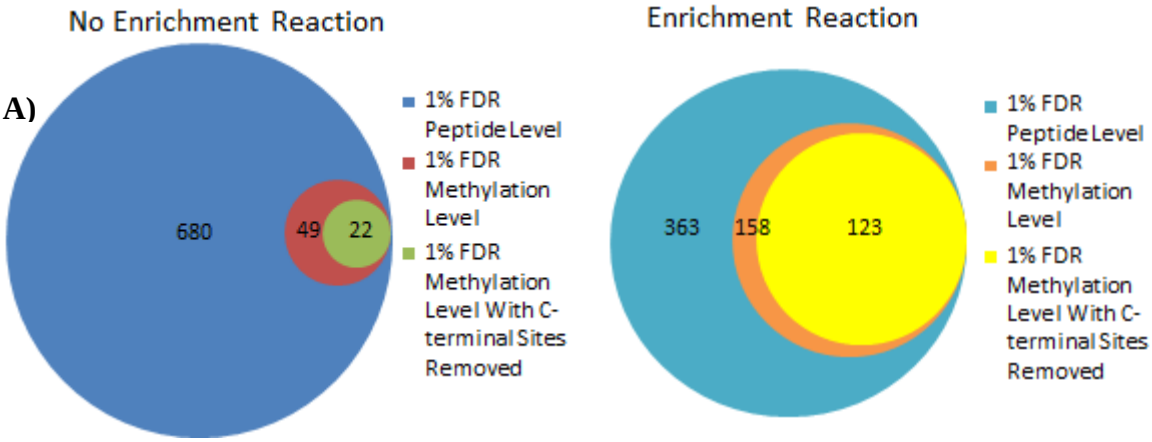
Overall the methylated proteins identified by the ProMENADe-enriched samples were found to be significantly enriched for the cellular components of: the heterogeneous nuclear ribonucleoprotein complex, ribonucleoprotein complex, eukaryotic translation elongation factor 1 complex, chromatin and the spliceosome. The methylated proteins identified by the non-enriched samples were significantly enriched in the cellular component of heterogeneous nuclear ribonucleoprotein complex (Figure 6B).

iv. Discussion for ProMENADe Reaction Identifies More Confident Methylation Sites

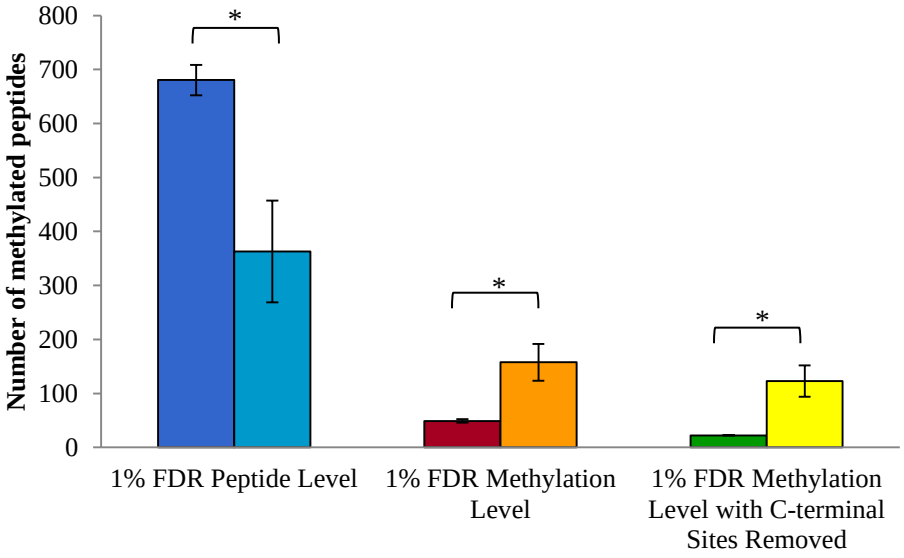
Analysis performed with a 1% FDR at the peptide level yields more sites in the sample without ProMENADe enrichment. This course of analysis, 1% FDR at the peptide level, is a less stringent approach to identify PTMs and is a similar analysis method to the work of others [27, 28, 147-151]. Without enrichment reaction at a 1% FDR at the peptide level, 680 unique methylation sites were identified. This number remains greater

Figure 5: The number of methylated peptides identified with and without the enrichment reaction. The HEK293T cells were lysed in 1X RIPA buffer and proteins were precipitated overnight with acetone at -20°C, reduced with dithiothreitol (DTT), and alkylated with iodoacetamide (IAA), and tryptically digested over night as described in the Materials and Methods sections III and VI . Three samples of 0.5 mg whole cell lysate underwent the ProMENADe reaction in parallel with three samples of 0.5 mg of whole cell lysate which did not undergo the ProMENADe reaction, which were the non-enriched controls, and were analyzed by mass spectrometry. The peptides were identified using Mascot version 2.3. A) The analysis summary for determining the number of methylated peptides at more strict confidence levels. The first level is the 1% false discovery rate (FDR) at the peptide level. The second level of confidence is using the 1% FDR at the level of the methylation modification. The last level of confidence is using the 1% FDR at the methylation level followed by removing sites with C-terminal methylation. B) The average number methylated peptides identified with and without the enrichment protocol using 0.5 mg of starting material with a 1% FDR on the peptide level, 1% FDR on the methylation level and with a 1% FDR on the methylation level with all C-terminal methylated peptides removed for potential esterification false positives. T-test * $p < 0.05$, n=3.

A)


No Enrichment Reaction
680
49
22
1% FDR Peptide Level
1% FDR Methylation Level
1% FDR Methylation Level With C-terminal Sites Removed
Enrichment Reaction
363
158
123
1% FDR Peptide Level
1% FDR Methylation Level
1% FDR Methylation Level With C-terminal Sites Removed

B)


Number of methylated peptides
800
700
600
500
400
300
200
100
0
*
*
*
1% FDR Peptide Level
1% FDR Methylation Level
1% FDR Methylation Level with C-terminal Sites Removed

than the compilation of 501 lysine and arginine methylation sites of Bremang *et al.* (2013) [151]. At a 1% FDR at the peptide level for the ProMENADe-enriched samples however, only 363 methylation sites were identified (Figure 5A). This is very likely due to peptide hydrolysis during the highly acidic conditions of the MDA derivatization reaction or sample loss during the basic conditions of the OPA derivatization reaction in the ProMENADe-enriched sample.

The stringency of analysis was increased so that a 1% FDR on the methylation modification was used to identify more stringent methylation sites. With a 1% FDR at the level of methylation, the ProMENADe-enriched sample had significantly more methylation sites than a control sample without enrichment (Figure 5B). The ProMENADe-enriched samples yielded 158 methylation sites while the control sample yielded only 49 methylation sites. This level of stringency should be applied across all studies. The ProMENADe reaction yields more confident sites compared to other methods which use a 1% FDR at the peptide level [27, 150].

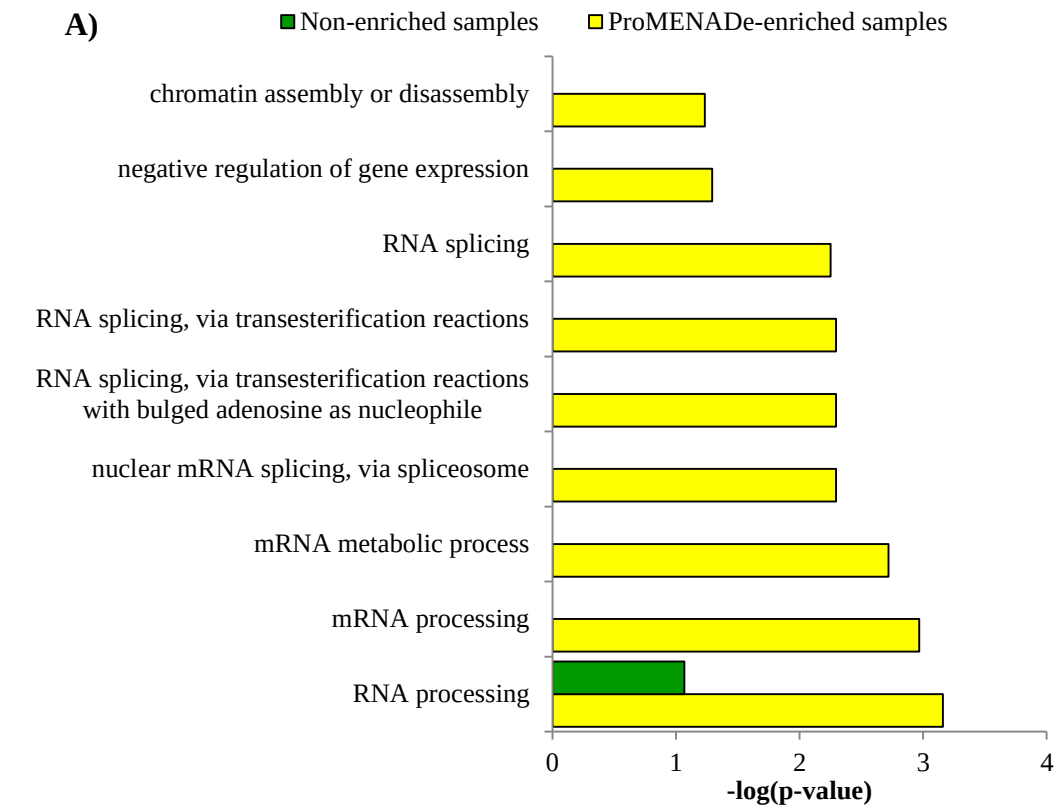
One drawback of our enrichment strategy is that many lysine and arginine residues at the peptide C-terminus were found to be methylated. This is against expectations as trypsin's efficiency is decreased when cleaving mono-methylated lysine and cleavage does not occur with di- and tri- methylated lysine [92]. As tryptic cleavage cannot occur efficiently at methylated residues, it would be unlikely to identify a peptide with methylation on the C-terminus. We then hypothesized that these C-terminal methylations could be the result of esterification caused by the strongly acidic conditions during the reaction with malondialdehyde with trace amounts of methanol remaining from its synthesis (Figure 2B).

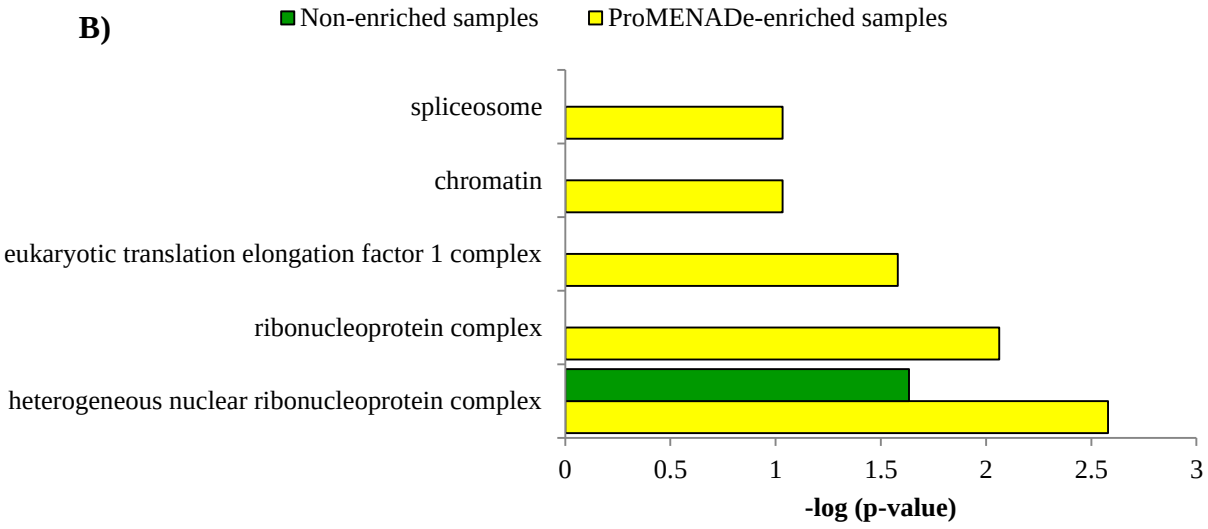
The Gene Ontology (GO) tool in the Database for Annotation, Visualization and Integrated Discovery v6.7 (DAVID) was used for analysis of the biological processes as well as the cellular components of methylated proteins in order to examine whether the ProMENADe methodology results in the identification of a different subset of methylated proteins.

For the ProMENADe-enriched samples, the biological processes of: macromolecular, protein, nucleosome and chromatin complex assembly and subunit organization, DNA packaging, microtubule processes, protein biogenesis and response, the localization, processing, splicing, transport, and metabolic processes of mRNA and RNA, nucleic acid transport, and translation were all found to be significantly enriched in the methylated protein population (Figure 6A). Meanwhile, the methylated proteins identified that did not undergo the enrichment reaction were more enriched in the processes of: microtubule based movement and process, protein complex assembly and biogenesis, and response to protein stimulus and unfolded protein (Figure 6A). These differences can be attributed to the small sample size of the non-enriched samples which is not accurate for DAVID analysis.

The biological processes identified are similar to other published results [27, 150]. The biological processes of RNA processing, splicing, localization, and transport, transcription, regulation of translation, and chromatin organization have been seen as enriched for proteins containing mono-methylated and di-methylated arginine [150]. Chromatin organization as well as RNA and DNA binding has been seen as enriched for proteins with methylated lysine residues [27].

Figure 6: Gene ontology analysis for the biological processes and cellular components enriched in the methylated proteins from the ProMENADe-enriched and non-enriched samples. A) The gene names of the identified methylated proteins at a 1% FDR at the level of methylation with C-terminal sites removed were exported and used for Gene Ontology (GO) analysis in Database for Annotation, Visualization and Integrated Discovery v6.7 (DAVID) of the biological processes significantly enriched in the methylated protein population of samples with and without ProMENADe enrichment. B) The gene names of the identified methylated proteins at a 1% FDR at the level of methylation with C-terminal sites removed were exported and used for GO analysis in DAVID of the cellular components significantly enriched in the methylated protein population of samples with and without ProMENADe enrichment.


A)
Non-enriched samples
ProMENADe-enriched samples
chromatin assembly or disassembly
negative regulation of gene expression
RNA splicing
RNA splicing, via transesterification reactions
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
nuclear mRNA splicing, via spliceosome
mRNA metabolic process
mRNA processing
RNA processing
0
1
2
3
4
-log(p-value)


B)
Non-enriched samples
ProMENADe-enriched samples
spliceosome
chromatin
eukaryotic translation elongation factor 1 complex
ribonucleoprotein complex
heterogeneous nuclear ribonucleoprotein complex
0
0.5
1
1.5
2
2.5
3
-log (p-value)

The methylated proteins identified by the ProMENADe enrichment were found to be enriched in nuclear components like chromatin, eukaryotic translation elongation factor 1 complex, heterogeneous nuclear ribonucleoprotein complex, and the spliceosome (Figure 6B). The non-enriched population of methylated proteins were enriched in the heterogeneous nuclear ribonucleoprotein complex (Figure 6B). These cellular components correspond to other studies where arginine methylated proteins were found distributed in the nucleus, nucleolus, ribonucleoprotein complex, spliceosome, transcriptional repressor complex, cytoplasm and cytoskeleton [150]. Proteins containing lysine methylation have been found most predominantly in the nucleus, and cytosol, but also found in the cytoskeleton, endoplasmic reticulum, plasma membrane, mitochondria, and extracellular space [27].

II. Simplification of the Protein Mixture to Increase MS Identification

Upon analysis of the data from the starting material samples and the proof of enrichment samples, it became evident that many of the previously identified methylated peptides were from high abundance proteins. In order to prove this we compared our sites identified from these tests to the "H. sapiens WHOLE_ORGANISM" dataset from the Protein Abundance Across Organisms Database (PaxDb). This database provides the identity and quantification in parts per million (ppm) of protein from tissues and organs to the whole organism in human and other species. The proteins in the "H. sapiens WHOLE_ORGANISM" dataset from PaxDb were used for comparison and are normally distributed around the protein abundance of 0.1 to 1 ppm.

As predicted, a majority of the methylated proteins identified from our previous experiments (Results Section I, subsection i and ii) are known high abundance proteins (Figure 7). Greater than 90% of the identified methylated proteins were those found with an

abundance above 10 ppm (Figure 7). Their abundance distribution does not match that of the predicted proteome from PaxDb as the sample contains mostly high abundance proteins with few low abundance proteins being identified.

Moving forward we adopted a few strategies to uncover more methylation sites in less abundant proteins. The first strategy to uncover less abundant proteins was to employ subcellular fractionation to simplify the protein mixture into two simpler mixtures: the nucleus and everything else – termed "cytosol". These samples were subsequently enriched for methylation and analyzed by MS/MS (Figure 8A).

Since PTMs can block tryptic cleavage sites, and proteins may contain too few or too many lysine and arginine residues it may be difficult to identify all methylated peptides with a tryptic digestion approach [165]. The use of multiple proteases like trypsin, chymotrypsin, and Glu-C were employed for digestion to create a larger peptide population to increase chances of identifying novel methylation sites (Figure 8B). These proteases were chosen as they are complimentary proteases in that they cleave at unique amino acids. Trypsin cleaves at basic residues like lysine and arginine, chymotrypsin cleaves at aromatic residues like tyrosine, phenylalanine and tryptophan, while Glu-C cleaves at acidic residues like aspartic acid and glutamic acid.

These two methods were then combined so that we could compare tryptically, chymotryptically, and Glu-c digested nuclear and cytosolic components to a tryptically digested whole cell lysate (Figure 8C).

Figure 7: Identified proteins plotted with their abundance. Proteins from the human whole organism dataset in the Protein Abundance Across Organisms Database (PaxDb) are plotted with their cellular abundance measured in parts per million (ppm). The identified methylated proteins from the starting material dataset and the ProMENADe-enrichment and non-enrichment datasets from Results, Section I subsection i and ii, were mapped to their abundance according to the PaxDb dataset and plotted on the graph.

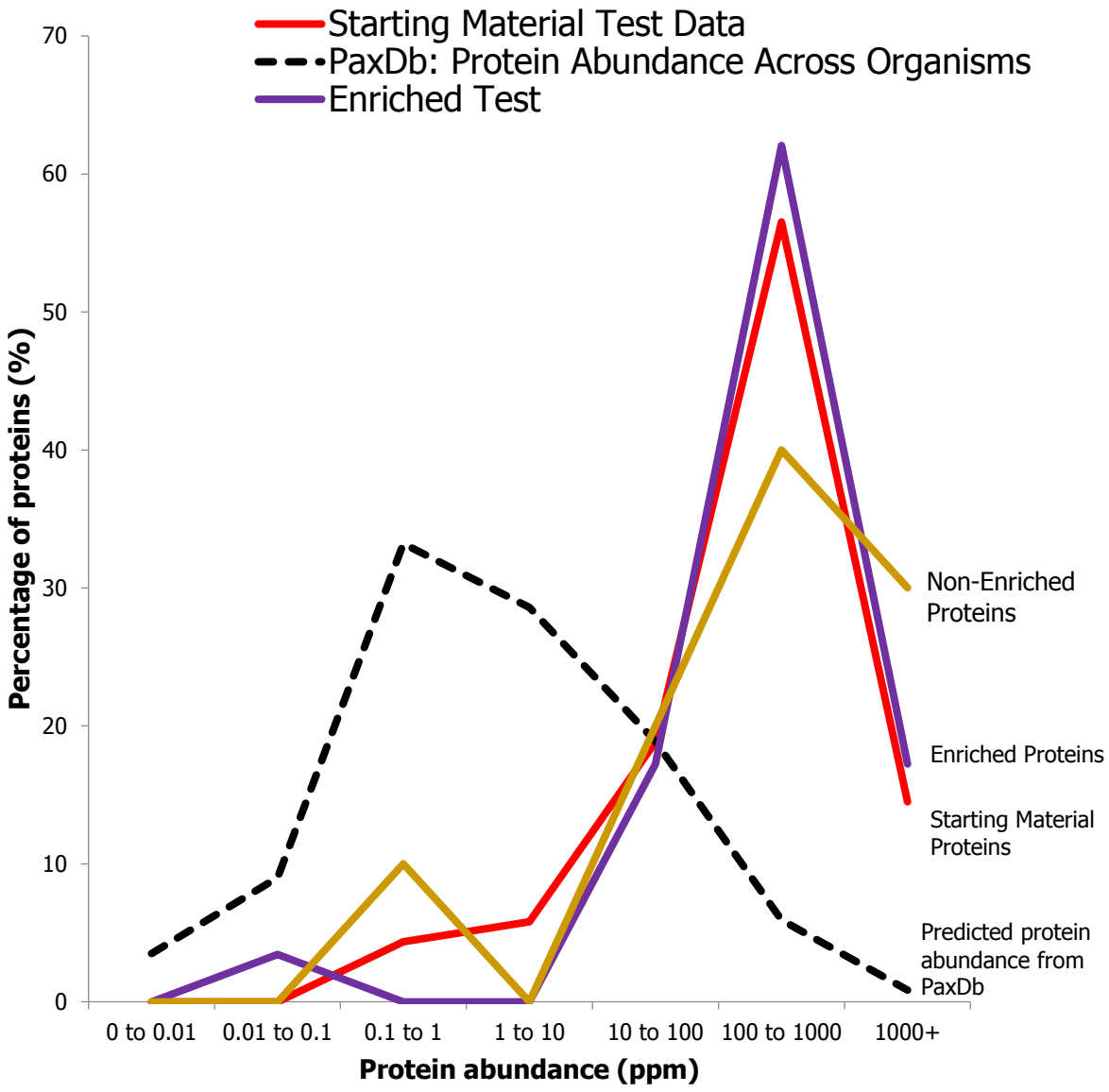
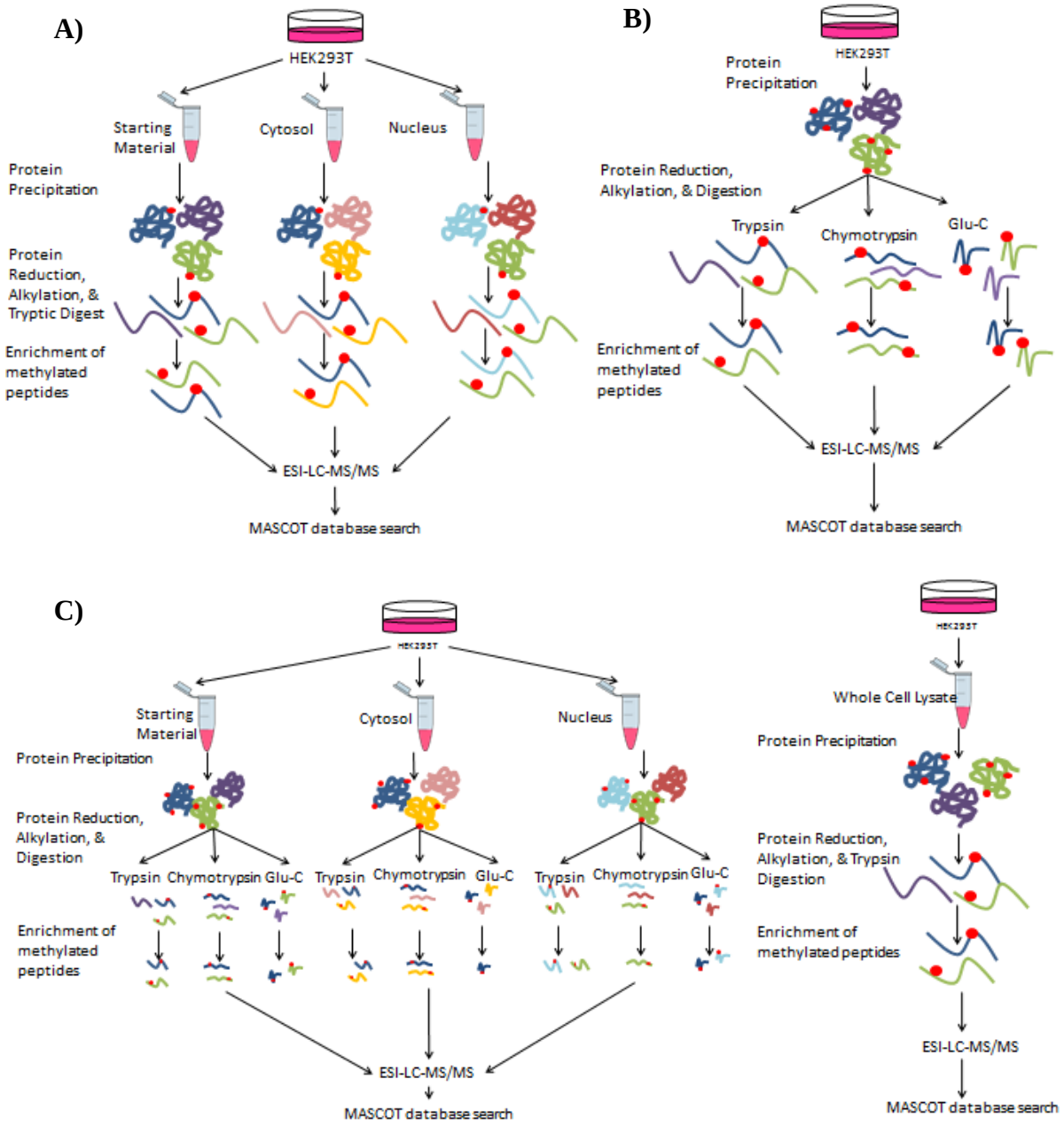

Starting Material Test Data
PaxDb: Protein Abundance Across Organisms
Enriched Test
70
60
50
40
30
20
10
0
Percentage of proteins (%)
0 to 0.01
0.01 to 0.1
0.1 to 1
1 to 10
10 to 100
100 to 1000
1000+
Protein abundance (ppm)
Non-Enriched Proteins
Enriched Proteins
Starting Material Proteins
Predicted protein abundance from PaxDb

Figure 8: Workflows for subcellular fractionation and multi-protease digest experiments. A) Subcellular fractionation on HEK293T cells were enriched for their nuclear and cytosolic proteins, the proteins were tryptically digested, and enriched for methylated peptides. B) The protein of HEK293T cells were digested by trypsin, chymotrypsin, and Glu-C, and the peptides were enriched for methylation. C) Subcellular fractionation on HEK293T cells were enriched for their nuclear and cytosolic proteins, the proteins were digested tryptically, chymotryptically, and with Glu-C. The resulting peptides were then enriched for methylation. Alongside, a whole cell lysate was tryptically digested and used for comparison of methylation identification.

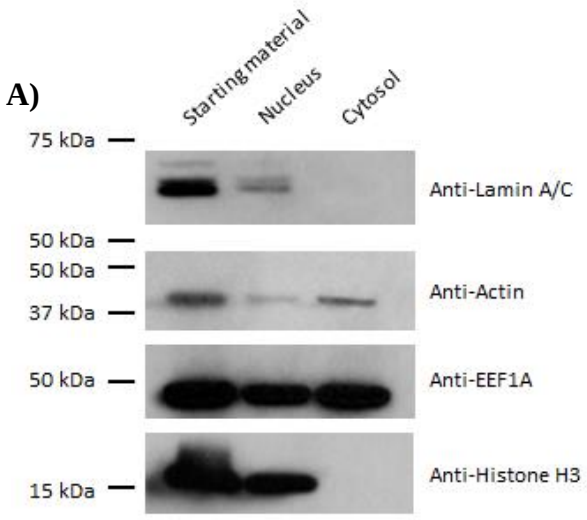

A)
HEK293T
Starting Material
Cytosol
Nucleus
Protein Precipitation
Protein Reduction, Alkylation, & Tryptic Digest
Enrichment of methylated peptides
ESI-LC-MS/MS
MASCOT database search
B)
HEK293T
Protein Precipitation
Protein Reduction, Alkylation, & Digestion
Trypsin
Chymotrypsin
Glu-C
Enrichment of methylated peptides
ESI-LC-MS/MS
MASCOT database search
C)
HEK293T
Starting Material
Cytosol
Nucleus
Protein Precipitation
Protein Reduction, Alkylation, & Digestion
Trypsin
Chymotrypsin
Glu-C
Enrichment of methylated peptides
ESI-LC-MS/MS
MASCOT database search
HEK293T
Whole Cell Lysate
Protein Precipitation
Protein Reduction, Alkylation, & Trypsin Digestion
Enrichment of methylated peptides
ESI-LC-MS/MS
MASCOT database search

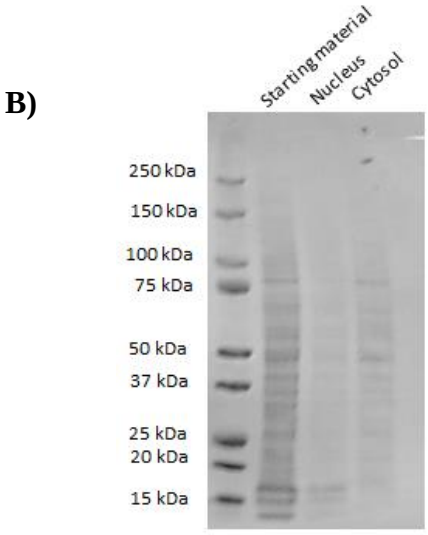
i. Subcellular Fractionation to Increase Methylation Site Identification by MS/MS

The Rapid, Efficient and Practical (REAP) method [161] was used for the subcellular fractionation of the HEK293T cells as described in Materials and Methods Section IV. The cells were separated into three fractions: the starting material, the nucleus and everything else, which has been termed "cytosol". The enrichment was visualized by immunoblotting using antibodies to detect the nuclear proteins, lamin A/C and histone H3, the cytosolic protein, actin, and elongation factor 1-alpha 1 (EEF1A1), a cytosolic and nuclear protein. This was performed according to the Materials and Methods Section V (Figure 9A). The proteins on the nitrocellulose membrane were stained with Ponceau for visualization of the loading control (Figure 9B). The proteins in the starting material, nuclear and cytosolic fractions were processed for proteomics as described in the Materials and Methods Section VI. This experiment was repeated three times.

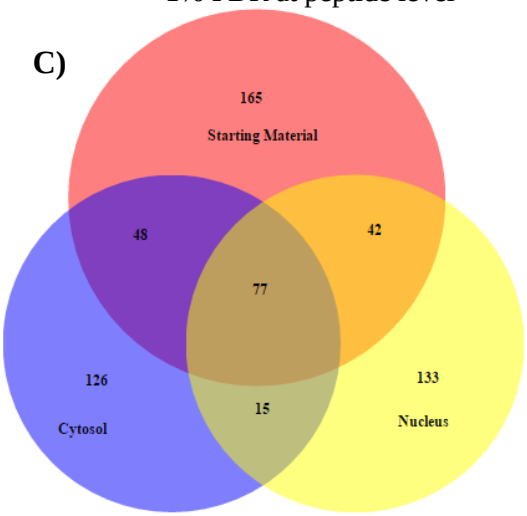
Overall the starting material sample identified 332 unique sites at a 1% FDR cut-off at the peptide level while performing subcellular fractionation and simplifying the whole cell lysate into the nuclear and cytosol components allowed the identification of 441 unique sites (Figure 9C). This corresponds to an 82.5% increase in identified methylation sites. At a cut-off of 1% FDR at the methylation level 111 sites were identified in the starting material while 150 were identified in the nuclear and cytosolic fractions combined (Figure 9D). This corresponds to a 59.5% increase in identified methylation sites. Lastly, with C-terminal methylation sites removed 76 sites were identified in the starting material and 92 sites were identified in the cytosolic and nuclear fractions combined (Figure 9E). This corresponds to a 39.5% increase in identified methylation sites.

Figure 9: Subcellular fractionation of HEK293T cells demonstrated by immunoblot and the identified methylated peptides per fraction. HEK293T cells were fractionated into the starting material the nucleus and the cytosol. The proteins were processed for proteomics and the methylated peptides were enriched for MS/MS analysis. A) Immunoblots using anti-lamin A/C and anti-Histone H3 to demonstrate the lanes expressing nuclear proteins. Immunoblots using anti-actin to demonstrate the lanes expressing cytosolic proteins. B) Total protein expressed in each lane visualized by Ponceau stain. C) Illustration of unique sites identified in the starting material, cytosolic, and nuclear fractions using a 1% FDR cut-off at the peptide level. D) Illustration of unique sites identified in the starting material, cytosolic, and nuclear fractions using a 1% FDR cut-off at the methylation level. E) Illustration of unique sites identified in the starting material, cytosolic, and nuclear fractions using a 1% FDR cut-off at the methylation level with C-terminal methylation sites removed. (n=3).

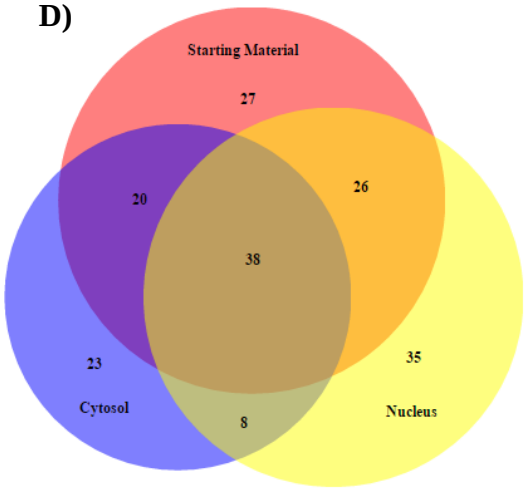


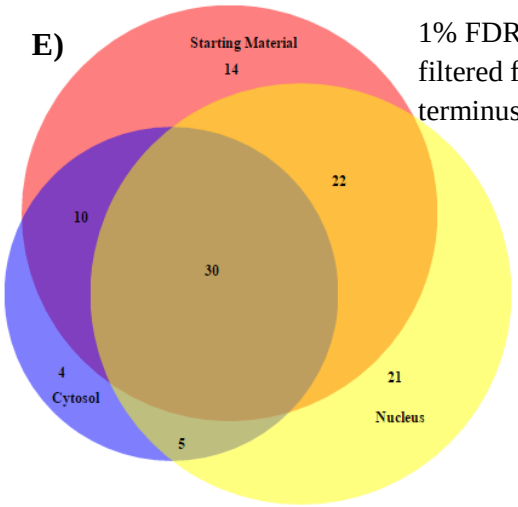


1% FDR at peptide level



1% FDR at methylation level





1% FDR at methylation level filtered for methylation at C-terminus

At the stringent level of analysis with 1% FDR at the methylation level filtered for C-terminal sites, 50% of the overlapping sites are for proteins located in both the cytosol and the nucleus. The other 50% of sites consist of 25% cytosolic proteins, 8% nuclear proteins, and 17% without an annotated cellular location. This indicates a relatively good enrichment by subcellular fractionation.

To elucidate whether the functions of the methylated proteins identified in each fraction differ, the biological processes and cellular components of these identified proteins for each fraction were analyzed by GO analysis in DAVID. In the nuclear fraction the biological processes of: chromatin assembly or disassembly and organization, DNA packaging, mRNA metabolic process, processing and nuclear splicing via spliceosome, nucleosome assembly and organization, protein-DNA complex assembly, and RNA processing and splicing are the significantly enriched (Figure 10A). Meanwhile, in the cytosolic fraction, the processes of: establishment of RNA localization, mRNA metabolic process, processing and transport, nucleic acid transport and RNA transport are significantly enriched (Figure 10A). The starting material, similar to the nuclear fraction, is significantly enriched in the biological processes of chromatin assembly or disassembly, mRNA metabolic process, processing and nuclear splicing via spliceosome, and RNA processing, and splicing (Figure 10A).

The cellular components for each fraction were analyzed by GO analysis in DAVID v6.7. In the nuclear fraction the cellular components of chromatin, heterogeneous nuclear ribonucleoprotein complex, nucleosome, protein-DNA complex, ribonucleoprotein complex, and spliceosome were significantly enriched while in the cytosolic fraction the cellular components of eukaryotic translation elongation factor 1 complex, and spliceosome were

significantly enriched (Figure 10B). Meanwhile the starting material was significantly enriched for the cellular components of: chromatin, eukaryotic translation elongation factor 1 complex, heterogeneous nuclear ribonucleoprotein complex, nucleosome, ribonucleoprotein complex, and spliceosome (Figure 10B).

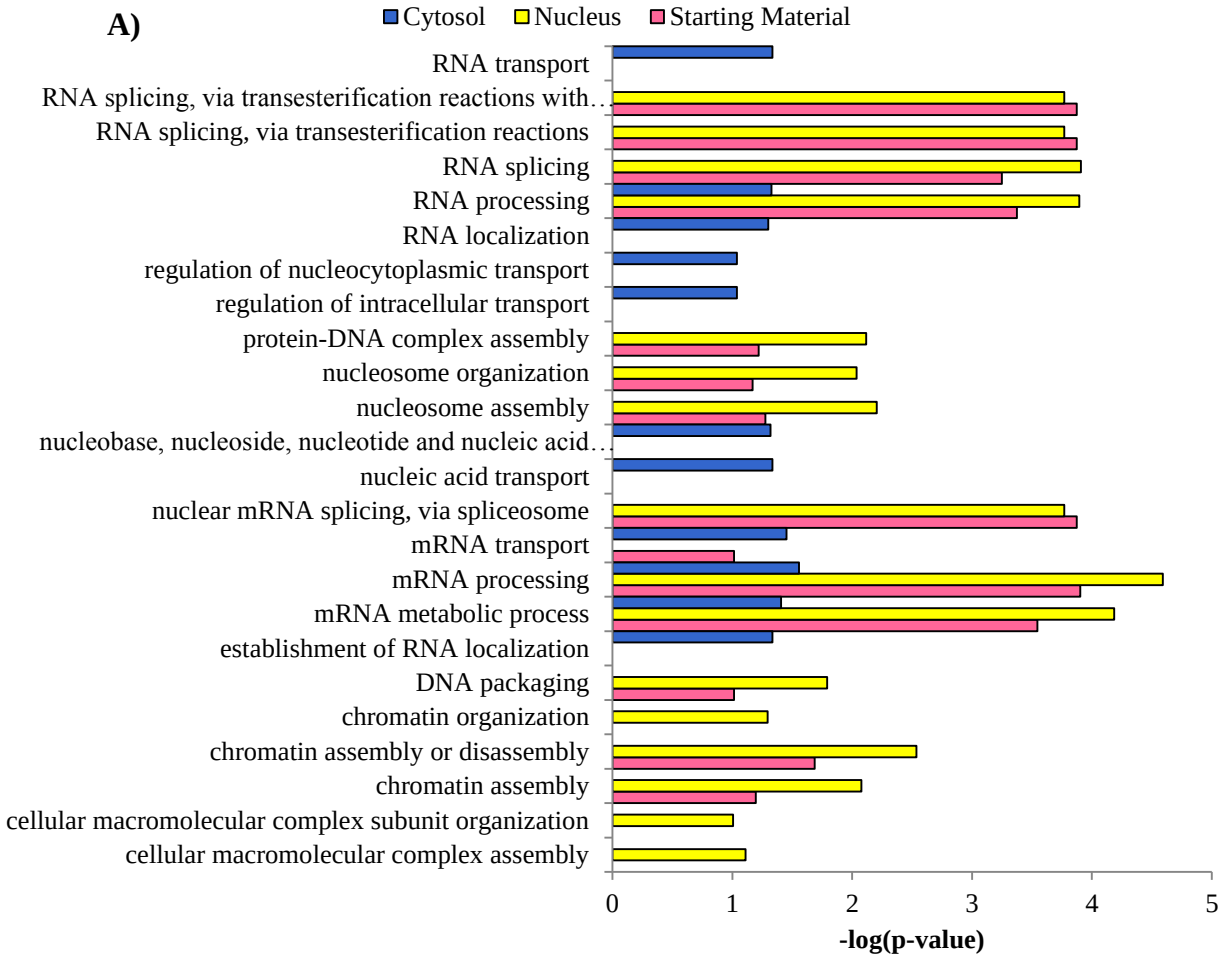
ii. Discussion for Subcellular Fractionation to Increase Methylation Site Identification by MS/MS

The enrichment was visualized by western blotting using antibodies to detect the nuclear proteins, lamin A/C and histone H3, the cytosolic protein, actin and EEF1A1, a cytosolic and nuclear protein. Lamin A/C and histone H3 were visualized solely in the starting material and nuclear fractions. Actin was seen mostly in the starting material and cytosolic fractions with minimal presence in the nuclear fraction. This could be due to the presence of nuclear actin [166]. The protein EEF1A1 was seen in all of the fractions which is expected due to its known location in cytosolic and nuclear regions (Figure 9A). In the total protein gel it is evident that more protein was loaded in the starting material over the nucleus and cytosolic fractions explaining the increase in intensity for the cellular markers in the starting material over the cytosolic and nuclear enriched fractions (Figure 9B).

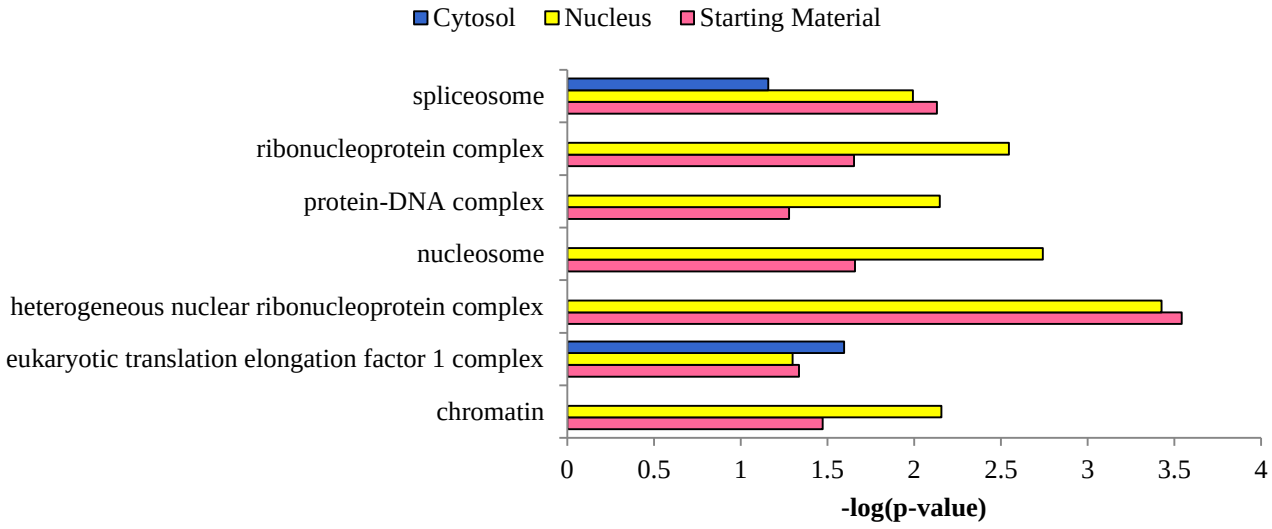
In all the varying levels of analysis, subcellular fractionation was found to increase the overall identification of methylation sites indicating the usefulness of its application to increase site identification. At 1% FDR at peptide level it increased the sites identified by 82.5%, at 1% FDR at methylation level it increased the sites identified by 59.5% and upon filtering the 1% FDR methylation level data for C-terminal methylation it increased the sites identified by 39.5%.

Figure 10: Gene ontology analysis for the biological processes and cellular components enriched in the methylated proteins from the starting material, cytosolic and nuclear fractions. A) The gene names of the identified methylated peptides at a 1% FDR at the level of methylation with C-terminal sites removed were exported and used for Gene Ontology (GO) analysis in Database for Annotation, Visualization and Integrated Discovery v6.7 (DAVID) of the biological processes significantly enriched in the starting material, cytosol and nuclear fractions. B) The gene names of the identified methylated peptides at a 1% FDR at the level of methylation with C-terminal sites removed were exported and used for GO analysis DAVID of the cellular components significantly enriched in the starting material, cytosol and nuclear fractions.

A)


Cytosol
Nucleus
Starting Material
RNA transport
RNA splicing, via transesterification reactions with…
RNA splicing, via transesterification reactions
RNA splicing
RNA processing
RNA localization
regulation of nucleocytoplasmic transport
regulation of intracellular transport
protein-DNA complex assembly
nucleosome organization
nucleosome assembly
nucleobase, nucleoside, nucleotide and nucleic acid…
nucleic acid transport
nuclear mRNA splicing, via spliceosome
mRNA transport
mRNA processing
mRNA metabolic process
establishment of RNA localization
DNA packaging
chromatin organization
chromatin assembly or disassembly
chromatin assembly
cellular macromolecular complex subunit organization
cellular macromolecular complex assembly
0
1
2
3
4
5
-log(p-value)

B)


Cytosol
Nucleus
Starting Material
spliceosome
ribonucleoprotein complex
protein-DNA complex
nucleosome
heterogeneous nuclear ribonucleoprotein complex
eukaryotic translation elongation factor 1 complex
chromatin
0
0.5
1
1.5
2
2.5
3
3.5
4
-log(p-value)

At a FDR of 1% at the methylation level the overlapping methylation sites identified between the cytosolic and nuclear fractions were composed of 50% proteins located in both the cytosol and nucleus, 25% cytosolic proteins, 8% nuclear proteins and 17% of unknown origin. This shows that the two fractions are enriched when compared to a whole cell lysate.

Overall, similar biological processes were significantly enriched in the nuclear and cytosolic fractions indicating that the methylated proteins identified in each fraction perform or are related to similar functions independent of cellular location (Figure 10A). In terms of cellular components, the fractions were relatively similar (Figure 10B). This could be because the dataset input into DAVID was that with filtering for C-terminal methylation. This drastically decreased the number of sites identified, and thus proteins identified at that confidence interval giving a smaller list of proteins exclusive to the cytosolic component and less differences seen between nuclear and cytosolic fractions.

Overall, the number of unique sites is higher in the cytosol and nuclear fractions combined compared to the starting material which indicates that simplifying the protein mixture into two smaller subcellular components simplifies it sufficiently to identify more sites.

iii. Digestion with Multiple Proteases to Increase Methylation Site Identification by MS/MS

Mass spectrometry identifies charged peptides ranging in size from 6-20 amino acids long. As proteins may contain too few or too many lysine and arginine residues this could yield peptides too short or too long for mass spectrometry making it difficult to identify all methylated peptides using a tryptic digestion approach. Additionally, PTMs can block tryptic cleavage sites which further increase the difficulty of identifying tryptic peptides. In order to increase the sequence coverage of proteins, a multiple enzyme approach was used for

digestion. The proteases used were trypsin, chymotrypsin and Glu-C which are complimentary for amino acid cleavage. The methylated peptides were enriched using ProMENADe and the samples were processed for MS as described in the Materials and Methods Section VI. The samples pre- and post-digestion were run and a gel and stained with Coomassie blue in order to visualize protein digestion. Digestion using trypsin, chymotrypsin and Glu-C went to completion (Supplementary Figure 1 A, B, C).

At a 1% FDR at the peptide level, 353 tryptically digested, 84 chymotryptically digested, and 66 Glu-C digested methylated peptides were identified (Figure 11A). Adding in digestion with chymotrypsin and Glu-C yielded an additional 42.5% more sites. At a 1% FDR at the methylation level 149 tryptic methylated peptides, 20 chymotryptic methylated peptides, and 10 Glu-C methylated peptides were identified (Figure 11B). This multi-protease approach yielded 20.1% more sites. Lastly, upon removal of the C-terminal methylation sites there were 111 tryptic methylated peptides, 20 chymotryptic, and 10 Glu-C (Figure 11C). This allowed the identification of 27% more sites. The chymotryptic and Glu-C generated methylated peptides are unaffected by C-terminal methylation removal as these enzymes cleave after aromatic, and acidic residues which are not the methylated residues of interest.

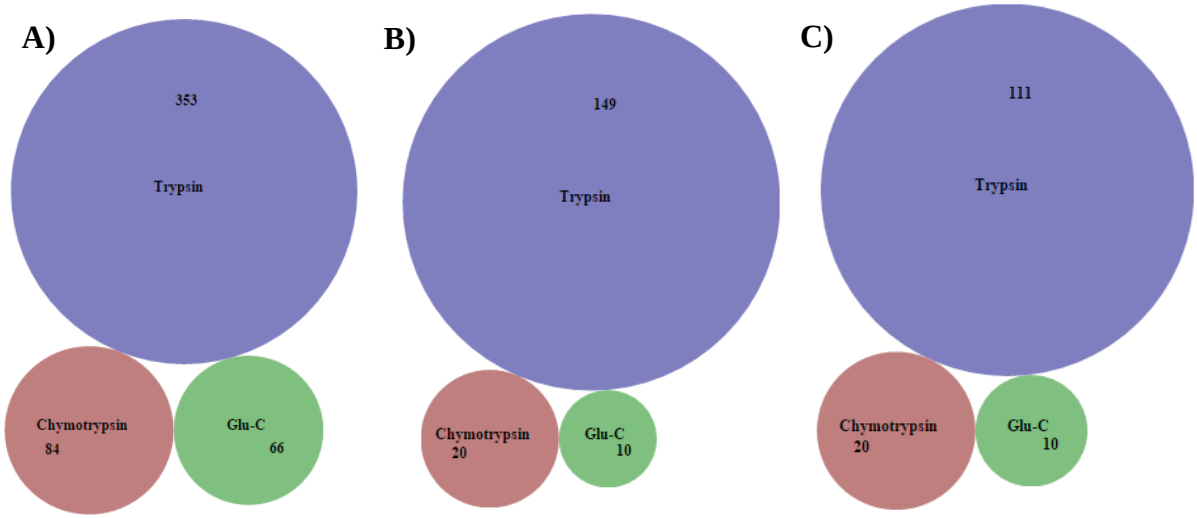
In order to explore whether the methylated peptide pool from each digest had different characteristics, the isoelectric points (pI) of the peptides were plotted, their grand average of hydropathy (GRAVY) values were plotted and GO analysis was performed for biological processes and cellular compartment. The tryptic peptides had a higher pI than the chymotryptic and Glu-C peptides peaking with a majority of the peptides with a pI above 10 (Figure 11D). The chymotryptic peptides peaked at a pI around 9 to 10 while the Glu-C

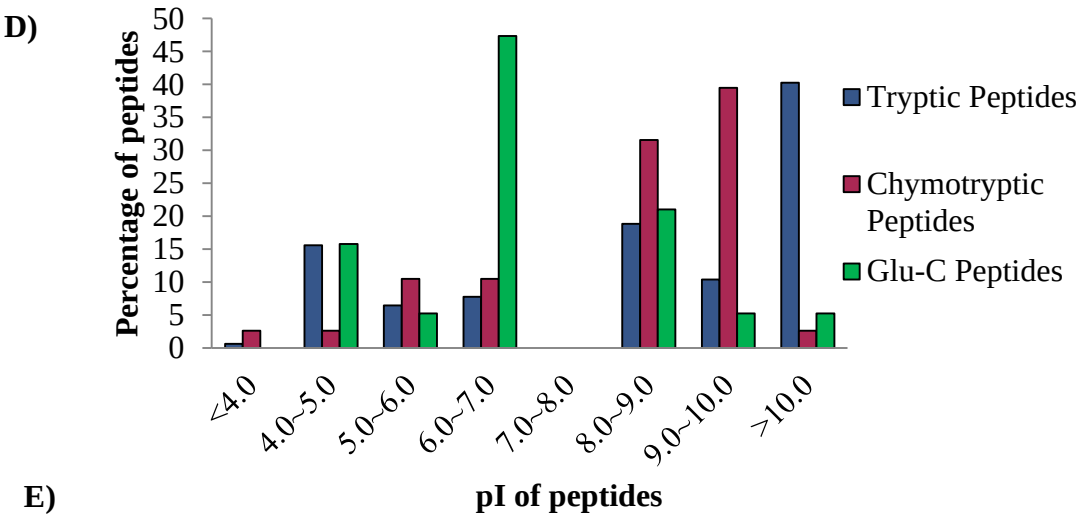
peptides were normally distributed at a pI around 6 to 7 (Figure 11D). Secondly the GRAVY values of the methylated peptides in the different digests were studied. The tryptic and chymotryptic peptides had normal distributions around -1 to -0.5 on the GRAVY scale indicating the peptides are hydrophilic. The Glu-C peptides however were normally distributed at -0.5 to 0 indicating a slightly more hydrophobic character than its tryptic and chymotryptic counterparts (Figure 11E).

The biological processes of the different digests were analyzed by GO analysis in DAVID v6.7. The significantly enriched biological processes for the tryptic and chymotryptic peptides were the same processes of: mRNA metabolic process, processing and nuclear splicing via the spliceosome, and RNA processing and splicing (Figure 12A). The Glu-C digest was significantly enriched for the biological processes of response to protein stimulus and response to unfolded protein (Figure 12A).

Lastly, the cellular compartments of the different tryptic, chymotryptic and Glu-C digests were analyzed by GO analysis in DAVID v6.7. The tryptic digest was found to be significantly enriched for the compartments of eukaryotic translation elongation factor 1 complex, heterogeneous nuclear ribonucleoprotein complex, ribonucleoprotein complex and the spliceosome while the chymotryptic methylated peptides were enriched for the compartments of the nucleolus, the ribonucleoprotein complex and the spliceosome. The Glu-C digests did not yield any significantly enriched cellular compartments (Figure 12B).

Figure 11: Identified methylated proteins upon digestion with trypsin, chymotrypsin and Glu-C proteases and the peptide characteristics. A) Illustration of methylation sites identified upon digestion with trypsin, chymotrypsin, or Glu-C (n=3) with a 1% FDR at the peptide level. B) Illustration of methylation sites identified upon digestion with trypsin, chymotrypsin, or Glu-C (n=3) with a 1% FDR at the methylation level. C) Illustration of methylation sites identified upon digestion with trypsin, chymotrypsin, or Glu-C (n=3) with a 1% FDR at the methylation level and C-terminal methylation sites removed. D) Isoelectric point of the methylated peptides identified after digestion with trypsin, chymotrypsin, or Glu-C. E) GRAVY values of the methylated peptides identified after digestion with trypsin, chymotrypsin, or Glu-C.


A)
353
Trypsin
Chymotrypsin
84
Glu-C
66
B)
149
Trypsin
Chymotrypsin
20
Glu-C
10
C)
111
Trypsin
Chymotrypsin
20
Glu-C
10


D)
Percentage of peptides
50
45
40
35
30
25
20
15
10
5
0
Tryptic Peptides
Chymotryptic Peptides
Glu-C Peptides
<4.0
4.0~5.0
5.0~6.0
6.0~7.0
7.0~8.0
8.0~9.0
9.0~10.0
>10.0
pI of peptides

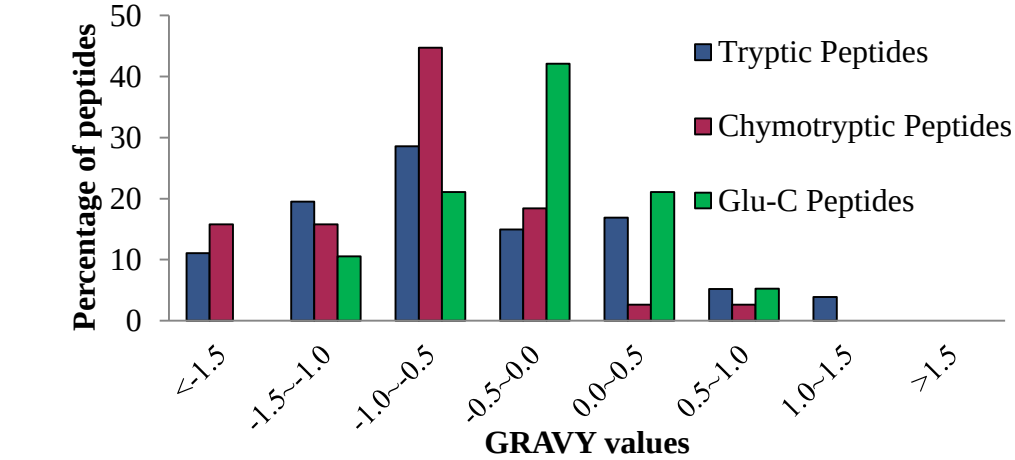
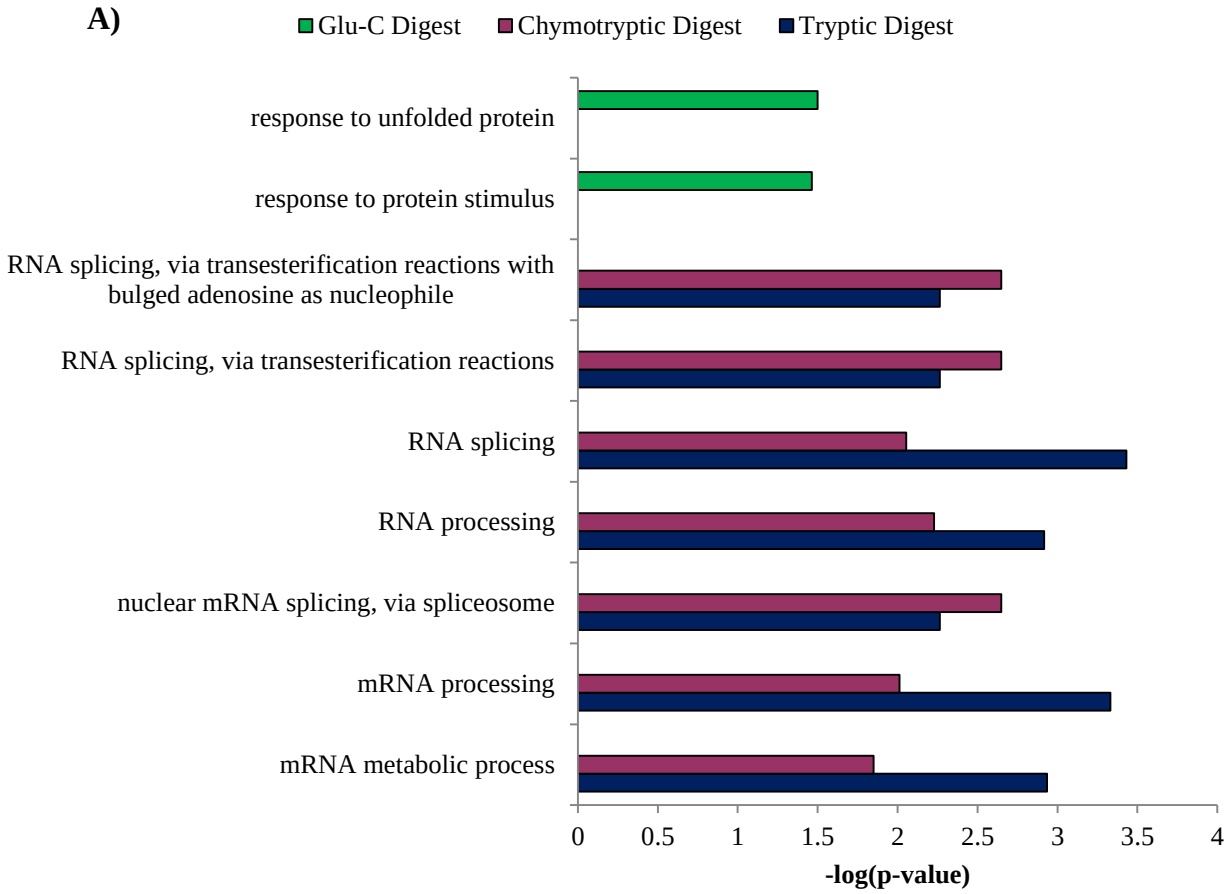
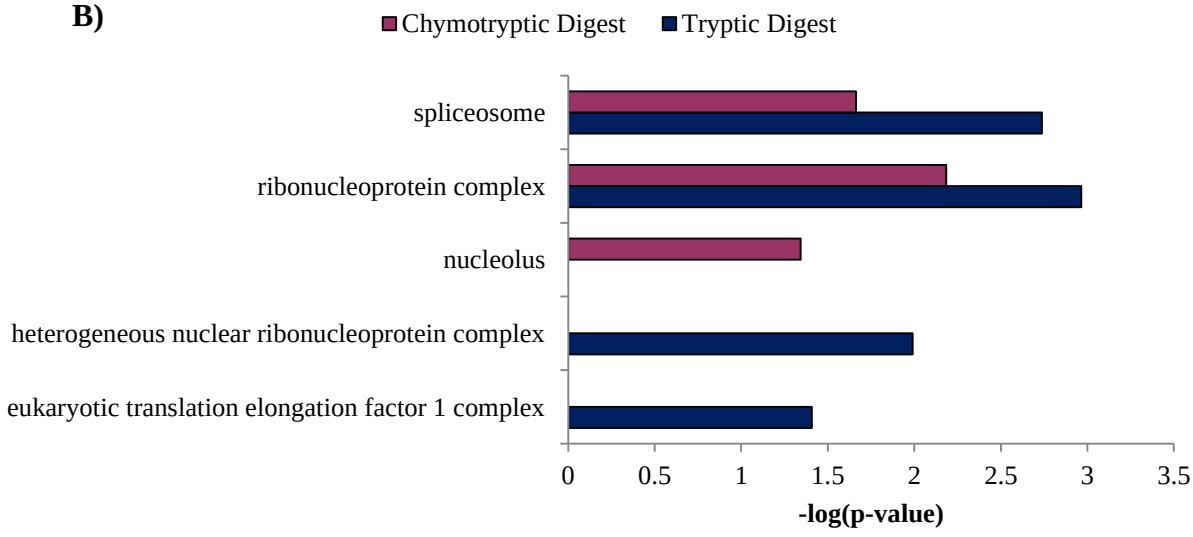

E)
Percentage of peptides
50
40
30
20
10
0
Tryptic Peptides
Chymotryptic Peptides
Glu-C Peptides
<-1.5
-1.5~-1.0
-1.0~-0.5
-0.5~0.0
0.0~0.5
0.5~1.0
1.0~1.5
>1.5
GRAVY values

Figure 12: Gene ontology analysis for the biological processes and cellular components enriched in the methylated proteins upon tryptic, chymotryptic, and Glu-C digestion. A) The gene names of the identified methylated peptides at a 1% FDR at the level of methylation with C-terminal sites removed were exported and used for Gene Ontology (GO) analysis in Database for Annotation, Visualization and Integrated Discovery v6.7 (DAVID) of the biological processes significantly enriched in the identified methylated proteins in the samples corresponding to digestion with trypsin, chymotrypsin, or Glu-C. B) The gene names of the identified methylated peptides at a 1% FDR at the level of methylation with C-terminal sites removed were exported and used for Gene Ontology (GO) analysis in Database for Annotation, Visualization and Integrated Discovery v6.7 (DAVID) of the biological processes significantly enriched in the identified methylated proteins in the samples corresponding to digestion with trypsin, chymotrypsin, or Glu-C.

A)


Glu-C Digest
Chymotryptic Digest
Tryptic Digest
response to unfolded protein
response to protein stimulus
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
RNA splicing, via transesterification reactions
RNA splicing
RNA processing
nuclear mRNA splicing, via spliceosome
mRNA processing
mRNA metabolic process
0
0.5
1
1.5
2
2.5
3
3.5
4
-log(p-value)

B)


Chymotryptic Digest
Tryptic Digest
spliceosome
ribonucleoprotein complex
nucleolus
heterogeneous nuclear ribonucleoprotein complex
eukaryotic translation elongation factor 1 complex
0
0.5
1
1.5
2
2.5
3
3.5
-log(p-value)

iv. Discussion for Digestion with Multiple Proteases to Increase Methylation Site Identification by MS/MS

A multi-enzyme digestion approach yielded 42.5% more sites at a 1% FDR at the peptide level, 20.1% more sites at a 1% FDR at the methylation level and 27% more sitesupon filtering data for peptide C-terminal methylation. The chymotryptic and Glu-C generated methylated peptides are unaffected by C-terminal methylation removal as these enzymes cleave after aromatic, and acidic residues which are not the methylated residues of interest. A multi-enzyme approach is a good solution to our C-terminal esterification as it will not be mistaken for C-terminal methylation.

There was no overlap between the tryptic, chymotryptic and Glu-C methylated peptides (Figure 11 A, B, C). This demonstrates the importance of increasing sequence coverage using multiple proteases for protein digestion, as many tryptic peptides may not be compatible for mass spectrometry analysis [167, 168].

The tryptic peptides had higher isoelectric points (pI) than the chymotryptic and Glu-C (Figure 11D). This was expected since methylated tryptic peptides will contain at least two basic amino acids because lysine and arginine will be the methylated residue as well as the residue at the peptide C-terminal which for chymotryptic and Glu-C peptides only one residue, the methylated one, is a basic amino acid. Glu-C peptides were expected to have the lower pI values for their peptides as Glu-C cleaves at the acidic residues of aspartic acid and glutamic acid guaranteeing the presence of at least one acidic residue (Figure 11 D). It was expected that the chymotryptic peptides would be the most hydrophobic as they cleave at aromatic residues thus guaranteeing at least one in the peptude sequence, however, it was

found that the Glu-C peptides had the highest distribution for the GRAVY value (Figure 11E).

The biological processes of the Glu-C peptides differed from the tryptic and chymotryptic digests (Figure 12A). The biological processes of the tryptic and chymotryptic peptides were similar to the earlier processes found while Glu-C had the biological processes of: response to protein stimulus and protein unfolding as its most significant processes (Figure 12A). This was due to the low number of genes used for DAVID analysis making the data appear significantly enriched in the small dataset. The Glu-C digest had so few methylated proteins identified that it did not yield an enriched cellular compartment (Figure 12B). The differences in the enriched processes and compartments is probably due to the few peptides identified in the Glu-C digests making it appear different from the tryptic and chymotryptic digests.

The use of chymotrypsin and Glu-C for digestion yielded unique methylation sites which did not overlap with a tryptic digest. These methylation sites would not have been identified with a tryptic digest approach demonstrating the benefits of using complimentary proteases for protein digestion.

v. Comparison of Tryptically-Digested Whole Cell Lysate to Nuclear and Cytosolic Fractions Digested by Trypsin, Chymotrypsin and Glu-C

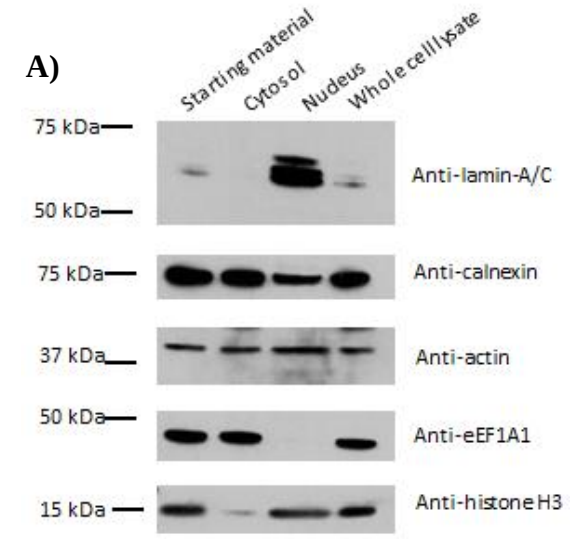
Subcellular fraction was performed on HEK293T separating the lysate into two fractions: the nucleus and the cytosol as described in the Materials and Methods Section IV. These samples were prepared alongside a whole cell lysate for comparison of the experimental approach of a whole cell lysate tryptically digested to subcellular fractionated samples digested with trypsin, chymotrypsin and Glu-C. The ProMENADe protocol and MS

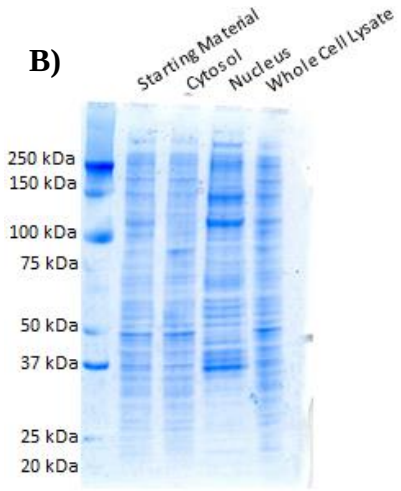
processing was employed as in the Materials and Methods Section VI. The subcellular fractions were confirmed by immunoblotting for lamin A/C and histone H3 to indicate a nuclear fraction, and actin to indicate the cytosolic fraction (Figure 13A) as in Materials and Methods Section V. Total protein loaded was visualized with Coomassie staining on a gel. The protein profiles of the cytosolic and nuclear fractions differ from each other and an emphasis on certain bands can be seen upon comparison to starting material and whole cell lysate samples (Figure 13B). This test was a preliminary test and thus experimental repeats have yet to be performed.

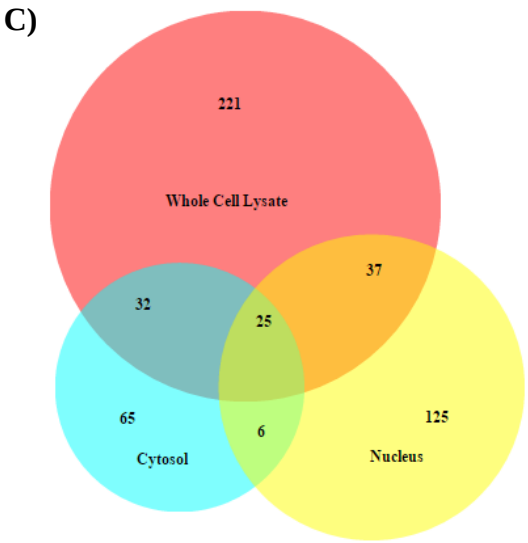
In the whole cell lysate a total of 315 unique peptides were identified while a multi-protease digest of nuclear and cytosolic samples together yielded 290 unique peptides at a 1% FDR at the peptide level (Figure 13C). This experiment identified 62.2% more methylation sites. At a 1% FDR at the methylation level 93 unique peptides were identified in a whole cell lysate while 80 were identified in a multi-protease digest of nuclear and cytosolic samples (Figure 13D) which lead to 35.5% more sites being identified. At a 1% FDR at the methylation level with C-terminal methylation sites removed the whole cell lysate has 53 unique methylation sites total while the nuclear and cytosolic fraction combined yield 58 unique methylation sites (Figure 13E). This increased the identification of methylation sites by 47.2%

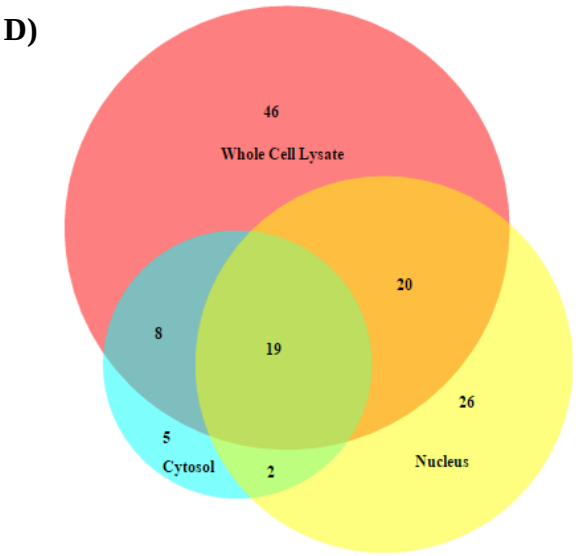
The biological processes of the different samples were analyzed by the GO tool in DAVID v6.7. In the tryptically digested whole cell lysate population the biological processes of: mRNA metabolism, processing and nuclear splicing via the spliceosome, and RNA processing and splicing was significantly enriched (Figure 14A). In the triply digested nuclear proteins the biological processes of: mRNA metabolic process, processing, splicing,

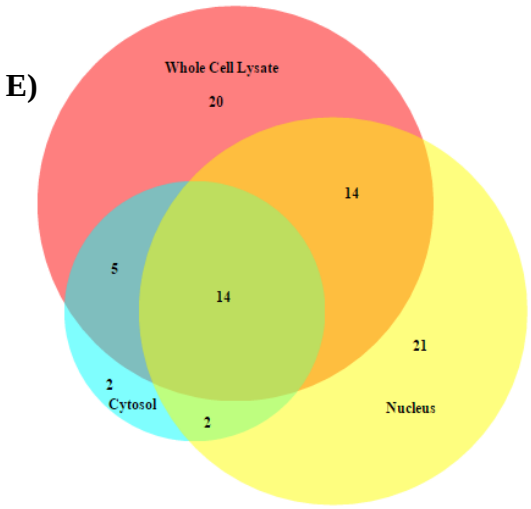
Figure 13: Subcellular fractionation of HEK293T cells demonstrated by immunoblot and their identified methylated peptides for each fraction. A) Western blots using anti-lamin A/C and anti-Histone H3 to demonstrate the lanes expressing nuclear proteins. Western blots using anti-actin and anti-EEF1A1 to demonstrate the lanes expressing cytosolic proteins. Anti-calnexin is used to determine the fraction containing endoplasmic reticulum. B) Total protein expressed in each lane visualized by Coomassie stain. C) Illustration of unique sites identified in the whole cell lysate, cytosolic, and nuclear fractions using a 1% FDR cut-off at the peptide level. D) Illustration of unique sites identified in the whole cell lysate, cytosolic, and nuclear fractions using a 1% FDR cut-off at the methylation level. E) Illustration of unique sites identified in the whole cell lysate, cytosolic, and nuclear fractions using a 1% FDR cut-off at the methylation level with all C-terminal methylation sites removed. (n=1)


A)
Starting material
Cytosol
Nucleus
Whole cell lysate
75 kDa
50 kDa
Anti-lamin-A/C
75 kDa
Anti-calnexin
37 kDa
Anti-actin
50 kDa
Anti-eEF1A1
15 kDa
Anti-histone H3


B)
Starting Material
Cytosol
Nucleus
Whole Cell Lysate
250 kDa
150 kDa
100 kDa
75 kDa
50 kDa
37 kDa
25 kDa
20 kDa


C)
221
Whole Cell Lysate
37
32
25
65
6
125
Cytosol
Nucleus


D)
46
Whole Cell Lysate
20
8
19
26
5
2
Cytosol
Nucleus


E)
Whole Cell Lysate
20
14
5
14
21
2
Cytosol
2
Nucleus

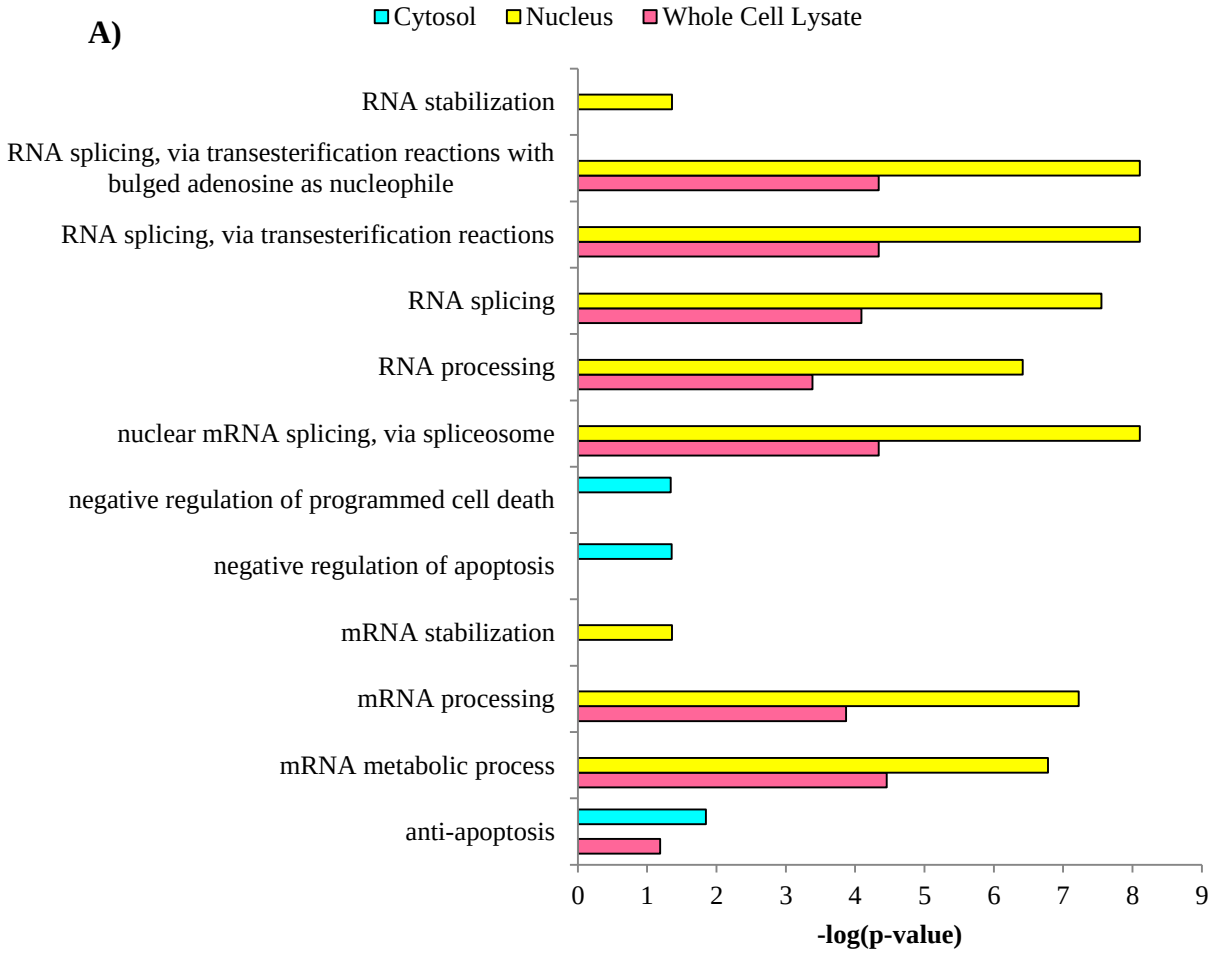
stabilization, and nuclear splicing via the spliceosome, and RNA processing splicing and stabilization were significantly enriched while in the triply digested cytosolic proteins the biological processes of: anti-apoptosis, negative regulation of apoptosis, and negative regulation of programmed cell death were the most significantly enriched (Figure 14A).

The cellular components of the samples were subsequently analyzed by the GO tool in DAVID v6.7. In the tryptically digested whole cell lysate population the cellular components of: eukaryotic translation elongation factor 1 complex, heterogeneous ribonucleoprotein complex, intracellular organelle lumen, nucleoplasm, organelle lumen, ribonucleoprotein complex and spliceosome were most significant (Figure 14B). In the triply digested nuclear proteins the biological processes of: heterogeneous ribonucleoprotein complex, nucleolus, ribonucleoprotein complex and spliceosome were significantly enriched while the cytosolic proteins were not significantly enriched for any cellular component (Figure 14B).

Following these experiments to simplify the protein mixture the new datasets were plotted according to their protein abundance with the "H. sapiens WHOLE_ORGANISM" dataset from PaxDb as in Results Section I. The subcellular fractionation dataset and multi-protease digestion dataset yielded more low abundant proteins and better represented the predicted proteome from PaxDb in terms of the distribution of abundance of the proteins identified (Figure 15). The preliminary dataset with both subcellular fractionation and multi-protease digestion yielded a high amount of low abundant proteins as well.

Figure 14: Gene ontology analysis for the biological processes and cellular components enriched in the methylated proteins in a tryptically digested whole cell lysate compared to a multi-protease digested nucleus and cytosol. A) The gene names of the identified methylated peptides at a 1% FDR at the level of methylation with C-terminal sites removed were exported and used for Gene Ontology (GO) analysis in Database for Annotation, Visualization and Integrated Discovery v6.7 (DAVID) of the biological processes significantly enriched in the identified methylated proteins in the samples corresponding to a tryptically digested whole cell lysate, or the combination of nucleus and cytosolic fractions digested with trypsin, chymotrypsin, and Glu-C. B) The gene names of the identified methylated peptides at a 1% FDR at the level of methylation with C-terminal sites removed were exported and used for GO analysis in DAVID of the cellular components significantly enriched in the identified methylated proteins in the samples corresponding to a tryptically digested whole cell lysate, or the combination of nucleus and cytosolic fractions digested with trypsin, chymotrypsin, and Glu-C.

A)


Cytosol
Nucleus
Whole Cell Lysate
RNA stabilization
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
RNA splicing, via transesterification reactions
RNA splicing
RNA processing
nuclear mRNA splicing, via spliceosome
negative regulation of programmed cell death
negative regulation of apoptosis
mRNA stabilization
mRNA processing
mRNA metabolic process
anti-apoptosis
0
1
2
3
4
5
6
7
8
9
-log(p-value)

B)

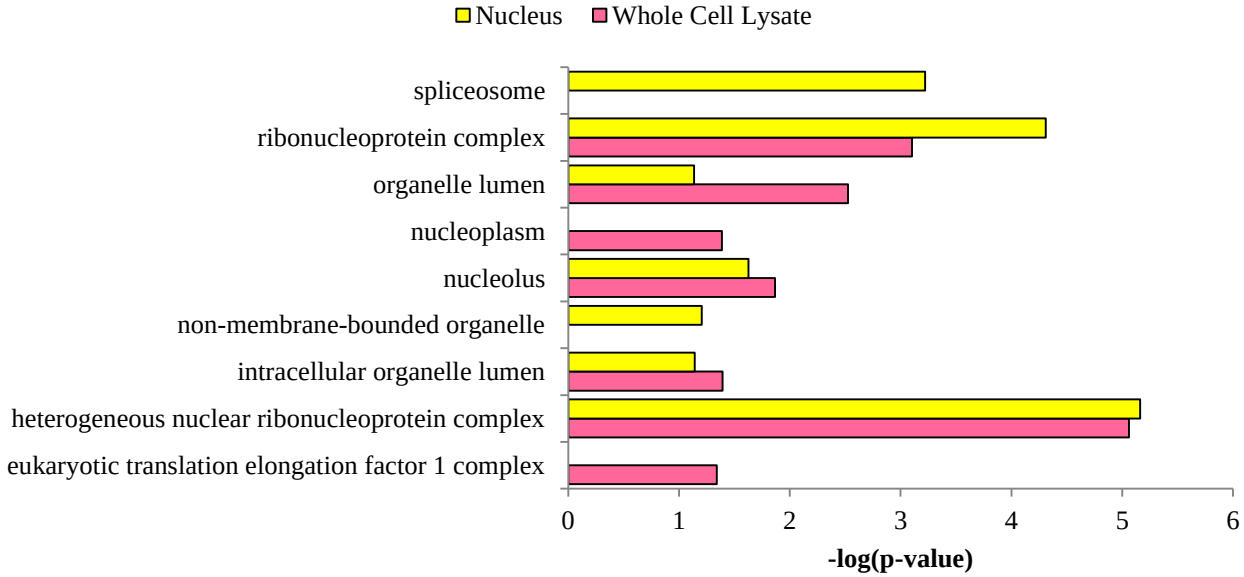
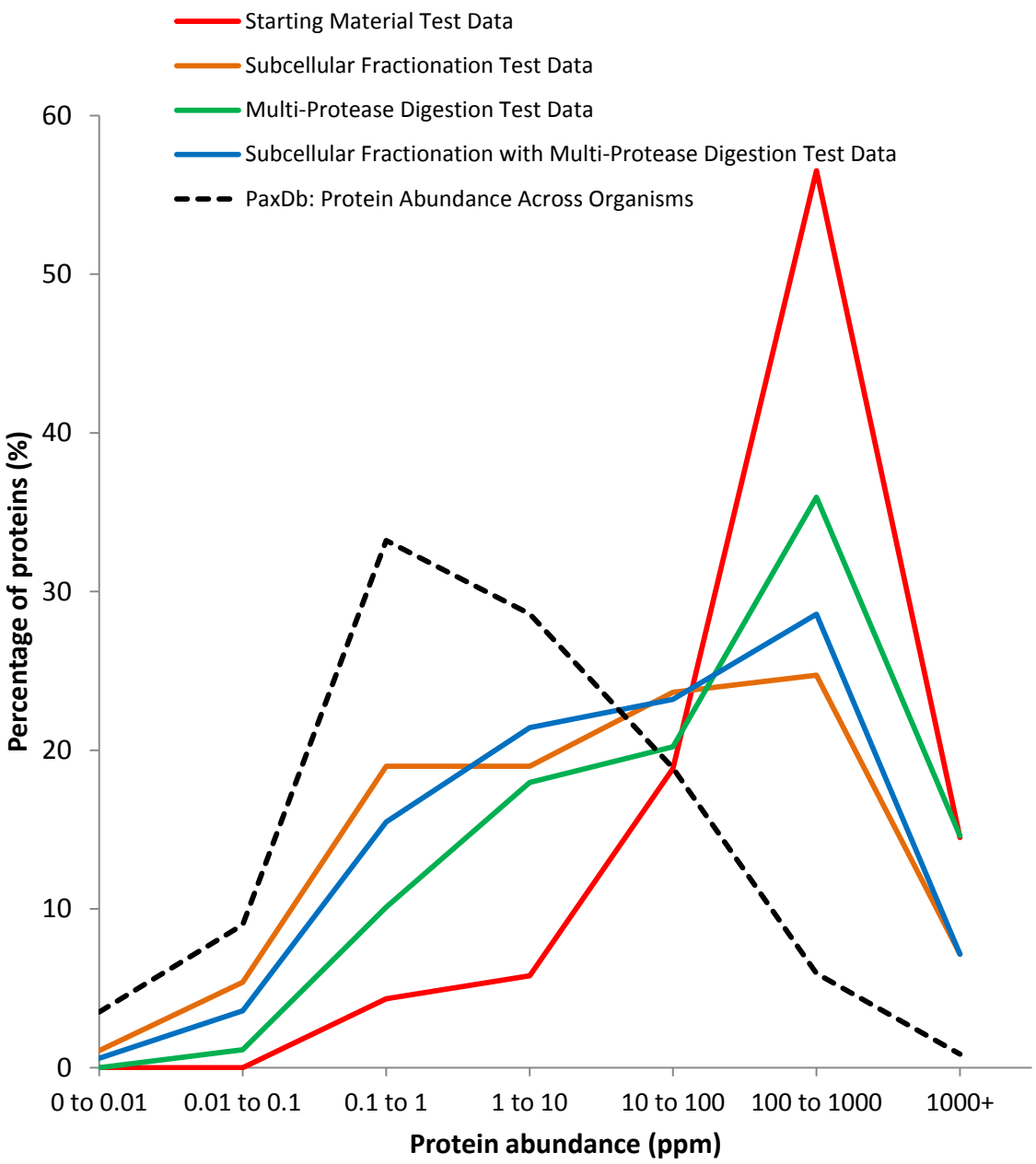

Nucleus
Whole Cell Lysate
spliceosome
ribonucleoprotein complex
organelle lumen
nucleoplasm
nucleolus
non-membrane-bounded organelle
intracellular organelle lumen
heterogeneous nuclear ribonucleoprotein complex
eukaryotic translation elongation factor 1 complex
0
1
2
3
4
5
6
-log(p-value)

Figure 15: Percentage of proteins plotted against their abundance for proteins in the Protein Abundance Across Organisms Database and in the different experiments. Proteins from the human whole organism dataset in the Protein Abundance Across Organisms Database (PaxDb) are plotted with their cellular abundance measured in parts per million (ppm). The identified methylated proteins from the data from the starting material experiment, subcellular fractionation experiment, multi-protease digest experiment and subcellular fractionation with multi-protease digest experiment are all compared to the predicted proteome of the PaxDb whole organism human proteins and their expression.


Starting Material Test Data
Subcellular Fractionation Test Data
Multi-Protease Digestion Test Data
Subcellular Fractionation with Multi-Protease Digestion Test Data
PaxDb: Protein Abundance Across Organisms
60
50
40
30
20
10
0
Percentage of proteins (%)
0 to 0.01
0.01 to 0.1
0.1 to 1
1 to 10
10 to 100
100 to 1000
1000+
Protein abundance (ppm)

vi. Discussion for the Comparison of Tryptically-Digested Whole Cell Lysate to Nuclear and Cytosolic Fractions Digested by Trypsin, Chymotrypsin and Glu-C

The subcellular fractions were confirmed by immunoblotting for lamin A/C and histone H3 to indicate a nuclear fraction, and actin to indicate the cytosolic fraction (Figure 13A). Lamin A/C and histone H3 were present in the starting material, nucleus, and whole cell lysate fractions with clear enrichment in the nucleus. Actin, although used as a cytosolic marker was present across all fractions. This could once again be due to the presence of nuclear actin [166]. Secondly, it could indicate an incomplete purification of the nuclear fraction.

Elongation factor was identified across all fractions except the nucleus (Figure 13A). This was unexpected as it should appear in both cytosolic and nuclear locations. Repeating the experiment could yield different results and ths could be an anomaly of one trial. A Coomassie stain of the total protein gel demonstrated the different banding patterns, and thus unique proteins between the cytosolic and nuclear fractions (Figure 13B).

Contrary to expectations, the tryptically digested whole cell lysate yielded more unique methylated peptides than the nucleus and cytosolic fractions digested by trypsin, chymotrypsin and Glu-C (Figure 13 C, D, E). This can be the result of the method identifying mostly high abundant proteins in all samples resulting in little variation upon subcellular fractionation. This can also be the result of only one experimental trial without repeat. Repeating this experiment twice more would yield more conclusive results.

In this dataset the tryptic digests yielded more peptides than chymotryptic and Glu-C digests (Appendix 4). In a sample where 3 mg of whole cell lysate is tryptically digested compared to 1.5 mg of nucleus and 1.5 mg of cytosol where 0.5 mg is digested by trypsin,

0.5 mg chymotrypsin, and 0.5 mg Glu-C, there remain more peptides in the whole cell lysate digests increasing chances of methylation identification compared to fewer peptides in the other digests.

When compared to the "H. sapiens WHOLE_ORGANISM" on PaxDb, the HEK293T starting material test samples consisted of a majority of highly abundant proteins. Subcellular fractionation and multi-protease digestion drastically increased the number of proteins identified, as well as the amount of low abundant proteins identified. The preliminary dataset of subcellular fractionation samples digested with multiple proteases also increased the number of low abundant methylated proteins identified (Figure 15). The subcellular fractionation and multi-protease digestion datasets better represented the predicted proteome from PaxDb in terms of the distribution of abundance of the proteins identified (Figure 15). This shows us that these techniques were useful for making our sample more representative.

III. Heavy Methionine Labeling in Cell Culture to Reliably Identify Methylated Peptides

An alternate way to reliably identify methylated proteins is to propagate cells in media containing heavy labeled methionine ($^{13}CD_3$). The cells will uptake the heavy methionine and convert it into heavy S-adenosyl-L-methionine [169]. This will result in the heavy labeling of the methyl groups on proteins, as well as heavy methionine residues to identify and confirm *in vivo* methylated proteins [169].

We cultured HEK293T cells in both heavy and light media as in the Materials and Methods Section II. The cells were lysed using the protocol in Materials and Methods

Section II. A 1:1 spike-in of heavy to light methylated proteins was mixed, digested, processed for MS as in Materials and Methods Section VI without the ProMENADe enrichment reaction for proof of concept, and analyzed by mass spectrometry (Figure 16A). Presence of both the heavy and light methylated counterparts was analyzed manually and indicates a positive methylation identification. This experiment confirmed 23 peptides, like K55 on EEF1A1, for methylation (Figure 16B).

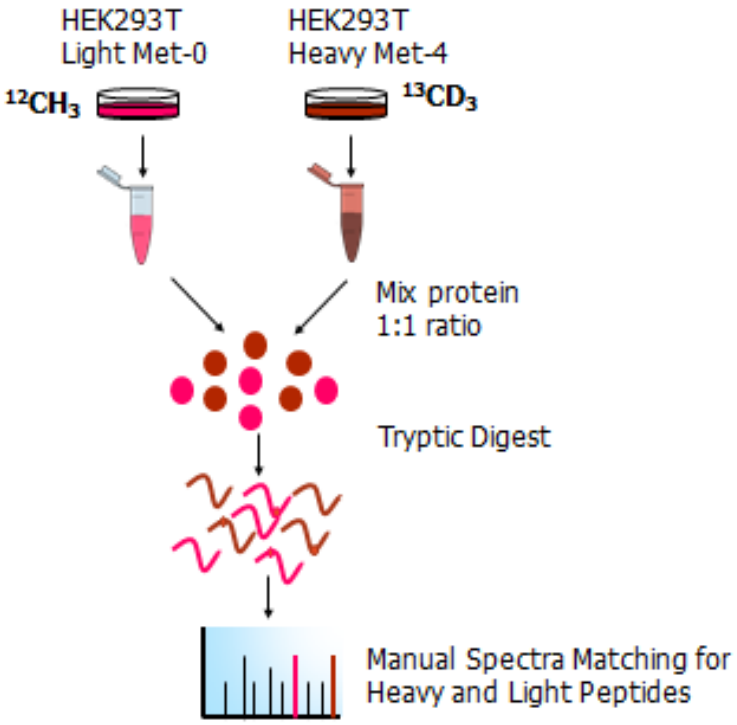
i. Discussion

This metabolic labeling approach can be used to address the problem of the ProMENADe methodology where there could be esterification on the peptide C-terminal. Although trypsin has difficulty cleaving mono-methylated lysine and arginine, it is still present on the peptide C-terminals in a digest [92]. Esterification on the C-terminal will not have a heavy-labeled counterpart and thus will not be identified as a true positive whereas methylation would have a heavy counterpart.

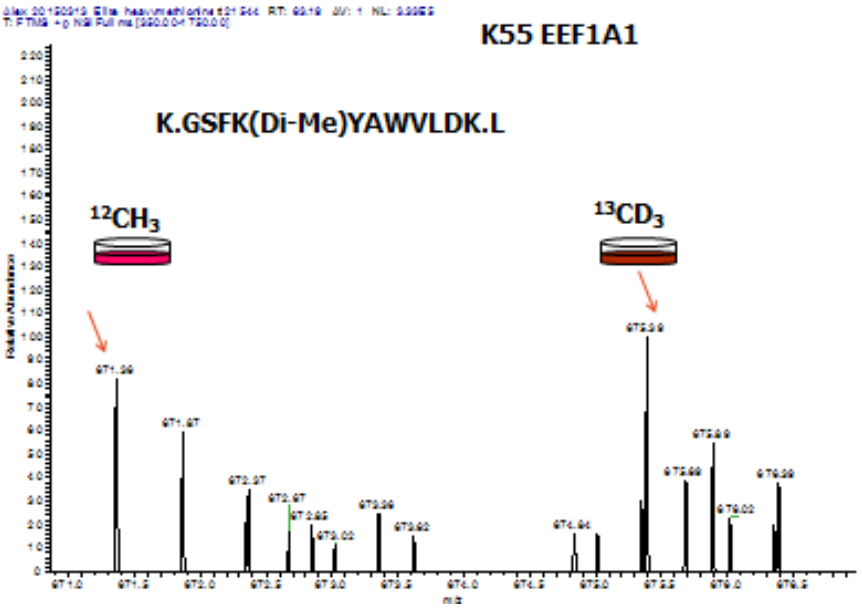
Implementation of the heavy methionine labeling of protein in HEK293T cells has allowed us to confirm methylation of 23 peptides *in vivo*. These peptides were manually identified and matched for their heavy and light counterparts for confirmation. Automation of the methodology to match the corresponding heavy and light peptides would allow for quicker verification of a larger number of peptides. The next step for this experiment is to enrich the heavy and light mixed samples for methylation with ProMENADe. This can be accomplished upon development of the Mascot software to enable more variable modifications for database searching.

Figure 16: Spectra of heavy and light confirmed methylated peptide for K55 of EEF1A1. A) HEK293T cells were grown in both heavy and light media were processed for MS. Methylated peptides were manually matched to confirm *in vivo* methylation in HEK293T cells. B) Di-methylation of K55 (internal lysine) of peptide KGSFKYAWVLDK of EEF1A1 verified by heavy and light peaks.

A)


HEK293T
Light Met-0
HEK293T
Heavy Met-4
$^{12}CH_3$
$^{13}CD_3$
Mix protein
1:1 ratio
Tryptic Digest
Manual Spectra Matching for
Heavy and Light Peptides

B)


K55 EEF1A1
K.GSFK(Di-Me)YAWVLDK.L
$^{12}CH_3$
$^{13}CD_3$

n=1

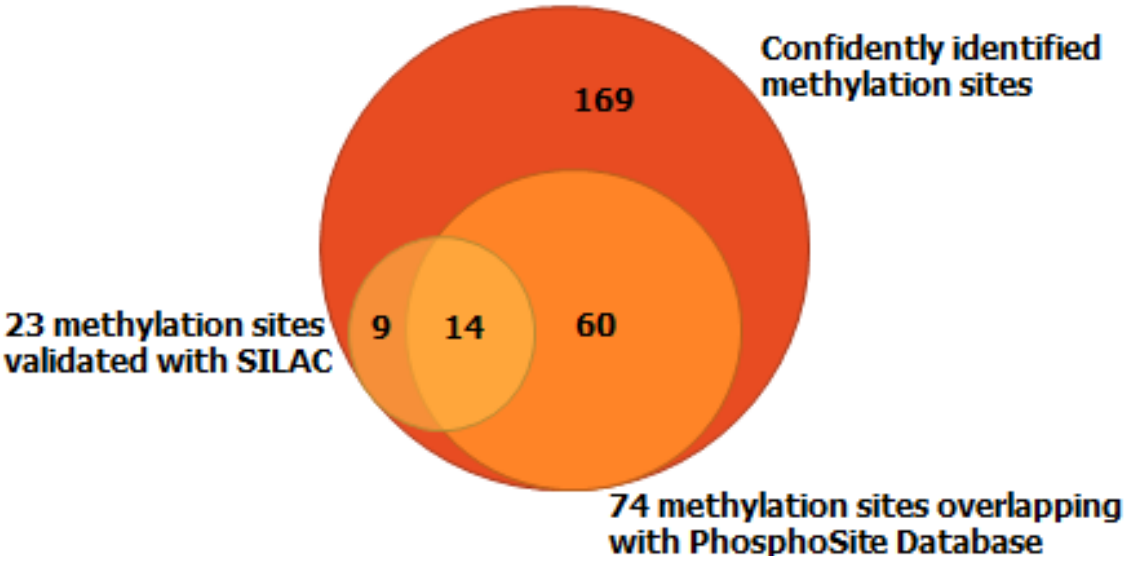
4. CONCLUSIONS AND FUTURE DIRECTIONS

In this work the use of a more stringent analysis of 1% FDR at the level of methylation has shown that the ProMENADe enrichment protocol significantly enriches for methylated peptides over a non-enriched sample. Removing the C-terminal methylation sites is a further stringent step to prevent the misidentification of esterified peptides as methylated. The FDR of 1% for methylation should be applied across the methylation field to increase the stringency in methylation site identification. The increase in stringency drastically decreases the number of identified methylation sites but increases the identification confidence.

The datasets across all of the experiments were compiled into one giant dataset to determine the total unique sites identified. At the 1% peptide level FDR 2620 methylation sites were identified, 260 methylation sites at the 1% methylation level FDR, and 169 sites upon removal of C-terminal methylation sites. When comparing with the current literature in the field, the 1% peptide level FDR is most commonly used for analysis. The ProMENADe approach yielded 2620 sites with a 1% peptide FDR which is greater than the current reports in the field [27, 28, 150, 151].

Similar to previous studies, GO analysis has revealed that the methylated proteins are involved in biological processes involving RNA, transcription, translation and chromatin modification [27, 150]. These methylated proteins are also found in predominantly nuclear and cytosolic locations [27, 150].

Figure 17: Compilation of confidently identified methylation sites. Analysis at a 1% FDR for methylation filtered for C-terminal methylation across all experiments performed yielded a total of 169 unique methylation sites. 23 of these sites were validated with metabolic labeling. 74 of these sites overlap with the methylation dataset in the PhosphoSite database. These experiments have yielded 95 novel sites to the field.


Confidently identified
methylation sites
169
23 methylation sites
validated with SILAC
9
14
60
74 methylation sites overlapping
with PhosphoSite Database

Further analysis with the compiled dataset for a 1% methylation FDR filtered for C-terminal methylation revealed that 74 of the sites identified overlap with the PhosphoSite database (Figure 17). This meant that combining the results from all of the experiments performed yielded 95 novel methylation sites to the field. Twenty-three of these sites were confirmed with metabolic labeling with heavy methionine.

Simplifying the whole cell lysate with subcellular fractionation prior to enrichment increased the identification of methylation sites by 39.5% while using multiple proteases for digestion increased our identification by 27%. Lastly, combining these two methods yielded an increase in 47.2%. All of these experiments also aided in identifying more low abundant proteins making our samples more representative of the cellular proteins (Figure 15).

The incorporation of heavy methionine into the cells allowed for confirmation of 23 *in vivo* methylation site identifications (Figure 16). This number can be further increased upon the implementation of the ProMENADe enrichment for heavy and light methionine-labeled cells.

Moving forward, the technology can be further improved. The esterification by-product reaction will be quenched by adding an excess of carboxylic acid to the reaction mixture to lower the esterification at peptide C-terminal. Additionally, increasing the chromatography gradient on the mass spectrometer, the use of more proteases for digestion, and subcellular fractionation into other organelles like plasma membrane, mitochondria, endoplasmic reticulum can aid in the identification of more methylation sites.

The misregulation of methyltransferase expression is widely implicated in embryonic development and cancer [82, 101, 103, 105-114, 116-125, 170]. In many of these cases there

are not any known methylation targets. This methodology could be applied to examine the differences in methylated proteins in these states allowing us to see potential methylation targets of the implicated methyltransferases. The methyltransferases or their methylation targets could then be used as potential therapeutics for cancer. This information allows us to further define the role of methylation and methyltransferases in disease.

This ProMENADe enrichment strategy for methylated proteins can be a key tool in the field of methylation allowing for the enrichment and identification of methylated proteins.

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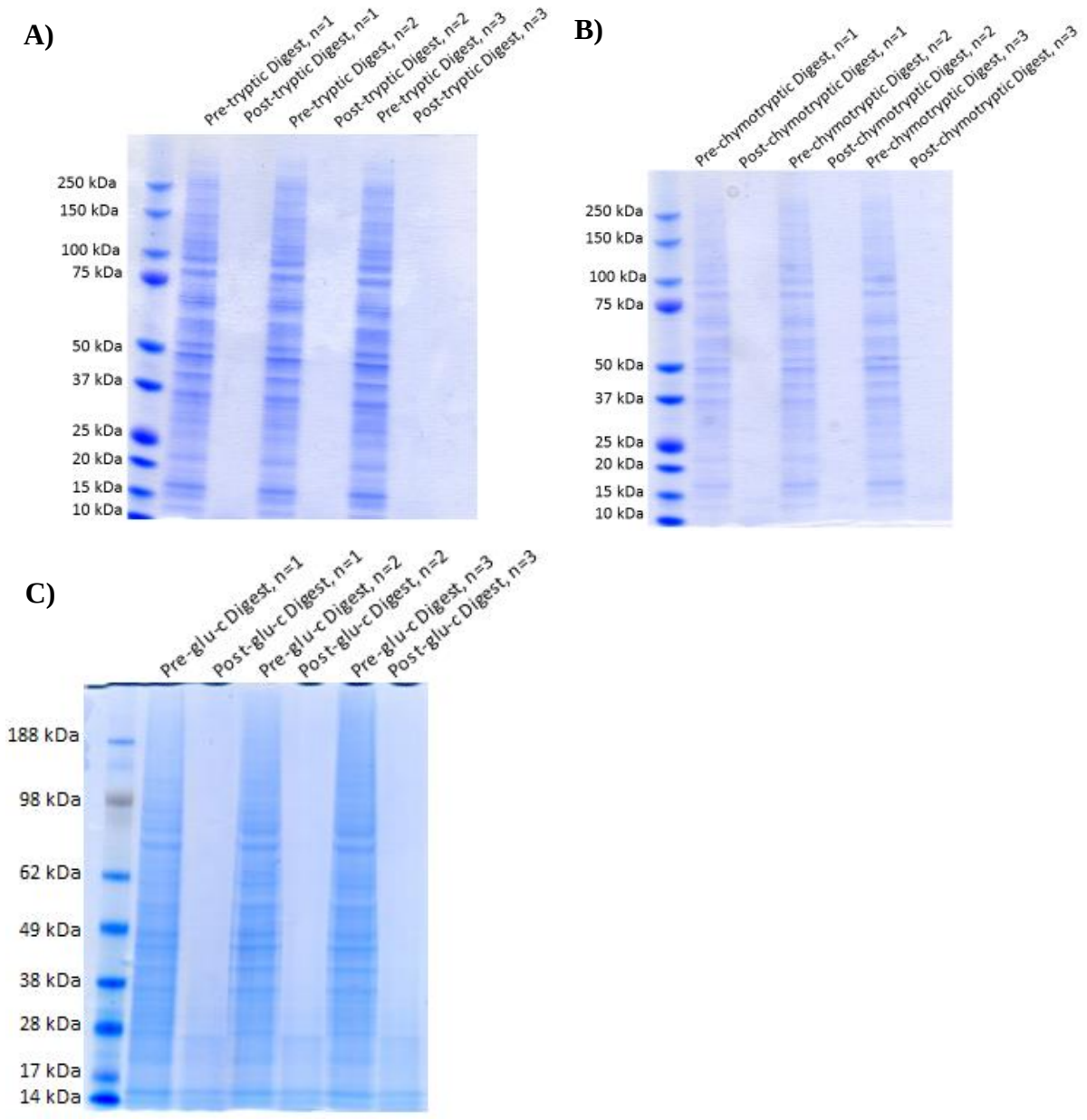
APPENDICES

Appendix 1: Supplementary Results

Supplementary Figure 1: Protein staining of samples pre- and post-digestion with Coomassie demonstrates completion of protein digestion. A) Trypsin digestion of HEK293T cellular protein in a 1:20 enzyme to protein ratio in 50 mM ammonium bicarbonate buffer at pH 8.5. B) Chymotrypsin digestion of HEK293T in cellular protein in a 1:20 enzyme to protein ratio in 50 mM ammonium bicarbonate buffer at pH 8.5. C) Glu-C digestion of HEK293T cellular protein in a 1:20 enzyme to protein ratio in 50 mM sodium phosphate buffer at pH 8.


A)
Pre-tryptic Digest, n=1
Post-tryptic Digest, n=1
Pre-tryptic Digest, n=2
Post-tryptic Digest, n=2
Pre-tryptic Digest, n=3
Post-tryptic Digest, n=3
250 kDa
150 kDa
100 kDa
75 kDa
50 kDa
37 kDa
25 kDa
20 kDa
15 kDa
10 kDa
B)
Pre-chymotryptic Digest, n=1
Post-chymotryptic Digest, n=1
Pre-chymotryptic Digest, n=2
Post-chymotryptic Digest, n=2
Pre-chymotryptic Digest, n=3
Post-chymotryptic Digest, n=3
250 kDa
150 kDa
100 kDa
75 kDa
50 kDa
37 kDa
25 kDa
20 kDa
15 kDa
10 kDa
C)
Pre-glu-c Digest, n=1
Post-glu-c Digest, n=1
Pre-glu-c Digest, n=2
Post-glu-c Digest, n=2
Pre-glu-c Digest, n=3
Post-glu-c Digest, n=3
188 kDa
98 kDa
62 kDa
49 kDa
38 kDa
28 kDa
17 kDa
14 kDa

Appendix 2: List of methylation sites identified by MS/MS in ranging amounts of starting material from 0.2 mg to 10 mg.

Sites identified at the 1% peptide FDR confidence level for the starting material test.

K/R	Site	Type	Mascot Score	Protein Name	Gene Name
K	333	Mono	23.02	ATP-binding cassette sub-family F member 1 (Fragment)	ABCF1
R	332	Mono	23.02	ATP-binding cassette sub-family F member 1 (Fragment)	ABCF1
K	333	Di	23.02	ATP-binding cassette sub-family F member 1 (Fragment)	ABCF1
R	332	Di	23.02	ATP-binding cassette sub-family F member 1 (Fragment)	ABCF1
K	333	Tri	23.02	ATP-binding cassette sub-family F member 1 (Fragment)	ABCF1
K	4	Mono	29.8	Target of Nesh-SH3 (Fragment)	ABI3BP
R	47	Mono	12.26	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 1 (Fragment)	ACAP1
R	7	Mono	31.06	Long-chain-fatty-acid--CoA ligase 1 (Fragment)	ACSL1
R	238	Di	13.46	Acyl-coenzyme A synthetase ACSM1, mitochondrial (Fragment)	ACSM1
K	239	Tri	13.46	Acyl-coenzyme A synthetase ACSM1, mitochondrial (Fragment)	ACSM1
K	129	Mono	69.41	Actin, alpha skeletal muscle	ACTA1
K	293	Di	46.68	Actin, aortic smooth muscle	ACTA2
K	87	Mono	16	Actin, cytoplasmic 2 (Fragment)	ACTB
R	40	Mono	30.16	Beta-actin-like protein 2	ACTBL2
R	63	Mono	20.11	Beta-actin-like protein 2	ACTBL2
R	38	Mono	30.16	Beta-actin-like protein 2	ACTBL2
R	38	Di	30.16	Beta-actin-like protein 2	ACTBL2
R	40	Di	30.16	Beta-actin-like protein 2	ACTBL2
K	682	Mono	21.63	Actinin alpha 1 isoform 3	ACTN1
K	684	Mono	21.63	Actinin alpha 1 isoform 3	ACTN1
K	684	Di	21.63	Actinin alpha 1 isoform 3	ACTN1
K	682	Di	21.63	Actinin alpha 1 isoform 3	ACTN1
K	682	Tri	21.63	Actinin alpha 1 isoform 3	ACTN1
K	684	Tri	21.63	Actinin alpha 1 isoform 3	ACTN1
R	89	Mono	38.09	Actinin, alpha 2, isoform CRA_b	ACTN2
R	740	Mono	53.2	Alpha-actinin-3	ACTN3
K	140	Di	66.04	Alpha-actinin-4	ACTN4
K	69	Mono	44.34	Actin-related protein 3B	ACTR3B
R	278	Mono	14.24	A disintegrin and metalloproteinase with thrombospondin motifs 10	ADAMTS10
K	262	Mono	27.37	ADAMTS-like protein 1	ADAMTSL1
K	509	Di	12.56	ADAMTS-like protein 1	ADAMTSL1
R	829	Mono	34.14	ADAMTS-like protein 4	ADAMTSL4
K	9	Di	13.43	AF4/FMR2 family member 1 (Fragment)	AFF1
R	383	Mono	12.9	Acylglycerol kinase, mitochondrial	AGK
R	385	Mono	12.9	Acylglycerol kinase, mitochondrial	AGK
R	383	Di	12.9	Acylglycerol kinase, mitochondrial	AGK
R	385	Di	12.9	Acylglycerol kinase, mitochondrial	AGK

K	217	Tri	29.25	5-phosphohydroxy-L-lysine phospho-lyase (Fragment)	AGXT2L2
R	70	Mono	49.77	Aldo-keto reductase family 1 member B10	AKR1B10
K	139	Mono	18.77	1,5-anhydro-D-fructose reductase	AKR1E2
K	143	Mono	18.77	1,5-anhydro-D-fructose reductase	AKR1E2
K	139	Di	18.77	1,5-anhydro-D-fructose reductase	AKR1E2
K	143	Di	18.77	1,5-anhydro-D-fructose reductase	AKR1E2
K	443	Mono	64.25	Serum albumin	ALB
K	113	Di	14.54	Retinal dehydrogenase 1	ALDH1A1
K	4063	Mono	42.41	Alstrom syndrome protein 1	ALMS1
K	120	Di	14.84	Putative ALMS1-like protein	ALMS1P
R	148	Mono	13.38	THO complex subunit 4	ALYREF
K	141	Mono	13.38	THO complex subunit 4	ALYREF
R	211	Di	76.07	THO complex subunit 4	ALYREF
R	57	Di	35.39	THO complex subunit 4	ALYREF
R	204	Di	50.09	THO complex subunit 4	ALYREF
R	70	Di	82.91	THO complex subunit 4	ALYREF
R	45	Di	84.8	THO complex subunit 4	ALYREF
K	82	Tri	18.12	AMP deaminase 3	AMPD3
R	137	Di	16.69	Ankyrin-3 (Fragment)	ANK3
K	8	Di	32.44	Ankyrin repeat and FYVE domain-containing protein 1 (Fragment)	ANKFY1
R	893	Mono	31.77	Ankyrin repeat domain-containing protein 11	ANKRD11
K	211	Tri	16.69	Ankyrin repeat domain-containing protein 17	ANKRD17
K	249	Di	12.1	Ankyrin repeat domain-containing protein 2	ANKRD2
R	270	Di	32.04	Ankyrin repeat domain-containing protein 6	ANKRD6
R	63	Mono	79.97	Putative annexin A2-like protein	ANXA2P2
K	286	Tri	28.71	Putative annexin A2-like protein	ANXA2P2
K	457	Mono	89.02	AP-2 complex subunit beta	AP2B1
K	570	Tri	15.08	Apoptosis-resistant E3 ubiquitin protein ligase 1 (Fragment)	AREL1
K	713	Di	15.28	Rho GTPase-activating protein 24	ARHGAP24
K	708	Tri	15.28	Rho GTPase-activating protein 24	ARHGAP24
R	174	Mono	31.26	Ankyrin repeat and SOCS box protein 17	ASB17
K	49	Mono	13.17	Set1/Ash2 histone methyltransferase complex subunit ASH2	ASH2L
K	143	Mono	15.19	Atlastin-2	ATL2
R	151	Mono	15.19	Atlastin-2	ATL2
R	5	Mono	18.93	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2
X	1	Mono	18.93	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2
K	7	Mono	18.93	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2
R	5	Di	18.93	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2
X	1	Di	18.93	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2
K	7	Di	18.93	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2
K	7	Tri	18.93	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2
K	719	Mono	29.46	Plasma membrane calcium-transporting ATPase 4 (Fragment)	ATP2B2
K	158	Mono	14.67	Probable phospholipid-transporting ATPase IA	ATP8A1

K	845	Mono	12.95	Transcriptional regulator ATRX	ATRX
K	845	Di	13.06	Transcriptional regulator ATRX	ATRX
R	8	Di	35.33	Advillin	AVIL
R	84	Mono	15.08	Beta-1,3-galactosyltransferase 5	B3GALT5
K	87	Di	15.08	Beta-1,3-galactosyltransferase 5	B3GALT5
K	335	Mono	19.18	HMG box transcription factor BBX (Fragment)	BBX
K	333	Mono	19.18	HMG box transcription factor BBX (Fragment)	BBX
K	333	Di	19.18	HMG box transcription factor BBX (Fragment)	BBX
K	335	Di	19.18	HMG box transcription factor BBX (Fragment)	BBX
K	333	Tri	19.18	HMG box transcription factor BBX (Fragment)	BBX
K	335	Tri	19.18	HMG box transcription factor BBX (Fragment)	BBX
R	61	Di	21.96	Breast carcinoma-amplified sequence 1	BCAS1
K	313	Mono	12.01	Branched-chain-amino-acid aminotransferase	BCAT2
R	4	Mono	29.62	B-cell CLL/lymphoma 7 protein family member C (Fragment)	BCL7C
R	7	Mono	29.62	B-cell CLL/lymphoma 7 protein family member C (Fragment)	BCL7C
K	504	Tri	15.59	Peregrin	BRPF1
R	100	Di	35.41	Bromodomain and WD repeat-containing protein 1 (Fragment)	BRWD1
K	470	Di	14.64	BUD13 homolog	BUD13
K	783	Di	17.89	Centrosomal protein C10orf90	C10orf90
K	132	Di	14.18	Uncharacterized protein C11orf42	C11orf42
R	14	Di	79.19	Isoform 2 of UPF0696 protein C11orf68	C11orf68
K	2	Di	28.26	Uncharacterized protein C11orf84 (Fragment)	C11orf84
R	4	Di	28.26	Uncharacterized protein C11orf84 (Fragment)	C11orf84
R	132	Mono	17.64	Uncharacterized protein C20orf201	C20orf201
R	1820	Mono	27.67	Uncharacterized protein C2orf16	C2orf16
R	2	Mono	27.57	UPF0561 protein C2orf68 (Fragment)	C2orf68
X	1	Mono	27.57	UPF0561 protein C2orf68 (Fragment)	C2orf68
X	1	Tri	21.41	UPF0561 protein C2orf68 (Fragment)	C2orf68
R	20	Mono	29.22	C6orf136 protein (Fragment)	C6orf136
R	8	Mono	12.48	Uncharacterized protein C7orf61 (Fragment)	C7orf61
X	1	Di	12.84	Uncharacterized protein C7orf63 (Fragment)	C7orf63
K	266	Di	18.12	Calcium binding tyrosine-(Y)-phosphorylation regulated (Fibrousheathin 2), isoform CRA_a	CABYR
K	738	Mono	12.58	Voltage-dependent T-type calcium channel subunit alpha-1G	CACNA1G
R	737	Mono	12.58	Voltage-dependent T-type calcium channel subunit alpha-1G	CACNA1G
K	738	Di	12.58	Voltage-dependent T-type calcium channel subunit alpha-1G	CACNA1G
R	737	Di	12.58	Voltage-dependent T-type calcium channel subunit alpha-1G	CACNA1G
K	6	Di	12.83	Voltage-dependent calcium channel subunit alpha-2/delta-4 (Fragment)	CACNA2D4
R	348	Di	15.19	Caldesmon (Fragment)	CALD1
K	163	Mono	44.41	Calmodulin	CALM2
R	174	Mono	44.41	Calmodulin	CALM2
R	174	Di	44.41	Calmodulin	CALM2
K	163	Di	44.41	Calmodulin	CALM2
K	163	Tri	91.17	Calmodulin	CALM2

R	112	Mono	32.51	Calmodulin-like protein 3	CALML3
K	116	Mono	32.51	Calmodulin-like protein 3	CALML3
K	778	Mono	12.87	Calmodulin-regulated spectrin-associated protein 1	CAMSAP1
R	15	Mono	16.98	Cullin-associated NEDD8-dissociated protein 2 (Fragment)	CAND2
K	157	Di	16.96	Calpain-12 (Fragment)	CAPN12
R	23	Mono	55.12	Calpain-2 catalytic subunit	CAPN2
K	344	Di	12.01	Calpain-7	CAPN7
K	66	Di	12.01	Calpain-7 (Fragment)	CAPN7
K	503	Di	31.78	Caspase recruitment domain-containing protein 11	CARD11
K	671	Di	15.65	Caspase recruitment domain-containing protein 14	CARD14
K	472	Tri	16.46	CASP8-associated protein 2	CASP8AP2
K	133	Mono	13.33	Cation channel sperm-associated protein subunit gamma	CATSPERG
K	143	Mono	44.2	Chromobox protein homolog 3	CBX3
K	31	Mono	25.45	Chromobox protein homolog 7	CBX7
R	76	Di	28.02	Protein chibby homolog 1 (Fragment)	CBY1
R	5	Mono	33.42	Coiled-coil domain-containing protein 137 (Fragment)	CCDC137
K	304	Mono	42.76	Coiled-coil domain-containing protein 146	CCDC146
R	306	Mono	42.76	Coiled-coil domain-containing protein 146	CCDC146
R	306	Di	42.76	Coiled-coil domain-containing protein 146	CCDC146
K	304	Di	42.76	Coiled-coil domain-containing protein 146	CCDC146
R	157	Di	30.92	Coiled-coil domain-containing protein 154	CCDC154
R	505	Di	32.3	Coiled-coil domain-containing protein 173	CCDC173
K	3	Mono	24.79	Coiled-coil domain-containing protein 18	CCDC18
K	703	Di	12	Coiled-coil domain-containing protein 33	CCDC33
K	129	Tri	29.81	Coiled-coil domain-containing protein 42A	CCDC42
R	23	Mono	13.71	Coiled-coil domain-containing protein 51 (Fragment)	CCDC51
K	226	Di	15.78	Coiled-coil domain-containing protein 73	CCDC73
K	234	Di	15.78	Coiled-coil domain-containing protein 73	CCDC73
K	228	Di	15.78	Coiled-coil domain-containing protein 73	CCDC73
X	1	Di	23.93	Coiled-coil domain-containing protein 73 (Fragment)	CCDC73
K	228	Tri	15.78	Coiled-coil domain-containing protein 73	CCDC73
K	234	Tri	15.78	Coiled-coil domain-containing protein 73	CCDC73
K	226	Tri	15.78	Coiled-coil domain-containing protein 73	CCDC73
R	76	Mono	33.11	Coiled-coil domain-containing protein 91 (Fragment)	CCDC91
K	9	Mono	47.76	T-complex protein 1 subunit delta	CCT4
K	388	Mono	19.56	T-complex protein 1 subunit zeta-2	CCT6B
K	325	Mono	13.33	Natural killer cell receptor 2B4	CD244
K	76	Tri	28.79	Cell division cycle 5-like protein	CDC5L
K	571	Mono	18.12	Cadherin-related family member 4	CDHR4
K	11	Mono	13.84	Cyclin-dependent kinase 16	CDK16
R	9	Mono	13.84	Cyclin-dependent kinase 16	CDK16
K	11	Di	13.84	Cyclin-dependent kinase 16	CDK16
R	9	Di	13.84	Cyclin-dependent kinase 16	CDK16

R	187	Mono	17.24	Threonylcarbamoyladenosine tRNA methylthiotransferase	CDKAL1
R	17	Mono	12.06	Protein CDV3 homolog (Fragment)	CDV3
R	1738	Mono	30.19	Centromere protein F	CENPF
R	661	Di	39.58	Centrosomal protein of 164 kDa	CEP164
K	312	Di	30.01	Centrosomal protein of 192 kDa	CEP192
K	1567	Tri	13.14	Centrosomal protein of 290 kDa	CEP290
R	72	Mono	13.86	Centrosomal protein of 97 kDa	CEP97
K	78	Tri	13.86	Centrosomal protein of 97 kDa	CEP97
K	68	Di	12.7	Carboxylesterase 4A	CES4A
K	91	Di	34.89	Cofilin-1	CFL1
K	91	Tri	37.54	Cofilin-1	CFL1
R	2	Mono	13.09	N-chimaerin (Fragment)	CHN1
K	223	Mono	60.38	Creatine kinase M-type	CKM
K	3	Mono	48.08	Clathrin heavy chain 1 (Fragment)	CLTC
K	3	Tri	48.08	Clathrin heavy chain 1 (Fragment)	CLTC
K	111	Mono	27.74	CKLF-like MARVEL transmembrane domain-containing protein 1	CMTM1
K	78	Di	25.3	Collagen alpha-1(XIX) chain	COL19A1
R	247	Mono	22.82	Collagen alpha-1(XX) chain	COL20A1
R	408	Di	13.38	Coronin-1A	CORO1A
K	161	Mono	13.33	Carboxypeptidase A2	CPA2
K	39	Di	27.53	Complexin-1 (Fragment)	CPLX1
K	6	Tri	35.58	Carnitine O-palmitoyltransferase 1, muscle isoform	CPT1B
K	209	Tri	35.58	Carnitine O-palmitoyltransferase 1, muscle isoform	CPT1B
X	1	Mono	17.5	Cellular retinoic acid-binding protein 1 (Fragment)	CRABP1
R	617	Mono	24.77	Rootletin (Fragment)	CROCC
R	453	Di	28.02	Rootletin (Fragment)	CROCC
R	470	Mono	15.08	Cysteine sulfinic acid decarboxylase (Fragment)	CSAD
K	473	Di	15.08	Cysteine sulfinic acid decarboxylase (Fragment)	CSAD
K	86	Mono	27.5	Catenin alpha-2 (Fragment)	CTNNA2
K	724	Mono	27.46	Cullin-5	CUL5
K	243	Mono	19.76	Pre-mRNA-splicing factor CWC22 homolog	CWC22
R	328	Mono	32.59	C-X-C chemokine receptor type 3	CXCR3
R	326	Mono	32.59	C-X-C chemokine receptor type 3	CXCR3
K	168	Mono	13.36	Putative uncharacterized protein CXorf58	CXorf58
R	62	Mono	18.39	Aspartyl aminopeptidase	DAP
R	61	Mono	18.39	Aspartyl aminopeptidase	DAP
R	61	Di	18.39	Aspartyl aminopeptidase	DAP
R	62	Di	18.39	Aspartyl aminopeptidase	DAP
R	27	Di	30.29	DAZ-associated protein 1 (Fragment)	DAZAP1
R	176	Di	32.36	Protein DBF4 homolog A	DBF4
K	51	Tri	28.01	m7GpppX diphosphatase	DCPS
R	182	Mono	37.26	DC-STAMP domain-containing protein 2	DCST2
K	158	Mono	28.01	Deoxycytidylate deaminase (Fragment)	DCTD

K	161	Mono	28.01	Deoxycytidylate deaminase (Fragment)	DCTD
R	7	Mono	13.15	Neuronal migration protein doublecortin (Fragment)	DCX
R	428	Mono	51.71	Probable ATP-dependent RNA helicase DDX17	DDX17
R	742	Mono	17.24	Nucleolar RNA helicase 2	DDX21
R	13	Mono	12.49	Spliceosome RNA helicase DDX39B	DDX39B
X	1	Mono	13.1	Probable ATP-dependent RNA helicase DDX46 (Fragment)	DDX46
K	283	Mono	52.74	ATP-dependent RNA helicase DDX50	DDX50
K	389	Mono	12.53	ATP-dependent RNA helicase DDX55	DDX55
K	392	Mono	12.53	ATP-dependent RNA helicase DDX55	DDX55
K	389	Di	12.53	ATP-dependent RNA helicase DDX55	DDX55
K	392	Di	12.53	ATP-dependent RNA helicase DDX55	DDX55
K	389	Tri	12.53	ATP-dependent RNA helicase DDX55	DDX55
K	392	Tri	12.53	ATP-dependent RNA helicase DDX55	DDX55
R	455	Mono	12.56	Putative ATP-dependent RNA helicase DHX30	DHX30
R	452	Mono	12.56	Putative ATP-dependent RNA helicase DHX30	DHX30
R	56	Di	21.28	Probable ATP-dependent RNA helicase DHX58 (Fragment)	DHX58
R	1550	Di	13.36	Dynein heavy chain 12, axonemal (Fragment)	DNAH12
K	2028	Mono	13.26	Dynein heavy chain 7, axonemal	DNAH7
K	4310	Di	12.48	Dynein heavy chain 8, axonemal	DNAH8
K	7	Mono	13.06	Dynein intermediate chain 1, axonemal	DNAI1
R	394	Mono	29.82	DNAI2 protein	DNAI2
R	14	Di	31.5	Dynein heavy chain domain-containing protein 1 (Fragment)	DNHD1
R	630	Mono	40.14	Dedicator of cytokinesis protein 3	DOCK3
R	628	Mono	40.14	Dedicator of cytokinesis protein 3	DOCK3
R	628	Di	40.14	Dedicator of cytokinesis protein 3	DOCK3
R	630	Di	40.14	Dedicator of cytokinesis protein 3	DOCK3
R	14	Mono	33.52	Protein DPCD (Fragment)	DPCD
R	1914	Mono	12.01	Desmoplakin	DSP
R	1912	Mono	12.01	Desmoplakin	DSP
R	1914	Di	12.01	Desmoplakin	DSP
R	1912	Di	12.01	Desmoplakin	DSP
R	21	Di	20.22	tRNA-dihydrouridine(20) synthase [NAD(P)+]-like	DUS2L
K	50	Mono	12.13	Enhancer of mRNA-decapping protein 3 (Fragment)	EDC3
K	79	Mono	47.52	Elongation factor 1-alpha 1 (Fragment)	EEF1A1
R	166	Mono	45.12	Elongation factor 1-alpha 1	EEF1A1
K	84	Mono	47.52	Elongation factor 1-alpha 1 (Fragment)	EEF1A1
K	165	Mono	63.82	Elongation factor 1-alpha 1	EEF1A1
K	84	Di	47.52	Elongation factor 1-alpha 1 (Fragment)	EEF1A1
K	318	Di	38.31	Elongation factor 1-alpha 1	EEF1A1
K	55	Di	65.56	Elongation factor 1-alpha 1 (Fragment)	EEF1A1
K	36	Di	36.92	Elongation factor 1-alpha 1 (Fragment)	EEF1A1
K	165	Di	72.16	Elongation factor 1-alpha 1	EEF1A1
K	79	Di	47.52	Elongation factor 1-alpha 1 (Fragment)	EEF1A1

R	166	Di	45.12	Elongation factor 1-alpha 1	EEF1A1
K	84	Tri	47.52	Elongation factor 1-alpha 1 (Fragment)	EEF1A1
K	165	Tri	72.08	Elongation factor 1-alpha 1	EEF1A1
K	318	Tri	47.11	Elongation factor 1-alpha 1	EEF1A1
K	36	Tri	43.36	Elongation factor 1-alpha 1 (Fragment)	EEF1A1
K	79	Tri	77.26	Elongation factor 1-alpha 1 (Fragment)	EEF1A1
R	166	Mono	17.05	Elongation factor 1-alpha 2	EEF1A2
K	165	Mono	52.72	Elongation factor 1-alpha 2	EEF1A2
K	84	Mono	47.52	Elongation factor 1-alpha 2	EEF1A2
K	79	Mono	47.52	Elongation factor 1-alpha 2	EEF1A2
K	79	Di	47.52	Elongation factor 1-alpha 2	EEF1A2
K	165	Di	61.07	Elongation factor 1-alpha 2	EEF1A2
K	84	Di	47.52	Elongation factor 1-alpha 2	EEF1A2
K	165	Tri	40.31	Elongation factor 1-alpha 2	EEF1A2
K	318	Tri	38.54	Elongation factor 1-alpha 2	EEF1A2
K	79	Tri	33.94	Elongation factor 1-alpha 2	EEF1A2
K	197	Di	32.09	Elongation factor 1-beta	EEF1B2
K	407	Mono	38.12	Elongation factor 2	EEF2
K	525	Tri	34.36	Elongation factor 2	EEF2
K	514	Tri	15.08	Eukaryotic translation initiation factor 2-alpha kinase 3 (Fragment)	EIF2AK3
K	165	Tri	13.14	Eukaryotic translation initiation factor 2-alpha kinase 4	EIF2AK4
R	926	Mono	28.72	Eukaryotic translation initiation factor 3 subunit A	EIF3A
R	3	Mono	15.35	Eukaryotic translation initiation factor 3 subunit L	EIF3L
K	7	Tri	15.35	Eukaryotic translation initiation factor 3 subunit L	EIF3L
K	248	Di	50.51	Eukaryotic initiation factor 4A-II	EIF4A2
R	8	Di	29.21	Eukaryotic translation initiation factor 4 gamma 1 (Fragment)	EIF4G1
R	19	Di	61.19	Eukaryotic translation initiation factor 4H	EIF4H
R	166	Di	41.44	Eukaryotic translation initiation factor 4H	EIF4H
K	9	Mono	12.11	Isoform 2 of Enkurin domain-containing protein 1	ENKD1
R	50	Di	31.57	Enkurin domain-containing protein 1 (Fragment)	ENKD1
R	806	Mono	15.61	E1A-binding protein p400 (Fragment)	EP400
R	412	Mono	17.64	Receptor tyrosine-protein kinase erbB-2	ERBB2
R	269	Mono	22.42	TFIIH basal transcription factor complex helicase XPD subunit (Fragment)	ERCC2
K	607	Tri	13.52	DNA excision repair protein ERCC-6	ERCC6
R	433	Di	84.02	RNA-binding protein EWS	EWSR1
R	577	Di	110.91	RNA-binding protein EWS	EWSR1
R	289	Mono	14.98	Exocyst complex component 8	EXOC8
R	288	Mono	14.98	Exocyst complex component 8	EXOC8
K	47	Mono	22.67	Fatty acid-binding protein, intestinal	FABP2
R	302	Mono	12.4	Protein FAM161A (Fragment)	FAM161A
K	654	Tri	14.82	KIAA0423, isoform CRA_a	FAM179B
K	6	Di	12.46	Protein FAM186A (Fragment)	FAM186A
R	118	Mono	12.4	Protein FAM207A (Fragment)	FAM207A

K	126	Di	13.71	Protein FAM227B	FAM227B
X	1	Mono	14.48	Protein FAM35A (Fragment)	FAM35A
R	394	Mono	12.09	Putative protein FAM47D	FAM47DP
K	71	Mono	12.95	Protein FAM60A (Fragment)	FAM60A
K	319	Mono	13.16	Protein FAM81A	FAM81A
K	7	Mono	15.27	Protein FAM81B (Fragment)	FAM81B
K	3011	Di	18.06	Protocadherin Fat 4	FAT4
X	1	Di	12.67	F-box only protein 15 (Fragment)	FBXO15
K	51	Mono	15.8	Fermitin family homolog 2 (Fragment)	FERMT2
K	55	Mono	15.8	Fermitin family homolog 2 (Fragment)	FERMT2
R	329	Di	28.7	Fibroblast growth factor receptor-like 1	FGFRL1
R	327	Di	28.7	Fibroblast growth factor receptor-like 1	FGFRL1
K	44	Mono	13.33	Fukutin	FKTN
R	141	Mono	19.64	FERM and PDZ domain-containing protein 4	FRMPD4
R	3	Mono	28.98	DOMON domain-containing protein FRRS1L	FRRS1L
R	5	Mono	28.98	DOMON domain-containing protein FRRS1L	FRRS1L
R	216	Di	87.88	RNA-binding protein FUS	FUS
R	218	Di	87.88	RNA-binding protein FUS	FUS
R	101	Mono	30.3	Alpha-(1,3)-fucosyltransferase	FUT7
R	434	Mono	28.33	Fragile X mental retardation syndrome-related protein 1	FXR1
K	25	Di	13.15	G0/G1 switch protein 2	G0S2
R	253	Di	64.82	Ras GTPase-activating protein-binding protein 1	G3BP1
R	468	Di	40.24	Ras GTPase-activating protein-binding protein 2	G3BP2
K	1197	Mono	12	GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1
K	1195	Mono	12	GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1
K	193	Di	15.24	2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT
R	157	Mono	12.4	Gem-associated protein 8 (Fragment)	GEMIN8
K	103	Mono	15.39	ADP-ribosylation factor-binding protein GGA1 (Fragment)	GGA1
R	68	Di	40.7	PERQ amino acid-rich with GYF domain-containing protein 2 (Fragment)	GIGYF2
R	149	Di	40.7	PERQ amino acid-rich with GYF domain-containing protein 2 (Fragment)	GIGYF2
R	64	Di	40.7	PERQ amino acid-rich with GYF domain-containing protein 2 (Fragment)	GIGYF2
R	153	Di	40.7	PERQ amino acid-rich with GYF domain-containing protein 2 (Fragment)	GIGYF2
R	264	Mono	18.22	G kinase-anchoring protein 1	GKAP1
K	265	Mono	18.22	G kinase-anchoring protein 1	GKAP1
R	15	Mono	16.06	Nucleoporin GLE1	GLE1
K	19	Tri	16.06	Nucleoporin GLE1	GLE1
K	17	Di	13.99	Guanine nucleotide-binding protein G(olf) subunit alpha (Fragment)	GNAL
K	21	Tri	27.55	Guanine nucleotide-binding protein G(t) subunit alpha-3	GNAT3
R	98	Mono	14.43	Putative golgin subfamily A member 2B	GOLGA2P5
K	381	Di	13.98	Golgin subfamily A member 5	GOLGA5
K	166	Di	12.49	G patch domain-containing protein 1	GPATCH1
R	154	Di	27.55	G-protein coupled receptor 20	GPR20
R	159	Di	27.55	G-protein coupled receptor 20	GPR20

K	46	Di	27.79	Isoform 2 of Gremlin-1	GREM1
R	344	Mono	12.96	Glutamate receptor ionotropic, delta-2	GRID2
K	443	Mono	12.56	Metabotropic glutamate receptor 5	GRM5
R	52	Mono	12.48	Metabotropic glutamate receptor 7 (Fragment)	GRM7
K	53	Di	12.48	Metabotropic glutamate receptor 7 (Fragment)	GRM7
R	346	Di	28.57	Interferon-induced very large GTPase 1	GVINP1
R	18	Mono	27.5	Histone H2A.x	H2AFX
K	37	Mono	27.41	Histone H3	H3F3A
K	80	Mono	70.85	Histone H3	H3F3A
K	28	Di	27.41	Histone H3	H3F3A
K	80	Di	59.06	Histone H3	H3F3A
K	28	Tri	50.16	Histone H3	H3F3A
K	57	Tri	39.27	Histone H3	H3F3A
R	70	Di	62.35	Intracellular hyaluronan-binding protein 4	HABP4
X	1	Tri	13.43	DNA-(apurinic or apyrimidinic site) lyase (Fragment)	HAP1
R	110	Di	40.9	HCG1652096, isoform CRA_a	hCG_1652096
R	656	Di	60.52	HCG2044799	hCG_2044799
R	623	Di	30.83	DNA helicase B	HELB
K	4513	Mono	12.17	Probable E3 ubiquitin-protein ligase HERC1	HERC1
K	159	Di	29.02	Protein HEXIM1	HEXIM1
K	160	Di	29.02	Protein HEXIM1	HEXIM1
R	156	Di	29.02	Protein HEXIM1	HEXIM1
K	78	Mono	30.7	Histone H1.5	HIST1H1B
K	17	Di	39.58	Histone H1.2	HIST1H1C
K	21	Di	39.58	Histone H1.2	HIST1H1C
R	18	Mono	27.5	Histone H2A type 1-A	HIST1H2AA
K	37	Mono	67.25	Histone H3.1	HIST1H3A
K	38	Mono	54.09	Histone H3.1	HIST1H3A
K	28	Mono	60.42	Histone H3.1	HIST1H3A
K	37	Di	71.98	Histone H3.1	HIST1H3A
K	28	Di	84.91	Histone H3.1	HIST1H3A
K	38	Di	54.09	Histone H3.1	HIST1H3A
K	37	Tri	39.32	Histone H3.1	HIST1H3A
K	28	Tri	59.7	Histone H3.1	HIST1H3A
K	38	Tri	39.32	Histone H3.1	HIST1H3A
R	24	Mono	49.78	Histone H4	HIST1H4A
K	92	Mono	39.19	Histone H4	HIST1H4A
R	96	Mono	28.71	Histone H4	HIST1H4A
K	78	Mono	27.41	Histone H4	HIST1H4A
K	21	Mono	49.78	Histone H4	HIST1H4A
K	32	Mono	34.88	Histone H4	HIST1H4A
K	78	Di	44.01	Histone H4	HIST1H4A
K	21	Di	60.18	Histone H4	HIST1H4A

R	24	Di	49.78	Histone H4	HIST1H4A
R	89	Mono	84.07	Histone H2A type 2-B	HIST2H2AB
K	35	Mono	17.52	Histone H2B	HIST2H2BF
R	34	Mono	17.52	Histone H2B	HIST2H2BF
K	58	Mono	30.66	Histone H2B	HIST2H2BF
K	58	Tri	33.97	Histone H2B	HIST2H2BF
R	93	Mono	31.66	Histone H2B type 3-B	HIST3H2BB
R	100	Mono	49.79	Histone H2B type 3-B	HIST3H2BB
K	336	Mono	13.33	HLA class I histocompatibility antigen, Cw-14 alpha chain	HLA-C
R	291	Di	107.87	Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0
R	215	Mono	29.78	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1
R	213	Mono	29.78	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1
R	31	Mono	101.78	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1
K	112	Mono	70.75	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1
R	215	Di	70.67	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1
R	225	Di	80.63	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1
R	213	Di	79.79	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1
R	206	Di	51.27	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1
R	196	Di	70.67	Heterogeneous nuclear ribonucleoprotein A1-like 2	HNRNPA1L2
R	194	Di	79.79	Heterogeneous nuclear ribonucleoprotein A1-like 2	HNRNPA1L2
R	52	Mono	94.56	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3
R	52	Di	101.78	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3
R	270	Mono	29.87	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB
R	270	Di	37.06	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB
R	245	Di	61.75	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB
R	248	Di	61.75	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB
R	293	Di	33.18	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD
K	68	Mono	28.29	Heterogeneous nuclear ribonucleoprotein H (Fragment)	HNRNPH1
R	233	Mono	42.95	Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2
R	268	Di	33.27	Heterogeneous nuclear ribonucleoprotein K	HNRNPK
R	296	Di	39.51	Heterogeneous nuclear ribonucleoprotein K	HNRNPK
R	271	Di	33.27	Heterogeneous nuclear ribonucleoprotein K	HNRNPK
R	739	Di	46.42	Heterogeneous nuclear ribonucleoprotein U	HNRNPU
R	733	Di	46.42	Heterogeneous nuclear ribonucleoprotein U	HNRNPU
K	161	Mono	69.72	Heterogeneous nuclear ribonucleoprotein D-like	HNRPDL
K	162	Mono	69.72	Heterogeneous nuclear ribonucleoprotein D-like	HNRPDL
R	408	Di	48.35	Heterogeneous nuclear ribonucleoprotein D-like	HNRPDL
R	30	Mono	32.08	Heat shock factor 2-binding protein (Fragment)	HSF2BP
R	202	Di	43.45	Putative heat shock protein HSP 90-alpha A2	HSP90AA2
K	30	Mono	43.6	Endoplasmin (Fragment)	HSP90B1
R	145	Mono	31.06	Heat shock 70 kDa protein 1A/1B	HSPA1A
R	378	Mono	36.39	Heat shock 70 kDa protein 1A/1B	HSPA1A
K	189	Di	67.98	Heat shock 70 kDa protein 1-like	HSPA1L

R	663	Mono	46.99	Heat shock 70 kDa protein 4L	HSPA4L
K	213	Di	67.98	78 kDa glucose-regulated protein	HSPA5
K	154	Di	46.56	78 kDa glucose-regulated protein	HSPA5
K	585	Tri	50.19	78 kDa glucose-regulated protein	HSPA5
K	330	Mono	16.34	Heat shock 70 kDa protein 6	HSPA6
R	248	Di	30.59	Heat shock 70 kDa protein 6	HSPA6
R	249	Di	30.59	Heat shock 70 kDa protein 6	HSPA6
K	187	Di	67.98	Heat shock cognate 71 kDa protein (Fragment)	HSPA8
K	146	Di	67.98	Heat shock cognate 71 kDa protein (Fragment)	HSPA8
K	206	Mono	39.65	Stress-70 protein, mitochondrial	HSPA9
K	233	Mono	46.9	60 kDa heat shock protein, mitochondrial (Fragment)	HSPD1
K	85	Di	13.62	Insulin-degrading enzyme	IDE
K	538	Tri	31.38	Isoform 4 of Interleukin-1 receptor accessory protein	IL1RAP
K	8	Tri	32.86	Interleukin-2 receptor subunit alpha (Fragment)	IL2RA
K	9	Mono	30.08	Interleukin enhancer-binding factor 3 (Fragment)	ILF3
K	25	Mono	30.08	Interleukin enhancer-binding factor 3 (Fragment)	ILF3
K	9	Di	51.17	Interleukin enhancer-binding factor 3 (Fragment)	ILF3
K	25	Di	36.28	Interleukin enhancer-binding factor 3 (Fragment)	ILF3
K	9	Tri	51.17	Interleukin enhancer-binding factor 3 (Fragment)	ILF3
K	25	Tri	36.28	Interleukin enhancer-binding factor 3 (Fragment)	ILF3
R	406	Mono	46.29	Inosine-5'-monophosphate dehydrogenase	IMPDH1
R	321	Mono	20.36	Inosine-5'-monophosphate dehydrogenase	IMPDH1
K	437	Mono	26.32	Inosine-5'-monophosphate dehydrogenase	IMPDH1
K	435	Mono	26.32	Inosine-5'-monophosphate dehydrogenase	IMPDH1
K	437	Di	26.32	Inosine-5'-monophosphate dehydrogenase	IMPDH1
K	435	Di	26.32	Inosine-5'-monophosphate dehydrogenase	IMPDH1
K	460	Di	30.01	Type II inositol 1,4,5-trisphosphate 5-phosphatase	INPP5B
K	510	Mono	16	Integrator complex subunit 2	INTS2
K	502	Mono	16	Integrator complex subunit 2	INTS2
R	508	Mono	16	Integrator complex subunit 2	INTS2
R	922	Di	18.4	Integrator complex subunit 4	INTS4
K	324	Mono	25.18	ITGA10 protein	ITGA10
R	999	Mono	29.59	Integrin alpha-7	ITGA7
R	2096	Di	12	Inositol 1,4,5-trisphosphate receptor type 1	ITPR1
R	2007	Di	12	Inositol 1,4,5-trisphosphate receptor type 3	ITPR3
R	88	Di	26.77	Jun dimerization protein 2 (Fragment)	JDP2
K	6	Tri	23.2	Lysine--tRNA ligase (Fragment)	KARS
K	248	Tri	12.06	Potassium voltage-gated channel subfamily S member 3	KCNS3
K	282	Mono	14.97	Lysine-specific histone demethylase 1B	KDM1B
R	284	Mono	14.97	Lysine-specific histone demethylase 1B	KDM1B
K	282	Di	14.97	Lysine-specific histone demethylase 1B	KDM1B
R	284	Di	14.97	Lysine-specific histone demethylase 1B	KDM1B
R	68	Mono	29.04	Lysine-specific demethylase 5C	KDM5C

R	1456	Di	33.61	Lysine-specific demethylase 5C	KDM5C
R	348	Di	33.9	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1
R	346	Di	39.05	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1
K	385	Tri	29.73	Mitochondrial ribonuclease P protein 3	KIAA0391
K	177	Mono	13.17	Uncharacterized protein KIAA0947	KIAA0947
K	28	Di	27.43	Junctional protein associated with coronary artery disease	KIAA1462
R	443	Di	29.74	Uncharacterized protein KIAA1522	KIAA1522
K	1329	Mono	14.64	Basic helix-loop-helix domain-containing protein KIAA2018	KIAA2018
R	670	Mono	12.82	Kinesin-like protein KIF21A	KIF21A
K	669	Mono	12.82	Kinesin-like protein KIF21A	KIF21A
R	670	Di	12.82	Kinesin-like protein KIF21A	KIF21A
K	669	Di	12.82	Kinesin-like protein KIF21A	KIF21A
K	669	Tri	12.82	Kinesin-like protein KIF21A	KIF21A
R	658	Mono	12.82	Kinesin-like protein KIF21B	KIF21B
R	659	Mono	12.82	Kinesin-like protein KIF21B	KIF21B
R	202	Mono	23.62	Kinesin-like protein KIF26B	KIF26B
K	203	Mono	23.62	Kinesin-like protein KIF26B	KIF26B
R	202	Di	23.62	Kinesin-like protein KIF26B	KIF26B
K	203	Di	23.62	Kinesin-like protein KIF26B	KIF26B
K	203	Tri	23.62	Kinesin-like protein KIF26B	KIF26B
K	586	Tri	13.29	Chromosome-associated kinesin KIF4B	KIF4B
K	223	Mono	29.62	Krueppel-like factor 10	KLF10
R	306	Mono	23.2	Isoform 3 of Krueppel-like factor 12	KLF12
K	975	Di	12.49	Histone-lysine N-methyltransferase MLL3 (Fragment)	KMT2C
R	431	Mono	35.17	Keratin, type I cytoskeletal 27	KRT27
R	355	Di	55.18	Keratin, type II cytoskeletal 75	KRT75
R	415	Mono	12.26	Keratin, type II cytoskeletal 78	KRT78
R	414	Mono	12.26	Keratin, type II cytoskeletal 78	KRT78
R	415	Di	12.26	Keratin, type II cytoskeletal 78	KRT78
R	414	Di	12.26	Keratin, type II cytoskeletal 78	KRT78
R	401	Mono	36.83	Keratin, type II cytoskeletal 8	KRT8
R	10	Di	12.01	Laminin subunit alpha-3 (Fragment)	LAMA3
R	4	Di	12.01	Laminin subunit alpha-3 (Fragment)	LAMA3
K	1519	Di	15.08	Laminin subunit beta-1	LAMB1
K	1516	Tri	15.08	Laminin subunit beta-1	LAMB1
R	59	Di	55.73	La-related protein 4B (Fragment)	LARP4B
R	61	Di	55.73	La-related protein 4B (Fragment)	LARP4B
K	543	Tri	12.13	La-related protein 7	LARP7
K	739	Tri	28.71	Serine/threonine-protein kinase LATS1	LATS1
K	190	Di	15.83	Lebercilin	LCA5
K	1737	Di	23.62	Lactase-phlorizin hydrolase	LCT
K	5	Tri	80.19	L-lactate dehydrogenase A chain	LDHA
K	264	Mono	27.76	L-lactate dehydrogenase	LDHC

R	12	Mono	17.75	Leukocyte receptor cluster member 1	LENG1
K	7	Tri	17.75	Leukocyte receptor cluster member 1	LENG1
K	6	Tri	17.75	Leukocyte receptor cluster member 1	LENG1
K	8	Di	16.98	Galectin-2 (Fragment)	LGALS2
K	306	Di	38.21	Leucine-rich repeat-containing G protein-coupled receptor 5	LGR5
K	6	Di	15.48	LIM and calponin homology domains-containing protein 1 (Fragment)	LIMCH1
R	290	Di	28.34	Lipase maturation factor 1	LMF1
K	749	Tri	28.01	Ligand-dependent nuclear receptor-interacting factor 1	LRIF1
R	22	Mono	13.59	Leucine-rich repeat protein 1	LRR1
K	24	Tri	13.59	Leucine-rich repeat protein 1	LRR1
R	288	Di	13.4	Leucine-rich repeat neuronal protein 1	LRRN1
R	317	Mono	27.53	Melanoma-associated antigen B18	MAGEB18
K	445	Di	20.48	MAGE-like 2	MAGEL2
R	428	Mono	31.15	Alpha-mannosidase 2	MAN2A1
R	1220	Di	29.32	Microtubule-associated protein 1B	MAP1B
R	1177	Mono	14.49	Mitogen-activated protein kinase kinase kinase 6	MAP3K6
K	1183	Di	14.49	Mitogen-activated protein kinase kinase kinase 6	MAP3K6
R	119	Mono	12.4	Ensconsin	MAP7
K	1116	Mono	12.11	Microtubule-associated serine/threonine-protein kinase 2	MAST2
K	252	Tri	41.5	Matrilin-4	MATN4
K	56	Mono	13.33	Cyclic GMP-AMP synthase	MB21D1
R	490	Mono	12.48	Guanine nucleotide exchange factor DBS	MCF2L
K	496	Tri	12.48	Guanine nucleotide exchange factor DBS	MCF2L
R	14	Di	33.08	DNA replication licensing factor MCM4 (Fragment)	MCM4
R	10	Di	37.87	DNA replication licensing factor MCM4 (Fragment)	MCM4
R	11	Di	37.87	DNA replication licensing factor MCM4 (Fragment)	MCM4
R	221	Di	16.3	Calcium uniporter protein, mitochondrial	MCU
K	103	Mono	16.7	Mediator of RNA polymerase II transcription subunit 10	MED10
R	211	Mono	22.42	Methionine aminopeptidase 1D, mitochondrial	METAP1D
K	86	Mono	12.11	Methyltransferase-like protein 16 (Fragment)	METTL16
R	268	Mono	12.4	Misshapen-like kinase 1 (Fragment)	MINK1
R	112	Di	27.54	Meckel syndrome type 1 protein	MKS1
R	205	Mono	16.3	Modulator of apoptosis 1	MOAP1
R	91	Mono	24.77	Mov10, Moloney leukemia virus 10, homolog (Mouse), isoform CRA_a	MOV10
R	37	Di	55.07	M-phase-specific PLK1-interacting protein	MPLKIP
R	71	Mono	22.84	39S ribosomal protein L30, mitochondrial	MRPL30
K	36	Di	17.33	39S ribosomal protein L54, mitochondrial (Fragment)	MRPL54
R	141	Mono	23.62	Myotubularin-related protein 9	MTMR9
R	141	Mono	31.47	Myelin expression factor 2	MYEF2
R	1114	Mono	45.27	Myosin-10	MYH10
R	1945	Mono	38.9	Myosin-14	MYH14
R	1923	Mono	44.52	Myosin-9	MYH9
K	1538	Di	48.97	Myosin-9	MYH9

K	626	Tri	28.01	Unconventional myosin-VIIb	MYO7B
R	19	Di	27.73	Myb-related transcription factor, partner of profilin	MYPOP
K	17	Di	27.73	Myb-related transcription factor, partner of profilin	MYPOP
R	146	Di	14.98	N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae), isoform CRA_a	NAA20
K	150	Tri	14.98	N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae), isoform CRA_a	NAA20
K	2	Di	13.33	N-alpha-acetyltransferase 50	NAA50
K	2	Mono	17.5	NGFI-A-binding protein 1 (Fragment)	NAB1
K	4	Mono	31.31	NAD kinase (Fragment)	NADK
K	4	Di	31.31	NAD kinase (Fragment)	NADK
R	164	Mono	17.33	Nicotinate phosphoribosyltransferase	NAPRT1
K	2	Tri	33.52	Kinetochore protein NDC80 homolog (Fragment)	NDC80
K	490	Di	13.82	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 2	NDST2
K	48	Di	16.96	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	NDUFA7
R	196	Mono	30.93	Complex I intermediate-associated protein 30, mitochondrial	NDUFAF1
R	191	Mono	30.93	Complex I intermediate-associated protein 30, mitochondrial	NDUFAF1
R	20	Di	34.53	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2
R	379	Mono	40.81	Isoform 2 of Serine/threonine-protein kinase Nek2	NEK2
K	50	Tri	38.49	Serine/threonine-protein kinase Nek3	NEK3
K	135	Mono	27.67	Negative elongation factor B	NELFB
R	516	Di	35.76	Ninein-like protein	NINL
K	520	Tri	35.76	Ninein-like protein	NINL
R	5	Mono	17.64	Nucleoside diphosphate kinase 6 (Fragment)	NME6
K	114	Mono	30.62	Thioredoxin domain-containing protein 3 (Fragment)	NME8
K	198	Mono	27.97	Non-POU domain-containing octamer-binding protein (Fragment)	NONO
K	187	Tri	33.81	Non-POU domain-containing octamer-binding protein (Fragment)	NONO
K	16	Di	28.31	Nucleolar protein 56 (Fragment)	NOP56
K	34	Di	16.62	Nuclear receptor subfamily 2 group C member 2 (Fragment)	NR2C2
K	88	Mono	42.19	GTPase NRas	NRAS
R	396	Di	28.88	5'-nucleotidase domain-containing protein 2	NT5DC2
R	8	Mono	14.29	Nefastin-1 (Fragment)	NUCB2
K	7	Mono	14.29	Nefastin-1 (Fragment)	NUCB2
K	1159	Tri	18.77	Nucleoporin NUP188 homolog	NUP188
R	26	Mono	29.18	Occludin/ELL domain-containing protein 1 (Fragment)	OCEL1
K	205	Tri	33.44	Protein odr-4 homolog	ODR4
K	387	Tri	31.73	Hepatocyte nuclear factor 6	ONECUT1
R	38	Di	22.84	Dynamin-like 120 kDa protein, mitochondrial (Fragment)	OPA1
K	264	Di	15.28	Long-wave-sensitive opsin 1	OPN1LW
K	308	Di	28.38	Olfactory receptor 11H4	OR11H4
K	308	Tri	30.99	Olfactory receptor 11H4	OR11H4
K	231	Tri	15.04	Olfactory receptor 13G1	OR13G1
K	85	Di	16.71	Olfactory receptor 2T11	OR2T11
R	307	Di	30.49	Olfactory receptor 4K5	OR4K5
R	316	Mono	27.55	Olfactory receptor 6J1	OR6J1

R	448	Di	99.77	Polyadenylate-binding protein 1	PABPC1
K	361	Mono	62.54	Polyadenylate-binding protein 1-like	PABPC1L
R	489	Di	59.41	Poly(A) binding protein, cytoplasmic 4 (Inducible form), isoform CRA_e	PABPC4
K	361	Di	62.54	Poly(A) binding protein, cytoplasmic 4 (Inducible form), isoform CRA_e	PABPC4
K	284	Tri	20.16	Poly(A) binding protein, cytoplasmic 4 (Inducible form), isoform CRA_e	PABPC4
R	23	Mono	66.1	Polyadenylate-binding protein 2	PABPN1
R	17	Mono	105.87	Polyadenylate-binding protein 2	PABPN1
R	23	Di	90.95	Polyadenylate-binding protein 2	PABPN1
R	17	Di	132.91	Polyadenylate-binding protein 2	PABPN1
K	438	Mono	17.82	Protein-arginine deiminase type-1	PADI1
K	393	Mono	13.37	Iron/zinc purple acid phosphatase-like protein	PAPL
K	288	Di	20.84	Poly (ADP-ribose) polymerase family, member 9, isoform CRA_b	PARP9
R	346	Di	127.53	Poly(rC)-binding protein 1	PCBP1
R	95	Mono	33.43	Poly(rC)-binding protein 2	PCBP2
R	101	Mono	33.43	Poly(rC)-binding protein 2	PCBP2
R	95	Di	33.43	Poly(rC)-binding protein 2	PCBP2
R	101	Di	33.43	Poly(rC)-binding protein 2	PCBP2
R	5	Mono	12.25	Protocadherin gamma-A10	PCDHGA10
R	403	Mono	28.91	Pre-mRNA cleavage complex 2 protein Pcf11 (Fragment)	PCF11
R	89	Mono	40.85	Protein-L-isoaspartate O-methyltransferase	PCMT1
K	41	Di	15.76	28 kDa heat- and acid-stable phosphoprotein	PDAP1
R	35	Di	15.76	28 kDa heat- and acid-stable phosphoprotein	PDAP1
K	516	Mono	13.92	Protein RRP5 homolog	PDCD11
K	515	Mono	13.92	Protein RRP5 homolog	PDCD11
K	515	Di	13.92	Protein RRP5 homolog	PDCD11
K	516	Di	13.92	Protein RRP5 homolog	PDCD11
K	1586	Di	15.28	Protein RRP5 homolog	PDCD11
X	1	Mono	14.44	Dual 3',5'-cyclic-AMP and -GMP phosphodiesterase 11A (Fragment)	PDE11A
X	1	Di	14.44	Dual 3',5'-cyclic-AMP and -GMP phosphodiesterase 11A (Fragment)	PDE11A
K	268	Mono	15.83	Platelet-derived growth factor D	PDGFD
R	42	Di	40.9	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	PDPR
X	1	Tri	18.39	PDZ domain-containing protein 7 (Fragment)	PDZD7
K	80	Mono	13.33	Putative PDZ domain-containing protein 1P	PDZK1P1
K	64	Mono	80.93	Uncharacterized protein (Fragment)	PE=2
K	64	Di	32.01	Uncharacterized protein (Fragment)	PE=2
K	4	Di	28.83	Uncharacterized protein (Fragment)	PE=4
K	5	Di	13.23	Uncharacterized protein (Fragment)	PE=4
K	256	Mono	28.38	Putative olfactory receptor GPCRLTM7	PE=5
K	37	Mono	32.89	Putative Rab-43-like protein ENSP00000330714	PE=5
K	256	Di	30.99	Putative olfactory receptor GPCRLTM7	PE=5
K	139	Tri	14.55	Platelet endothelial cell adhesion molecule	PECAM1
X	1	Tri	44.4	Proline-, glutamic acid- and leucine-rich protein 1 (Fragment)	PELP1
K	278	Tri	31.11	Period circadian protein homolog 2	PER2

K	71	Mono	32.76	Protein PET117 homolog, mitochondrial	PET117
K	38	Mono	18.92	Peroxisomal membrane protein 11A	PEX11A
K	35	Mono	18.92	Peroxisomal membrane protein 11A	PEX11A
R	2	Mono	13.09	Isoform 4 of Phosphatase and actin regulator 3	PHACTR3
K	547	Tri	16.62	PH domain leucine-rich repeat-containing protein phosphatase 1	PHLPP1
R	819	Di	28.02	p53-induced protein with a death domain	PIDD
R	8	Mono	35.36	GPI ethanolamine phosphate transferase 1 (Fragment)	PIGN
K	540	Mono	17.33	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha	PIK3C2A
R	465	Mono	27.42	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit delta isoform	PIK3CD
K	1203	Mono	29.59	Membrane-associated phosphatidylinositol transfer protein 1	PITPNM1
R	551	Mono	13.87	Membrane-associated phosphatidylinositol transfer protein 3	PITPNM3
K	550	Mono	13.87	Membrane-associated phosphatidylinositol transfer protein 3	PITPNM3
K	545	Mono	13.87	Membrane-associated phosphatidylinositol transfer protein 3	PITPNM3
R	551	Di	13.87	Membrane-associated phosphatidylinositol transfer protein 3	PITPNM3
K	550	Di	13.87	Membrane-associated phosphatidylinositol transfer protein 3	PITPNM3
R	1164	Di	27.33	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-2 (Fragment)	PLCH2
K	710	Di	18.29	Phospholipase D1	PLD1
K	165	Di	28.54	Plastin-3	PLS3
R	1077	Mono	13.74	Plexin-B3	PLXNB3
R	17	Di	18.77	Mitochondrial-processing peptidase subunit beta	PMPCB
R	16	Di	18.77	Mitochondrial-processing peptidase subunit beta	PMPCB
K	403	Mono	34.78	PNMA-like protein 1	PNMAL1
R	928	Mono	28.15	DNA polymerase	POLA1
R	927	Mono	30.49	DNA polymerase	POLA1
R	927	Di	28.15	DNA polymerase	POLA1
K	929	Di	28.15	DNA polymerase	POLA1
R	928	Di	28.15	DNA polymerase	POLA1
K	929	Tri	30.49	DNA polymerase	POLA1
K	1045	Mono	37.97	DNA-directed RNA polymerase	POLR2B
R	101	Mono	13.34	Popeye domain-containing protein 3 (Fragment)	POPDC3
R	255	Mono	13.34	Popeye domain-containing protein 3	POPDC3
K	100	Mono	15.55	Popeye domain-containing protein 3 (Fragment)	POPDC3
K	254	Mono	15.55	Popeye domain-containing protein 3	POPDC3
R	408	Mono	17.24	HCG2033702, isoform CRA_a	PPAN
K	125	Di	33.89	Peptidyl-prolyl cis-trans isomerase A-like 4G	PPIAL4G
R	118	Di	27.54	Periplakin	PPL
R	341	Mono	35.78	Probable protein phosphatase 1N (Fragment)	PPM1N
R	449	Mono	29.34	Protein phosphatase 1 regulatory subunit 37	PPP1R37
R	449	Di	29.34	Protein phosphatase 1 regulatory subunit 37	PPP1R37
K	448	Di	29.34	Protein phosphatase 1 regulatory subunit 37	PPP1R37
K	448	Tri	29.34	Protein phosphatase 1 regulatory subunit 37	PPP1R37
R	3	Di	13.76	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B beta isoform (Fragment)	PPP2R2B
R	8	Di	13.76	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B beta isoform (Fragment)	PPP2R2B

K	288	Mono	53.78	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B gamma isoform	PPP2R2C
K	5	Di	12.49	Serine/threonine-protein phosphatase 2A activator (Fragment)	PPP2R4
K	558	Di	28.71	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D
R	196	Mono	103.6	cAMP-dependent protein kinase type II-beta regulatory subunit	PRKAR2B
K	176	Mono	103.6	cAMP-dependent protein kinase type II-beta regulatory subunit	PRKAR2B
K	47	Mono	20.94	Protein kinase C beta type (Fragment)	PRKCB
K	51	Di	20.94	Protein kinase C beta type (Fragment)	PRKCB
R	216	Di	13.36	Protein kinase C delta type	PRKCD
R	207	Di	13.36	Protein kinase C delta type	PRKCD
K	69	Tri	38.45	Pre-mRNA-processing-splicing factor 8 (Fragment)	PRPF8
K	17	Tri	41.06	Peripherin (Fragment)	PRPH
R	1164	Di	29.28	Protein PRRC2A	PRRC2A
K	447	Mono	28.68	Protein PRRC2B	PRRC2B
K	957	Mono	29.33	Protein PRRC2B	PRRC2B
K	955	Mono	29.33	Protein PRRC2B	PRRC2B
K	2086	Mono	30.4	Protein PRRC2C	PRRC2C
R	2089	Mono	30.4	Protein PRRC2C	PRRC2C
K	359	Mono	12.17	Inactive serine protease 35	PRSS35
K	360	Mono	12.17	Inactive serine protease 35	PRSS35
K	360	Di	12.17	Inactive serine protease 35	PRSS35
K	359	Di	12.17	Inactive serine protease 35	PRSS35
X	1	Tri	15.82	26S proteasome non-ATPase regulatory subunit 6 (Fragment)	PSMD6
R	566	Di	18.28	Tyrosine-protein phosphatase non-receptor type 23	PTPN23
R	471	Mono	14.12	Receptor-type tyrosine-protein phosphatase U	PTPRU
R	991	Di	22.42	Receptor-type tyrosine-protein phosphatase U	PTPRU
K	113	Mono	13.14	Polymerase I and transcript release factor	PTRF
R	287	Mono	31.08	Paxillin	PXN
R	282	Mono	31.08	Paxillin	PXN
R	287	Di	30.77	Paxillin	PXN
R	282	Di	30.77	Paxillin	PXN
K	107	Mono	50.28	Pyrroline-5-carboxylate reductase 2	PYCR2
K	106	Mono	50.28	Pyrroline-5-carboxylate reductase 2	PYCR2
K	1604	Mono	28.31	Glutamine-rich protein 2	QRICH2
R	1606	Mono	28.31	Glutamine-rich protein 2	QRICH2
K	1604	Di	28.31	Glutamine-rich protein 2	QRICH2
R	1606	Di	28.31	Glutamine-rich protein 2	QRICH2
K	1604	Tri	28.31	Glutamine-rich protein 2	QRICH2
K	58	Mono	12.9	Ras-related protein Rab-13	RAB13
K	13	Mono	32.89	Ras-related protein Rab-30 (Fragment)	RAB30
K	86	Di	12.9	Ras-related protein Rab-33A	RAB33A
K	72	Mono	32.89	Ras-related protein Rab-3B	RAB3B
R	69	Mono	33.88	Ras-related protein Rab-7b	RAB7B
R	195	Mono	12.61	Ras-related protein Rab-7b	RAB7B

K	875	Mono	12.01	Ankycorbin	RAI14
K	873	Mono	12.01	Ankycorbin	RAI14
K	873	Di	12.01	Ankycorbin	RAI14
K	875	Di	12.01	Ankycorbin	RAI14
K	34	Di	52.13	RNA-binding protein Raly (Fragment)	RALY
K	34	Di	52.13	RNA-binding Raly-like protein	RALYL
K	466	Di	12.56	Rap guanine nucleotide exchange factor 6	RAPGEF6
K	136	Mono	39.74	Pre-mRNA-splicing factor RBM22	RBM22
R	105	Di	83.94	Putative RNA-binding protein 3	RBM3
R	50	Di	40.28	RNA-binding motif protein, X chromosome, N-terminally processed	RBMX
R	52	Di	36.44	RNA-binding motif protein, X chromosome, N-terminally processed	RBMX
R	21	Mono	13.01	Plasma retinol-binding protein(1-182)	RBP4
R	18	Mono	13.01	Plasma retinol-binding protein(1-182)	RBP4
R	83	Mono	33.16	Reticulocalbin-1	RCN1
K	81	Mono	57.27	Reticulocalbin-1	RCN1
K	104	Mono	19.18	DNA repair protein REV1	REV1
K	107	Mono	19.18	DNA repair protein REV1	REV1
K	107	Di	19.18	DNA repair protein REV1	REV1
K	104	Di	19.18	DNA repair protein REV1	REV1
K	107	Tri	19.18	DNA repair protein REV1	REV1
K	104	Tri	19.18	DNA repair protein REV1	REV1
R	84	Mono	34.14	Inactive rhomboid protein 1 (Fragment)	RHBDF1
X	1	Mono	37.38	Synembryn-A (Fragment)	RIC8A
R	7	Mono	35.14	Synembryn-B (Fragment)	RIC8B
R	6	Di	28.19	Rapamycin-insensitive companion of mTOR (Fragment)	RICTOR
K	595	Mono	27.73	CARMIL2b	RLTPR
R	6	Di	40.54	Ribonuclease kappa (Fragment)	RNASEK
R	24	Di	33.61	E3 ubiquitin-protein ligase RNF125	RNF125
K	655	Di	16.23	E3 ubiquitin-protein ligase BRE1A	RNF20
K	391	Mono	22.15	E3 ubiquitin-protein ligase RNF216	RNF216
K	414	Di	14.98	E3 ubiquitin-protein ligase RNF216	RNF216
K	413	Di	14.98	E3 ubiquitin-protein ligase RNF216	RNF216
R	409	Mono	19.44	Protein fantom	RPGRIP1L
K	411	Mono	19.44	Protein fantom	RPGRIP1L
K	411	Di	19.44	Protein fantom	RPGRIP1L
R	409	Di	19.44	Protein fantom	RPGRIP1L
K	411	Tri	19.44	Protein fantom	RPGRIP1L
R	98	Mono	35.83	60S ribosomal protein L13a (Fragment)	RPL13A
K	2	Di	29.18	60S ribosomal protein L26 (Fragment)	RPL26
R	26	Mono	49.96	60S ribosomal protein L26-like 1 (Fragment)	RPL26L1
K	5	Mono	54.46	60S ribosomal protein L29	RPL29
R	128	Mono	33.22	40S ribosomal protein S14	RPS14
R	137	Mono	39.8	40S ribosomal protein S15	RPS15

R	58	Mono	36.77	40S ribosomal protein S4, Y isoform 1 (Fragment)	RPS4Y1
R	65	Di	12.83	R-spondin-2 (Fragment)	RSPO2
K	517	Mono	32.76	Relaxin receptor 1	RXFP1
R	7	Mono	22.05	Serine--tRNA ligase, mitochondrial	SARS2
R	1036	Mono	30.94	Splicing factor, arginine/serine-rich 15	SCAF4
K	2	Di	13.33	Secretoglobin family 1C member 1	SCGB1C1
R	324	Mono	28.17	Amiloride-sensitive sodium channel subunit beta	SCNN1B
R	200	Di	18	Protein SCO1 homolog, mitochondrial	SCO1
R	2	Mono	27.31	SCY1-like protein 2 (Fragment)	SCYL2
K	134	Mono	30.89	SEC14-like protein 3	SEC14L3
X	1	Mono	13.23	Protein transport protein Sec31A (Fragment)	SEC31A
K	10	Tri	32.34	Protein transport protein Sec61 subunit alpha isoform 2	SEC61A2
K	142	Di	13.95	Semaphorin-6A	SEMA6A
K	979	Di	13.13	Semaphorin-6D	SEMA6D
K	190	Di	39.67	Glia-derived nexin (Fragment)	SERPINE2
K	660	Mono	12.47	SET-binding protein	SETBP1
R	244	Di	77.81	Splicing factor 3B subunit 2 (Fragment)	SF3B2
R	246	Di	77.81	Splicing factor 3B subunit 2 (Fragment)	SF3B2
R	221	Di	42.11	Splicing factor 3B subunit 2 (Fragment)	SF3B2
R	779	Mono	33.04	Scm-like with four MBT domains protein 2	SFMBT2
R	777	Mono	33.04	Scm-like with four MBT domains protein 2	SFMBT2
R	779	Di	33.04	Scm-like with four MBT domains protein 2	SFMBT2
R	777	Di	38.22	Scm-like with four MBT domains protein 2	SFMBT2
R	693	Mono	49.67	Splicing factor, proline- and glutamine-rich	SFPQ
R	2	Mono	35.93	Splicing factor, proline- and glutamine-rich (Fragment)	SFPQ
R	9	Di	68.83	Splicing factor, proline- and glutamine-rich	SFPQ
R	693	Di	42.64	Splicing factor, proline- and glutamine-rich	SFPQ
R	94	Mono	30.55	Serine/arginine-rich-splicing factor 2	SFRS2
K	193	Di	28.71	Alpha-sarcoglycan	SGCA
X	1	Tri	14.72	N-sulphoglucosamine sulphohydrolase (Fragment)	SGSH
R	366	Mono	24.41	SH3 domain-containing protein 19	SH3D19
K	675	Tri	45.03	Single-minded homolog 1	SIM1
K	85	Mono	20.23	Spindle and kinetochore-associated protein 3	SKA3
K	92	Di	20.23	Spindle and kinetochore-associated protein 3	SKA3
R	9	Mono	29.72	Histone RNA hairpin-binding protein (Fragment)	SLBP
K	128	Di	16.38	Calcium-binding mitochondrial carrier protein SCaMC-2	SLC25A25
K	124	Di	16.38	Calcium-binding mitochondrial carrier protein SCaMC-2	SLC25A25
R	31	Mono	26.49	ADP/ATP translocase 1	SLC25A4
K	23	Mono	66.94	ADP/ATP translocase 1	SLC25A4
R	56	Mono	17.78	Mitochondrial coenzyme A transporter SLC25A42	SLC25A42
K	49	Tri	29.86	ADP/ATP translocase 2	SLC25A5
K	52	Tri	60.15	ADP/ATP translocase 2	SLC25A5
K	52	Tri	59.95	ADP/ATP translocase 3 (Fragment)	SLC25A6

K	25	Mono	15.22	Solute carrier family 35 member G2	SLC35G2
K	33	Mono	12.47	Choline transporter-like protein 2 (Fragment)	SLC44A2
K	287	Di	29.63	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	SMARCE1
K	570	Mono	12.47	Structural maintenance of chromosomes protein 2	SMC2
R	566	Di	12.47	Structural maintenance of chromosomes protein 2	SMC2
R	180	Di	14.25	Telomerase-binding protein EST1A (Fragment)	SMG6
K	6	Mono	24.52	Protein SMG8 (Fragment)	SMG8
R	136	Di	12.83	Staphylococcal nuclease domain-containing protein 1	SND1
R	4	Di	29.83	Small nuclear ribonucleoprotein E	SNRPE
R	6	Mono	27.54	Alpha-1-syntrophin	SNTA1
R	5	Mono	27.54	Alpha-1-syntrophin	SNTA1
R	559	Mono	13.09	SNW domain-containing protein 1	SNW1
K	315	Di	29.72	SNW domain-containing protein 1	SNW1
K	63	Di	12.48	Suppressor of cytokine-signaling 2	SOCS2
K	104	Mono	15.07	Spermatogenesis-associated protein 24	SPATA24
K	107	Mono	15.07	Spermatogenesis-associated protein 24	SPATA24
K	104	Di	15.07	Spermatogenesis-associated protein 24	SPATA24
K	107	Di	15.07	Spermatogenesis-associated protein 24	SPATA24
K	104	Tri	15.07	Spermatogenesis-associated protein 24	SPATA24
K	107	Tri	15.07	Spermatogenesis-associated protein 24	SPATA24
R	797	Di	13.81	Hemofiltrate peptide HF6478 (Fragment)	SPINK5
K	113	Mono	27.86	Spectrin alpha chain, erythrocytic 1	SPTA1
R	1007	Di	16.18	Spectrin beta chain, non-erythrocytic 4	SPTBN4
R	386	Di	32.22	Spectrin beta chain, non-erythrocytic 4	SPTBN4
R	1004	Di	16.18	Spectrin beta chain, non-erythrocytic 4	SPTBN4
R	903	Di	32.77	SLIT-ROBO Rho GTPase-activating protein 3	SRGAP3
R	326	Di	28.17	Serine/arginine repetitive matrix protein 1	SRRM1
K	732	Mono	14.79	Serine/arginine repetitive matrix protein 2 (Fragment)	SRRM2
R	97	Di	37.03	Serine/arginine-rich-splicing factor 1	SRSF1
R	109	Mono	13.09	CDNA FLJ25552 fis, clone JTH02127	SRXN1
K	106	Di	12.26	Sex-determining region Y protein	SRY
K	640	Mono	14.79	FACT complex subunit SSRP1	SSRP1
K	204	Di	12.57	Alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3-N-acetyl-galactosaminide alpha-2,6-sialyltransferase	ST6GALNAC4
K	205	Di	12.57	Alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3-N-acetyl-galactosaminide alpha-2,6-sialyltransferase	ST6GALNAC4
K	205	Tri	12.57	Alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3-N-acetyl-galactosaminide alpha-2,6-sialyltransferase	ST6GALNAC4
K	204	Tri	12.57	Alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3-N-acetyl-galactosaminide alpha-2,6-sialyltransferase	ST6GALNAC4
K	349	Di	34.16	Striatin-interacting protein 1	STRIP1
K	233	Tri	27.69	Striatin-3	STRN3
R	3	Mono	15.14	Isoform 7 of SUN domain-containing protein 1	SUN1
R	251	Di	21.85	Transcription initiation protein SPT3 homolog	SUPT3H
K	3437	Di	12.93	Nesprin-2	SYNE2
K	964	Tri	13.52	Nesprin-2	SYNE2

K	1230	Mono	13.16	Ras GTPase-activating protein SynGAP (Fragment)	SYNGAP1
K	266	Mono	13.33	Synaptotagmin-4	SYT4
R	69	Di	30.36	Synaptotagmin-like protein 5	SYTL5
R	68	Mono	15.96	Transcription initiation factor TFIID subunit 12	TAF12
K	207	Mono	29.44	TATA-binding protein-associated factor 2N (Fragment)	TAF15
R	203	Mono	29.44	TATA-binding protein-associated factor 2N (Fragment)	TAF15
R	124	Di	35.06	TATA-binding protein-associated factor 2N (Fragment)	TAF15
R	192	Di	30.04	TATA-binding protein-associated factor 2N (Fragment)	TAF15
R	150	Di	40.48	TATA-binding protein-associated factor 2N (Fragment)	TAF15
R	184	Di	36.03	TATA-binding protein-associated factor 2N (Fragment)	TAF15
R	182	Di	66.95	TATA-binding protein-associated factor 2N (Fragment)	TAF15
R	203	Di	29.44	TATA-binding protein-associated factor 2N (Fragment)	TAF15
R	157	Di	40.48	TATA-binding protein-associated factor 2N (Fragment)	TAF15
K	207	Di	29.44	TATA-binding protein-associated factor 2N (Fragment)	TAF15
R	483	Di	81.26	TATA-binding protein-associated factor 2N	TAF15
K	3	Mono	32.6	Serine/threonine-protein kinase TAO3 (Fragment)	TAOK3
K	57	Mono	29.3	Serine/threonine-protein kinase TAO3	TAOK3
R	515	Di	34.03	TBC1 domain family member 2A	TBC1D2
K	7	Mono	13.36	TBC1 domain family member 3 (Fragment)	TBC1D3
K	4	Mono	13.36	TBC1 domain family member 3 (Fragment)	TBC1D3
R	32	Di	12.02	Transcription factor 23	TCF23
R	23	Di	36.09	T-cell leukemia/lymphoma protein 1A (Fragment)	TCL1A
K	642	Mono	13.06	Treacle protein	TCOF1
R	757	Di	18.03	Methylcytosine dioxygenase TET1	TET1
K	99	Tri	15.48	Testis-expressed sequence 36 protein	TEX36
R	385	Di	45.49	Protein TFG	TFG
R	3	Di	15.35	Tuftelin-interacting protein 11 (Fragment)	TFIP11
K	7	Tri	15.35	Tuftelin-interacting protein 11 (Fragment)	TFIP11
K	423	Mono	22.05	Transforming growth factor-beta receptor-associated protein 1	TGFBRAP1
K	425	Mono	22.05	Transforming growth factor-beta receptor-associated protein 1	TGFBRAP1
R	464	Mono	12.53	Protein-glutamine gamma-glutamyltransferase Z	TGM7
R	464	Di	12.53	Protein-glutamine gamma-glutamyltransferase Z	TGM7
K	461	Di	12.53	Protein-glutamine gamma-glutamyltransferase Z	TGM7
K	461	Tri	12.53	Protein-glutamine gamma-glutamyltransferase Z	TGM7
K	202	Di	76.12	Thyroid hormone receptor-associated protein 3	THRAP3
K	173	Di	28.03	Thyroid hormone receptor-associated protein 3	THRAP3
K	532	Tri	12.12	Thyroid hormone receptor-associated protein 3	THRAP3
R	188	Di	35.68	Thrombospondin type-1 domain-containing protein 4	THSD4
R	86	Di	30.18	Fructose-2,6-bisphosphatase TIGAR	TIGAR
K	26	Mono	19.07	Tigger transposable element-derived protein 4	TIGD4
R	6	Di	18.77	Metalloproteinase inhibitor 4	TIMP4
K	575	Tri	24.28	Transketolase	TKT
R	5	Mono	27.97	Transketolase-like protein 1 (Fragment)	TKTL1

K	6	Mono	27.97	Transketolase-like protein 1 (Fragment)	TKTL1
R	5	Di	27.97	Transketolase-like protein 1 (Fragment)	TKTL1
K	6	Di	27.97	Transketolase-like protein 1 (Fragment)	TKTL1
K	6	Tri	27.97	Transketolase-like protein 1 (Fragment)	TKTL1
R	813	Mono	30.82	Transmembrane protein 132A	TMEM132A
R	256	Mono	14.74	Transmembrane protein 198	TMEM198
K	31	Tri	14.55	Transmembrane protein 26	TMEM26
K	286	Di	27.71	Tropomodulin-1	TMOD1
K	329	Di	31.41	Transmembrane protease serine 5	TMPRSS5
K	5	Di	16.46	Troponin T, slow skeletal muscle (Fragment)	TNNT1
K	7	Tri	12.53	Trinucleotide repeat-containing gene 18 protein (Fragment)	TNRC18
K	4	Tri	12.53	Trinucleotide repeat-containing gene 18 protein (Fragment)	TNRC18
K	425	Mono	16.18	DNA topoisomerase 2-alpha	TOP2A
K	426	Mono	16.18	DNA topoisomerase 2-alpha	TOP2A
K	888	Mono	16.51	Tumor suppressor p53-binding protein 1	TP53BP1
R	61	Di	48.04	Transformer-2 protein homolog beta (Fragment)	TRA2B
K	257	Mono	40.34	TRAF3-interacting protein 1	TRAF3IP1
K	252	Di	40.34	TRAF3-interacting protein 1	TRAF3IP1
K	171	Mono	32.06	Trafficking kinesin-binding protein 2	TRAK2
K	109	Di	23	Trafficking protein particle complex subunit 12 (Fragment)	TRAPPC12
R	745	Di	13.07	TLR4 interactor with leucine rich repeats	TRIL
K	178	Di	13.74	Tripartite motif-containing protein 5	TRIM5
X	1	Mono	29.98	Activating signal cointegrator 1 (Fragment)	TRIP4
R	4	Di	13.46	Activating signal cointegrator 1 (Fragment)	TRIP4
X	1	Tri	13.46	Activating signal cointegrator 1 (Fragment)	TRIP4
R	25	Mono	39.57	tRNA (adenine(58)-N(1))-methyltransferase, mitochondrial (Fragment)	TRMT61B
R	107	Di	33.61	TMF-regulated nuclear protein 1	TRNP1
K	657	Di	12.01	Transient receptor potential cation channel subfamily M member 7	TRPM7
K	5	Di	15.08	Tetratricopeptide repeat protein 12 (Fragment)	TTC12
K	2	Tri	15.08	Tetratricopeptide repeat protein 12 (Fragment)	TTC12
K	6	Mono	12.95	Isoform 3 of Tetratricopeptide repeat protein 21A	TTC21A
K	6	Di	13.06	Isoform 3 of Tetratricopeptide repeat protein 21A	TTC21A
R	662	Mono	14.74	Tetratricopeptide repeat protein 6	TTC6
K	664	Di	14.74	Tetratricopeptide repeat protein 6	TTC6
K	688	Di	27.94	Transcription termination factor 1	TTF1
K	170	Tri	30.78	Transcription termination factor 2	TTF2
K	6132	Tri	14.84	Titin	TTN
R	460	Mono	14.79	Tubulin alpha-1C chain	TUBA1C
R	79	Mono	68.16	Tubulin alpha-3C/D chain	TUBA3C
K	112	Mono	28.41	Tubulin alpha-3C/D chain	TUBA3C
R	121	Mono	18.37	Tubulin alpha-3C/D chain	TUBA3C
R	324	Mono	36.65	Tubulin alpha-4A chain	TUBA4A
R	28	Mono	65.66	Tubulin beta chain	TUBB

R	46	Mono	65.66	Tubulin beta chain	TUBB
R	84	Mono	41.62	HCG1983504, isoform CRA_f	TUBB3
R	90	Mono	37.43	HCG1983504, isoform CRA_f	TUBB3
R	318	Mono	49.2	Tubulin beta-4A chain	TUBB4A
X	1	Mono	68.08	Tubulin beta-6 chain (Fragment)	TUBB6
R	390	Mono	35.46	Tubulin beta-6 chain	TUBB6
X	1	Di	68.08	Tubulin beta-6 chain (Fragment)	TUBB6
R	246	Mono	29.19	Tubulin beta-8 chain	TUBB8
R	308	Mono	51.95	Tubulin beta-8 chain	TUBB8
K	330	Mono	35.91	Alpha-taxilin	TXLNA
R	264	Di	15.76	Alpha-taxilin	TXLNA
K	53	Mono	20.24	Thioredoxin-interacting protein	TXNIP
K	39	Mono	28.75	Splicing factor U2AF 35 kDa subunit	U2AF1
K	48	Mono	58.77	Protein UBBP4 (Fragment)	UBBP4
R	54	Mono	34.95	Protein UBBP4 (Fragment)	UBBP4
R	50	Mono	58.77	Protein UBBP4 (Fragment)	UBBP4
K	48	Di	40.06	Protein UBBP4 (Fragment)	UBBP4
R	50	Di	40.06	Protein UBBP4 (Fragment)	UBBP4
K	48	Tri	39.83	Protein UBBP4 (Fragment)	UBBP4
K	101	Mono	15.72	Ubiquitin-conjugating enzyme E2 D1	UBE2D1
K	101	Mono	15.72	Ubiquitin-conjugating enzyme E2 D4	UBE2D4
R	6	Mono	29.51	E3 ubiquitin-protein ligase UBR4	UBR4
R	2	Di	29.51	E3 ubiquitin-protein ligase UBR4	UBR4
R	2394	Mono	15.25	E3 ubiquitin-protein ligase UBR5	UBR5
K	3	Di	13.13	Isoform 5 of UBX domain-containing protein 11	UBXN11
K	61	Di	16.23	UDP-glucuronosyltransferase 1-7 (Fragment)	UGT1A7
K	204	Di	16.23	UDP-glucuronosyltransferase 1-9	UGT1A9
K	471	Mono	14.64	Ubiquitin carboxyl-terminal hydrolase	USP19
R	434	Mono	16.18	Ubiquitin carboxyl-terminal hydrolase 20	USP20
R	435	Mono	16.18	Ubiquitin carboxyl-terminal hydrolase 20	USP20
R	5	Mono	30.3	Ubiquitin carboxyl-terminal hydrolase 36 (Fragment)	USP36
R	949	Di	29.55	USP48 protein	USP48
R	112	Mono	16.35	Ubiquitin carboxyl-terminal hydrolase 8	USP8
K	10	Di	13.13	U3 small nucleolar RNA-associated protein 18 homolog	UTP18
K	85	Mono	30.53	Vesicle-associated membrane protein 1	VAMP1
K	7	Mono	29.57	Vesicle-associated membrane protein 3	VAMP3
K	238	Mono	39.46	Voltage-dependent anion-selective channel protein 2	VDAC2
R	410	Mono	36.83	Vimentin	VIM
R	228	Mono	36.83	Vimentin	VIM
R	42	Di	28.75	Vacuolar protein sorting-associated protein 13A (Fragment)	VPS13A
K	50	Tri	28.75	Vacuolar protein sorting-associated protein 13A (Fragment)	VPS13A
K	328	Tri	19.44	von Willebrand factor A domain-containing protein 5B1	VWA5B1
K	111	Mono	12.13	T1-TrpRS (Fragment)	WARS

K	7	Tri	13.36	WD repeat-containing protein 49 (Fragment)	WDR49
R	7	Mono	29.45	WD repeat-containing protein 52 (Fragment)	WDR52
K	794	Mono	18.46	WD repeat-containing protein 65	WDR65
K	1051	Mono	20.78	WD repeat-containing protein 65	WDR65
R	1044	Di	20.78	WD repeat-containing protein 65	WDR65
K	209	Mono	42.25	X-ray repair cross-complementing protein 5	XRCC5
K	97	Mono	19.44	Protein YIPF1	YIPF1
K	96	Mono	16.8	Protein YIPF1	YIPF1
K	96	Di	19.44	Protein YIPF1	YIPF1
K	97	Di	16.8	Protein YIPF1	YIPF1
K	97	Tri	19.44	Protein YIPF1	YIPF1
R	43	Mono	46.25	14-3-3 protein eta (Fragment)	YWHAH
K	212	Mono	100.4	14-3-3 protein theta	YWHAQ
R	55	Mono	75.91	14-3-3 protein theta (Fragment)	YWHAQ
R	55	Di	46.25	14-3-3 protein theta (Fragment)	YWHAQ
R	629	Mono	53.82	Isoform 2 of Zinc finger B-box domain-containing protein 1	ZBBX
R	4	Di	13.4	Zinc finger and BTB domain-containing protein 49 (Fragment)	ZBTB49
R	291	Di	13.64	DBF4-type zinc finger-containing protein 2	ZDBF2
K	295	Tri	13.64	DBF4-type zinc finger-containing protein 2	ZDBF2
R	249	Mono	31.91	Protein zer-1 homolog	ZER1
R	255	Di	31.91	Protein zer-1 homolog	ZER1
R	7	Mono	30.92	AN1-type zinc finger protein 6 (Fragment)	ZFAND6
R	7	Di	28.08	AN1-type zinc finger protein 6 (Fragment)	ZFAND6
K	9	Di	30.92	AN1-type zinc finger protein 6 (Fragment)	ZFAND6
K	9	Tri	28.08	AN1-type zinc finger protein 6 (Fragment)	ZFAND6
K	1006	Mono	12.36	Zinc finger FYVE domain-containing protein 16	ZFYVE16
R	19	Di	27.41	Zinc finger protein 287 (Fragment)	ZNF287
K	937	Di	15.08	Zinc finger protein 536 (Fragment)	ZNF536
K	934	Tri	15.08	Zinc finger protein 536 (Fragment)	ZNF536
R	1346	Di	16.8	Zinc finger protein 646	ZNF646
K	1342	Tri	16.8	Zinc finger protein 646	ZNF646
R	7	Di	39.18	Zinc finger protein 785 (Fragment)	ZNF785
R	8	Di	39.18	Zinc finger protein 785 (Fragment)	ZNF785
K	210	Mono	13.01	Zinc finger protein 786	ZNF786
R	204	Mono	13.01	Zinc finger protein 786	ZNF786
K	258	Di	20.14	Zinc finger and SCAN domain-containing protein 5A	ZSCAN5A
R	265	Di	20.14	Zinc finger and SCAN domain-containing protein 5A	ZSCAN5A
R	259	Di	20.14	Zinc finger and SCAN domain-containing protein 5A	ZSCAN5A

Appendix 3: List of methylation sites identified by MS/MS in a ProMENADe-enriched and non-enriched samples.

Sites identified at the 1% peptide FDR confidence level for the ProMENADe-enriched and non-enriched samples. The numbers on the right of the table indicate peptide hits for each site in each sample.

K/R	Site	Type	Mascot Score	Protein Name	Gene Name	ProMENADe-enriched	Non-enriched
R	6	Mono	11.57	Probable E3 ubiquitin-protein ligase MARCH10	March10	0	4
R	778	Mono	18.87	Probable E3 ubiquitin-protein ligase MARCH10	March10	28	140
K	143	Di	26.93	Septin-1 (Fragment)	Sept1	0	13
K	322	Mono	16.86	Septin-4	Sept4	0	2
K	209	Mono	26.93	Septin 10, isoform CRA_c	Sept10	0	13
K	113	Mono	14.74	Acyl-CoA synthetase family member 4	AASDH	0	2
K	114	Mono	14.74	Acyl-CoA synthetase family member 4	AASDH	0	2
K	113	Di	14.74	Acyl-CoA synthetase family member 4	AASDH	0	2
K	114	Di	14.74	Acyl-CoA synthetase family member 4	AASDH	0	2
K	114	Tri	14.74	Acyl-CoA synthetase family member 4	AASDH	0	2
K	113	Tri	14.74	Acyl-CoA synthetase family member 4	AASDH	0	2
R	443	Mono	31.03	ATP-binding cassette sub-family A member 1	ABCA1	0	1
R	690	Di	12.01	ATP-binding cassette sub-family A member 6	ABCA6	0	6
R	314	Di	14.98	Abhydrolase domain-containing protein 16A	ABHD16A	0	5
R	6	Di	16.83	Target of Nesh-SH3 (Fragment)	ABI3BP	0	2
R	71	Mono	33.23	Active breakpoint cluster region-related protein	ABR	0	2
K	78	Di	33.23	Active breakpoint cluster region-related protein	ABR	0	2
R	21	Di	18.63	Isobutyryl-CoA dehydrogenase, mitochondrial	ACAD8	0	3
K	6	Mono	19.38	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2 (Fragment)	ACAP2	0	2
R	7	Mono	13.33	Angiotensin-converting enzyme	ACE	0	1
K	16	Mono	12.49	Isoform 2 of 2-amino-3-carboxymuconate-6-semialdehyde decarboxylase	ACMSD	0	1
K	95	Mono	13.92	Acyl-coenzyme A thioesterase 1	ACOT1	17	67
R	96	Mono	13.92	Acyl-coenzyme A thioesterase 1	ACOT1	17	67
K	95	Di	13.92	Acyl-coenzyme A thioesterase 1	ACOT1	17	67
R	96	Di	13.92	Acyl-coenzyme A thioesterase 1	ACOT1	17	67
K	217	Di	16.2	Acyl-coenzyme A thioesterase 11	ACOT11	0	5
R	6	Mono	16.22	Cytosolic acyl coenzyme A thioester hydrolase	ACOT7	1	0
X	1	Di	12.46	Long-chain-fatty-acid--CoA ligase 1 (Fragment)	ACSL1	0	1
K	129	Mono	29.23	Actin, alpha skeletal muscle	ACTA1	1	0
K	293	Di	38.79	Actin, aortic smooth muscle	ACTA2	4	1
K	292	Mono	38.03	Beta-actin-like protein 2	ACTBL2	0	4
R	204	Mono	36.22	Actin-like protein 6B	ACTL6B	0	1
R	331	Mono	13.29	Actin-like protein 9	ACTL9	3	0
R	740	Mono	46.81	Alpha-actinin-3	ACTN3	1	8

R	752	Mono	32.18	Alpha-actinin-3	ACTN3	1	11
R	105	Mono	13.78	Adenosine deaminase-like protein	ADAL	0	4
R	109	Mono	13.78	Adenosine deaminase-like protein	ADAL	0	4
R	39	Mono	13.05	Disintegrin and metalloproteinase domain-containing protein 10 (Fragment)	ADAM10	0	1
R	278	Mono	14.36	A disintegrin and metalloproteinase with thrombospondin motifs 10	ADAMTS10	2	0
K	326	Mono	14.3	A disintegrin and metalloproteinase with thrombospondin motifs 5	ADAMTS5	0	9
K	324	Mono	14.3	A disintegrin and metalloproteinase with thrombospondin motifs 5	ADAMTS5	0	9
K	326	Di	14.3	A disintegrin and metalloproteinase with thrombospondin motifs 5	ADAMTS5	0	9
K	324	Di	14.3	A disintegrin and metalloproteinase with thrombospondin motifs 5	ADAMTS5	0	9
K	809	Di	19.71	Adenylate cyclase type 2	ADCY2	0	1
K	237	Di	12.35	Androglobin	ADGB	0	4
K	161	Tri	36.74	Adenylosuccinate lyase	ADSL	0	8
R	8	Di	13.62	Adipocyte enhancer-binding protein 1 (Fragment)	AEBP1	0	4
K	6	Di	17.82	Amino-terminal enhancer of split (Fragment)	AES	0	4
K	694	Mono	22.37	Actin filament-associated protein 1-like 1	AFAP1L1	0	6
R	696	Mono	22.37	Actin filament-associated protein 1-like 1	AFAP1L1	0	6
K	694	Di	22.37	Actin filament-associated protein 1-like 1	AFAP1L1	0	6
R	696	Di	22.37	Actin filament-associated protein 1-like 1	AFAP1L1	0	6
R	661	Mono	33.95	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 2	AGAP2	4	0
K	660	Mono	33.95	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 2	AGAP2	4	0
K	84	Di	16.12	Angiogenic factor with G patch and FHA domains 1 (Fragment)	AGGF1	0	1
K	3346	Mono	13.55	Neuroblast differentiation-associated protein AHNAK	AHNAK	0	3
K	3348	Mono	13.55	Neuroblast differentiation-associated protein AHNAK	AHNAK	0	3
R	288	Mono	14.96	Aryl hydrocarbon receptor repressor	AHRR	0	1
K	290	Di	14.73	Apoptosis-inducing factor 3	AIFM3	1	0
K	286	Mono	13.19	Protein AK9	AK9	0	4
R	284	Mono	13.19	Protein AK9	AK9	0	4
R	284	Di	13.19	Protein AK9	AK9	0	4
K	286	Di	13.19	Protein AK9	AK9	0	4
K	560	Di	31.86	A-kinase anchor protein 11	AKAP11	0	1
R	368	Mono	30.04	A-kinase anchor protein 17A	AKAP17A	0	2
R	449	Mono	13.28	A-kinase anchor protein 4	AKAP4	0	4
K	447	Mono	13.07	A-kinase anchor protein 4	AKAP4	0	4
R	70	Mono	39.59	Aldo-keto reductase family 1 member B10	AKR1B10	1	0
X	1	Tri	12.84	5-aminolevulinate synthase, erythroid-specific, mitochondrial (Fragment)	ALAS2	0	1
K	443	Mono	51.11	Serum albumin	ALB	6	1
K	362	Tri	11.83	Retinal dehydrogenase 1	ALDH1A1	0	6
R	117	Di	12.36	Fatty aldehyde dehydrogenase (Fragment)	ALDH3A2	0	21
X	1	Di	16.85	Dol-P-Man:Man(7)GlcNAc(2)-PP-Dol alpha-1,6-mannosyltransferase (Fragment)	ALG12	0	1
R	43	Mono	12.96	UDP-N-acetylglucosamine transferase subunit ALG13 homolog (Fragment)	ALG13	0	1
K	264	Mono	29.3	ALK tyrosine kinase receptor	ALK	0	5
K	130	Mono	28.53	Alpha-ketoglutarate-dependent dioxygenase alkB homolog 6	ALKBH6	0	4
R	61	Di	36.62	Alpha-ketoglutarate-dependent dioxygenase alkB homolog 7	ALKBH7	0	1

K	4024	Tri	13.64	Alstrom syndrome protein 1	ALMS1	0	16
K	132	Tri	42.25	Alpha-protein kinase 1	ALPK1	0	2
K	955	Mono	12.12	Isoform 4 of Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 11 protein	ALS2CR11	0	8
K	951	Mono	12.76	Isoform 4 of Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 11 protein	ALS2CR11	0	8
R	211	Di	53.18	THO complex subunit 4	ALYREF	3	0
R	45	Di	66.19	THO complex subunit 4	ALYREF	5	0
K	82	Tri	35.43	AMP deaminase 3	AMPD3	0	4
K	339	Tri	15.58	Angiopoietin-related protein 3	ANGPTL3	0	2
K	1329	Mono	30.52	Ankyrin-2 (Fragment)	ANK2	0	1
K	931	Di	16.15	Ankyrin repeat and FYVE domain-containing protein 1	ANKFY1	0	1
K	1849	Mono	15.25	Ankyrin repeat domain-containing protein 12	ANKRD12	0	1
K	623	Mono	14.2	Ankyrin repeat domain-containing protein 18B	ANKRD18B	0	1
K	621	Mono	14.2	Ankyrin repeat domain-containing protein 18B	ANKRD18B	0	1
K	318	Tri	13.14	Ankyrin repeat domain-containing protein 18B	ANKRD18B	0	1
K	200	Di	15.93	Anoctamin	ANO1	0	5
K	203	Di	15.93	Anoctamin	ANO1	0	5
R	527	Di	17.41	Anoctamin	ANO2	0	4
K	525	Tri	17.41	Anoctamin	ANO2	0	4
K	180	Mono	19.63	Anoctamin-5	ANO5	0	2
R	63	Mono	45.86	Putative annexin A2-like protein	ANXA2P2	4	6
K	457	Mono	71.26	AP-2 complex subunit beta	AP2B1	3	0
K	93	Mono	41.58	AP-2 complex subunit beta	AP2B1	1	0
R	76	Di	13.3	AP-2 complex subunit sigma	AP2S1	0	4
K	55	Mono	13.84	Apolipoprotein C-IV	APOC4	0	4
R	153	Mono	17.18	Apolipoprotein O	APOO	0	4
R	258	Mono	12.18	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 3	ARAP3	0	1
R	122	Mono	20.23	ADP-ribosylation factor 4	ARF4	0	6
K	639	Tri	12.09	Rho GTPase-activating protein 11A	ARHGAP11A	0	7
K	152	Mono	11.92	Rho GTPase-activating protein 12 (Fragment)	ARHGAP12	0	1
K	151	Di	11.92	Rho GTPase-activating protein 12 (Fragment)	ARHGAP12	0	1
K	152	Tri	11.92	Rho GTPase-activating protein 12 (Fragment)	ARHGAP12	0	1
R	364	Mono	20.66	Rho GTPase activating protein 22, isoform CRA_a	ARHGAP22	0	10
K	170	Tri	16.78	Rho GTPase-activating protein 29	ARHGAP29	0	1
R	157	Di	30.07	Rho GTPase-activating protein 40 (Fragment)	ARHGAP40	0	1
R	21	Di	15.35	Rho GTPase-activating protein 40 (Fragment)	ARHGAP40	0	1
R	826	Mono	13.39	Rho GTPase-activating protein 5	ARHGAP5	0	6
R	827	Mono	13.39	Rho GTPase-activating protein 5	ARHGAP5	0	6
R	827	Di	13.39	Rho GTPase-activating protein 5	ARHGAP5	0	6
R	826	Di	13.39	Rho GTPase-activating protein 5	ARHGAP5	0	6
K	455	Di	14.73	Rho guanine nucleotide exchange factor 4	ARHGEF4	0	2
K	368	Di	16.88	Armadillo repeat-containing X-linked protein 1	ARMCX1	0	2
K	223	Tri	21.35	Isoform BMAL1C of Aryl hydrocarbon receptor nuclear translocator-like protein 1	ARNTL	0	1
K	161	Mono	26.01	Aryl hydrocarbon receptor nuclear translocator-like protein 2 (Fragment)	ARNTL2	0	2

K	89	Mono	14.74	Neutral ceramidase soluble form	ASAH2	0	1
R	174	Mono	22.28	Neutral ceramidase	ASAH2	0	4
R	251	Mono	12.4	Asparagine synthetase [glutamine-hydrolyzing]	ASNS	0	4
R	768	Di	27.74	Abnormal spindle-like microcephaly-associated protein	ASPM	0	1
R	296	Di	29.98	ATPase family AAA domain-containing protein 3A (Fragment)	ATAD3A	0	2
K	406	Mono	23.77	Atlastin-1	ATL1	0	21
R	151	Mono	14.19	Atlastin-2	ATL2	1	0
K	143	Mono	14.19	Atlastin-2	ATL2	1	0
R	5	Mono	26.16	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2	3	7
K	7	Mono	26.16	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2	3	7
X	1	Mono	26.16	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2	3	7
K	7	Di	26.16	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2	3	7
R	5	Di	26.16	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2	3	7
K	7	Tri	26.16	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2	3	7
K	89	Mono	35.51	Sodium/potassium-transporting ATPase subunit alpha-2	ATP1A2	0	6
R	235	Mono	46.09	Sodium/potassium-transporting ATPase subunit alpha-4	ATP1A4	0	3
K	667	Tri	13.2	Sodium/potassium-transporting ATPase subunit alpha-4	ATP1A4	0	1
R	81	Di	15.07	Plasma membrane calcium-transporting ATPase 1	ATP2B1	1	10
K	79	Tri	22.52	ATP synthase subunit d, mitochondrial	ATP5H	0	2
K	245	Tri	21.25	V-type proton ATPase 116 kDa subunit a isoform 1	ATP6V0A1	0	1
K	158	Mono	23.83	Probable phospholipid-transporting ATPase IA	ATP8A1	0	1
K	96	Tri	12.01	ATR-interacting protein	ATRIP	0	2
K	2	Mono	20.7	Ataxin-1-like	ATXN1L	0	6
R	7	Di	20.7	Ataxin-1-like	ATXN1L	0	6
R	8	Di	35.76	Advillin	AVIL	3	0
K	335	Tri	12.84	Beta-1,4-galactosyltransferase 2	B4GALT2	0	6
K	303	Mono	18.53	Beta-1,4-galactosyltransferase 6	B4GALT6	0	2
X	1	Di	15.12	Large proline-rich protein BAG6 (Fragment)	BAG6	1	0
R	28	Mono	19.11	Bardet-Biedl syndrome 7 protein	BBS7	0	6
R	601	Di	18.52	Breast cancer anti-estrogen resistance protein 3	BCAR3	0	9
K	116	Di	29.3	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	0	5
R	448	Mono	15.37	Breakpoint cluster region protein	BCR	0	1
R	447	Mono	15.37	Breakpoint cluster region protein	BCR	0	1
K	795	Tri	12.35	Breakpoint cluster region protein	BCR	0	4
K	43	Mono	18.28	Bridging integrator 3	BIN3	0	1
K	769	Mono	17.8	Bloom syndrome protein	BLM	0	4
K	1389	Mono	14.59	Biorientation of chromosomes in cell division protein 1-like 1	BOD1L1	0	1
K	121	Mono	14.38	Bactericidal permeability-increasing protein	BPI	0	3
K	123	Mono	14.38	Bactericidal permeability-increasing protein	BPI	0	3
K	247	Di	12.36	BRCA1-associated protein	BRAP	0	2
R	989	Di	16.61	Bromodomain-containing protein 1	BRD1	0	1
R	339	Mono	12.99	Ribosome biogenesis protein BRX1 homolog	BRIX1	0	1
K	338	Mono	12.99	Ribosome biogenesis protein BRX1 homolog	BRIX1	0	1

R	341	Mono	12.99	Ribosome biogenesis protein BRX1 homolog	BRIX1	0	1
K	6	Mono	19.18	Serine/threonine-protein kinase BRSK1 (Fragment)	BRSK1	0	4
R	302	Mono	31.99	Bromodomain and WD repeat-containing protein 1 (Fragment)	BRWD1	0	1
R	100	Di	36.14	Bromodomain and WD repeat-containing protein 1 (Fragment)	BRWD1	2	0
R	2230	Di	19.76	Isoform B of Bromodomain and WD repeat-containing protein 1	BRWD1	6	26
R	331	Mono	13.14	Butyrophilin subfamily 1 member A1	BTN1A1	0	1
K	333	Di	13.14	Butyrophilin subfamily 1 member A1	BTN1A1	0	1
K	586	Mono	19.58	Uncharacterized protein C11orf35	C11orf35	0	2
R	14	Di	103.94	Isoform 2 of UPF0696 protein C11orf68	C11orf68	9	0
K	115	Di	13.66	UPF0235 protein C15orf40 (Fragment)	C15orf40	0	1
K	116	Di	13.66	UPF0235 protein C15orf40 (Fragment)	C15orf40	0	1
K	116	Tri	13.66	UPF0235 protein C15orf40 (Fragment)	C15orf40	0	1
K	115	Tri	13.66	UPF0235 protein C15orf40 (Fragment)	C15orf40	0	1
R	237	Mono	14.95	HCG40828, isoform CRA_a	C15orf60	0	4
K	334	Tri	12.89	UPF0183 protein C16orf70	C16orf70	0	2
R	124	Mono	18.55	Putative uncharacterized protein C16Orf98	C16orf98	0	2
R	269	Mono	16.21	Uncharacterized protein C17orf59	C17orf59	0	1
K	30	Mono	29.08	Uncharacterized protein C18orf63	C18orf63	0	1
K	207	Tri	12.49	Uncharacterized protein C18orf63	C18orf63	1	0
R	65	Mono	15.36	Protein C19orf12	C19orf12	0	18
R	117	Di	32.51	Uncharacterized protein C19orf52	C19orf52	0	2
R	46	Mono	19.53	UPF0692 protein C19orf54 (Fragment)	C19orf54	0	20
K	6	Mono	13.31	UPF0515 protein C19orf66 (Fragment)	C19orf66	0	1
R	6	Mono	13.22	Betatrophin (Fragment)	C19orf80	0	1
K	4	Di	18.17	Uncharacterized protein C1orf198 (Fragment)	C1orf198	3	6
R	6	Mono	20.6	UPF0732 protein C1orf227	C1orf227	0	3
K	549	Mono	14.52	Uncharacterized protein C1orf94	C1orf94	0	9
K	7	Mono	23.83	Uncharacterized protein C21orf59	C21orf59	0	1
R	291	Mono	13.42	tRNA-splicing ligase RtcB homolog	C22orf28	0	1
R	291	Di	19.97	tRNA-splicing ligase RtcB homolog	C22orf28	0	9
K	77	Di	12.44	Uncharacterized protein C22orf42	C22orf42	2	10
K	74	Di	12.44	Uncharacterized protein C22orf42	C22orf42	2	10
K	77	Tri	12.44	Uncharacterized protein C22orf42	C22orf42	2	10
K	74	Tri	12.44	Uncharacterized protein C22orf42	C22orf42	2	10
K	406	Di	15.25	C2 domain-containing protein 2	C2CD2	0	1
R	537	Mono	17.88	C2 domain-containing protein 3	C2CD3	0	3
R	2	Mono	17.99	UPF0561 protein C2orf68 (Fragment)	C2orf68	37	36
X	1	Mono	17.99	UPF0561 protein C2orf68 (Fragment)	C2orf68	37	36
X	1	Tri	16.76	UPF0561 protein C2orf68 (Fragment)	C2orf68	37	36
K	72	Tri	13.62	UPF0538 protein C2orf76	C2orf76	0	1
R	247	Di	15.81	Putative uncharacterized protein C3orf49	C3orf49	9	12
K	50	Di	19.58	Uncharacterized protein C6orf118	C6orf118	0	2
R	420	Di	18.44	Isoform 2 of Uncharacterized protein C9orf117	C9orf117	0	11

K	308	Di	12.09	Uncharacterized protein C9orf43	C9orf43	0	7
R	140	Di	16.78	Carbonic anhydrase-related protein 11	CA11	0	12
R	3	Mono	15.66	Calcium-binding protein 39-like	CAB39L	0	5
R	7	Di	15.66	Calcium-binding protein 39-like	CAB39L	0	5
K	356	Di	22.42	Calcineurin-binding protein cabin-1 (Fragment)	CABIN1	0	3
K	793	Mono	17.45	Voltage-dependent T-type calcium channel subunit alpha-1H	CACNA1H	0	1
R	1278	Mono	14.28	Voltage-dependent T-type calcium channel subunit alpha-1I	CACNA1I	0	9
R	26	Mono	18.77	Cactin	CACTIN	0	1
R	19	Di	18.77	Cactin	CACTIN	0	1
K	163	Mono	30.22	Calmodulin	CALM2	2	0
R	174	Mono	30.22	Calmodulin	CALM2	2	0
R	174	Di	30.22	Calmodulin	CALM2	2	0
K	163	Di	30.22	Calmodulin	CALM2	2	0
K	163	Tri	55.95	Calmodulin	CALM2	3	4
R	7	Mono	12.67	Calreticulin (Fragment)	CALR	0	1
X	1	Tri	12.67	Calreticulin (Fragment)	CALR	0	1
X	1	Tri	11.76	Calmodulin-binding transcription activator 1 (Fragment)	CAMTA1	0	1
R	1065	Mono	29.41	Cullin-associated NEDD8-dissociated protein 2	CAND2	0	1
R	15	Mono	19.58	Cullin-associated NEDD8-dissociated protein 2 (Fragment)	CAND2	1	6
R	1064	Mono	29.41	Cullin-associated NEDD8-dissociated protein 2	CAND2	0	1
K	157	Di	20.77	Calpain-12 (Fragment)	CAPN12	1	0
K	671	Di	17.05	Caspase recruitment domain-containing protein 14	CARD14	0	1
R	461	Mono	17.44	Carnosine synthase 1	CARNS1	0	4
K	607	Mono	17.08	Caskin-1	CASKIN1	0	1
K	66	Mono	20.54	Caspase-8 subunit p10 (Fragment)	CASP8	0	7
R	4	Di	22.27	Caspase-9 subunit p35 (Fragment)	CASP9	0	3
R	240	Mono	13.84	Protein CBFA2T2	CBFA2T2	0	15
R	235	Mono	13.84	Protein CBFA2T2	CBFA2T2	0	15
R	241	Mono	13.84	Protein CBFA2T2	CBFA2T2	0	15
K	143	Mono	43.78	Chromobox protein homolog 3	CBX3	1	0
K	304	Mono	26.16	Coiled-coil domain-containing protein 146	CCDC146	3	7
R	306	Mono	26.16	Coiled-coil domain-containing protein 146	CCDC146	3	7
R	306	Di	26.16	Coiled-coil domain-containing protein 146	CCDC146	3	7
K	304	Di	26.16	Coiled-coil domain-containing protein 146	CCDC146	3	7
R	99	Di	16.32	Coiled-coil domain-containing protein 171	CCDC171	0	2
R	570	Mono	15.59	Coiled-coil domain-containing protein 180	CCDC180	0	14
K	117	Tri	18.81	CCDC19 protein	CCDC19	0	2
R	361	Mono	15.59	Coiled-coil domain-containing protein 30	CCDC30	0	14
R	361	Di	11.83	Coiled-coil domain-containing protein 30	CCDC30	0	6
K	918	Tri	15.1	Coiled-coil domain-containing protein 40	CCDC40	0	13
R	23	Mono	12.02	Coiled-coil domain-containing protein 51 (Fragment)	CCDC51	1	11
K	89	Mono	12.01	Coiled-coil domain-containing protein 63	CCDC63	0	1
R	150	Mono	13.26	Coiled-coil domain-containing protein 68 (Fragment)	CCDC68	0	5

R	611	Mono	19.11	Coiled-coil domain-containing protein 73	CCDC73	0	6
K	728	Mono	12.04	Coiled-coil domain-containing protein 73	CCDC73	0	1
K	204	Di	12.85	Coiled-coil domain-containing protein 73	CCDC73	0	1
R	1058	Mono	37.64	Coiled-coil domain-containing protein 88B	CCDC88B	0	1
R	1325	Mono	12.46	Coiled-coil domain-containing protein 88B	CCDC88B	0	1
R	1322	Di	12.46	Coiled-coil domain-containing protein 88B	CCDC88B	0	1
R	334	Mono	14.67	Protein Daple	CCDC88C	0	3
X	1	Mono	30.02	Coiled-coil domain-containing protein 91 (Fragment)	CCDC91	0	3
R	469	Mono	15.27	Coiled-coil alpha-helical rod protein 1	CCHCR1	0	3
R	88	Mono	12.31	C-C motif chemokine 19	CCL19	0	7
R	85	Mono	12.31	C-C motif chemokine 19	CCL19	0	7
K	67	Mono	15.09	Cyclin-I	CCNI	0	3
K	170	Mono	31.05	C-C chemokine receptor type 7	CCR7	0	1
R	325	Mono	14.45	C-C chemokine receptor type 11	CCRL1	2	1
R	57	Mono	18.72	T-complex protein 1 subunit beta	CCT2	0	1
K	9	Mono	36.55	T-complex protein 1 subunit delta	CCT4	0	1
R	148	Mono	29.95	Natural killer cell receptor 2B4	CD244	0	14
R	150	Di	29.95	Natural killer cell receptor 2B4	CD244	0	14
R	6	Mono	13.22	Leukocyte antigen CD37 (Fragment)	CD37	0	1
K	76	Tri	13.99	Cell division cycle 5-like protein	CDC5L	0	1
K	1929	Mono	21.7	Cadherin-23	CDH23	0	7
K	44	Di	24.53	Cadherin-3	CDH3	0	2
K	155	Mono	19.01	Cyclin-dependent kinase 18 (Fragment)	CDK18	0	1
R	156	Mono	13.05	Cyclin-dependent kinase 5	CDK5	0	13
K	233	Mono	13.23	CDK5 regulatory subunit-associated protein 2	CDK5RAP2	0	1
R	6	Mono	22.99	Cyclin-dependent kinase-like 1 (Fragment)	CDKL1	0	11
R	23	Mono	14.71	Cyclin-dependent kinase-like 1	CDKL1	0	22
X	1	Mono	22.99	Cyclin-dependent kinase-like 1 (Fragment)	CDKL1	0	11
R	923	Di	24.52	Cyclin-dependent kinase-like 5	CDKL5	0	2
R	7	Di	14.67	Serine/threonine-protein kinase Chk2	CDS1	0	3
R	5	Di	13.01	Serine/threonine-protein kinase Chk2	CDS1	0	3
R	16	Mono	12.56	Chromodomain Y-like protein 2	CDYL2	0	1
K	15	Mono	12.56	Chromodomain Y-like protein 2	CDYL2	0	1
K	2406	Tri	13.17	Centromere-associated protein E	CENPE	0	1
K	2409	Tri	13.17	Centromere-associated protein E	CENPE	0	1
K	703	Mono	21	Centrosomal protein of 112 kDa	CEP112	1	2
K	853	Tri	17.25	Centrosomal protein of 164 kDa	CEP164	0	1
R	886	Di	15.85	Centrosomal protein of 290 kDa	CEP290	0	1
R	332	Di	12.15	Centrosome-associated protein 350 (Fragment)	CEP350	1	0
K	4	Mono	15.25	Centrosomal protein of 63 kDa (Fragment)	CEP63	0	1
R	314	Mono	20.17	Centrosomal protein of 78 kDa	CEP78	0	5
K	549	Mono	26.77	Centrosomal protein of 89 kDa	CEP89	0	8
K	516	Mono	13.52	Centrosomal protein of 95 kDa	CEP95	7	13

R	308	Di	13.87	Centrosomal protein of 95 kDa	CEP95	0	1
R	289	Mono	11.82	Ceramide kinase-like protein	CERKL	0	1
K	414	Mono	11.64	Carboxylesterase 4A	CES4A	1	0
R	843	Mono	30.95	Cingulin	CGN	0	6
R	847	Di	30.95	Cingulin	CGN	0	6
R	95	Mono	16.2	Coiled-coil-helix-coiled-coil-helix domain-containing protein 6, mitochondrial (Fragment)	CHCHD6	0	1
R	894	Mono	20.78	Chromodomain-helicase-DNA-binding protein 5 (Fragment)	CHD5	0	3
K	43	Tri	17.61	Serine/threonine-protein kinase Chk1 (Fragment)	CHEK1	0	1
K	197	Mono	33.92	Serine/threonine-protein kinase Chk2 (Fragment)	CHEK2	0	1
K	11	Mono	13.2	Charged multivesicular body protein 1a	CHMP1A	0	1
R	585	Di	30.27	Chondroitin sulfate synthase 2	CHPF	0	1
K	436	Mono	29.37	Muscarinic acetylcholine receptor M5	CHRM5	2	0
R	438	Mono	29.37	Muscarinic acetylcholine receptor M5	CHRM5	2	0
K	436	Di	29.37	Muscarinic acetylcholine receptor M5	CHRM5	2	0
R	438	Di	29.37	Muscarinic acetylcholine receptor M5	CHRM5	2	0
R	307	Di	26.45	Carbohydrate sulfotransferase 1	CHST1	0	3
K	311	Tri	26.45	Carbohydrate sulfotransferase 1	CHST1	0	3
R	177	Mono	29.26	Carbohydrate sulfotransferase 5	CHST5	0	1
K	172	Di	29.26	Carbohydrate sulfotransferase 5	CHST5	0	1
R	440	Mono	16.21	Carbohydrate sulfotransferase 7	CHST7	0	1
R	528	Mono	11.85	Chromosome transmission fidelity protein 18 homolog	CHTF18	0	1
R	532	Mono	11.85	Chromosome transmission fidelity protein 18 homolog	CHTF18	0	1
R	20	Di	34.48	Cirhin (Fragment)	CIRH1A	1	0
R	696	Di	13.15	Isoform 4 of Citron Rho-interacting kinase	CIT	0	3
K	594	Di	20.41	Cytoskeleton-associated protein 2	CKAP2	0	4
K	51	Di	12.31	Creatine kinase B-type (Fragment)	CKB	0	2
K	3	Mono	43.6	Clathrin heavy chain 1 (Fragment)	CLTC	1	0
K	3	Tri	43.6	Clathrin heavy chain 1 (Fragment)	CLTC	1	0
K	50	Di	16.81	Putative cytidine monophosphate-N-acetylneuraminic acid hydroxylase-like protein	CMAHP	0	1
R	235	Di	13.5	Carboxymethylenebutenolidase homolog	CMBL	0	5
X	1	Di	18.84	Protein CMSS1 (Fragment)	CMSS1	0	1
R	32	Mono	18.76	Connector enhancer of kinase suppressor of ras 3	CNKSR3	0	4
K	5	Mono	14.74	Calponin-1 (Fragment)	CNN1	0	1
R	2311	Di	19.4	CCR4-NOT transcription complex subunit 1	CNOT1	0	2
K	12	Di	16.82	CCR4-NOT transcription complex subunit 11 (Fragment)	CNOT11	0	1
R	874	Mono	17.8	Contactin-6	CNTN6	0	4
R	871	Mono	17.8	Contactin-6	CNTN6	0	4
K	211	Di	28	Centriolin (Fragment)	CNTRL	0	1
K	320	Tri	12.13	Collagen alpha-1(XXIII) chain	COL23A1	0	5
R	1496	Di	13.02	Collagen alpha-6(VI) chain	COL6A6	0	3
K	82	Di	15.6	Procollagen galactosyltransferase 2	COLGALT2	0	6
R	149	Mono	29.02	COMM domain-containing protein 9	COMMD9	0	1
R	144	Di	29.02	COMM domain-containing protein 9	COMMD9	0	1

K	175	Mono	29.54	Coatomer subunit gamma-2	COPG2	0	1
K	266	Mono	14.1	Coenzyme Q6 homolog, monooxygenase (Yeast), isoform CRA_a	COQ6	0	2
R	268	Mono	14.1	Coenzyme Q6 homolog, monooxygenase (Yeast), isoform CRA_a	COQ6	0	2
R	222	Di	12.7	Cytochrome c oxidase assembly protein COX15 homolog	COX15	0	16
K	113	Mono	25.8	Cytochrome c oxidase subunit 5A, mitochondrial	COX5A	0	5
K	32	Mono	25.8	Cytochrome c oxidase subunit 5A, mitochondrial	COX5A	0	5
R	4	Mono	12.31	Cytochrome c oxidase subunit 5B, mitochondrial	COX5B	0	1
R	352	Mono	14.38	Carboxypeptidase B2	CPB2	0	3
K	349	Mono	14.38	Carboxypeptidase B2	CPB2	0	3
K	221	Mono	13.99	CPNE5 protein	CPNE5	0	1
R	598	Mono	17.25	Carnitine O-palmitoyltransferase 1, liver isoform	CPT1A	0	2
X	1	Mono	20.29	Cellular retinoic acid-binding protein 1 (Fragment)	CRABP1	0	1
K	2	Mono	11.99	Cysteine-rich secretory protein LCCL domain-containing 1 (Fragment)	CRISPLD1	0	6
R	617	Mono	27.16	Rootletin (Fragment)	CROCC	9	25
R	355	Di	32.35	Cartilage acidic protein 1 (Fragment)	CRTAC1	0	5
R	68	Di	11.8	Tyrosine-protein kinase CSK (Fragment)	CSK	0	6
K	76	Tri	11.8	Tyrosine-protein kinase CSK (Fragment)	CSK	0	6
K	28	Tri	13.38	CUB and sushi domain-containing protein 1	CSMD1	0	1
X	1	Di	16.69	Casein kinase I isoform epsilon (Fragment)	CSNK1E	0	1
R	6	Di	14.43	Cystatin-9	CST9	0	1
R	495	Di	41.48	Cleavage stimulation factor subunit 2	CSTF2	0	1
R	224	Mono	22.73	CTP synthase 1	CTPS1	0	4
K	163	Mono	15.15	Chymotrypsin B2 chain A (Fragment)	CTRB2	0	3
R	47	Di	13.05	Isoform 2 of Cullin-7	CUL7	0	1
K	243	Mono	18.68	Pre-mRNA-splicing factor CWC22 homolog	CWC22	14	60
R	51	Mono	24.17	UPF0428 protein CXorf56	CXorf56	0	5
R	98	Mono	18.57	1,25-dihydroxyvitamin D(3) 24-hydroxylase, mitochondrial	CYP24A1	0	8
K	100	Mono	18.57	1,25-dihydroxyvitamin D(3) 24-hydroxylase, mitochondrial	CYP24A1	0	8
K	100	Di	18.57	1,25-dihydroxyvitamin D(3) 24-hydroxylase, mitochondrial	CYP24A1	0	8
R	98	Di	18.57	1,25-dihydroxyvitamin D(3) 24-hydroxylase, mitochondrial	CYP24A1	0	8
K	100	Tri	18.57	1,25-dihydroxyvitamin D(3) 24-hydroxylase, mitochondrial	CYP24A1	0	8
R	85	Mono	29.39	Cytochrome P450 2A7	CYP2A7	0	1
R	181	Mono	29.63	Cytochrome P450 2U1	CYP2U1	0	1
R	68	Mono	14.27	25-hydroxycholesterol 7-alpha-hydroxylase	CYP7B1	0	6
K	71	Mono	14.27	25-hydroxycholesterol 7-alpha-hydroxylase	CYP7B1	0	6
K	678	Tri	23.16	Sn1-specific diacylglycerol lipase alpha	DAGLA	0	1
R	61	Mono	14.34	Aspartyl aminopeptidase	DAP	1	1
R	62	Mono	14.34	Aspartyl aminopeptidase	DAP	1	1
R	61	Di	14.34	Aspartyl aminopeptidase	DAP	1	1
R	62	Di	14.34	Aspartyl aminopeptidase	DAP	1	1
K	57	Mono	22.35	DAZ-associated protein 1 (Fragment)	DAZAP1	1	3
K	98	Tri	26.93	Decorin	DCN	0	5
R	428	Mono	55.12	Probable ATP-dependent RNA helicase DDX17	DDX17	2	26

K	199	Mono	15.98	ATP-dependent RNA helicase DDX39A	DDX39	8	6
R	134	Di	30.33	Spliceosome RNA helicase DDX39B	DDX39B	0	2
R	282	Di	12.88	Probable ATP-dependent RNA helicase DDX60	DDX60	0	4
K	275	Mono	37.86	Probable ATP-dependent RNA helicase DDX60-like (Fragment)	DDX60L	0	1
R	273	Mono	37.86	Probable ATP-dependent RNA helicase DDX60-like (Fragment)	DDX60L	0	1
R	11	Di	27.78	Peroxisomal 2,4-dienoyl-CoA reductase (Fragment)	DECR2	0	1
R	5	Di	31.15	DENN domain-containing protein 5A (Fragment)	DENND5A	0	1
K	788	Mono	24.56	DEP domain-containing protein 5	DEPDC5	13	22
K	790	Mono	24.56	DEP domain-containing protein 5	DEPDC5	13	22
K	790	Di	24.56	DEP domain-containing protein 5	DEPDC5	13	22
K	788	Di	24.56	DEP domain-containing protein 5	DEPDC5	13	22
K	790	Tri	24.56	DEP domain-containing protein 5	DEPDC5	13	22
K	788	Tri	24.56	DEP domain-containing protein 5	DEPDC5	13	22
K	5	Mono	12.1	DNA fragmentation factor subunit beta (Fragment)	DFFB	0	1
K	4	Mono	12.1	DNA fragmentation factor subunit beta (Fragment)	DFFB	0	1
K	116	Di	16.11	Microprocessor complex subunit DGCR8 (Fragment)	DGCR8	0	4
K	88	Di	15.13	7-dehydrocholesterol reductase (Fragment)	DHCR7	0	1
R	5	Mono	14.08	Deoxyhypusine synthase (Fragment)	DHPS	0	4
R	251	Mono	19.53	Dehydrogenase/reductase SDR family member 12	DHRS12	0	20
R	452	Mono	12.89	Putative ATP-dependent RNA helicase DHX30	DHX30	2	0
R	455	Mono	12.89	Putative ATP-dependent RNA helicase DHX30	DHX30	2	0
R	4	Di	14.43	Probable ATP-dependent RNA helicase DHX40 (Fragment)	DHX40	0	1
R	56	Di	15.55	Probable ATP-dependent RNA helicase DHX58 (Fragment)	DHX58	4	36
K	1158	Di	13.14	Diaphanous homolog 1 (Drosophila), isoform CRA_a	DIAPH1	0	1
K	433	Mono	29.96	Death-inducer obliterator 1	DIDO1	0	3
K	41	Di	21.98	Disco-interacting protein 2 homolog B (Fragment)	DIP2B	0	4
R	634	Mono	21.44	Disrupted in schizophrenia 1 protein	DISC1	0	1
R	693	Di	16.78	Protein dispatched homolog 2	DISP2	0	12
K	258	Mono	19.01	Deleted in lung and esophageal cancer protein 1	DLEC1	0	7
K	259	Mono	19.01	Deleted in lung and esophageal cancer protein 1	DLEC1	0	7
R	257	Mono	19.01	Deleted in lung and esophageal cancer protein 1	DLEC1	0	7
K	259	Di	19.01	Deleted in lung and esophageal cancer protein 1	DLEC1	0	7
K	258	Di	19.01	Deleted in lung and esophageal cancer protein 1	DLEC1	0	7
R	257	Di	19.01	Deleted in lung and esophageal cancer protein 1	DLEC1	0	7
K	258	Tri	19.01	Deleted in lung and esophageal cancer protein 1	DLEC1	0	7
K	259	Tri	19.01	Deleted in lung and esophageal cancer protein 1	DLEC1	0	7
R	80	Mono	19.11	Discs, large homolog 3 (Neuroendocrine-dlg, Drosophila), isoform CRA_b	DLG3	0	6
K	691	Di	12.36	Dynein heavy chain 11, axonemal	DNAH11	0	2
K	551	Mono	15.16	Dynein heavy chain 12, axonemal (Fragment)	DNAH12	0	1
R	29	Mono	15.89	Dynein heavy chain 14, axonemal (Fragment)	DNAH14	0	1
K	767	Mono	13.32	Dynein heavy chain 14, axonemal (Fragment)	DNAH14	0	2
K	33	Mono	15.89	Dynein heavy chain 14, axonemal (Fragment)	DNAH14	0	1
R	7	Di	20.24	Dynein heavy chain 14, axonemal (Fragment)	DNAH14	3	38

K	1183	Mono	25.03	Dynein heavy chain 17, axonemal	DNAH17	0	4
K	827	Tri	13.59	Dynein heavy chain 17, axonemal	DNAH17	0	1
K	931	Tri	17.08	Dynein heavy chain 3, axonemal	DNAH3	0	1
K	675	Mono	12.1	Dynein heavy chain 7, axonemal	DNAH7	0	1
K	677	Mono	12.1	Dynein heavy chain 7, axonemal	DNAH7	0	1
R	1794	Di	20.24	Dynein heavy chain 8, axonemal	DNAH8	3	38
K	1209	Mono	30.09	Dynein heavy chain 9, axonemal	DNAH9	1	10
K	1638	Di	12.99	Dynein heavy chain 9, axonemal	DNAH9	0	4
K	223	Mono	41.98	DnaJ homolog subfamily A member 2	DNAJA2	0	2
R	103	Di	22.79	DnaJ homolog subfamily C member 17	DNAJC17	0	3
K	421	Di	16.69	Dynamin-3	DNM3	0	1
K	590	Di	15.94	DOCK10.2	DOCK10.2	13	72
R	628	Mono	45.2	Dedicator of cytokinesis protein 3	DOCK3	0	2
R	630	Mono	45.2	Dedicator of cytokinesis protein 3	DOCK3	0	2
R	630	Di	45.2	Dedicator of cytokinesis protein 3	DOCK3	0	2
R	628	Di	45.2	Dedicator of cytokinesis protein 3	DOCK3	0	2
R	14	Mono	33.99	Protein DPCD (Fragment)	DPCD	13	38
R	114	Di	24.56	Desmocollin-1	DSC1	3	0
R	2522	Mono	29.37	Desmoplakin	DSP	2	0
R	1912	Mono	11.82	Desmoplakin	DSP	1	0
R	1914	Mono	11.82	Desmoplakin	DSP	1	0
R	1914	Di	11.82	Desmoplakin	DSP	1	0
R	1912	Di	11.82	Desmoplakin	DSP	1	0
K	2523	Di	29.37	Desmoplakin	DSP	2	0
R	2522	Di	29.37	Desmoplakin	DSP	2	0
R	1885	Di	29.02	Desmoplakin	DSP	0	1
K	2523	Tri	29.37	Desmoplakin	DSP	2	0
R	5137	Mono	12.89	Dystonin	DST	2	15
R	5131	Mono	12.89	Dystonin	DST	2	15
K	360	Tri	17.48	Dual serine/threonine and tyrosine protein kinase	DSTYK	0	2
K	518	Mono	14.98	Dystrobrevin beta	DTNB	0	1
R	214	Mono	14.39	Ethylmalonyl-CoA decarboxylase (Fragment)	ECHDC1	0	1
K	146	Mono	20.86	Isoform 4 of Endothelin-1 receptor	EDNRA	0	1
R	166	Mono	45.45	Elongation factor 1-alpha 1	EEF1A1	1	3
K	30	Mono	47.26	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	3	0
K	439	Mono	35.79	Elongation factor 1-alpha 1	EEF1A1	2	0
K	165	Mono	45.45	Elongation factor 1-alpha 1	EEF1A1	1	3
K	55	Mono	27.73	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	1	0
K	36	Mono	27.85	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	1	0
K	318	Di	33.5	Elongation factor 1-alpha 1	EEF1A1	4	0
K	55	Di	61.97	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	8	4
K	36	Di	34.7	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	3	0
K	165	Di	59.94	Elongation factor 1-alpha 1	EEF1A1	15	0

R	166	Di	45.45	Elongation factor 1-alpha 1	EEF1A1	1	3
K	439	Tri	33.82	Elongation factor 1-alpha 1	EEF1A1	1	0
K	165	Tri	59.85	Elongation factor 1-alpha 1	EEF1A1	19	0
K	318	Tri	43.99	Elongation factor 1-alpha 1	EEF1A1	16	0
K	36	Tri	41.67	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	6	0
K	79	Tri	61.49	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	3	0
K	165	Mono	29.18	Elongation factor 1-alpha 2	EEF1A2	2	0
K	439	Mono	35.79	Elongation factor 1-alpha 2	EEF1A2	2	0
K	318	Di	33.72	Elongation factor 1-alpha 2	EEF1A2	1	0
K	165	Di	51.2	Elongation factor 1-alpha 2	EEF1A2	3	0
K	318	Tri	37.93	Elongation factor 1-alpha 2	EEF1A2	7	0
K	439	Tri	33.82	Elongation factor 1-alpha 2	EEF1A2	1	0
K	407	Mono	28.44	Elongation factor 2	EEF2	1	0
K	525	Tri	30.17	Elongation factor 2	EEF2	3	0
X	1	Di	20.42	EF-hand calcium-binding domain-containing protein 2 (Fragment)	EFCAB2	0	1
R	304	Mono	23.33	EF-hand calcium-binding domain-containing protein 4A	EFCAB4A	0	1
K	215	Di	13.02	EF-hand domain-containing protein 1	EFHC1	0	2
R	767	Mono	19.97	Pikachurin	EGFLAM	0	9
R	767	Di	18.76	Pikachurin	EGFLAM	0	1
R	41	Mono	13.38	Etoposide-induced protein 2.4 homolog	EI24	0	1
K	126	Mono	12.99	EP300-interacting inhibitor of differentiation 2B	EID2B	0	4
K	265	Mono	15.25	Eukaryotic translation initiation factor 2 subunit 1 (Fragment)	EIF2S1	0	1
R	926	Mono	33.95	Eukaryotic translation initiation factor 3 subunit A	EIF3A	1	0
K	928	Mono	12.1	Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	0	1
K	930	Mono	12.1	Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	0	1
K	3	Mono	15.25	Eukaryotic translation initiation factor 4 gamma 2 (Fragment)	EIF4G2	0	1
R	19	Di	41.16	Eukaryotic translation initiation factor 4H	EIF4H	3	0
K	1016	Tri	17.56	Eukaryotic translation initiation factor 5B	EIF5B	0	1
R	86	Mono	25.75	Enhancer of yellow 2 transcription factor homolog	ENY2	0	4
K	864	Tri	27.75	Ephrin type-A receptor 5	EPHA5	0	1
R	112	Mono	15.51	Epoxide hydrolase 1 (Fragment)	EPHX1	0	1
K	1019	Mono	18.8	Bifunctional glutamate/proline--tRNA ligase	EPRS	0	5
K	1020	Mono	18.8	Bifunctional glutamate/proline--tRNA ligase	EPRS	0	5
R	68	Mono	18.46	Receptor tyrosine-protein kinase erbB-2	ERBB2	0	1
K	319	Di	13.49	ELKS/Rab6-interacting/CAST family member 1	ERC1	0	3
R	269	Mono	25.15	TFIIH basal transcription factor complex helicase XPD subunit (Fragment)	ERCC2	0	5
K	404	Tri	16.75	DNA excision repair protein ERCC-6-like	ERCC6L	0	6
K	228	Mono	12.49	Erlin-1 (Fragment)	ERLIN1	0	1
R	39	Di	12.81	Homeobox protein ESX1	ESX1	1	0
K	7	Tri	17.42	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial (Fragment)	ETFDH	0	2
R	577	Di	41.4	RNA-binding protein EWS	EWSR1	1	0
R	723	Mono	12.16	Exosome component 10	EXOSC10	0	1
R	91	Di	11.79	Exosome complex component RRP4	EXOSC2	0	1

R	92	Di	11.79	Exosome complex component RRP4	EXOSC2	0	1
R	93	Di	11.79	Exosome complex component RRP4	EXOSC2	0	1
R	108	Mono	11.61	Exosome complex component RRP45 (Fragment)	EXOSC9	0	1
X	1	Mono	15.79	Exostosin-like 3 (Fragment)	EXTL3	0	2
K	1800	Mono	11.72	Coagulation factor V	F5	0	1
K	6	Mono	37.69	Fatty acid-binding protein, epidermal	FABP5	0	1
K	37	Mono	13.64	Fas apoptotic inhibitory molecule 1 (Fragment)	FAIM	0	6
K	513	Mono	15.79	Niban-like protein 1	FAM129B	0	2
R	9	Mono	15.52	Protein FAM149A (Fragment)	FAM149A	0	1
R	76	Di	21.16	Protein FAM156A/FAM156B (Fragment)	FAM156A	0	2
K	126	Tri	12.58	Soluble lamin-associated protein of 75 kDa (Fragment)	FAM169A	0	1
R	478	Mono	17.23	Protein FAM178A	FAM178A	0	1
K	1416	Tri	29.65	KIAA0423, isoform CRA_a	FAM179B	0	3
R	213	Mono	15.51	Protein FAM186B	FAM186B	0	1
R	243	Mono	12.29	Glycosaminoglycan xylosylkinase	FAM20B	0	1
R	295	Di	19.93	Protein FAM217A	FAM217A	0	1
X	1	Di	19.76	Protein FAM219B (Fragment)	FAM219B	6	26
K	192	Mono	16.06	Family with sequence similarity 46, member A, isoform CRA_a	FAM46A	0	3
K	279	Mono	20.98	Protein FAM5C	FAM5C	0	7
K	226	Tri	18.09	Protein FAM5C	FAM5C	0	8
R	555	Mono	28.11	Protein FAM63B	FAM63B	0	1
K	85	Di	11.74	Protein FAM65B	FAM65B	0	1
R	91	Di	13.96	Protein FAM74A7	FAM74A7	0	1
R	92	Di	13.96	Protein FAM74A7	FAM74A7	0	1
R	90	Di	13.96	Protein FAM74A7	FAM74A7	0	1
K	4164	Di	13.05	Protocadherin Fat 3	FAT3	0	2
K	285	Tri	12.87	Fibrillin-1	FBN1	0	1
K	28	Tri	12.35	FCH and double SH3 domains protein 2	FCHSD2	0	4
K	487	Mono	30.95	Fc receptor-like protein 4	FCRL4	0	2
K	431	Mono	12.96	Fermitin family homolog 2 (Fragment)	FERMT2	0	1
K	429	Mono	12.96	Fermitin family homolog 2 (Fragment)	FERMT2	0	1
R	82	Di	25.53	Fibroblast growth factor 2	FGF2	0	2
K	26	Di	18.02	FLJ00388 protein (Fragment)	FLJ00388	0	1
R	248	Mono	22.65	HCG1658703	FLJ11235	0	1
K	247	Mono	22.65	HCG1658703	FLJ11235	0	1
K	176	Mono	13.64	Intracellular domain VEGFR1 variant 21	FLT1	0	1
R	96	Mono	18.22	Formin-1	FMN1	0	1
R	94	Mono	18.22	Formin-1	FMN1	0	1
R	1755	Mono	20.01	Ugl-Y3	FN1	0	4
K	6	Tri	25.75	Formin-binding protein 1 (Fragment)	FNBP1	0	6
R	489	Mono	20.86	Fibronectin type III domain-containing protein 1 (Fragment)	FNDC1	0	10
R	490	Mono	20.86	Fibronectin type III domain-containing protein 1 (Fragment)	FNDC1	0	10
R	287	Di	14.71	Forkhead box protein O3	FOXO3	0	2

K	83	Mono	26.97	FAD-dependent oxidoreductase domain-containing protein 2 (Fragment)	FOXRED2	0	1
R	141	Mono	29.07	FERM and PDZ domain-containing protein 4	FRMPD4	0	14
K	130	Mono	12.03	Protein furry homolog-like	FRYL	0	1
R	976	Mono	28.37	Protein furry homolog-like	FRYL	0	1
R	975	Mono	28.37	Protein furry homolog-like	FRYL	0	1
K	198	Mono	14.74	Protein furry homolog-like	FRYL	0	1
K	5425	Mono	13.13	Fibrous sheath-interacting protein 2	FSIP2	0	2
R	38	Mono	12.31	pre-rRNA-processing protein FTSJ3 (Fragment)	FTSJ3	0	7
R	37	Mono	25.35	pre-rRNA-processing protein FTSJ3 (Fragment)	FTSJ3	0	6
R	398	Mono	13.19	pre-rRNA processing protein FTSJ3	FTSJ3	12	91
R	400	Mono	13.19	pre-rRNA processing protein FTSJ3	FTSJ3	12	91
R	37	Di	12.31	pre-rRNA-processing protein FTSJ3 (Fragment)	FTSJ3	0	7
R	38	Di	12.31	pre-rRNA-processing protein FTSJ3 (Fragment)	FTSJ3	0	7
R	380	Mono	32.64	Far upstream element-binding protein 1	FUBP1	0	1
R	216	Di	37.05	RNA-binding protein FUS	FUS	2	0
R	218	Di	37.05	RNA-binding protein FUS	FUS	2	0
R	141	Di	19.27	Frizzled-5	FZD5	0	6
R	253	Di	30.2	Ras GTPase-activating protein-binding protein 1	G3BP1	1	0
R	468	Di	35.88	Ras GTPase-activating protein-binding protein 2	G3BP2	2	0
K	2	Mono	18.64	Gamma-aminobutyric acid receptor-associated protein-like 1	GABARAPL1	0	9
R	47	Mono	15.16	Gamma-aminobutyric acid receptor-associated protein-like 1 (Fragment)	GABARAPL1	0	1
K	46	Mono	15.16	Gamma-aminobutyric acid receptor-associated protein-like 1 (Fragment)	GABARAPL1	0	1
R	242	Mono	13.72	GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	0	1
K	541	Mono	12.85	GTPase-activating Rap/Ran-GAP domain-like protein 3	GARNL3	0	1
K	467	Mono	12.78	Guanylate-binding protein 4	GBP4	0	11
R	466	Mono	12.78	Guanylate-binding protein 4	GBP4	0	11
K	470	Mono	12.78	Guanylate-binding protein 4	GBP4	0	11
K	467	Di	12.78	Guanylate-binding protein 4	GBP4	0	11
R	466	Di	12.78	Guanylate-binding protein 4	GBP4	0	11
K	470	Di	12.78	Guanylate-binding protein 4	GBP4	0	11
R	88	Di	30.04	Glutaryl-CoA dehydrogenase, mitochondrial (Fragment)	GCDH	0	2
R	166	Di	11.66	GC-rich sequence DNA-binding factor 2 (Fragment)	GCFC2	0	3
K	50	Mono	11.7	Chorion-specific transcription factor GCMa	GCM1	0	1
K	195	Di	21.16	Ganglioside-induced differentiation-associated protein 1	GDAP1	0	14
K	60	Di	24.56	Ganglioside-induced differentiation-associated protein 2	GDAP2	3	0
K	60	Tri	18.17	Ganglioside-induced differentiation-associated protein 2	GDAP2	0	4
R	20	Di	28.8	Growth/differentiation factor 11 (Fragment)	GDF11	0	1
R	44	Mono	13.88	Growth/differentiation factor 6	GDF6	0	5
K	173	Mono	17.45	Glial cell line-derived neurotrophic factor	GDNF	0	1
K	100	Di	17.35	ADP-ribosylation factor-binding protein GGA3	GGA3	0	1
R	68	Di	64.3	PERQ amino acid-rich with GYF domain-containing protein 2 (Fragment)	GIGYF2	2	0
R	64	Di	64.3	PERQ amino acid-rich with GYF domain-containing protein 2 (Fragment)	GIGYF2	2	0
R	149	Di	64.3	PERQ amino acid-rich with GYF domain-containing protein 2 (Fragment)	GIGYF2	2	0

R	153	Di	64.3	PERQ amino acid-rich with GYF domain-containing protein 2 (Fragment)	GIGYF2	2	0
K	276	Mono	30.94	GTPase IMAP family member 4	GIMAP4	1	0
K	321	Tri	12.13	Gypsy retrotransposon integrase-like protein 1	GIN1	0	5
K	69	Di	21.12	Beta-galactosidase-1-like protein (Fragment)	GLB1L	0	12
R	173	Mono	14.07	Zinc finger protein GLI4	GLI4	4	0
R	288	Di	14.71	Mannose-1-phosphate guanyltransferase beta	GMPPB	0	2
K	17	Di	38.85	Guanine nucleotide-binding protein G(olf) subunit alpha (Fragment)	GNAL	4	0
K	7	Tri	23.5	Guanine nucleotide-binding protein subunit gamma	GNG2	0	6
R	36	Di	23.31	Guanine nucleotide-binding protein subunit gamma	GNGT1	0	8
K	582	Mono	14.31	Dihydroxyacetone phosphate acyltransferase	GNPAT	0	2
K	583	Mono	14.04	Dihydroxyacetone phosphate acyltransferase	GNPAT	0	2
R	509	Di	19.93	Golgin subfamily A member 2	GOLGA2	0	1
K	237	Di	14.11	Putative golgin subfamily A member 6C	GOLGA6C	0	1
R	7	Mono	22.78	Isoform 2 of Golgin subfamily A member 6-like protein 9	GOLGA6L9	0	3
K	413	Tri	12.02	Putative golgin subfamily A member 8F/8G	GOLGA8F	0	6
R	337	Mono	22.78	Golgin subfamily A member 8I	GOLGA8I	0	3
K	8	Tri	40.35	Golgi SNAP receptor complex member 1 (Fragment)	GOSR1	3	11
R	277	Di	14.28	Glycerol-3-phosphate acyltransferase 1, mitochondrial	GPAM	0	1
K	36	Mono	33.1	G patch domain-containing protein 8 (Fragment)	GPATCH8	0	1
R	1155	Mono	12.96	G patch domain-containing protein 8	GPATCH8	0	2
K	1156	Mono	12.96	G patch domain-containing protein 8	GPATCH8	0	2
K	1159	Mono	12.96	G patch domain-containing protein 8	GPATCH8	0	2
R	1155	Di	12.96	G patch domain-containing protein 8	GPATCH8	0	2
K	1159	Di	12.96	G patch domain-containing protein 8	GPATCH8	0	2
K	1156	Di	12.96	G patch domain-containing protein 8	GPATCH8	0	2
K	1159	Tri	12.96	G patch domain-containing protein 8	GPATCH8	0	2
K	1156	Tri	12.96	G patch domain-containing protein 8	GPATCH8	0	2
R	312	Mono	13.21	GC-rich promoter binding protein 1, isoform CRA_c	GPBP1	0	14
K	30	Di	13.39	Glycerol-3-phosphate dehydrogenase 1-like protein (Fragment)	GPD1L	0	6
K	29	Di	13.39	Glycerol-3-phosphate dehydrogenase 1-like protein (Fragment)	GPD1L	0	6
K	8	Di	13.84	Molybdopterin molybdenumtransferase (Fragment)	GPHN	0	14
R	693	Mono	11.73	Probable G-protein coupled receptor 115	GPR115	0	1
R	154	Di	42.87	G-protein coupled receptor 20	GPR20	9	0
R	159	Di	42.87	G-protein coupled receptor 20	GPR20	9	0
R	294	Mono	15.01	G protein-regulated inducer of neurite outgrowth 3	GPRIN3	0	1
K	637	Di	17.22	Glutamate receptor 2	GRIA2	0	5
R	344	Mono	13.16	Glutamate receptor ionotropic, delta-2	GRID2	0	1
K	798	Mono	11.74	Glutamate receptor ionotropic, kainate 3	GRIK3	1	0
K	796	Mono	11.74	Glutamate receptor ionotropic, kainate 3	GRIK3	1	0
K	796	Di	11.74	Glutamate receptor ionotropic, kainate 3	GRIK3	1	0
K	798	Di	11.74	Glutamate receptor ionotropic, kainate 3	GRIK3	1	0
K	796	Tri	11.74	Glutamate receptor ionotropic, kainate 3	GRIK3	1	0
K	798	Tri	11.74	Glutamate receptor ionotropic, kainate 3	GRIK3	1	0

R	179	Mono	13.67	Glutamate receptor ionotropic, kainate 5	GRIK5	0	1
R	96	Mono	29.16	Glutamate receptor ionotropic, NMDA 3A	GRIN3A	0	5
R	145	Mono	21.67	GrpE protein homolog 2, mitochondrial	GRPEL2	0	7
K	142	Mono	21.67	GrpE protein homolog 2, mitochondrial	GRPEL2	0	7
K	2	Di	17.05	Maleylacetoacetate isomerase	GSTZ1	1	1
R	416	Di	11.66	General transcription factor II-I repeat domain-containing protein 1	GTF2IRD1	0	3
R	226	Di	11.99	GTP-binding protein 10	GTPBP10	0	9
K	1480	Di	16.81	Interferon-induced very large GTPase 1	GVINP1	0	1
K	204	Mono	13.4	Glucoside xylosyltransferase 2	GXYLT2	0	1
R	236	Mono	31.79	Glycogen [starch] synthase, liver	GYS2	0	1
K	231	Tri	31.79	Glycogen [starch] synthase, liver	GYS2	0	1
K	82	Mono	54.75	Histone H2A (Fragment)	H2AFJ	1	0
K	82	Tri	39.6	Histone H2A (Fragment)	H2AFJ	2	0
K	10	Mono	29.33	Histone H3	H3F3A	1	0
K	80	Mono	59.23	Histone H3	H3F3A	46	0
K	28	Mono	36.81	Histone H3	H3F3A	0	1
K	10	Di	49.85	Histone H3	H3F3A	1	0
K	28	Di	55.9	Histone H3	H3F3A	1	0
K	80	Di	46.25	Histone H3	H3F3A	10	0
K	80	Tri	45.45	Histone H3	H3F3A	7	0
K	222	Di	12.13	Trifunctional enzyme subunit alpha, mitochondrial	HADHA	0	5
K	166	Mono	16.68	3-ketoacyl-CoA thiolase	HADHB	0	1
R	303	Mono	13.56	Hyaluronan and proteoglycan link protein 1	HAPLN1	0	5
K	8	Mono	18.59	Hemoglobin subunit gamma-2	HBG2	0	3
R	9	Mono	18.59	Hemoglobin subunit gamma-2	HBG2	0	3
R	9	Di	18.59	Hemoglobin subunit gamma-2	HBG2	0	3
K	8	Di	18.59	Hemoglobin subunit gamma-2	HBG2	0	3
K	167	Di	29.59	Hepatocellular carcinoma-associated antigen 90	HCA90	0	1
R	110	Di	40.03	HCG1652096, isoform CRA_a	hCG_1652096	1	0
K	638	Mono	12.13	HCG2044799	hCG_2044799	0	1
R	656	Di	41.65	HCG2044799	hCG_2044799	3	0
K	33	Mono	26.33	HCG2045747	hCG_2045747	0	3
R	27	Di	26.33	HCG2045747	hCG_2045747	0	3
R	71	Mono	23.25	Hepatoma-derived growth factor-related protein 2 (Fragment)	HDGFRP2	0	1
K	3	Mono	11.95	Heme-binding protein 2 (Fragment)	HEBP2	1	11
X	1	Mono	11.95	Heme-binding protein 2 (Fragment)	HEBP2	1	11
K	727	Tri	12.15	E3 ubiquitin-protein ligase HECTD1 (Fragment)	HECTD1	0	3
R	867	Mono	23.43	Helicase POLQ-like	HELQ	0	7
R	1319	Di	32.13	Probable E3 ubiquitin-protein ligase HERC1	HERC1	0	1
K	340	Mono	13.52	Probable ATP-dependent DNA helicase HFM1	HFM1	0	3
K	214	Di	13.55	Heparan-alpha-glucosaminide N-acetyltransferase	HGSNAT	0	5
K	78	Mono	15.97	Histone H1.5	HIST1H1B	12	32
K	118	Mono	36.28	Histone H1.3	HIST1H1D	0	1

K	119	Mono	54.75	Histone H2A type 1-B/E	HIST1H2AB	1	0
K	119	Tri	39.6	Histone H2A type 1-B/E	HIST1H2AB	2	0
K	37	Mono	30.78	Histone H3.1	HIST1H3A	0	1
K	28	Mono	54.25	Histone H3.1	HIST1H3A	7	0
K	28	Di	63.02	Histone H3.1	HIST1H3A	20	0
K	28	Tri	39.63	Histone H3.1	HIST1H3A	6	0
K	92	Mono	71.29	Histone H4	HIST1H4A	2	0
K	78	Mono	42.98	Histone H4	HIST1H4A	4	0
K	32	Mono	28.33	Histone H4	HIST1H4A	1	0
R	89	Mono	34.92	Histone H2A type 2-B	HIST2H2AB	6	10
K	58	Mono	52.12	Histone H2B	HIST2H2BF	7	0
K	109	Tri	27.79	Histone H2B	HIST2H2BF	1	0
K	58	Tri	39.16	Histone H2B	HIST2H2BF	4	0
R	169	Mono	84.61	HLA class I histocompatibility antigen, B-48 alpha chain	HLA-B	0	5
K	41	Mono	15.59	HLA class II histocompatibility antigen, DRB1-4 beta chain	HLA-DRB1	0	3
K	41	Tri	15.59	HLA class II histocompatibility antigen, DR beta 4 chain	HLA-DRB4	0	3
R	35	Di	24.52	Hydroxymethylglutaryl-CoA synthase, mitochondrial	HMGCS2	0	3
R	291	Di	91.24	Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	3	26
R	31	Mono	106.62	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	12	8
K	112	Mono	58.47	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	3	1
R	225	Di	36.41	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	2	0
R	225	Di	41.84	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	2	0
R	213	Di	71.39	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	1	0
R	206	Di	80.99	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	2	0
R	215	Di	71.39	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	1	0
R	196	Di	66.31	Heterogeneous nuclear ribonucleoprotein A1-like 2	HNRNPA1L2	27	0
R	194	Di	66.31	Heterogeneous nuclear ribonucleoprotein A1-like 2	HNRNPA1L2	27	0
R	213	Mono	38.73	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	1	3
R	52	Mono	100.61	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	3	6
R	52	Di	106.62	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	12	8
R	245	Mono	28.26	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	1	0
R	245	Di	40.93	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	1	0
R	13	Di	12.4	Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment)	HNRNPC	0	1
R	226	Mono	29.85	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	0	1
R	220	Mono	29.85	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	0	1
R	220	Di	31.91	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	0	1
R	226	Di	29.85	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	0	1
K	99	Mono	43.37	Heterogeneous nuclear ribonucleoprotein R	HNRNPR	1	0
R	739	Di	28.05	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	1	0
R	733	Di	28.05	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	1	0
K	161	Mono	72.9	Heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	2	4
K	162	Mono	72.9	Heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	2	4
R	408	Di	44.46	Heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	1	0

K	214	Mono	16.06	Hermansky-Pudlak syndrome 5 protein	HPS5	0	3
R	72	Di	12.23	Heparan sulfate glucosamine 3-O-sulfotransferase 5	HS3ST5	0	1
K	73	Tri	12.23	Heparan sulfate glucosamine 3-O-sulfotransferase 5	HS3ST5	0	1
R	9	Mono	11.61	Peroxisomal multifunctional enzyme type 2	HSD17B4	0	5
K	546	Tri	28.39	Heat shock protein HSP 90-alpha	HSP90AA1	1	0
R	202	Di	34.29	Putative heat shock protein HSP 90-alpha A2	HSP90AA2	1	0
K	30	Mono	38.02	Endoplasmin (Fragment)	HSP90B1	0	2
R	378	Mono	44.89	Heat shock 70 kDa protein 1A/1B	HSPA1A	0	6
K	470	Di	29.7	Heat shock 70 kDa protein 1A/1B	HSPA1A	0	1
K	470	Tri	28.87	Heat shock 70 kDa protein 1A/1B	HSPA1A	1	0
K	189	Di	63.55	Heat shock 70 kDa protein 1-like	HSPA1L	0	3
K	461	Mono	41.28	Heat shock-related 70 kDa protein 2	HSPA2	0	4
K	188	Mono	52.38	Heat shock-related 70 kDa protein 2	HSPA2	0	1
R	472	Mono	41.28	Heat shock-related 70 kDa protein 2	HSPA2	0	4
K	612	Mono	34.64	Heat shock-related 70 kDa protein 2	HSPA2	0	4
K	189	Mono	52.38	Heat shock-related 70 kDa protein 2	HSPA2	0	1
K	188	Di	52.38	Heat shock-related 70 kDa protein 2	HSPA2	0	1
K	189	Di	52.38	Heat shock-related 70 kDa protein 2	HSPA2	0	1
R	290	Mono	15.67	78 kDa glucose-regulated protein	HSPA5	0	4
R	289	Mono	15.67	78 kDa glucose-regulated protein	HSPA5	0	4
K	294	Mono	15.67	78 kDa glucose-regulated protein	HSPA5	0	4
K	213	Di	63.55	78 kDa glucose-regulated protein	HSPA5	0	3
K	154	Di	45.89	78 kDa glucose-regulated protein	HSPA5	3	0
K	585	Tri	50.38	78 kDa glucose-regulated protein	HSPA5	4	0
K	330	Mono	16.81	Heat shock 70 kDa protein 6	HSPA6	26	53
K	142	Mono	29.74	Heat shock 70 kDa protein 6	HSPA6	0	2
K	147	Mono	52.38	Heat shock cognate 71 kDa protein (Fragment)	HSPA8	0	1
K	146	Mono	52.38	Heat shock cognate 71 kDa protein (Fragment)	HSPA8	0	1
R	233	Mono	80.28	Heat shock cognate 71 kDa protein	HSPA8	0	4
K	187	Di	63.55	Heat shock cognate 71 kDa protein (Fragment)	HSPA8	0	3
K	146	Di	63.55	Heat shock cognate 71 kDa protein (Fragment)	HSPA8	0	3
K	147	Di	52.38	Heat shock cognate 71 kDa protein (Fragment)	HSPA8	0	1
K	325	Tri	43.43	Heat shock cognate 71 kDa protein	HSPA8	1	0
K	56	Tri	22.86	Heat shock cognate 71 kDa protein (Fragment)	HSPA8	1	0
K	405	Mono	17.15	60 kDa heat shock protein, mitochondrial	HSPD1	1	0
R	111	Mono	12.83	5-hydroxytryptamine receptor 5A	HTR5A	0	1
R	216	Di	14.28	5-hydroxytryptamine receptor 6	HTR6	0	9
R	2662	Mono	25.23	E3 ubiquitin-protein ligase HUWE1 (Fragment)	HUWE1	0	2
R	1114	Mono	17.44	E3 ubiquitin-protein ligase HUWE1 (Fragment)	HUWE1	0	4
R	4423	Mono	30.71	Hydrocephalus-inducing protein homolog	HYDIN	0	3
R	2505	Di	18.46	Hydrocephalus-inducing protein homolog	HYDIN	0	1
R	6	Di	16.22	Isoleucine--tRNA ligase, mitochondrial	IARS2	1	0
R	85	Di	12.47	Chromosome 1 open reading frame 69	IBA57	2	39

R	97	Mono	23.08	Uncharacterized protein IDI2-AS1	IDI2-AS1	0	3
K	319	Mono	12.1	Interferon alpha/beta receptor 1	IFNAR1	0	1
K	318	Mono	12.1	Interferon alpha/beta receptor 1	IFNAR1	0	1
R	141	Mono	17.25	Interleukin-13	IL13	0	2
K	402	Mono	15.31	Pro-interleukin-16 (Fragment)	IL16	0	1
R	309	Mono	23.01	Interleukin-5 receptor subunit alpha	IL5RA	0	2
R	321	Mono	39.86	Inosine-5'-monophosphate dehydrogenase	IMPDH1	0	11
K	437	Mono	13.73	Inosine-5'-monophosphate dehydrogenase	IMPDH1	2	4
K	435	Mono	13.73	Inosine-5'-monophosphate dehydrogenase	IMPDH1	2	4
K	437	Di	13.73	Inosine-5'-monophosphate dehydrogenase	IMPDH1	2	4
K	435	Di	13.73	Inosine-5'-monophosphate dehydrogenase	IMPDH1	2	4
K	691	Mono	15.37	InaD-like protein	INADL	0	1
K	165	Mono	30.74	InaD-like protein	INADL	0	1
K	691	Tri	13.05	InaD-like protein	INADL	0	8
K	694	Tri	13.05	InaD-like protein	INADL	0	8
R	922	Di	24.5	Integrator complex subunit 4	INTS4	0	18
K	344	Tri	15.1	Integrator complex subunit 6	INTS6	0	7
R	85	Mono	35.74	Importin-8 (Fragment)	IPO8	2	0
K	380	Mono	15.25	IQ domain-containing protein G	IQCG	0	1
K	817	Mono	11.64	Ras GTPase-activating-like protein IQGAP1	IQGAP1	1	0
K	324	Mono	23.36	ITGA10 protein	ITGA10	5	4
R	523	Mono	12.87	Integrin alpha-6	ITGA6	0	9
K	525	Mono	12.87	Integrin alpha-6	ITGA6	0	9
R	424	Mono	35.17	Inter-alpha-trypsin inhibitor heavy chain H5	ITIH5	0	15
R	428	Mono	35.17	Inter-alpha-trypsin inhibitor heavy chain H5	ITIH5	0	15
R	428	Di	35.17	Inter-alpha-trypsin inhibitor heavy chain H5	ITIH5	0	15
R	424	Di	35.17	Inter-alpha-trypsin inhibitor heavy chain H5	ITIH5	0	15
R	132	Mono	20.45	Inositol 1,4,5-trisphosphate receptor-interacting protein-like 2	ITPRIPL2	0	2
R	275	Mono	12.53	Jerky protein homolog-like	JRKL	0	2
K	533	Mono	25.8	Junction plakoglobin	JUP	0	5
R	43	Di	15.49	Potassium voltage-gated channel subfamily A member 2	KCNA2	0	9
K	234	Tri	18.46	Potassium voltage-gated channel subfamily A member 7	KCNA7	0	1
K	603	Tri	15.01	Potassium voltage-gated channel subfamily KQT member 5	KCNQ5	3	22
R	258	Di	13.3	BTB/POZ domain-containing protein KCTD21	KCTD21	0	4
K	74	Mono	29.83	KDEL motif-containing protein 1	KDELC1	3	15
R	61	Mono	18.57	Lysine-specific demethylase 6A	KDM6A	0	8
K	200	Mono	12.35	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	0	4
R	320	Di	31.09	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	1	0
R	346	Di	32.98	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	2	0
R	348	Di	30.27	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	3	0
R	325	Di	40.06	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	2	0
K	164	Di	15.68	Pumilio domain-containing protein KIAA0020	KIAA0020	6	5
R	445	Mono	16.25	Mitochondrial ribonuclease P protein 3	KIAA0391	0	7

K	1633	Tri	22.36	Isoform 3 of Protein TALPID3	KIAA0586	0	7
R	880	Di	12.16	Uncharacterized protein KIAA1107	KIAA1107	0	1
K	679	Mono	25.75	Coiled-coil domain-containing protein KIAA1407	KIAA1407	0	4
K	678	Mono	25.75	Coiled-coil domain-containing protein KIAA1407	KIAA1407	0	4
K	679	Di	25.75	Coiled-coil domain-containing protein KIAA1407	KIAA1407	0	4
K	678	Di	25.75	Coiled-coil domain-containing protein KIAA1407	KIAA1407	0	4
K	679	Tri	25.75	Coiled-coil domain-containing protein KIAA1407	KIAA1407	0	4
K	678	Tri	25.75	Coiled-coil domain-containing protein KIAA1407	KIAA1407	0	4
R	967	Mono	16.3	Protein RIC1 homolog (Fragment)	KIAA1432	0	1
R	7	Mono	13.24	Uncharacterized protein KIAA1522	KIAA1522	0	1
R	8	Mono	13.24	Uncharacterized protein KIAA1522	KIAA1522	0	1
K	444	Mono	20.14	Protein CIP2A	KIAA1524	0	1
K	355	Mono	23.5	KIAA1715 protein	KIAA1715	0	4
R	356	Mono	23.5	KIAA1715 protein	KIAA1715	0	4
R	356	Di	23.5	KIAA1715 protein	KIAA1715	0	4
K	355	Di	23.5	KIAA1715 protein	KIAA1715	0	4
R	758	Di	17.87	WD repeat-containing protein KIAA1875	KIAA1875	4	0
K	93	Mono	23.92	DBIRD complex subunit KIAA1967 (Fragment)	KIAA1967	0	2
K	525	Mono	12.43	Uncharacterized coiled-coil domain-containing protein KIAA1984	KIAA1984	0	1
K	612	Tri	12.84	Uncharacterized protein KIAA2026 (Fragment)	KIAA2026	0	6
K	373	Mono	11.94	Kinesin-like protein KIF14	KIF14	0	1
K	370	Mono	11.94	Kinesin-like protein KIF14	KIF14	0	1
K	373	Di	11.94	Kinesin-like protein KIF14	KIF14	0	1
K	370	Di	11.94	Kinesin-like protein KIF14	KIF14	0	1
K	373	Tri	11.94	Kinesin-like protein KIF14	KIF14	0	1
K	370	Tri	11.94	Kinesin-like protein KIF14	KIF14	0	1
K	610	Mono	24.29	Kinesin-like protein KIF15	KIF15	0	1
K	813	Di	15.89	Kinesin-like protein KIF17	KIF17	0	14
K	590	Mono	14.21	Kinesin-like protein KIF23	KIF23	0	16
K	34	Tri	16	Kinesin-like protein KIF24	KIF24	0	2
K	442	Mono	15.24	Kinesin-like protein KIF9	KIF9	0	1
K	439	Mono	15.24	Kinesin-like protein KIF9	KIF9	0	1
K	329	Tri	26.44	Kin of IRRE-like protein 1	KIRREL	0	22
R	811	Di	11.79	Beta-klotho	KLB	0	1
R	812	Di	11.79	Beta-klotho	KLB	0	1
R	306	Mono	11.96	Isoform 3 of Krueppel-like factor 12	KLF12	1	6
K	405	Di	15.12	Kelch-like protein 15	KLHL15	0	1
R	288	Mono	17.23	Kelch-like protein 17	KLHL17	0	1
R	566	Mono	28.1	Kelch-like protein 6	KLHL6	0	1
K	115	Mono	36.42	Keratin, type I cytoskeletal 13 (Fragment)	KRT13	0	1
R	280	Mono	18.02	Keratin-like protein KRT222	KRT222	0	3
R	60	Mono	38.95	Keratin, type II cytoskeletal 5 (Fragment)	KRT5	0	1
K	711	Mono	21.78	Kinectin	KTN1	0	21

K	708	Mono	21.78	Kinectin	KTN1	0	21
K	711	Di	21.78	Kinectin	KTN1	0	21
K	708	Di	21.78	Kinectin	KTN1	0	21
K	1982	Tri	22.86	Laminin subunit alpha-2	LAMA2	1	0
K	1227	Tri	12.15	Laminin subunit beta-1	LAMB1	0	3
R	743	Mono	15.59	Laminin subunit beta-3	LAMB3	0	14
K	1555	Mono	21.44	Laminin subunit beta-4	LAMB4	0	1
K	1557	Mono	21.44	Laminin subunit beta-4	LAMB4	0	1
R	92	Mono	13.22	Ragulator complex protein LAMTOR4	LAMTOR4	0	2
R	89	Mono	13.1	Ragulator complex protein LAMTOR4	LAMTOR4	0	11
R	89	Di	13.22	Ragulator complex protein LAMTOR4	LAMTOR4	0	2
R	77	Mono	15.62	Glycosyltransferase-like protein LARGE1 (Fragment)	LARGE	0	3
R	16	Mono	29.83	La-related protein 4B (Fragment)	LARP4B	0	2
R	33	Di	24.14	Ligand-dependent nuclear receptor corepressor-like protein	LCORL	0	1
K	1825	Mono	12.85	Lactase-phlorizin hydrolase	LCT	1	5
K	1829	Mono	12.85	Lactase-phlorizin hydrolase	LCT	1	5
K	156	Tri	30.45	L-lactate dehydrogenase (Fragment)	LDHB	0	1
K	264	Mono	12.02	L-lactate dehydrogenase	LDHC	1	0
R	133	Mono	19.11	Isoform 2 of Leptin receptor overlapping transcript-like 1	LEPROTL1	0	6
R	451	Mono	22.19	Leucine-rich repeat LGI family member 4	LGI4	0	1
K	84	Mono	16.58	Lutropin-choriogonadotropic hormone receptor	LHCGR	0	4
R	259	Mono	13.07	LIM/homeobox protein Lhx1	LHX1	0	1
R	115	Di	29.26	Protein lin-7 homolog B (Fragment)	LIN7B	0	11
R	217	Mono	16.12	Lethal(2) giant larvae protein homolog 1	LLGL1	0	7
K	22	Mono	12.99	LIM and cysteine-rich domains protein 1	LMCD1	0	1
R	25	Mono	12.99	LIM and cysteine-rich domains protein 1	LMCD1	0	1
R	23	Mono	12.99	LIM and cysteine-rich domains protein 1	LMCD1	0	1
K	22	Di	12.99	LIM and cysteine-rich domains protein 1	LMCD1	0	1
R	23	Di	12.99	LIM and cysteine-rich domains protein 1	LMCD1	0	1
R	25	Di	12.99	LIM and cysteine-rich domains protein 1	LMCD1	0	1
R	156	Mono	13.48	Leiomodin-1	LMOD1	0	9
K	160	Mono	13.48	Leiomodin-1	LMOD1	0	9
R	70	Di	28.99	Protein LOC100652732 (Fragment)	LOC100652732	0	1
R	236	Di	15.81	Lysyl oxidase homolog 3	LOXL3	9	12
K	43	Mono	12.85	Lysophosphatidylcholine acyltransferase 1	LPCAT1	0	1
R	113	Di	21.16	Lipoma-preferred partner (Fragment)	LPP	0	2
K	160	Di	21.51	Leucine-rich repeat and guanylate kinase domain-containing protein	LRGUK	0	5
K	1733	Di	17.58	Low-density lipoprotein receptor-related protein 1B	LRP1B	0	3
R	3290	Mono	15.55	Low-density lipoprotein receptor-related protein 2	LRP2	0	7
K	544	Mono	30.95	Low-density lipoprotein receptor-related protein 5	LRP5	0	2
K	510	Di	12.36	Low-density lipoprotein receptor-related protein 6	LRP6	0	2
R	25	Mono	17.23	Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	0	1
R	33	Mono	16.77	Leucine-rich repeat-containing protein 31	LRRC31	0	5

R	26	Mono	16.77	Leucine-rich repeat-containing protein 31	LRRC31	0	5
K	93	Tri	16.58	Leucine-rich repeat-containing protein 40	LRRC40	0	4
K	193	Mono	23.14	Leucine-rich repeat-containing protein 4B (Fragment)	LRRC4B	0	2
R	26	Mono	17.22	Leucine-rich repeat-containing protein 73	LRRC73	0	3
K	57	Mono	19.97	Leucine-rich repeat-containing protein 8C	LRRC8C	0	9
K	405	Di	13.33	Leucine-rich repeat and IQ domain-containing protein 3	LRRIQ3	0	3
R	19	Di	15.41	Leucine-rich repeat and transmembrane domain-containing protein 2 (Fragment)	LRTM2	0	3
R	267	Di	24.25	U7 snRNA-associated Sm-like protein LSm11	LSM11	0	22
K	328	Tri	12.35	T-lymphocyte surface antigen Ly-9	LY9	0	4
R	86	Mono	18.76	LYR motif-containing protein 4	LYRM4	0	1
R	136	Mono	18.96	Protein LZIC	LZIC	0	3
K	7	Tri	12.49	Protein mab-21-like 1	MAB21L1	0	1
K	665	Tri	24.68	Metastasis-associated in colon cancer protein 1	MACC1	0	1
K	2204	Mono	17.05	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	MACF1	1	1
K	34	Mono	14.57	Mastermind-like domain-containing protein 1 (Fragment)	MAMLD1	2	0
R	428	Mono	31.24	Alpha-mannosidase 2	MAN2A1	7	0
R	634	Mono	17.16	MAP1S light chain	MAP1S	0	1
K	264	Di	17.49	Mitogen-activated protein kinase kinase kinase 6 (Fragment)	MAP3K6	2	15
K	199	Mono	14.96	Mitogen-activated protein kinase kinase kinase 9	MAP3K9	0	12
R	236	Mono	24.29	Mitogen-activated protein kinase kinase kinase 9	MAP3K9	0	1
K	558	Mono	25.08	Microtubule-associated protein 9	MAP9	0	1
R	82	Di	13.64	Mitogen-activated protein kinase 12	MAPK12	0	1
R	374	Mono	16.7	Mitogen-activated protein kinase 7	MAPK7	0	1
R	740	Di	12.56	MAP/microtubule affinity-regulating kinase 4	MARK4	0	7
R	264	Mono	48.32	S-adenosylmethionine synthase isoform type-1	MAT1A	0	23
K	476	Tri	12.83	Megakaryocyte-associated tyrosine kinase, isoform CRA_a	MATK	0	1
K	7	Mono	17.08	Matrilin-2 (Fragment)	MATN2	0	1
K	7	Di	28.42	Matrilin-2 (Fragment)	MATN2	0	1
K	252	Tri	41.83	Matrilin-4	MATN4	0	1
K	86	Mono	15.01	Myc-associated zinc finger protein	MAZ	0	1
R	1392	Mono	16.38	Methyl-CpG-binding domain protein 5	MBD5	0	4
R	1395	Di	16.38	Methyl-CpG-binding domain protein 5	MBD5	0	4
R	86	Mono	12.4	Muscleblind-like protein 1 (Fragment)	MBNL1	0	4
K	71	Tri	42.25	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial (Fragment)	MCCC1	0	2
K	75	Tri	12.35	Isoform 3 of Proto-oncogene DBL	MCF2	0	4
K	27	Di	16.81	Multiple C2 and transmembrane domain-containing protein 1 (Fragment)	MCTP1	0	1
R	641	Mono	17	Multiple C2 and transmembrane domain-containing protein 2	MCTP2	0	2
K	643	Mono	17	Multiple C2 and transmembrane domain-containing protein 2	MCTP2	0	2
R	644	Mono	17	Multiple C2 and transmembrane domain-containing protein 2	MCTP2	0	2
R	291	Di	19.4	Mediator of DNA damage checkpoint protein 1	MDC1	0	2
K	363	Mono	12.33	Putative malate dehydrogenase 1B	MDH1B	0	1
R	2	Di	28.27	Isoform 3 of Mediator of RNA polymerase II transcription subunit 8	MED8	0	1
R	211	Mono	25.15	Methionine aminopeptidase 1D, mitochondrial	METAP1D	0	5

R	70	Mono	17.92	Methyltransferase-like protein 10	METTL10	0	2
R	233	Mono	12.97	Methyltransferase-like protein 24	METTL24	1	0
X	1	Tri	15.77	Methyltransferase-like protein 25 (Fragment)	METTL25	0	1
R	365	Di	23.69	Methyltransferase-like protein 8	METTL8	0	1
R	21	Mono	16.32	Malignant fibrous histiocytoma-amplified sequence 1	MFHAS1	0	2
R	164	Mono	19.61	Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase B	MGAT5B	0	2
R	502	Mono	30.04	E3 ubiquitin-protein ligase MIB2	MIB2	0	2
K	115	Mono	29.37	Protein-methionine sulfoxide oxidase MICAL1 (Fragment)	MICAL1	2	0
R	116	Mono	29.37	Protein-methionine sulfoxide oxidase MICAL1 (Fragment)	MICAL1	2	0
R	116	Di	29.37	Protein-methionine sulfoxide oxidase MICAL1 (Fragment)	MICAL1	2	0
K	115	Di	29.37	Protein-methionine sulfoxide oxidase MICAL1 (Fragment)	MICAL1	2	0
K	115	Tri	29.37	Protein-methionine sulfoxide oxidase MICAL1 (Fragment)	MICAL1	2	0
R	631	Di	11.8	WD repeat-containing protein mio	MIOS	0	1
R	3119	Mono	13.26	Antigen KI-67	MKI67	0	5
R	125	Mono	29.35	Isoform 2 of Multiple myeloma tumor-associated protein 2	MMTAG2	0	1
R	128	Mono	29.35	Isoform 2 of Multiple myeloma tumor-associated protein 2	MMTAG2	0	1
R	4	Di	14.96	Myeloid cell nuclear differentiation antigen (Fragment)	MNDA	0	1
R	41	Mono	18.76	MAPK/MAK/MRK overlapping kinase	MOK	0	4
K	795	Mono	22.21	MORC family CW-type zinc finger protein 2	MORC2	0	1
R	790	Mono	22.21	MORC family CW-type zinc finger protein 2	MORC2	0	1
R	113	Mono	12.14	Proto-oncogene serine/threonine-protein kinase mos	MOS	0	1
R	91	Mono	27.16	Mov10, Moloney leukemia virus 10, homolog (Mouse), isoform CRA_a	MOV10	9	25
K	285	Di	14.39	MAGUK p55 subfamily member 5	MPP5	0	1
R	1316	Di	33.75	Myosin phosphatase Rho-interacting protein (Fragment)	MPRIP	0	1
R	43	Mono	25.53	3-mercaptopyruvate sulfurtransferase	MPST	0	2
K	1316	Mono	12.89	Maestro heat-like repeat-containing protein family member 1	MROH1	0	2
R	71	Mono	14.37	39S ribosomal protein L30, mitochondrial	MRPL30	0	2
K	79	Mono	30.09	39S ribosomal protein L4, mitochondrial (Fragment)	MRPL4	1	10
X	1	Mono	24.01	39S ribosomal protein L49, mitochondrial (Fragment)	MRPL49	0	2
K	36	Di	12.1	39S ribosomal protein L54, mitochondrial (Fragment)	MRPL54	2	0
K	860	Mono	13.3	DNA mismatch repair protein Msh3	MSH3	0	1
R	863	Mono	13.3	DNA mismatch repair protein Msh3	MSH3	0	1
R	25	Mono	45.61	Metastasis-associated protein MTA2	MTA2	0	2
R	10	Mono	18.27	Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	0	5
K	58	Mono	19.13	Methylenetetrahydrofolate reductase	MTHFR	0	1
R	245	Mono	11.83	Myotubularin-related protein 11	MTMR11	0	6
R	246	Mono	11.83	Myotubularin-related protein 11	MTMR11	0	6
R	246	Di	11.83	Myotubularin-related protein 11	MTMR11	0	6
R	245	Di	11.83	Myotubularin-related protein 11	MTMR11	0	6
K	12291	Mono	11.97	Mucin-16	MUC16	0	7
K	12293	Mono	11.97	Mucin-16	MUC16	0	7
K	148	Tri	12.09	Myb-binding protein 1A (Fragment)	MYBBP1A	0	7
R	72	Mono	12.78	N-cym protein	MYCNOS	0	3

R	73	Di	12.78	N-cym protein	MYCNOS	0	3
R	141	Mono	18.26	Myelin expression factor 2	MYEF2	2	0
K	86	Tri	13.75	Myogenic factor 5	MYF5	0	1
R	163	Mono	28.5	Myosin-10 (Fragment)	MYH10	1	0
R	1114	Mono	27.74	Myosin-10	MYH10	0	2
R	820	Di	11.66	Myosin-15	MYH15	0	3
R	661	Mono	13.17	Myosin light chain kinase 3	MYLK3	0	1
R	7	Di	12.06	Putative unconventional myosin-XVB (Fragment)	MYO15B	0	1
R	9	Di	12.06	Putative unconventional myosin-XVB (Fragment)	MYO15B	0	1
R	858	Mono	14.77	Unconventional myosin-If	MYO1F	0	3
K	905	Tri	18.81	Myosin-IIIa	MYO3A	0	2
R	314	Mono	17.19	Unconventional myosin-Vb (Fragment)	MYO5B	0	1
K	313	Mono	17.19	Unconventional myosin-Vb (Fragment)	MYO5B	0	1
K	1283	Mono	14.97	Unconventional myosin-VIIa	MYO7A	0	1
R	1285	Mono	14.97	Unconventional myosin-VIIa	MYO7A	0	1
K	1649	Mono	17.34	Myomesin-1	MYOM1	0	2
R	8	Mono	12.65	Myomesin-1	MYOM1	0	3
R	61	Mono	18.57	Myozenin-2	MYOZ2	0	8
K	59	Di	18.57	Myozenin-2	MYOZ2	0	8
K	59	Tri	18.09	Myozenin-2	MYOZ2	0	8
K	7	Mono	40.41	Isoform 2 of Myopalladin	MYPN	0	1
K	153	Mono	12.32	Myopalladin	MYPN	2	1
R	782	Mono	13.49	Histone H2A deubiquitinase MYSM1	MYSM1	0	3
R	782	Di	13.49	Histone H2A deubiquitinase MYSM1	MYSM1	0	3
K	783	Di	13.49	Histone H2A deubiquitinase MYSM1	MYSM1	0	3
K	783	Tri	13.49	Histone H2A deubiquitinase MYSM1	MYSM1	0	3
X	1	Tri	13.62	Mitotic-spindle organizing protein 2A (Fragment)	MZT2A	0	3
K	2	Mono	20.29	NGFI-A-binding protein 1 (Fragment)	NAB1	0	1
K	63	Di	34.86	Nucleosome assembly protein 1-like 4 (Fragment)	NAP1L4	1	0
R	164	Mono	12.1	Nicotinate phosphoribosyltransferase	NAPRT1	2	0
R	350	Mono	28.1	Neurobeachin-like protein 2	NBEAL2	0	1
K	87	Mono	17.08	Neuroblastoma breakpoint family member 20	NBPF10	0	1
K	591	Di	13.59	Neural cell adhesion molecule 1	NCAM1	0	1
K	302	Di	14.44	Neural cell adhesion molecule 2	NCAM2	0	2
K	302	Tri	17.42	Neural cell adhesion molecule 2	NCAM2	0	2
R	21	Di	21.45	Nck-associated protein 1-like	NCKAP1L	0	4
K	280	Mono	21.44	Nicalin (Fragment)	NCLN	0	1
K	278	Mono	21.44	Nicalin (Fragment)	NCLN	0	1
R	52	Mono	13.72	Nuclear receptor coactivator 7 (Fragment)	NCOA7	0	7
K	51	Di	13.72	Nuclear receptor coactivator 7 (Fragment)	NCOA7	0	7
R	52	Di	13.72	Nuclear receptor coactivator 7 (Fragment)	NCOA7	0	7
K	51	Tri	13.72	Nuclear receptor coactivator 7 (Fragment)	NCOA7	0	7
K	490	Di	14.89	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 2	NDST2	3	25

K	48	Di	20.77	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	NDUFA7	1	0
R	17	Mono	41.19	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	0	1
R	111	Mono	24.85	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	0	4
K	1062	Di	12.64	Nebulin	NEB	0	1
K	235	Tri	20.3	Nebulin	NEB	0	1
K	292	Tri	12.35	N-terminal EF-hand calcium-binding protein 1	NECAB1	0	4
K	105	Mono	20.22	Adaptin ear-binding coat-associated protein 2	NECAP2	0	15
K	106	Mono	20.22	Adaptin ear-binding coat-associated protein 2	NECAP2	0	15
K	106	Di	20.22	Adaptin ear-binding coat-associated protein 2	NECAP2	0	15
K	105	Di	20.22	Adaptin ear-binding coat-associated protein 2	NECAP2	0	15
K	105	Tri	20.22	Adaptin ear-binding coat-associated protein 2	NECAP2	0	15
K	106	Tri	20.22	Adaptin ear-binding coat-associated protein 2	NECAP2	0	15
R	379	Mono	42.87	Isoform 2 of Serine/threonine-protein kinase Nek2	NEK2	0	6
K	50	Tri	38.5	Serine/threonine-protein kinase Nek3	NEK3	0	2
R	91	Di	12.46	Serine/threonine-protein kinase Nek5	NEK5	0	1
R	24	Mono	12.11	Serine/threonine-protein kinase Nek9 (Fragment)	NEK9	0	1
K	184	Di	12.71	Nexilin (Fragment)	NEXN	0	12
R	32	Mono	21.81	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase (Fragment)	NGLY1	0	6
R	35	Mono	21.81	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase (Fragment)	NGLY1	0	6
R	35	Di	21.81	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase (Fragment)	NGLY1	0	6
R	32	Di	21.81	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase (Fragment)	NGLY1	0	6
K	566	Tri	13.75	Nidogen-2 (Fragment)	NID2	0	2
K	565	Tri	13.75	Nidogen-2 (Fragment)	NID2	0	2
K	1364	Tri	13.73	Ninein-like protein	NINL	0	8
R	2598	Mono	12.35	Nipped-B-like protein	NIPBL	2	10
K	2605	Mono	12.35	Nipped-B-like protein	NIPBL	2	10
K	223	Mono	22.21	Homeobox protein Nkx-2.1	NKX2-1	0	1
R	218	Mono	22.21	Homeobox protein Nkx-2.1	NKX2-1	0	1
K	905	Mono	27.92	NACHT, LRR and PYD domains-containing protein 5	NLRP5	2	0
K	1040	Mono	15.31	NACHT, LRR and PYD domains-containing protein 7	NLRP7	0	1
R	229	Di	26.21	NACHT, LRR and PYD domains-containing protein 8	NLRP8	0	4
R	36	Mono	20.45	Nucleoside diphosphate kinase 3 (Fragment)	NME3	0	2
K	22	Mono	20.28	Nucleoside diphosphate kinase 3 (Fragment)	NME3	6	54
K	198	Mono	18.08	Non-POU domain-containing octamer-binding protein (Fragment)	NONO	2	36
R	920	Mono	18.34	Nitric oxide synthase, brain	NOS1	0	12
K	918	Mono	18.34	Nitric oxide synthase, brain	NOS1	0	12
K	918	Di	21.12	Nitric oxide synthase, brain	NOS1	0	12
R	920	Di	18.34	Nitric oxide synthase, brain	NOS1	0	12
R	2047	Mono	14.26	Neurogenic locus notch homolog protein 2	NOTCH2	0	1
R	2051	Mono	14.26	Neurogenic locus notch homolog protein 2	NOTCH2	0	1
R	2051	Di	14.26	Neurogenic locus notch homolog protein 2	NOTCH2	0	1
R	2047	Di	14.26	Neurogenic locus notch homolog protein 2	NOTCH2	0	1
K	90	Mono	13.23	RNA-binding protein Nova-1	NOVA1	0	1

K	16	Tri	29.38	Nuclear protein localization protein 4 homolog	NPLOC4	0	1
K	16	Mono	27.85	Nucleophosmin (Fragment)	NPM1	1	0
K	16	Tri	37.8	Nucleophosmin (Fragment)	NPM1	2	0
K	54	Tri	34.9	Nucleophosmin	NPM1	1	0
K	171	Tri	12.39	Nucleoplasmin-2	NPM2	0	1
R	2	Di	19.88	Ribosome biogenesis protein NSA2 homolog (Fragment)	NSA2	0	6
K	43	Di	23.33	Nuclear speckle-splicing regulatory protein 1 (Fragment)	NSRP1	0	1
R	39	Mono	24.65	Cytosolic purine 5'-nucleotidase	NT5C2	0	7
R	396	Di	14.73	5'-nucleotidase domain-containing protein 2	NT5DC2	1	0
K	290	Mono	25.08	NudC domain-containing protein 3	NUDCD3	0	1
K	765	Mono	13.99	Nuclear mitotic apparatus protein 1 (Fragment)	NUMA1	0	1
K	59	Mono	25.27	Nucleoporin-62 C-terminal-like protein (Fragment)	NUP62CL	0	2
K	67	Mono	11.77	Nuclear pore complex protein Nup88 (Fragment)	NUP88	0	3
K	68	Mono	11.77	Nuclear pore complex protein Nup88 (Fragment)	NUP88	0	3
K	67	Di	11.77	Nuclear pore complex protein Nup88 (Fragment)	NUP88	0	3
K	68	Di	11.77	Nuclear pore complex protein Nup88 (Fragment)	NUP88	0	3
K	261	Mono	12.47	Nuclear RNA export factor 1 (Fragment)	NXF1	0	3
R	57	Mono	11.82	Neurexophilin-2	NXPH2	0	1
R	33	Di	28.99	Protein NYNRIN	NYNRIN	0	1
K	83	Di	18.34	Odorant-binding protein 2a	OBP2A	0	12
R	1305	Mono	15.47	Obscurin	OBSCN	0	1
R	989	Mono	16.32	Obscurin	OBSCN	0	2
R	5	Di	24.14	Outer dense fiber protein 2-like (Fragment)	ODF2L	0	1
R	10	Mono	19.13	Noelin (Fragment)	OLFM1	0	3
R	38	Di	14.37	Dynamin-like 120 kDa protein, mitochondrial (Fragment)	OPA1	0	2
K	245	Mono	13.82	Olfactory receptor 10J1	OR10J1	0	4
R	244	Mono	13.82	Olfactory receptor 10J1	OR10J1	0	4
K	245	Di	13.82	Olfactory receptor 10J1	OR10J1	0	4
R	244	Di	13.82	Olfactory receptor 10J1	OR10J1	0	4
K	284	Di	28.67	Olfactory receptor 1L1	OR1L1	0	1
K	234	Di	28.67	Olfactory receptor 1L3	OR1L3	0	1
K	271	Di	28.67	Olfactory receptor 1L6	OR1L6	0	1
K	227	Mono	21.44	Olfactory receptor 1M1	OR1M1	0	1
K	326	Mono	30.14	Olfactory receptor 1N2	OR1N2	0	5
R	302	Di	19.76	Olfactory receptor 2AE1	OR2AE1	6	26
K	85	Di	20.72	Olfactory receptor 2T11	OR2T11	0	9
K	87	Tri	12.8	Olfactory receptor 4A5	OR4A5	0	1
K	328	Mono	15.41	Olfactory receptor 5AL1	OR5AL1	0	1
K	311	Mono	26.97	Olfactory receptor 6C65	OR6C65	0	1
K	234	Di	28.67	Olfactory receptor 6N1	OR6N1	0	1
K	234	Tri	28.67	Olfactory receptor 7G3	OR7G3	0	1
K	308	Mono	25.12	Olfactory receptor 8U9	OR8U9	1	7
K	160	Mono	16.22	Protein odd-skipped-related 1	OSR1	0	10

R	164	Mono	16.22	Protein odd-skipped-related 1	OSR1	0	10
K	161	Mono	16.22	Protein odd-skipped-related 1	OSR1	0	10
R	126	Di	26.53	Otoferlin (Fragment)	OTOF	0	1
R	50	Mono	15.2	Otogelin-like protein (Fragment)	OTOGL	9	12
K	9	Tri	14.69	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	OXCT1	0	3
K	6	Mono	15.85	Polyadenylate-binding protein 1 (Fragment)	PABPC1	0	1
R	448	Di	82.97	Polyadenylate-binding protein 1	PABPC1	4	0
K	361	Mono	59.69	Polyadenylate-binding protein 1-like	PABPC1L	1	13
K	104	Mono	41.3	Polyadenylate-binding protein 3	PABPC3	0	2
R	41	Mono	23.01	Poly(A) binding protein, cytoplasmic 4 (Inducible form), isoform CRA_e	PABPC4	0	21
R	489	Di	70.11	Poly(A) binding protein, cytoplasmic 4 (Inducible form), isoform CRA_e	PABPC4	3	0
K	361	Di	59.69	Poly(A) binding protein, cytoplasmic 4 (Inducible form), isoform CRA_e	PABPC4	1	13
R	23	Di	80.58	Polyadenylate-binding protein 2	PABPN1	1	0
R	17	Di	102.06	Polyadenylate-binding protein 2	PABPN1	4	0
R	10	Di	13.3	P antigen family member 1	PAGE1	0	4
K	458	Tri	21.35	Inactive serine protease PAMR1	PAMR1	0	1
R	866	Di	16.26	Poly [ADP-ribose] polymerase 10	PARP10	0	1
K	396	Mono	20.31	PAX3- and PAX7-binding protein 1	PAXBP1	0	1
R	212	Di	29.95	Pre-B-cell leukemia transcription factor 4	PBX4	0	14
R	645	Mono	37.83	Protocadherin gamma-B4	PCDHGB4	0	7
R	753	Mono	13.36	Methyl-CpG-binding domain protein 1	PCM1	0	1
R	89	Mono	33.43	Protein-L-isoaspartate O-methyltransferase	PCMT1	0	1
K	136	Tri	12.13	Procollagen C-endopeptidase enhancer 2 (Fragment)	PCOLCE2	0	5
K	118	Tri	16.78	Proprotein convertase subtilisin/kexin type 7	PCSK7	0	3
R	138	Di	14.43	Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1B	PDE1B	0	1
K	62	Di	29.3	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	0	5
R	172	Di	12.81	3-phosphoinositide-dependent protein kinase 1	PDPK1	0	6
K	169	Di	12.81	3-phosphoinositide-dependent protein kinase 1	PDPK1	0	6
R	42	Di	40.03	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	PDPR	1	0
R	26	Di	13.09	HCG401289, isoform CRA_e	PDXK	0	1
R	27	Di	13.09	HCG401289, isoform CRA_e	PDXK	0	1
X	1	Tri	14.34	PDZ domain-containing protein 7 (Fragment)	PDZD7	1	1
R	558	Mono	20.66	E3 ubiquitin-protein ligase PDZRN3	PDZRN3	0	10
R	52	Mono	13.84	Ig lambda chain V-IV region MOL	PE=1	0	15
R	54	Mono	49.87	Ig lambda chain V-II region VIL	PE=1	0	10
R	52	Mono	13.84	Ig lambda chain V-IV region Bau	PE=1	0	15
R	276	Mono	18.46	HERV-H_2q24.1 provirus ancestral Env polyprotein	PE=2	0	1
R	31	Mono	54.62	Uncharacterized protein (Fragment)	PE=2	0	1
R	66	Mono	22.13	Golgin subfamily A member 2-like protein 4	PE=2	0	12
K	64	Mono	74.29	Uncharacterized protein (Fragment)	PE=2	12	0
R	703	Di	18.52	Uncharacterized protein (Fragment)	PE=2	0	9
K	2	Mono	15.01	Uncharacterized protein	PE=3	0	1
K	7	Mono	12.36	Uncharacterized protein (Fragment)	PE=3	0	21

R	265	Mono	51.74	Putative UPF0609 protein C4orf27-like	PE=3	0	1
K	106	Di	25.08	Uncharacterized protein	PE=3	0	1
R	41	Mono	29.94	Uncharacterized protein	PE=4	0	1
R	32	Mono	11.87	Uncharacterized protein	PE=4	0	1
R	53	Di	16.25	Uncharacterized protein	PE=4	0	7
R	9	Mono	15.63	Putative uncharacterized protein LOC389458	PE=5	0	3
K	44	Mono	33.1	Putative uncharacterized protein FLJ44553	PE=5	0	1
R	5	Mono	15.63	Putative uncharacterized protein LOC389458	PE=5	0	3
R	261	Di	14.71	Putative uncharacterized protein LOC100996504	PE=5	0	2
K	140	Mono	24.56	Platelet endothelial cell adhesion molecule	PECAM1	13	22
K	139	Mono	24.56	Platelet endothelial cell adhesion molecule	PECAM1	13	22
K	139	Di	24.56	Platelet endothelial cell adhesion molecule	PECAM1	13	22
K	140	Di	24.56	Platelet endothelial cell adhesion molecule	PECAM1	13	22
K	139	Tri	24.56	Platelet endothelial cell adhesion molecule	PECAM1	13	22
K	140	Tri	24.56	Platelet endothelial cell adhesion molecule	PECAM1	13	22
K	429	Mono	16.06	Pescadillo homolog	PES1	0	3
R	430	Di	12.86	Pescadillo homolog	PES1	0	1
K	38	Mono	18.37	Peroxisomal membrane protein 11A	PEX11A	0	4
K	35	Mono	18.37	Peroxisomal membrane protein 11A	PEX11A	0	4
K	239	Tri	12.86	Phosphoglycerate kinase	PGK1	0	1
K	267	Tri	12.86	Phosphoglycerate kinase 2	PGK2	0	1
R	222	Mono	24.02	PHD finger protein 10	PHF10	0	2
R	517	Di	27.92	Protein Jade-2	PHF15	0	11
R	517	Di	27.92	PHD finger protein 15, isoform CRA_b	PHF15	0	11
R	517	Di	27.92	PHD finger protein 15, isoform CRA_d	PHF15	0	11
R	517	Di	27.92	Isoform 2 of Protein Jade-2	PHF15	0	11
R	669	Mono	29.06	PH-interacting protein	PHIP	0	1
R	658	Di	29.06	PH-interacting protein	PHIP	0	1
R	892	Di	17.56	Pleckstrin homology-like domain family B member 1	PHLDB1	0	8
R	24	Mono	23.85	E3 SUMO-protein ligase PIAS3 (Fragment)	PIAS3	0	2
K	25	Mono	23.85	E3 SUMO-protein ligase PIAS3 (Fragment)	PIAS3	0	2
R	473	Di	19.27	Isoform 5 of p53-induced protein with a death domain	PIDD	0	6
R	60	Mono	41.71	GPI transamidase component PIG-S	PIGS	0	8
R	484	Mono	15.24	GPI transamidase component PIG-S	PIGS	0	1
K	540	Mono	12.1	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha	PIK3C2A	2	0
R	7	Mono	19.8	Phosphatidylinositol 3-kinase catalytic subunit type 3 (Fragment)	PIK3C3	0	1
K	1	Di	17.63	Phosphatidylinositol 3-kinase regulatory subunit alpha (Fragment)	PIK3R1	0	2
K	6	Tri	17.63	Phosphatidylinositol 3-kinase regulatory subunit alpha (Fragment)	PIK3R1	0	2
R	380	Di	18.01	Phosphatidylinositol 4-phosphate 5-kinase-like protein 1	PIP5KL1	0	7
K	255	Tri	29.65	Serine/threonine-protein kinase N1 (Fragment)	PKN1	0	3
R	25	Mono	17.51	Zinc finger protein PLAG1	PLAG1	0	1
K	178	Mono	13.75	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1	PLCG1	0	1
K	175	Mono	13.75	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1	PLCG1	0	1

K	318	Di	21.44	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-2	PLCH2	0	1
K	316	Di	21.44	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-2	PLCH2	0	1
X	1	Mono	13.02	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase zeta-1 (Fragment)	PLCZ1	0	1
R	42	Mono	11.93	Pleckstrin-2	PLEK2	0	1
K	1139	Mono	13.57	Pleckstrin homology domain-containing family A member 7	PLEKHA7	0	1
K	1140	Mono	13.57	Pleckstrin homology domain-containing family A member 7	PLEKHA7	0	1
K	123	Mono	18.23	Pleckstrin homology domain-containing family B member 1	PLEKHB1	0	1
K	452	Di	13.23	Perilipin-4	PLIN4	0	1
R	399	Mono	23.8	Serine/threonine-protein kinase PLK2	PLK2	0	3
K	624	Mono	14.84	Polyamine modulated factor 1 binding protein 1, isoform CRA_b	PMFBP1	0	1
K	633	Di	18.8	PNMA-like protein 2	PNMAL2	0	1
R	90	Mono	25.53	Pinin	PNN	0	2
K	324	Mono	11.64	Proline-rich nuclear receptor coactivator 1	PNRC1	1	0
K	408	Di	21.51	DNA polymerase	POLA1	0	5
K	72	Mono	14.41	Polymerase delta-interacting protein 3	POLDIP3	3	13
R	75	Mono	14.41	Polymerase delta-interacting protein 3	POLDIP3	3	13
K	927	Di	23.92	DNA-directed RNA polymerase	POLR2B	0	2
R	108	Di	16.72	DNA-directed RNA polymerase III subunit RPC7 (Fragment)	POLR3G	0	1
R	101	Mono	13.53	Popeye domain-containing protein 3 (Fragment)	POPDC3	33	69
R	255	Mono	13.53	Popeye domain-containing protein 3	POPDC3	33	69
K	100	Mono	14.5	Popeye domain-containing protein 3 (Fragment)	POPDC3	33	69
K	254	Mono	14.5	Popeye domain-containing protein 3	POPDC3	33	69
R	7	Di	17.38	Liprin-alpha-2 (Fragment)	PPFIA2	0	3
K	5	Tri	17.38	Liprin-alpha-2 (Fragment)	PPFIA2	0	3
R	579	Mono	19.32	Peptidyl-prolyl cis-trans isomerase G	PPIG	0	3
R	581	Mono	14.03	Protein phosphatase 1D	PPM1D	0	14
K	91	Di	13.64	Protein phosphatase 1 regulatory subunit 3C	PPP1R3C	0	6
K	162	Mono	12.69	Neurabin-1	PPP1R9A	0	3
K	165	Mono	12.69	Neurabin-1	PPP1R9A	0	3
K	163	Mono	12.69	Neurabin-1	PPP1R9A	0	3
K	288	Mono	48.54	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B gamma isoform	PPP2R2C	3	2
R	6	Di	13.22	Serine/threonine-protein phosphatase 2A regulatory subunit B'' subunit gamma (Fragment)	PPP2R3C	0	1
R	199	Mono	13.05	Serine/threonine-protein phosphatase 2A activator	PPP2R4	0	1
R	26	Di	27.74	Serine/threonine-protein phosphatase (Fragment)	PPP5C	0	1
K	138	Mono	21.46	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 2 protein	PREX2	0	2
K	673	Di	13.12	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 2 protein	PREX2	0	1
R	167	Mono	13.59	Putative 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxylase	PRHOXNB	0	1
K	396	Mono	29.93	5'-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1	1	0
K	52	Mono	12.16	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)	PRKAR2A	0	1
R	56	Mono	12.16	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)	PRKAR2A	0	1
R	56	Di	12.16	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)	PRKAR2A	0	1
K	52	Di	12.16	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)	PRKAR2A	0	1
K	326	Tri	12.84	cAMP-dependent protein kinase type II-beta regulatory subunit	PRKAR2B	0	6

R	187	Di	30.33	Protein kinase C epsilon type	PRKCE	0	2
K	1140	Mono	12.1	DNA-dependent protein kinase catalytic subunit	PRKDC	0	1
K	1141	Mono	12.1	DNA-dependent protein kinase catalytic subunit	PRKDC	0	1
R	81	Di	14.73	Protamine-3	PRM3	1	0
K	69	Tri	35.88	Pre-mRNA-processing-splicing factor 8 (Fragment)	PRPF8	5	0
K	61	Tri	12.86	Proline-rich protein 15-like protein	PRR15L	0	1
R	243	Mono	17	Proline-rich protein 18	PRR18	0	1
K	126	Mono	32.65	Trypsin-1	PRSS1	1	0
R	639	Mono	15.67	Neurotrypsin	PRSS12	0	4
K	1420	Mono	15.27	Periaxin	PRX	0	1
R	385	Di	27.91	Periaxin	PRX	0	1
R	1051	Di	12.58	PH and SEC7 domain-containing protein 4	PSD4	0	1
R	72	Di	15.81	Proteasome subunit beta type (Fragment)	PSMA4	9	12
R	112	Mono	18.92	Proteasome subunit beta type-8	PSMB8	0	4
K	109	Mono	18.92	Proteasome subunit beta type-8	PSMB8	0	4
K	197	Mono	15.41	26S proteasome non-ATPase regulatory subunit 12	PSMD12	0	1
K	36	Di	19.38	26S proteasome non-ATPase regulatory subunit 12	PSMD12	0	2
K	376	Tri	12.84	26S proteasome non-ATPase regulatory subunit 12	PSMD12	0	6
K	343	Mono	13.55	Phosphotriesterase-related protein	PTER	0	5
K	247	Mono	12.16	Prostaglandin G/H synthase 1	PTGS1	0	1
K	234	Mono	12.16	Prostaglandin G/H synthase 2	PTGS2	0	1
R	32	Di	15.16	Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	0	1
R	35	Di	15.16	Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	0	1
R	566	Di	20.28	Tyrosine-protein phosphatase non-receptor type 23	PTPN23	1	5
R	126	Mono	14.98	PTPRS protein	PTPRS	0	4
R	991	Di	25.15	Receptor-type tyrosine-protein phosphatase U	PTPRU	0	5
R	1339	Mono	13.4	Peroxidasin-like protein	PXDNL	4	0
K	167	Di	14.04	Paxillin	PXN	0	2
K	106	Mono	56.08	Pyrroline-5-carboxylate reductase 2	PYCR2	1	0
K	107	Mono	56.08	Pyrroline-5-carboxylate reductase 2	PYCR2	1	0
R	27	Mono	18.09	Queuine tRNA-ribosyltransferase subunit QTRTD1 (Fragment)	QTRTD1	0	1
R	166	Mono	17.03	R3H domain-containing protein 1	R3HDM1	0	1
R	69	Mono	38.79	Ras-related protein Rab-7b	RAB7B	1	30
K	104	Mono	13.76	Rab-like protein 6	RABL6	7	99
K	106	Mono	13.76	Rab-like protein 6	RABL6	7	99
R	24	Di	17.83	Rac GTPase-activating protein 1 (Fragment)	RACGAP1	0	1
R	511	Mono	23.13	Double-strand-break repair protein rad21-like protein 1	RAD21L1	0	2
R	850	Mono	13.26	DNA repair protein RAD50	RAD50	0	5
K	875	Mono	11.82	Ankycorbin	RAI14	1	0
K	873	Mono	11.82	Ankycorbin	RAI14	1	0
R	556	Mono	18.9	Ankycorbin	RAI14	0	1
K	558	Mono	18.9	Ankycorbin	RAI14	0	1
K	875	Di	11.82	Ankycorbin	RAI14	1	0

K	873	Di	11.82	Ankycorbin	RAI14	1	0
K	62	Mono	11.64	Ras-specific guanine nucleotide-releasing factor RalGPS2 (Fragment)	RALGPS2	1	0
K	65	Mono	11.64	Ras-specific guanine nucleotide-releasing factor RalGPS2 (Fragment)	RALGPS2	1	0
K	65	Di	11.64	Ras-specific guanine nucleotide-releasing factor RalGPS2 (Fragment)	RALGPS2	1	0
K	62	Di	11.64	Ras-specific guanine nucleotide-releasing factor RalGPS2 (Fragment)	RALGPS2	1	0
K	34	Di	42.7	RNA-binding protein Raly (Fragment)	RALY	0	2
K	34	Di	42.7	RNA-binding Raly-like protein	RALYL	0	2
K	214	Di	13.14	RNA-binding Raly-like protein	RALYL	0	1
R	41	Mono	18.02	Ran-specific GTPase-activating protein (Fragment)	RANBP1	0	3
R	1235	Mono	18.02	E3 SUMO-protein ligase RanBP2	RANBP2	0	3
K	356	Mono	29.08	Ran-binding protein 3-like	RANBP3L	0	1
K	368	Mono	13.57	Ran-binding protein 6	RANBP6	0	1
K	244	Tri	37.41	Retinoic acid receptor beta (Fragment)	RARB	0	1
K	419	Mono	11.89	Ras GTPase-activating protein 2	RASA2	0	1
R	280	Mono	34.01	Ras GTPase-activating protein 2	RASA2	0	3
R	43	Di	12.88	GTP-binding protein Rhes	RASD2	0	4
R	34	Mono	29.06	Ras-like protein family member 10A	RASL10A	1	0
R	52	Di	17.47	Ras-like protein family member 11B	RASL11B	0	1
R	141	Mono	15.63	HCG1647537, isoform CRA_b	RBAK	0	3
R	137	Mono	15.63	HCG1647537, isoform CRA_b	RBAK	0	3
K	1207	Mono	12.4	E3 ubiquitin-protein ligase RBBP6	RBBP6	0	1
R	55	Di	13.42	Uncharacterized protein	RBBP8	0	1
R	163	Di	21.2	RNA-binding protein 10	RBM10	0	4
R	366	Mono	14.39	Probable RNA-binding protein 19	RBM19	0	11
K	877	Tri	12.35	RNA-binding protein 27	RBM27	0	4
R	105	Di	83.51	Putative RNA-binding protein 3	RBM3	15	0
K	300	Mono	12.56	RNA-binding protein 34 (Fragment)	RBM34	0	1
R	53	Mono	29.83	RNA-binding protein 45 (Fragment)	RBM45	0	2
R	234	Di	28.89	RNA-binding motif protein, X chromosome, N-terminally processed	RBMX	1	0
R	384	Mono	12.18	Protein RCC2	RCC2	0	1
X	1	Mono	12.63	Reticulocalbin-1 (Fragment)	RCN1	1	7
K	9	Tri	12.63	Reticulocalbin-1 (Fragment)	RCN1	1	7
R	128	Mono	14.27	Reticulocalbin-3 (Fragment)	RCN3	0	1
K	193	Mono	17.8	ATP-dependent DNA helicase Q1 (Fragment)	RECQL	0	4
K	33	Mono	16.55	Receptor expression-enhancing protein 3	REEP3	0	1
K	42	Mono	15.68	Regenerating islet-derived protein 3-gamma	REG3G	0	1
K	45	Mono	15.68	Regenerating islet-derived protein 3-gamma	REG3G	0	1
K	45	Di	15.68	Regenerating islet-derived protein 3-gamma	REG3G	0	1
K	42	Di	15.68	Regenerating islet-derived protein 3-gamma	REG3G	0	1
K	45	Tri	15.68	Regenerating islet-derived protein 3-gamma	REG3G	0	1
K	42	Tri	15.68	Regenerating islet-derived protein 3-gamma	REG3G	0	1
K	312	Mono	15.25	Transcription factor p65 (Fragment)	RELA	0	1
K	496	Mono	13.92	RNA exonuclease 1 homolog	REXO1	17	67

R	495	Mono	13.92	RNA exonuclease 1 homolog	REXO1	17	67
R	498	Di	13.92	RNA exonuclease 1 homolog	REXO1	17	67
K	107	Mono	19.97	RNA exonuclease 4	REXO4	0	9
K	216	Tri	16.42	Replication factor C subunit 4	RFC4	0	5
R	11	Mono	51.45	Replication factor C subunit 5 (Fragment)	RFC5	0	1
R	965	Mono	17.18	MHC class II regulatory factor RFX1	RFX1	0	1
K	575	Di	13.75	Ral guanine nucleotide dissociation stimulator-like 2	RGL2	0	1
R	1398	Mono	18.02	RanBP2-like and GRIP domain-containing protein 3	RGPD3	0	3
K	473	Mono	13.22	Isoform 5 of Regulator of G-protein signaling 7	RGS7	0	1
R	360	Di	21.35	Regulator of G-protein-signaling 9	RGS9	0	8
K	19	Di	17.82	Regulator of G-protein-signaling 9	RGS9	0	4
R	201	Di	13.3	Ammonium transporter Rh type C	RHCG	0	4
R	602	Mono	12.96	Rho-related BTB domain-containing protein 2	RHOBTB2	0	1
R	475	Mono	13.26	Mitochondrial Rho GTPase 1	RHOT1	0	5
R	21	Mono	12.36	RIIa domain-containing protein 1	RIIAD1	0	2
K	97	Mono	15.25	RILP-like protein 1	RILPL1	0	1
R	530	Di	14.99	RIMS-binding protein 3C	RIMBP3C	0	2
R	1043	Mono	11.85	Regulating synaptic membrane exocytosis protein 2 (Fragment)	RIMS2	0	1
R	434	Mono	29.94	Isoform RIN1-delta of Ras and Rab interactor 1	RIN1	0	1
R	28	Mono	13.62	Ras and Rab interactor-like protein	RINL	0	3
K	25	Mono	13.62	Ras and Rab interactor-like protein	RINL	0	3
R	28	Di	13.62	Ras and Rab interactor-like protein	RINL	0	3
K	25	Di	13.62	Ras and Rab interactor-like protein	RINL	0	3
K	25	Tri	13.62	Ras and Rab interactor-like protein	RINL	0	3
R	6	Di	40.66	Ribonuclease kappa (Fragment)	RNASEK	1	0
R	167	Di	12.46	E3 ubiquitin-protein ligase RNF167	RNF167	0	1
K	6	Tri	24.06	Aminopeptidase B (Fragment)	RNPEP	0	1
R	1012	Mono	12.86	Rho-associated protein kinase 1	ROCK1	0	1
K	1013	Mono	12.86	Rho-associated protein kinase 1	ROCK1	0	1
R	801	Mono	12.86	Rho-associated protein kinase 2	ROCK2	0	1
K	802	Mono	12.86	Rho-associated protein kinase 2	ROCK2	0	1
R	49	Di	12.88	Receptor tyrosine kinase-like orphan receptor 2, isoform CRA_b	ROR2	0	4
R	55	Mono	13.24	Nuclear receptor ROR-alpha (Fragment)	RORA	0	1
R	51	Mono	13.24	Nuclear receptor ROR-alpha (Fragment)	RORA	0	1
R	51	Di	13.24	Nuclear receptor ROR-alpha (Fragment)	RORA	0	1
R	55	Di	13.24	Nuclear receptor ROR-alpha (Fragment)	RORA	0	1
R	26	Mono	50.02	60S ribosomal protein L26-like 1 (Fragment)	RPL26L1	3	4
K	41	Mono	12.33	60S ribosomal protein L5	RPL5	0	1
X	1	Mono	19.49	60S acidic ribosomal protein P2 (Fragment)	RPLP2	0	2
X	1	Di	19.49	60S acidic ribosomal protein P2 (Fragment)	RPLP2	0	2
K	387	Di	19.71	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	0	1
K	164	Mono	15.79	40S ribosomal protein S4, Y isoform 1 (Fragment)	RPS4Y1	0	3
R	58	Mono	38.4	40S ribosomal protein S4, Y isoform 1 (Fragment)	RPS4Y1	2	15

R	81	Mono	14.39	40S ribosomal protein S7	RPS7	0	1
R	6	Mono	17.12	RNA pseudouridylate synthase domain-containing protein 2	RPUSD2	0	9
R	5	Mono	17.12	RNA pseudouridylate synthase domain-containing protein 2	RPUSD2	0	9
K	42	Mono	27.89	Ras-related protein R-Ras	RRAS	1	2
K	27	Mono	27.89	Ras-related protein R-Ras2	RRAS2	1	2
K	63	Mono	30.14	REM2- and Rab-like small GTPase 1	RSG1	0	5
K	6	Di	24.56	Ribosomal L1 domain-containing protein 1 (Fragment)	RSL1D1	3	0
R	86	Di	11.92	Ribosomal L1 domain-containing protein 1 (Fragment)	RSL1D1	0	9
K	6	Tri	18.17	Ribosomal L1 domain-containing protein 1 (Fragment)	RSL1D1	0	4
R	219	Mono	24.02	Protein RTF2 homolog (Fragment)	RTFDC1	0	2
R	33	Di	18.52	Rhotekin-2	RTKN2	0	9
R	316	Mono	18.88	Reticulon-4 receptor (Fragment)	RTN4R	0	3
R	316	Di	13.61	Reticulon-4 receptor (Fragment)	RTN4R	0	1
K	125	Tri	15.22	RWD domain-containing protein 2A	RWDD2A	0	4
R	66	Mono	18.38	Ryanodine receptor 1 (Fragment)	RYR1	0	2
R	62	Di	18.38	Ryanodine receptor 1 (Fragment)	RYR1	0	2
R	455	Mono	14.96	Protein SAAL1	SAAL1	0	6
R	5	Di	30.07	Sacsin (Fragment)	SACS	0	2
K	2127	Di	14.17	Sacsin	SACS	0	8
K	746	Mono	14.74	Scaffold attachment factor B2	SAFB2	0	1
K	32	Di	16.06	Sterile alpha motif domain-containing protein 11 (Fragment)	SAMD11	0	3
K	1186	Mono	14.46	Sterile alpha motif domain-containing protein 9 (Fragment)	SAMD9	0	1
K	215	Mono	14.07	Secretogranin-2	SCG2	0	1
K	89	Mono	15.25	Secretogranin-3	SCG3	0	1
K	1190	Di	14.76	Sodium channel protein type 5 subunit alpha	SCN5A	0	2
R	2	Mono	11.82	Amiloride-sensitive sodium channel subunit delta	SCNN1D	26	53
K	8	Tri	11.82	Amiloride-sensitive sodium channel subunit delta	SCNN1D	26	53
R	200	Di	15.45	Protein SCO1 homolog, mitochondrial	SCO1	0	9
K	323	Di	18.34	Secretin receptor	SCTR	0	12
K	589	Mono	17.51	Signal peptide, CUB and EGF-like domain-containing protein 3	SCUBE3	2	8
R	628	Mono	22.78	Protein-associating with the carboxyl-terminal domain of ezrin	SCYL3	0	3
K	164	Mono	21.7	Syntenin-1	SDCBP	0	7
R	581	Mono	40.46	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	SDHA	0	1
R	356	Mono	12.15	Protein sidekick-2	SDK2	0	6
K	455	Di	17.8	Protein transport protein Sec16B	SEC16B	0	4
R	211	Mono	38.15	Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	0	1
R	38	Mono	17.74	Selenoprotein V	SELV	0	2
K	142	Di	18.87	Semaphorin-6A	SEMA6A	28	140
K	198	Mono	25.02	Alpha-1-antitrypsin	SERPINA1	0	4
K	132	Tri	14.69	Heparin cofactor 2	SERPIND1	0	2
K	660	Mono	23.49	SET-binding protein	SETBP1	0	4
K	661	Mono	14.04	SET-binding protein	SETBP1	0	2
R	524	Mono	18.27	Histone-lysine N-methyltransferase setd3	SETD3	0	5

R	2	Mono	40.39	Splicing factor, proline- and glutamine-rich (Fragment)	SFPQ	0	3
R	693	Di	31.22	Splicing factor, proline- and glutamine-rich	SFPQ	1	0
K	54	Mono	16.26	Splicing factor, suppressor of white-apricot homolog (Fragment)	SFSWAP	0	1
R	457	Di	15.36	Splicing factor, suppressor of white-apricot homolog (Fragment)	SFSWAP	0	18
R	571	Di	18.52	SH2 domain-containing protein 3C	SH2D3C	0	9
K	89	Mono	16	SH3 domain-binding protein 5	SH3BP5	0	2
K	244	Tri	15.88	SH3 domain-containing protein 19	SH3D19	0	3
K	34	Mono	17.81	Endophilin-A2	SH3GL1	0	1
K	176	Tri	31.03	Endophilin-B1	SH3GLB1	0	2
R	283	Di	11.74	E3 ubiquitin-protein ligase SH3RF1 (Fragment)	SH3RF1	1	0
R	284	Di	11.74	E3 ubiquitin-protein ligase SH3RF1 (Fragment)	SH3RF1	1	0
K	6	Tri	14.26	SHC-transforming protein 3	SHC3	0	1
K	675	Tri	45.81	Single-minded homolog 1	SIM1	1	6
K	85	Mono	22.59	Spindle and kinetochore-associated protein 3	SKA3	5	16
K	395	Mono	18.17	Spindle and kinetochore-associated protein 3	SKA3	0	2
K	92	Di	22.59	Spindle and kinetochore-associated protein 3	SKA3	5	16
R	755	Di	19.76	Superkiller viralicidic activity 2-like 2	SKIV2L2	6	26
R	8	Mono	11.74	Sodium/bile acid cotransporter 7	SLC10A7	2	14
R	6	Di	11.74	Sodium/bile acid cotransporter 7	SLC10A7	2	14
K	1061	Mono	15.67	Solute carrier family 12 (Sodium/potassium/chloride transporters), member 2, isoform CRA_a	SLC12A2	2	1
R	61	Mono	14.13	Solute carrier family 12 member 8 (Fragment)	SLC12A8	0	9
R	55	Mono	14.13	Solute carrier family 12 member 8 (Fragment)	SLC12A8	0	9
R	63	Mono	14.13	Solute carrier family 12 member 8 (Fragment)	SLC12A8	0	9
R	61	Di	14.13	Solute carrier family 12 member 8 (Fragment)	SLC12A8	0	9
R	63	Di	14.13	Solute carrier family 12 member 8 (Fragment)	SLC12A8	0	9
R	468	Mono	26.12	Monocarboxylate transporter 14 (Fragment)	SLC16A14	0	12
R	217	Mono	18.76	Sodium/potassium/calcium exchanger 4 (Fragment)	SLC24A4	0	1
R	147	Mono	16.1	Mitochondrial 2-oxoglutarate/malate carrier protein (Fragment)	SLC25A11	0	1
R	444	Mono	28.99	Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	0	1
K	23	Mono	47.66	ADP/ATP translocase 1	SLC25A4	25	14
R	56	Mono	40.54	Mitochondrial coenzyme A transporter SLC25A42	SLC25A42	0	4
K	52	Di	69.72	ADP/ATP translocase 2	SLC25A5	5	0
K	52	Tri	48.6	ADP/ATP translocase 2	SLC25A5	23	0
K	52	Tri	47.6	ADP/ATP translocase 3 (Fragment)	SLC25A6	4	0
K	233	Di	12.31	Bile acyl-CoA synthetase	SLC27A5	0	2
K	5	Tri	13.2	Putative sodium-coupled neutral amino acid transporter 10 (Fragment)	SLC38A10	0	1
K	33	Mono	23.49	Choline transporter-like protein 2 (Fragment)	SLC44A2	0	4
R	446	Mono	13.78	Proton-associated sugar transporter A	SLC45A1	0	4
K	444	Mono	13.78	Proton-associated sugar transporter A	SLC45A1	0	4
R	446	Di	13.78	Proton-associated sugar transporter A	SLC45A1	0	4
K	444	Di	13.78	Proton-associated sugar transporter A	SLC45A1	0	4
K	444	Tri	13.78	Proton-associated sugar transporter A	SLC45A1	0	4
K	869	Tri	34.58	Anion exchange protein 4	SLC4A9	0	1

K	479	Tri	12.35	Slit homolog 3 protein	SLIT3	0	4
K	8	Di	12.8	SAFB-like transcription modulator (Fragment)	SLTM	0	1
R	87	Di	28.99	Mothers against decapentaplegic homolog 4 (Fragment)	SMAD4	0	1
R	307	Mono	26.12	Probable global transcription activator SNF2L1 (Fragment)	SMARCA1	0	12
K	521	Mono	13.35	Probable global transcription activator SNF2L2 (Fragment)	SMARCA2	0	6
K	522	Mono	13.35	Probable global transcription activator SNF2L2 (Fragment)	SMARCA2	0	6
K	500	Mono	15.25	Probable global transcription activator SNF2L2 (Fragment)	SMARCA2	0	1
R	524	Mono	11.83	Probable global transcription activator SNF2L2 (Fragment)	SMARCA2	0	6
K	437	Di	13.14	Probable global transcription activator SNF2L2 (Fragment)	SMARCA2	0	1
R	57	Mono	15.36	Structural maintenance of chromosomes protein 1B	SMC1B	0	18
K	643	Mono	33.96	Structural maintenance of chromosomes protein 2	SMC2	0	4
R	281	Mono	13	Structural maintenance of chromosomes protein 4 (Fragment)	SMC4	1	3
K	719	Mono	25.49	Structural maintenance of chromosomes protein 6	SMC6	2	6
R	1602	Mono	17.23	Structural maintenance of chromosomes flexible hinge domain-containing protein 1	SMCHD1	0	1
K	700	Tri	17.25	Serine/threonine-protein kinase SMG1	SMG1	0	1
R	180	Di	18.19	Telomerase-binding protein EST1A (Fragment)	SMG6	0	4
K	7	Tri	30.43	Survival of motor neuron-related-splicing factor 30	SMNDC1	0	1
K	212	Mono	24.77	SET and MYND domain-containing protein 5	SMYD5	0	6
R	169	Mono	23.33	Synaptosomal-associated protein 47 (Fragment)	SNAP47	0	1
K	107	Di	13.64	Synphilin-1 (Fragment)	SNCAIP	0	6
K	319	Mono	13.07	Staphylococcal nuclease domain-containing protein 1	SND1	0	4
R	321	Mono	13.28	Staphylococcal nuclease domain-containing protein 1	SND1	0	4
R	1162	Mono	13.01	Sushi, nidogen and EGF-like domain-containing protein 1	SNED1	1	0
R	4	Di	32.56	Small nuclear ribonucleoprotein E	SNRPE	0	1
R	412	Mono	12.47	Protein SOGA3	SOGA3	1	6
R	1443	Mono	29.37	Sperm-associated antigen 17	SPAG17	2	0
K	1444	Mono	29.37	Sperm-associated antigen 17	SPAG17	2	0
K	1444	Di	29.37	Sperm-associated antigen 17	SPAG17	2	0
R	1443	Di	29.37	Sperm-associated antigen 17	SPAG17	2	0
K	1444	Tri	29.37	Sperm-associated antigen 17	SPAG17	2	0
X	1	Tri	19.43	Sperm-associated antigen 5 (Fragment)	SPAG5	0	2
K	282	Tri	13.17	Spermatogenesis-associated protein 1	SPATA1	0	1
K	279	Tri	13.17	Spermatogenesis-associated protein 1	SPATA1	0	1
K	104	Mono	20.4	Spermatogenesis-associated protein 24	SPATA24	2	4
K	107	Mono	20.4	Spermatogenesis-associated protein 24	SPATA24	2	4
K	104	Di	20.4	Spermatogenesis-associated protein 24	SPATA24	2	4
K	107	Di	20.4	Spermatogenesis-associated protein 24	SPATA24	2	4
K	104	Tri	20.4	Spermatogenesis-associated protein 24	SPATA24	2	4
K	107	Tri	20.4	Spermatogenesis-associated protein 24	SPATA24	2	4
R	605	Di	15.22	Isoform 2 of Spermatogenesis-associated protein 5-like protein 1	SPATA5L1	0	7
R	481	Mono	18.76	Cytospin-B	SPECC1	0	4
K	117	Mono	15.16	Cytospin-A (Fragment)	SPECC1L	0	1
R	110	Mono	15.16	Cytospin-A (Fragment)	SPECC1L	0	1

R	160	Mono	13.94	Kunitz-type protease inhibitor 1	SPINT1	5	0
K	307	Mono	12.31	Protein spinster homolog 2	SPNS2	0	1
K	537	Mono	13.62	Spectrin alpha chain, erythrocytic 1	SPTA1	0	1
K	281	Mono	14.23	Spectrin beta chain, erythrocytic	SPTB	0	4
R	386	Di	34.42	Spectrin beta chain, non-erythrocytic 4	SPTBN4	2	39
R	837	Di	21.27	SLIT-ROBO Rho GTPase activating protein 1, isoform CRA_a	SRGAP1	0	6
K	541	Mono	13.1	Serine/arginine repetitive matrix protein 5	SRRM5	0	1
R	543	Mono	13.1	Serine/arginine repetitive matrix protein 5	SRRM5	0	1
R	353	Mono	28.07	Serine/arginine-rich splicing factor 11	SRSF11	0	1
R	118	Di	14.43	Serine/arginine-rich splicing factor 12	SRSF12	0	1
R	403	Mono	27.74	Protein phosphatase Slingshot homolog 3	SSH3	0	1
K	418	Mono	24.18	Suppression of tumorigenicity 5 protein	ST5	0	3
R	600	Mono	12.11	Cohesin subunit SA-1	STAG1	0	1
K	382	Tri	13.52	Cohesin subunit SA-2 (Fragment)	STAG2	0	3
R	5	Di	19.4	Signal-transducing adaptor protein 2 (Fragment)	STAP2	0	2
K	110	Mono	14.11	Stathmin	STMN4	0	1
K	438	Mono	15.24	Storkhead-box protein 1	STOX1	0	1
K	436	Mono	15.24	Storkhead-box protein 1	STOX1	0	1
R	7	Di	30.37	Stereocilin (Fragment)	STRC	0	2
R	150	Mono	18.41	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial (Fragment)	SUCLG2	0	7
K	528	Mono	13.87	Extracellular sulfatase Sulf-2	SULF2	0	1
K	167	Mono	12.49	Sulfotransferase family cytosolic 2B member 1	SULT2B1	0	1
K	697	Tri	18.58	Supervillin	SVIL	0	4
R	145	Mono	13.42	Synaptonemal complex protein 1	SYCP1	0	1
R	145	Di	19.97	Synaptonemal complex protein 1	SYCP1	0	9
R	171	Mono	23.91	Synaptonemal complex protein 3	SYCP3	0	3
K	3128	Tri	13.2	Nesprin-2	SYNE2	0	1
R	211	Di	15.81	Synaptogyrin-3 (Fragment)	SYNGR3	9	12
K	593	Mono	14.8	Synemin	SYNM	0	1
K	8	Mono	13.44	Synaptotagmin-1 (Fragment)	SYT1	0	2
R	272	Mono	11.79	Tumor-associated calcium signal transducer 2	TACSTD2	0	3
R	192	Di	43.52	TATA-binding protein-associated factor 2N (Fragment)	TAF15	1	0
R	182	Di	63.07	TATA-binding protein-associated factor 2N (Fragment)	TAF15	4	0
R	203	Di	48.43	TATA-binding protein-associated factor 2N (Fragment)	TAF15	6	0
R	483	Di	83.81	TATA-binding protein-associated factor 2N	TAF15	12	0
R	8	Mono	21.27	Transcription initiation factor TFIID subunit 4 (Fragment)	TAF4	0	6
K	80	Tri	18.53	Transport and Golgi organization protein 6 homolog	TANGO6	0	2
K	1032	Mono	13.17	Probable methyltransferase TARBP1	TARBP1	0	1
K	92	Mono	12.1	Threonine--tRNA ligase, cytoplasmic	TARS	0	1
K	90	Mono	12.1	Threonine--tRNA ligase, cytoplasmic	TARS	0	1
R	163	Di	33.41	Threonine--tRNA ligase, mitochondrial	TARS2	0	1
R	6	Di	11.56	Taste receptor type 1 member 1 (Fragment)	TAS1R1	0	4
K	2	Mono	17.67	Threonine aspartase subunit beta (Fragment)	TASP1	0	1

K	6	Tri	12.97	Threonine aspartase subunit beta (Fragment)	TASP1	0	1
K	577	Tri	17.08	Tax1-binding protein 1	TAX1BP1	0	1
R	11	Mono	11.71	TBC1 domain family member 1 (Fragment)	TBC1D1	0	1
R	6	Mono	11.71	TBC1 domain family member 1 (Fragment)	TBC1D1	0	1
K	7	Mono	11.81	TBC1 domain family member 3 (Fragment)	TBC1D3	0	2
K	4	Mono	11.81	TBC1 domain family member 3 (Fragment)	TBC1D3	0	2
K	7	Di	11.81	TBC1 domain family member 3 (Fragment)	TBC1D3	0	2
K	4	Di	11.81	TBC1 domain family member 3 (Fragment)	TBC1D3	0	2
K	4	Tri	11.81	TBC1 domain family member 3 (Fragment)	TBC1D3	0	2
K	7	Tri	11.81	TBC1 domain family member 3 (Fragment)	TBC1D3	0	2
K	536	Mono	33.26	Thromboxane-A synthase	TBXAS1	0	1
K	700	Mono	29.03	Transcription elongation regulator 1	TCERG1	0	1
K	578	Mono	13.62	Transcription elongation regulator 1	TCERG1	0	1
R	702	Mono	29.03	Transcription elongation regulator 1	TCERG1	0	1
K	700	Di	29.03	Transcription elongation regulator 1	TCERG1	0	1
R	702	Di	29.03	Transcription elongation regulator 1	TCERG1	0	1
K	389	Di	31.78	Transcription elongation regulator 1-like protein	TCERG1L	0	1
K	33	Mono	15.15	Transcription factor 23	TCF23	0	3
R	32	Mono	15.15	Transcription factor 23	TCF23	0	3
R	32	Di	15.15	Transcription factor 23	TCF23	0	3
K	33	Di	15.15	Transcription factor 23	TCF23	0	3
X	1	Tri	13.41	Transcription factor 7 (Fragment)	TCF7	0	1
K	1437	Mono	27.9	Treacle protein	TCOF1	0	1
K	64	Tri	11.88	Treacle protein	TCOF1	1	6
K	393	Di	17.81	Teneurin-1	TENM1	0	8
R	2625	Mono	13.42	Teneurin-3	TENM3	0	1
K	1949	Tri	18.74	Teneurin-3	TENM3	0	5
K	288	Mono	12.13	Testis expressed sequence 9	TEX9	0	5
R	98	Mono	11.84	Transcription factor AP-2 gamma	TFAP2C	0	1
K	5	Mono	12.05	Transforming growth factor-beta-induced protein ig-h3 (Fragment)	TGFBI	0	3
K	2	Mono	18.46	Thyroid adenoma-associated protein (Fragment)	THADA	0	3
K	2	Di	18.46	Thyroid adenoma-associated protein (Fragment)	THADA	0	3
R	124	Mono	17.42	Isoform 3 of Thrombospondin type-1 domain-containing protein 4	THSD4	0	1
R	188	Di	32.67	Thrombospondin type-1 domain-containing protein 4	THSD4	3	0
R	79	Di	23.63	Treslin (Fragment)	TICRR	6	26
K	62	Mono	12.15	Tigger transposable element-derived protein 1	TIGD1	0	3
K	59	Tri	12.15	Tigger transposable element-derived protein 1	TIGD1	0	3
K	207	Mono	25.08	Tigger transposable element-derived protein 7	TIGD7	0	1
K	575	Tri	30.09	Transketolase	TKT	1	10
K	861	Tri	29.65	Talin-1	TLN1	0	3
R	63	Mono	13.28	T-cell leukemia homeobox protein 2 (Fragment)	TLX2	0	4
K	61	Mono	13.28	T-cell leukemia homeobox protein 2 (Fragment)	TLX2	0	4
K	61	Di	13.28	T-cell leukemia homeobox protein 2 (Fragment)	TLX2	0	4

R	63	Di	13.28	T-cell leukemia homeobox protein 2 (Fragment)	TLX2	0	4
K	42	Mono	12.27	Protein lifeguard 4	TMBIM4	0	9
K	215	Di	12.44	Transmembrane channel-like protein 2	TMC2	2	10
K	216	Di	12.44	Transmembrane channel-like protein 2	TMC2	2	10
K	215	Tri	12.44	Transmembrane channel-like protein 2	TMC2	2	10
K	216	Tri	12.44	Transmembrane channel-like protein 2	TMC2	2	10
R	68	Mono	27.91	Isoform 2 of Transmembrane and coiled-coil domain-containing protein 1	TMCO1	0	12
K	70	Tri	27.91	Isoform 2 of Transmembrane and coiled-coil domain-containing protein 1	TMCO1	0	12
K	4	Di	14.34	Transmembrane protein 126B (Fragment)	TMEM126B	0	4
R	240	Di	13.42	Transmembrane protein 156	TMEM156	0	1
R	217	Mono	11.74	Transmembrane protein 51	TMEM51	1	0
K	214	Mono	11.74	Transmembrane protein 51	TMEM51	1	0
K	214	Di	11.74	Transmembrane protein 51	TMEM51	1	0
R	217	Di	11.74	Transmembrane protein 51	TMEM51	1	0
K	214	Tri	11.74	Transmembrane protein 51	TMEM51	1	0
K	329	Di	27.92	Transmembrane protease serine 5	TMPRSS5	1	0
R	939	Mono	18.02	Transmembrane and TPR repeat-containing protein 1	TMTC1	1	0
K	166	Mono	28.9	Tumor necrosis factor ligand superfamily member 8	TNFSF8	0	2
K	234	Tri	13.32	Troponin T, fast skeletal muscle	TNNT3	0	2
K	28	Di	11.66	Transportin-2 (Fragment)	TNPO2	0	3
K	2160	Mono	12.79	Trinucleotide repeat-containing gene 18 protein	TNRC18	0	2
K	2156	Mono	12.79	Trinucleotide repeat-containing gene 18 protein	TNRC18	0	2
K	2156	Di	12.79	Trinucleotide repeat-containing gene 18 protein	TNRC18	0	2
K	2160	Di	12.79	Trinucleotide repeat-containing gene 18 protein	TNRC18	0	2
R	815	Mono	32.13	DNA topoisomerase 2-alpha	TOP2A	0	1
K	358	Mono	25.8	DNA topoisomerase 2 (Fragment)	TOP2B	0	5
R	57	Mono	11.85	DNA topoisomerase 3-alpha	TOP3A	0	1
R	59	Mono	11.85	DNA topoisomerase 3-alpha	TOP3A	0	1
R	57	Di	11.85	DNA topoisomerase 3-alpha	TOP3A	0	1
R	59	Di	11.85	DNA topoisomerase 3-alpha	TOP3A	0	1
R	86	Mono	17.83	TP53-regulating kinase	TP53RK	0	1
K	256	Mono	55.99	Triosephosphate isomerase	TPI1	2	0
K	106	Mono	31.32	Triosephosphate isomerase	TPI1	1	0
K	256	Tri	38.15	Triosephosphate isomerase	TPI1	1	0
R	61	Di	48.55	Transformer-2 protein homolog beta (Fragment)	TRA2B	2	1
K	257	Mono	36.18	TRAF3-interacting protein 1	TRAF3IP1	1	0
K	252	Di	36.18	TRAF3-interacting protein 1	TRAF3IP1	1	0
R	1097	Mono	28.92	Trafficking protein particle complex subunit 8	TRAPPC8	0	1
K	1099	Di	28.92	Trafficking protein particle complex subunit 8	TRAPPC8	0	1
R	263	Mono	13.02	Tripartite motif-containing protein 16	TRIM16	0	2
K	282	Di	12.4	Transcription intermediary factor 1-alpha	TRIM24	0	2
K	280	Di	12.4	Transcription intermediary factor 1-alpha	TRIM24	0	2
K	114	Di	12.87	Tripartite motif-containing protein 4 (Fragment)	TRIM4	0	1

K	463	Tri	36.41	Protein TRIM6-TRIM34	TRIM6-TRIM34	0	7
K	145	Mono	28.06	Tripartite motif-containing protein 77	TRIM77	0	1
K	72	Di	16.12	Tripartite motif-containing protein 77	TRIM77	0	1
R	439	Di	29.25	tRNA:m(4)X modification enzyme TRM13 homolog	TRMT13	0	2
R	25	Mono	32.82	tRNA (adenine(58)-N(1))-methyltransferase, mitochondrial (Fragment)	TRMT61B	0	1
K	98	Mono	30.21	Trophinin (Fragment)	TRO	1	0
R	510	Di	29.25	Isoform 8 of Transient receptor potential cation channel subfamily M member 3	TRPM3	0	2
R	264	Mono	15.67	Transient receptor potential cation channel subfamily M member 7	TRPM7	0	4
R	263	Mono	15.67	Transient receptor potential cation channel subfamily M member 7	TRPM7	0	4
K	572	Tri	11.97	Transient receptor potential cation channel subfamily M member 7	TRPM7	0	6
R	232	Mono	15.79	tRNA-splicing endonuclease subunit Sen2 (Fragment)	TSEN2	0	8
R	303	Di	19.93	Testis-specific serine kinase substrate	TSKS	0	1
K	229	Mono	19.58	Testis-specific serine/threonine-protein kinase 2	TSSK2	0	2
R	406	Di	23.18	Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein 2	TSTD2	0	2
K	60	Mono	20.05	Tetratricopeptide repeat protein 16	TTC16	1	3
K	584	Mono	12.56	Tetratricopeptide repeat protein 18	TTC18	0	1
R	182	Di	18.76	Tetratricopeptide repeat protein 26	TTC26	0	1
R	1675	Mono	43.18	E3 ubiquitin-protein ligase TTC3	TTC3	0	9
K	24	Tri	26.15	Tetratricopeptide repeat protein 39C	TTC39C	0	8
K	2197	Tri	15.09	Tetratricopeptide repeat protein 40	TTC40	0	3
K	608	Mono	17.8	Transcription termination factor 1	TTF1	0	4
R	83	Di	14.43	Tubulin polyglutamylase TTLL7	TTLL7	0	1
K	5075	Mono	12.7	Titin	TTN	0	16
K	5	Tri	46.3	Tubulin alpha-1A chain (Fragment)	TUBA1A	0	1
R	149	Mono	46.34	Tubulin alpha-1C chain	TUBA1C	0	2
R	460	Mono	35.93	Tubulin alpha-1C chain	TUBA1C	36	205
R	79	Mono	77.89	Tubulin alpha-3C/D chain	TUBA3C	2	10
R	324	Mono	39.16	Tubulin alpha-4A chain	TUBA4A	0	2
R	46	Mono	64.76	Tubulin beta chain	TUBB	6	9
R	28	Mono	64.76	Tubulin beta chain	TUBB	6	9
R	84	Mono	28.98	HCG1983504, isoform CRA_f	TUBB3	7	13
R	318	Mono	44.48	Tubulin beta-4A chain	TUBB4A	3	7
X	1	Mono	84.88	Tubulin beta-6 chain (Fragment)	TUBB6	0	15
R	390	Mono	36.66	Tubulin beta-6 chain	TUBB6	2	3
X	1	Di	72.33	Tubulin beta-6 chain (Fragment)	TUBB6	1	6
R	246	Mono	29.1	Tubulin beta-8 chain	TUBB8	0	2
R	308	Mono	49.12	Tubulin beta-8 chain	TUBB8	8	8
R	89	Mono	16.25	Golgi apparatus membrane protein TVP23 homolog A	TVP23A	0	7
K	53	Mono	20.06	Thioredoxin-interacting protein	TXNIP	1	0
R	356	Di	15.81	Thioredoxin reductase 1, cytoplasmic	TXNRD1	9	12
R	537	Di	15.81	Thioredoxin reductase 3 (Fragment)	TXNRD3	9	12
R	2	Di	30.36	Protein TXNRD3NB	TXNRD3NB	0	1
K	39	Mono	60.12	Splicing factor U2AF 35 kDa subunit	U2AF1	3	0

K	39	Mono	45.67	Isoform 2 of Splicing factor U2AF 35 kDa subunit	U2AF1	5	0
R	215	Di	19.4	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	UAP1L1	0	2
K	101	Mono	36.45	Ubiquitin-conjugating enzyme E2 D1	UBE2D1	0	16
K	101	Mono	36.45	Ubiquitin-conjugating enzyme E2 D4	UBE2D4	0	16
R	12	Di	30.04	Ubiquitin-like protein 4B	UBL4B	0	2
R	236	Mono	40.25	Ubiquilin-1	UBQLN1	0	1
K	88	Tri	15.37	Putative upstream-binding factor 1-like protein 6	UBTFL6	0	1
R	162	Mono	13.26	Ubiquitin carboxyl-terminal hydrolase isozyme L5	UCHL5	0	5
R	863	Mono	17.23	Netrin receptor UNC5B	UNC5B	0	1
K	64	Mono	13.14	Regulator of nonsense transcripts 2	UPF2	0	1
K	277	Tri	28.15	Regulator of nonsense transcripts 3A	UPF3A	0	1
K	362	Di	15.77	Ubiquitin carboxyl-terminal hydrolase 48	USP31	0	2
K	13	Tri	16.85	Ubiquitin carboxyl-terminal hydrolase 36	USP36	1	2
R	10	Di	17.64	Ubiquitin carboxyl-terminal hydrolase 49 (Fragment)	USP49	0	8
X	1	Tri	17.64	Ubiquitin carboxyl-terminal hydrolase 49 (Fragment)	USP49	0	8
R	810	Mono	16.32	Inactive ubiquitin carboxyl-terminal hydrolase 54	USP54	0	2
R	128	Di	12.47	Ubiquitin carboxyl-terminal hydrolase	USP7	1	6
K	193	Mono	16.06	Probable U3 small nucleolar RNA-associated protein 11	UTP11L	0	3
R	58	Mono	18.57	Histone demethylase UTY	UTY	0	8
K	85	Mono	49.46	Vesicle-associated membrane protein 1	VAMP1	0	3
K	207	Mono	17.45	Isoform 2 of Vesicle-associated membrane protein 7	VAMP7	0	11
R	210	Mono	17.45	Isoform 2 of Vesicle-associated membrane protein 7	VAMP7	0	11
R	189	Di	12.19	Valine--tRNA ligase	VARS	0	2
R	297	Mono	15.81	Vasorin	VASN	9	12
K	346	Mono	12.89	Synaptic vesicle membrane protein VAT-1 homolog-like	VAT1L	2	15
K	345	Mono	12.89	Synaptic vesicle membrane protein VAT-1 homolog-like	VAT1L	2	15
K	346	Di	12.89	Synaptic vesicle membrane protein VAT-1 homolog-like	VAT1L	2	15
K	345	Di	12.89	Synaptic vesicle membrane protein VAT-1 homolog-like	VAT1L	2	15
K	346	Tri	12.89	Synaptic vesicle membrane protein VAT-1 homolog-like	VAT1L	2	15
K	345	Tri	12.89	Synaptic vesicle membrane protein VAT-1 homolog-like	VAT1L	2	15
K	830	Tri	42.25	Vinculin	VCL	0	2
K	315	Tri	29.13	Transitional endoplasmic reticulum ATPase	VCP	2	0
K	238	Mono	56.57	Voltage-dependent anion-selective channel protein 2	VDAC2	7	12
R	78	Di	22.65	Villin-like protein	VILL	0	1
K	80	Di	22.65	Villin-like protein	VILL	0	1
R	42	Di	29.61	Vacuolar protein sorting-associated protein 13A (Fragment)	VPS13A	1	0
K	50	Tri	29.61	Vacuolar protein sorting-associated protein 13A (Fragment)	VPS13A	1	0
R	140	Mono	24.02	Chromosome 16 open reading frame 7, isoform CRA_b	VPS9D1	0	2
R	41	Di	20.92	Wiskott-Aldrich syndrome protein (Fragment)	WAS	0	1
R	190	Di	29.26	WAS protein family, member 3, isoform CRA_a	WASF3	0	11
R	442	Mono	15.78	WD repeat-containing protein 34	WDR34	0	14
R	86	Mono	14.28	WD repeat-containing protein 35	WDR35	0	9
R	129	Mono	18.72	WD repeat-containing protein 64	WDR64	0	1

R	17	Mono	15.36	WD repeat-containing protein 7 (Fragment)	WDR7	0	18
K	1486	Mono	13.57	WD repeat-containing protein 87	WDR87	0	1
K	1482	Mono	13.57	WD repeat-containing protein 87	WDR87	0	1
K	1917	Mono	17.05	WD repeat-containing protein 87	WDR87	1	1
R	134	Mono	16.79	Negative elongation factor A	WHSC2	0	2
K	61	Di	20.74	WAS/WASL-interacting protein family member 1	WIPF1	0	9
K	63	Di	20.74	WAS/WASL-interacting protein family member 1	WIPF1	0	9
K	61	Tri	20.74	WAS/WASL-interacting protein family member 1	WIPF1	0	9
K	63	Tri	20.74	WAS/WASL-interacting protein family member 1	WIPF1	0	9
R	35	Mono	18.87	WAS/WASL-interacting protein family member 2	WIPF2	28	140
K	68	Mono	20.74	WAS/WASL-interacting protein family member 2 (Fragment)	WIPF2	0	9
R	31	Mono	18.87	WAS/WASL-interacting protein family member 2	WIPF2	28	140
R	37	Mono	18.87	WAS/WASL-interacting protein family member 2	WIPF2	28	140
K	66	Mono	20.74	WAS/WASL-interacting protein family member 2 (Fragment)	WIPF2	0	9
K	68	Di	20.74	WAS/WASL-interacting protein family member 2 (Fragment)	WIPF2	0	9
K	66	Di	20.74	WAS/WASL-interacting protein family member 2 (Fragment)	WIPF2	0	9
K	66	Tri	20.74	WAS/WASL-interacting protein family member 2 (Fragment)	WIPF2	0	9
K	68	Tri	20.74	WAS/WASL-interacting protein family member 2 (Fragment)	WIPF2	0	9
K	267	Di	11.8	Protein Wnt-6	WNT6	0	2
R	279	Mono	21.7	Werner syndrome ATP-dependent helicase	WRN	1	15
R	280	Mono	21.7	Werner syndrome ATP-dependent helicase	WRN	1	15
R	279	Di	21.7	Werner syndrome ATP-dependent helicase	WRN	1	15
R	280	Di	21.7	Werner syndrome ATP-dependent helicase	WRN	1	15
K	101	Tri	15.1	Protein KIBRA (Fragment)	WWC1	0	13
K	138	Mono	37.3	WW domain-containing oxidoreductase	WWOX	0	1
R	106	Mono	14.78	WW domain-containing transcription regulator protein 1 (Fragment)	WWTR1	0	4
R	78	Di	12.58	5'-3' exoribonuclease 1	XRN1	0	1
R	103	Di	19.4	Protein yippee-like 5	YPEL5	0	2
R	138	Mono	24.73	YTH domain-containing protein 1	YTHDC1	0	3
R	1050	Mono	15.36	Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	0	18
K	129	Mono	45.31	14-3-3 protein eta (Fragment)	YWHAH	0	1
K	212	Mono	102.61	14-3-3 protein theta	YWHAQ	0	2
R	55	Mono	23.43	14-3-3 protein theta (Fragment)	YWHAQ	0	7
K	98	Mono	23.37	YY1-associated protein 1	YY1AP1	0	4
K	523	Mono	28.22	Zonadhesin	ZAN	0	1
R	30	Di	27.93	Zonadhesin	ZAN	9	0
R	629	Mono	54.39	Isoform 2 of Zinc finger B-box domain-containing protein 1	ZBBX	0	1
K	36	Mono	18.29	Z-DNA-binding protein 1	ZBP1	0	3
K	365	Mono	14.4	Zinc finger and BTB domain-containing protein 41	ZBTB41	0	1
K	921	Mono	15.24	Zinc finger CCCH domain-containing protein 18	ZC3H18	0	8
K	925	Mono	15.24	Zinc finger CCCH domain-containing protein 18	ZC3H18	0	8
K	925	Di	15.24	Zinc finger CCCH domain-containing protein 18	ZC3H18	0	8
R	914	Di	15.24	Zinc finger CCCH domain-containing protein 18	ZC3H18	0	8

K	921	Di	15.24	Zinc finger CCCH domain-containing protein 18	ZC3H18	0	8
K	921	Tri	15.24	Zinc finger CCCH domain-containing protein 18	ZC3H18	0	8
K	925	Tri	15.24	Zinc finger CCCH domain-containing protein 18	ZC3H18	0	8
R	786	Mono	13.75	Zinc finger CCCH domain-containing protein 6	ZC3H6	0	1
K	1848	Mono	12.86	DBF4-type zinc finger-containing protein 2	ZDBF2	0	5
K	153	Mono	16.81	AN1-type zinc finger protein 2A (Fragment)	ZFAND2A	0	1
K	153	Tri	12.02	AN1-type zinc finger protein 2A (Fragment)	ZFAND2A	0	6
K	161	Tri	24.89	AN1-type zinc finger protein 6	ZFAND6	0	13
R	578	Mono	16.73	Zinc finger protein 64 homolog, isoforms 3 and 4	ZFP64	0	1
R	581	Mono	16.73	Zinc finger protein 64 homolog, isoforms 3 and 4	ZFP64	0	1
R	581	Di	16.73	Zinc finger protein 64 homolog, isoforms 3 and 4	ZFP64	0	1
R	578	Di	16.73	Zinc finger protein 64 homolog, isoforms 3 and 4	ZFP64	0	1
K	198	Mono	14.75	Zinc finger matrin-type protein 3	ZMAT3	0	1
R	116	Di	12.47	Zinc finger protein 195 (Fragment)	ZNF195	1	6
K	7	Mono	11.93	Zinc finger protein 205 (Fragment)	ZNF205	0	1
R	409	Di	17.45	Zinc finger protein 222	ZNF222	0	1
R	175	Di	79.98	DBIRD complex subunit ZNF326	ZNF326	4	0
R	235	Di	60.64	DBIRD complex subunit ZNF326	ZNF326	5	0
K	62	Mono	13.51	Zinc finger protein 333	ZNF333	1	0
R	57	Di	16.41	Zinc finger protein 415	ZNF415	0	2
R	299	Di	14.15	Zinc finger protein 438	ZNF438	0	1
K	381	Tri	21.2	Zinc finger protein 438	ZNF438	0	2
R	317	Mono	18.89	Zinc finger protein 480	ZNF480	0	1
R	978	Di	16.1	Zinc finger protein 518B	ZNF518B	0	4
K	77	Di	12.86	Zinc finger protein 567	ZNF567	0	1
K	81	Tri	12.86	Zinc finger protein 567	ZNF567	0	1
K	79	Tri	12.86	Zinc finger protein 567	ZNF567	0	1
K	734	Mono	20.98	Zinc finger protein 616	ZNF616	0	7
K	153	Mono	17.08	Zinc finger protein 616	ZNF616	0	1
R	26	Mono	12.51	Zinc finger protein 618 (Fragment)	ZNF618	0	1
K	283	Mono	13.79	Zinc finger protein 711	ZNF711	0	4
K	66	Mono	12.26	Zinc finger protein 732	ZNF732	0	1
R	7	Di	36.93	Zinc finger protein 785 (Fragment)	ZNF785	5	0
R	8	Di	36.93	Zinc finger protein 785 (Fragment)	ZNF785	5	0
R	3	Mono	15.66	Zinc finger protein 816 (Fragment)	ZNF816	0	5
K	8	Di	15.66	Zinc finger protein 816 (Fragment)	ZNF816	0	5
K	429	Mono	12.32	Zinc finger protein 888	ZNF888	2	1

Appendix 4: List of methylation sites identified by MS/MS in starting material, cytosolic and nuclear fractions.

Sites identified at the 1% peptide FDR confidence level for the subcellular fractionation samples. The numbers on the right of the table indicate peptide hits for each site in each sample.

K/R	Site	Type	Mascot Score	Protein Name	Gene Name	Starting Material	Cytosol	Nucleus
R	778	Mono	29.61	Probable E3 ubiquitin-protein ligase MARCH10	March10	0	0	1
K	303	Di	13.98	Canalicular multispecific organic anion transporter 1	ABCC2	0	1	0
R	44	Mono	27.02	Abhydrolase domain-containing protein 15	ABHD15	0	0	1
R	36	Di	27.02	Abhydrolase domain-containing protein 15	ABHD15	0	0	1
K	51	Mono	24.76	Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	1	0	0
K	65	Mono	25.67	Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	0	1	0
K	74	Mono	25.67	Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	0	1	0
R	11	Mono	37.4	Very long-chain-specific acyl-CoA dehydrogenase, mitochondrial (Fragment)	ACADVL	0	4	0
R	6	Mono	16.22	Cytosolic acyl coenzyme A thioester hydrolase	ACOT7	1	0	0
K	129	Mono	69.15	Actin, alpha skeletal muscle	ACTA1	1	6	10
K	52	Mono	29.77	Actin, alpha skeletal muscle	ACTA1	0	1	0
K	250	Mono	25.96	Actin, alpha skeletal muscle	ACTA1	0	1	0
K	240	Mono	26	Actin, alpha skeletal muscle	ACTA1	1	0	0
K	63	Mono	33.47	Actin, alpha skeletal muscle	ACTA1	0	2	0
K	293	Di	37.36	Actin, aortic smooth muscle	ACTA2	4	3	0
K	113	Mono	28.38	Actin, cytoplasmic 2 (Fragment)	ACTB	0	1	0
R	63	Mono	19.09	Beta-actin-like protein 2	ACTBL2	0	2	0
R	331	Mono	13.29	Actin-like protein 9	ACTL9	3	0	0
R	83	Mono	27.9	Actinin, alpha 2, isoform CRA_b	ACTN2	0	1	0
R	89	Mono	27.9	Actinin, alpha 2, isoform CRA_b	ACTN2	0	1	0
K	86	Mono	27.9	Actinin, alpha 2, isoform CRA_b	ACTN2	0	1	0
R	93	Mono	27.9	Alpha-actinin-3	ACTN3	0	1	0
R	90	Mono	27.9	Alpha-actinin-3	ACTN3	0	1	0
K	96	Mono	27.9	Alpha-actinin-3	ACTN3	0	1	0
K	140	Di	82.75	Alpha-actinin-4	ACTN4	0	3	1
K	79	Mono	14.07	Disintegrin and metalloproteinase domain-containing protein 21	ADAM21	2	3	4
R	77	Mono	14.07	Disintegrin and metalloproteinase domain-containing protein 21	ADAM21	2	3	4
R	278	Mono	14.36	A disintegrin and metalloproteinase with thrombospondin motifs 10	ADAMTS10	3	0	0
R	829	Mono	34.33	ADAMTS-like protein 4	ADAMTSL4	0	1	2
K	196	Tri	24.5	tRNA-specific adenosine deaminase 1	ADAT1	0	0	1
K	121	Di	15.81	Alcohol dehydrogenase 4 (Fragment)	ADH4	0	0	1
R	117	Di	15.81	Alcohol dehydrogenase 4 (Fragment)	ADH4	0	0	1
K	284	Mono	27.26	Alcohol dehydrogenase class-3	ADH5	0	1	0
R	661	Mono	33.75	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 2	AGAP2	3	0	0
K	660	Mono	33.75	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 2	AGAP2	3	0	0
K	290	Di	15.44	Apoptosis-inducing factor 3	AIFM3	1	0	3

R	70	Mono	39.59	Aldo-keto reductase family 1 member B10	AKR1B10	1	2	1
K	443	Mono	51.11	Serum albumin	ALB	4	3	0
R	57	Di	29.69	THO complex subunit 4	ALYREF	1	0	6
R	204	Di	49.69	THO complex subunit 4	ALYREF	0	5	8
R	211	Di	70.85	THO complex subunit 4	ALYREF	5	4	12
R	70	Di	72.06	THO complex subunit 4	ALYREF	0	4	6
R	45	Di	66.35	THO complex subunit 4	ALYREF	5	5	17
R	460	Mono	24.96	Ankyrin repeat domain-containing protein 20A4	ANKRD20A4	0	0	1
R	63	Mono	51.87	Putative annexin A2-like protein	ANXA2P2	3	2	4
R	171	Mono	26.34	AP-1 complex subunit mu-1	AP1M1	8	0	0
K	456	Mono	29.1	AP-2 complex subunit beta	AP2B1	0	1	0
K	457	Mono	71.26	AP-2 complex subunit beta	AP2B1	2	2	0
K	93	Mono	41.58	AP-2 complex subunit beta	AP2B1	1	0	0
R	153	Mono	16.68	Apolipoprotein O	APOO	0	1	0
K	143	Mono	14.92	Atlastin-2	ATL2	1	0	2
R	151	Mono	14.92	Atlastin-2	ATL2	1	0	2
R	5	Mono	23.73	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2	2	1	0
X	1	Mono	23.73	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2	2	1	0
K	7	Mono	23.73	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2	2	1	0
R	5	Di	23.73	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2	2	1	0
X	1	Di	23.73	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2	2	1	0
K	7	Di	23.73	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2	2	1	0
K	7	Tri	23.73	Probable cation-transporting ATPase 13A2 (Fragment)	ATP13A2	2	1	0
K	719	Mono	33.11	Plasma membrane calcium-transporting ATPase 4 (Fragment)	ATP2B2	0	0	1
R	8	Di	38	Advillin	AVIL	2	1	6
X	1	Di	15.12	Large proline-rich protein BAG6 (Fragment)	BAG6	1	0	0
R	390	Mono	25.1	Bridging integrator 2	BIN2	0	0	1
K	1265	Tri	10.94	Ribosome biogenesis protein BMS1 homolog	BMS1	0	1	0
R	100	Di	36.14	Bromodomain and WD repeat-containing protein 1 (Fragment)	BRWD1	2	0	0
R	179	Di	12.92	Peripheral-type benzodiazepine receptor-associated protein 1	BZRAP1	0	0	1
K	401	Mono	24.86	Uncharacterized protein C10orf71	C10orf71	1	0	0
R	4	Di	10.94	Isoform 2 of UPF0668 protein C10orf76	C10orf76	0	0	1
K	18	Mono	32.91	Small acidic protein	C11orf58	0	2	0
R	14	Di	103.94	Isoform 2 of UPF0696 protein C11orf68	C11orf68	7	10	5
K	499	Mono	13.98	Uncharacterized protein C1orf168	C1orf168	0	1	0
R	2	Mono	29.24	Complement C2b fragment (Fragment)	C2	0	0	1
R	247	Di	15.81	Putative uncharacterized protein C3orf49	C3orf49	8	0	0
K	6	Di	11.24	Voltage-dependent calcium channel subunit alpha-2/delta-4 (Fragment)	CACNA2D4	1	1	1
K	163	Mono	30.22	Calmodulin	CALM2	2	0	0
R	174	Mono	30.22	Calmodulin	CALM2	2	0	0
R	174	Di	30.22	Calmodulin	CALM2	2	0	0
K	163	Di	30.22	Calmodulin	CALM2	2	0	0
K	163	Tri	55.95	Calmodulin	CALM2	3	1	0

R	15	Mono	25.56	Cullin-associated NEDD8-dissociated protein 2 (Fragment)	CAND2	1	1	2
R	23	Mono	29.51	Calpain-2 catalytic subunit	CAPN2	0	0	1
K	132	Mono	13.98	Caspase-8 subunit p10 (Fragment)	CASP8	0	1	0
K	505	Di	27.11	Zinc finger protein castor homolog 1	CASZ1	1	0	0
R	5	Mono	25.55	Protein CBFA2T3	CBFA2T3	0	0	1
K	143	Mono	61.96	Chromobox protein homolog 3	CBX3	1	0	2
K	1690	Di	26.47	Coiled-coil domain-containing protein 108	CCDC108	1	0	0
R	119	Mono	24.63	Coiled-coil domain-containing protein 13	CCDC13	0	0	1
K	304	Mono	23.73	Coiled-coil domain-containing protein 146	CCDC146	2	1	0
R	306	Mono	23.73	Coiled-coil domain-containing protein 146	CCDC146	2	1	0
R	306	Di	23.73	Coiled-coil domain-containing protein 146	CCDC146	2	1	0
K	304	Di	23.73	Coiled-coil domain-containing protein 146	CCDC146	2	1	0
K	228	Di	13.84	Coiled-coil domain-containing protein 73	CCDC73	0	1	0
K	226	Di	13.84	Coiled-coil domain-containing protein 73	CCDC73	0	1	0
K	234	Di	13.84	Coiled-coil domain-containing protein 73	CCDC73	0	1	0
K	228	Tri	13.84	Coiled-coil domain-containing protein 73	CCDC73	0	1	0
K	234	Tri	13.84	Coiled-coil domain-containing protein 73	CCDC73	0	1	0
K	226	Tri	13.84	Coiled-coil domain-containing protein 73	CCDC73	0	1	0
K	263	Mono	24.49	T-complex protein 1 subunit beta	CCT2	0	1	0
K	234	Mono	44.54	T-complex protein 1 subunit delta	CCT4	0	1	0
K	21	Mono	42.26	T-complex protein 1 subunit delta	CCT4	0	3	0
K	388	Mono	20.54	T-complex protein 1 subunit zeta-2	CCT6B	0	3	0
K	30	Tri	10.94	CDK5 regulatory subunit-associated protein 3	CDK5RAP3	0	1	0
R	71	Mono	32.35	CUGBP Elav-like family member 2	CELF2	0	0	1
R	332	Di	12.15	Centrosome-associated protein 350 (Fragment)	CEP350	1	0	0
K	68	Mono	39.75	Cofilin-1	CFL1	0	4	0
R	438	Mono	29.37	Muscarinic acetylcholine receptor M5	CHRM5	3	0	0
K	436	Mono	29.37	Muscarinic acetylcholine receptor M5	CHRM5	3	0	0
K	436	Di	29.37	Muscarinic acetylcholine receptor M5	CHRM5	3	0	0
R	438	Di	29.37	Muscarinic acetylcholine receptor M5	CHRM5	3	0	0
R	58	Di	38.12	Chromatin target of PRMT1 protein	CHTOP	0	0	3
R	148	Di	28.89	Chromatin target of PRMT1 protein	CHTOP	0	0	1
K	3	Mono	43.6	Clathrin heavy chain 1 (Fragment)	CLTC	1	0	0
K	3	Tri	43.6	Clathrin heavy chain 1 (Fragment)	CLTC	1	0	0
R	34	Mono	24.91	Isoform 2 of Cellular nucleic acid-binding protein	CNBP	1	0	0
R	32	Mono	24.91	Isoform 2 of Cellular nucleic acid-binding protein	CNBP	1	0	0
R	32	Di	24.91	Isoform 2 of Cellular nucleic acid-binding protein	CNBP	1	0	0
R	34	Di	24.91	Isoform 2 of Cellular nucleic acid-binding protein	CNBP	1	0	0
R	119	Mono	28.7	CCR4-NOT transcription complex subunit 8 (Fragment)	CNOT8	0	1	0
R	617	Mono	25.72	Rootletin (Fragment)	CROCC	8	4	0
K	7	Tri	13	Protein CASP	CUX1	0	1	0
K	243	Mono	18.82	Pre-mRNA-splicing factor CWC22 homolog	CWC22	11	10	14
R	455	Mono	11.2	Putative ATP-dependent RNA helicase DHX30	DHX30	1	0	0

R	452	Mono	11.2	Putative ATP-dependent RNA helicase DHX30	DHX30	1	0	0
R	796	Mono	26.6	Endoribonuclease Dicer	DICER1	0	0	1
K	202	Tri	31.22	Dynein heavy chain 2, axonemal (Fragment)	DNAH2	0	1	0
K	223	Mono	26.46	DnaJ homolog subfamily A member 2	DNAJA2	0	1	0
R	14	Mono	31.85	Protein DPCD (Fragment)	DPCD	8	10	10
R	114	Di	24.56	Desmocollin-1	DSC1	1	0	0
R	2522	Mono	29.37	Desmoplakin	DSP	3	0	0
R	1914	Mono	18.51	Desmoplakin	DSP	1	1	3
R	1912	Mono	18.51	Desmoplakin	DSP	1	1	3
R	2522	Di	29.37	Desmoplakin	DSP	3	0	0
R	1914	Di	18.51	Desmoplakin	DSP	1	1	3
R	1912	Di	18.51	Desmoplakin	DSP	1	1	3
K	2523	Di	29.37	Desmoplakin	DSP	3	0	0
K	2523	Tri	29.37	Desmoplakin	DSP	3	0	0
R	166	Mono	36.97	Elongation factor 1-alpha 1	EEF1A1	1	2	0
K	154	Mono	29.49	Elongation factor 1-alpha 1	EEF1A1	0	1	0
K	146	Mono	26.26	Elongation factor 1-alpha 1	EEF1A1	0	1	0
K	55	Mono	27.73	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	1	0	0
K	290	Mono	37.11	Elongation factor 1-alpha 1	EEF1A1	0	2	0
K	30	Mono	53.08	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	3	4	0
K	392	Mono	41.73	Elongation factor 1-alpha 1	EEF1A1	0	2	0
K	439	Mono	35.79	Elongation factor 1-alpha 1	EEF1A1	2	2	0
K	165	Mono	55.34	Elongation factor 1-alpha 1	EEF1A1	7	15	19
K	36	Mono	27.85	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	1	0	0
K	55	Di	61.97	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	7	6	0
K	36	Di	40.55	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	3	3	3
K	165	Di	59.94	Elongation factor 1-alpha 1	EEF1A1	11	36	34
K	318	Di	37.64	Elongation factor 1-alpha 1	EEF1A1	7	7	2
R	166	Di	36.97	Elongation factor 1-alpha 1	EEF1A1	1	2	0
K	439	Tri	33.82	Elongation factor 1-alpha 1	EEF1A1	1	0	0
K	165	Tri	76.44	Elongation factor 1-alpha 1	EEF1A1	13	32	38
K	79	Tri	61.49	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	4	6	0
K	318	Tri	46.28	Elongation factor 1-alpha 1	EEF1A1	15	50	27
K	36	Tri	45.91	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	18	36	20
K	165	Mono	53.67	Elongation factor 1-alpha 2	EEF1A2	1	1	4
K	439	Mono	35.79	Elongation factor 1-alpha 2	EEF1A2	2	2	0
K	165	Di	54.53	Elongation factor 1-alpha 2	EEF1A2	2	4	7
K	165	Tri	28.73	Elongation factor 1-alpha 2	EEF1A2	0	1	1
K	318	Tri	37.93	Elongation factor 1-alpha 2	EEF1A2	11	3	2
K	439	Tri	33.82	Elongation factor 1-alpha 2	EEF1A2	1	0	0
K	277	Mono	30.29	Elongation factor 1-gamma	EEF1G	0	1	0
K	512	Mono	25.76	Elongation factor 2	EEF2	0	1	0
K	258	Mono	32.34	Elongation factor 2	EEF2	0	1	0

K	407	Mono	29.58	Elongation factor 2	EEF2	0	3	0
K	525	Tri	30.53	Elongation factor 2	EEF2	7	5	3
R	606	Di	12.5	Eukaryotic translation initiation factor 3 subunit L	EIF3L	0	1	0
R	19	Di	61.77	Eukaryotic translation initiation factor 4H	EIF4H	2	5	0
R	269	Mono	22.84	TFIIH basal transcription factor complex helicase XPD subunit (Fragment)	ERCC2	0	1	0
R	39	Di	12.81	Homeobox protein ESX1	ESX1	1	0	0
K	147	Mono	24.91	Electron transfer flavoprotein subunit beta (Fragment)	ETFB	0	0	1
R	468	Di	36.39	RNA-binding protein EWS	EWSR1	0	0	1
R	433	Di	43.52	RNA-binding protein EWS	EWSR1	0	0	1
R	577	Di	88.19	RNA-binding protein EWS	EWSR1	0	3	8
R	289	Mono	12.83	Exocyst complex component 8	EXOC8	0	0	1
R	288	Mono	12.83	Exocyst complex component 8	EXOC8	0	0	1
K	276	Mono	25.05	Exosome complex component RRP42	EXOSC7	1	0	0
K	9	Di	26.02	Protein FAM127B	FAM127B	1	2	2
K	466	Mono	11.37	Protein fem-1 homolog C	FEM1C	1	0	0
K	42	Di	31.33	Fukutin	FKTN	12	5	11
K	44	Di	31.33	Fukutin	FKTN	12	5	11
K	14	Tri	10.94	Folate receptor beta (Fragment)	FOLR2	0	1	0
R	1834	Di	17.05	Fibrous sheath-interacting protein 2	FSIP2	0	1	0
R	216	Di	37.05	RNA-binding protein FUS	FUS	2	0	2
R	218	Di	37.05	RNA-binding protein FUS	FUS	2	0	2
R	253	Di	69.7	Ras GTPase-activating protein-binding protein 1	G3BP1	0	4	3
R	468	Di	40.16	Ras GTPase-activating protein-binding protein 2	G3BP2	1	1	4
K	42	Mono	41.23	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	0	2	0
K	60	Di	24.56	Ganglioside-induced differentiation-associated protein 2	GDAP2	1	0	0
K	189	Tri	12.11	Glial fibrillary acidic protein (Fragment)	GFAP	0	1	0
K	103	Mono	12.71	ADP-ribosylation factor-binding protein GGA1 (Fragment)	GGA1	10	0	3
R	68	Di	64.3	PERQ amino acid-rich with GYF domain-containing protein 2 (Fragment)	GIGYF2	1	0	0
R	64	Di	64.3	PERQ amino acid-rich with GYF domain-containing protein 2 (Fragment)	GIGYF2	1	0	0
R	149	Di	64.3	PERQ amino acid-rich with GYF domain-containing protein 2 (Fragment)	GIGYF2	1	0	0
R	153	Di	64.3	PERQ amino acid-rich with GYF domain-containing protein 2 (Fragment)	GIGYF2	1	0	0
R	264	Mono	22.87	G kinase-anchoring protein 1	GKAP1	0	0	2
K	265	Mono	22.87	G kinase-anchoring protein 1	GKAP1	0	0	2
R	15	Mono	18.43	Nucleoporin GLE1	GLE1	1	0	3
K	19	Tri	18.43	Nucleoporin GLE1	GLE1	1	0	3
R	173	Mono	14.07	Zinc finger protein GLI4	GLI4	4	0	0
R	36	Di	19.29	Putative oxidoreductase GLYR1 (Fragment)	GLYR1	0	0	2
K	17	Di	38.85	Guanine nucleotide-binding protein G(olf) subunit alpha (Fragment)	GNAL	3	0	1
R	159	Di	42.87	G-protein coupled receptor 20	GPR20	9	0	0
R	154	Di	42.87	G-protein coupled receptor 20	GPR20	9	0	0
R	809	Di	12.9	G-protein-coupled receptor 64	GPR64	0	2	0
K	798	Mono	11.74	Glutamate receptor ionotropic, kainate 3	GRIK3	1	0	0
K	796	Mono	11.74	Glutamate receptor ionotropic, kainate 3	GRIK3	1	0	0

K	798	Di	11.74	Glutamate receptor ionotropic, kainate 3	GRIK3	1	0	0
K	796	Di	11.74	Glutamate receptor ionotropic, kainate 3	GRIK3	1	0	0
K	798	Tri	11.74	Glutamate receptor ionotropic, kainate 3	GRIK3	1	0	0
K	796	Tri	11.74	Glutamate receptor ionotropic, kainate 3	GRIK3	1	0	0
K	739	Tri	12.5	Heat-stable enterotoxin receptor	GUCY2C	1	3	3
K	82	Mono	54.75	Histone H2A (Fragment)	H2AFJ	1	0	0
K	82	Tri	39.6	Histone H2A (Fragment)	H2AFJ	2	0	0
K	10	Mono	37.56	Histone H3	H3F3A	0	0	1
K	80	Mono	70.09	Histone H3	H3F3A	0	10	1
K	80	Di	46.25	Histone H3	H3F3A	9	1	6
K	28	Di	55.9	Histone H3	H3F3A	1	0	4
K	10	Di	55.41	Histone H3	H3F3A	0	0	1
K	80	Tri	67.76	Histone H3	H3F3A	6	6	87
R	656	Di	46.03	HCG2044799	hCG_2044799	3	4	7
R	101	Mono	11.7	HD domain-containing protein 2	HDDC2	0	0	1
K	107	Di	11.7	HD domain-containing protein 2	HDDC2	0	0	1
R	67	Mono	24.73	Isoform 4 of Protein-cysteine N-palmitoyltransferase HHAT	HHAT	0	0	1
K	78	Mono	33.3	Histone H1.5	HIST1H1B	0	0	5
K	118	Mono	40.61	Histone H1.3	HIST1H1D	1	0	4
K	119	Mono	54.75	Histone H2A type 1-B/E	HIST1H2AB	1	0	0
K	119	Tri	39.6	Histone H2A type 1-B/E	HIST1H2AB	2	0	0
K	37	Mono	64.85	Histone H3.1	HIST1H3A	0	0	1
K	38	Mono	33.89	Histone H3.1	HIST1H3A	0	0	1
K	28	Mono	54.25	Histone H3.1	HIST1H3A	7	0	12
K	28	Di	84.95	Histone H3.1	HIST1H3A	16	3	29
K	37	Di	37.92	Histone H3.1	HIST1H3A	0	0	2
K	38	Di	30.18	Histone H3.1	HIST1H3A	0	0	1
K	28	Tri	49.95	Histone H3.1	HIST1H3A	1	3	3
K	92	Mono	71.29	Histone H4	HIST1H4A	2	0	4
K	78	Mono	42.98	Histone H4	HIST1H4A	4	0	0
K	32	Mono	28.33	Histone H4	HIST1H4A	2	0	0
R	89	Mono	49.87	Histone H2A type 2-B	HIST2H2AB	0	0	1
K	58	Mono	52.12	Histone H2B	HIST2H2BF	6	0	0
K	109	Tri	27.79	Histone H2B	HIST2H2BF	1	0	0
K	58	Tri	39.16	Histone H2B	HIST2H2BF	3	0	0
R	291	Di	97.31	Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	6	0	11
R	31	Mono	106.62	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	10	0	37
K	112	Mono	65.93	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	0	0	6
K	298	Mono	25.13	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	0	0	1
R	225	Di	74.02	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	3	0	5
R	225	Di	32.93	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	1	0	0
R	215	Di	71.39	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	1	0	0
R	213	Di	71.39	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	1	0	0

R	206	Di	80.99	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	2	0	1
R	196	Di	69.17	Heterogeneous nuclear ribonucleoprotein A1-like 2	HNRNPA1L2	23	10	29
R	194	Di	71.39	Heterogeneous nuclear ribonucleoprotein A1-like 2	HNRNPA1L2	15	7	37
R	213	Mono	27.98	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	1	0	0
R	52	Mono	90.41	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	3	0	5
R	52	Di	106.62	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	10	0	37
R	22	Di	47.03	Heterogeneous nuclear ribonucleoprotein A3 (Fragment)	HNRNPA3	0	0	3
R	245	Mono	28.26	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	2	0	0
R	248	Mono	25.7	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	1	0	0
R	270	Di	35.3	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	0	0	6
R	245	Di	49.97	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	0	0	1
R	248	Di	49.97	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	0	0	1
R	226	Mono	25.2	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	1	0	0
R	220	Mono	25.2	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	1	0	0
R	220	Di	25.2	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	1	0	0
R	293	Di	35.42	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	0	0	6
R	226	Di	25.2	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	1	0	0
K	99	Mono	43.37	Heterogeneous nuclear ribonucleoprotein R	HNRNPR	1	0	1
R	739	Di	41.61	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	1	0	3
R	733	Di	41.61	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	1	0	3
R	762	Di	24.47	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	0	0	1
K	161	Mono	46.24	Heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	1	0	0
K	162	Mono	46.24	Heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	1	0	0
R	408	Di	49.24	Heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	1	0	7
K	499	Mono	36.68	Heat shock protein HSP 90-alpha	HSP90AA1	0	6	0
K	112	Mono	31.88	Heat shock protein HSP 90-alpha	HSP90AA1	0	1	0
K	100	Mono	33.45	Heat shock protein HSP 90-alpha (Fragment)	HSP90AA1	0	2	0
K	546	Tri	28.39	Heat shock protein HSP 90-alpha	HSP90AA1	1	0	0
R	202	Di	56.35	Putative heat shock protein HSP 90-alpha A2	HSP90AA2	1	7	0
K	95	Mono	33.45	Heat shock protein HSP 90-beta	HSP90AB1	0	2	0
K	148	Mono	41.76	Heat shock protein HSP 90-beta	HSP90AB1	0	5	0
K	107	Mono	31.88	Putative heat shock protein HSP 90-beta 2	HSP90AB2P	0	1	0
R	378	Mono	37.71	Heat shock 70 kDa protein 1A/1B	HSPA1A	1	3	17
K	470	Tri	36.45	Heat shock 70 kDa protein 1A/1B	HSPA1A	1	4	0
R	10	Di	27.29	Heat shock 70 kDa protein 4L	HSPA4L	1	0	0
K	154	Di	45.89	78 kDa glucose-regulated protein	HSPA5	2	2	1
K	585	Tri	59.56	78 kDa glucose-regulated protein	HSPA5	0	0	1
K	56	Mono	47.45	Heat shock cognate 71 kDa protein (Fragment)	HSPA8	0	4	0
R	233	Mono	28.6	Heat shock cognate 71 kDa protein	HSPA8	0	0	3
K	56	Tri	22.86	Heat shock cognate 71 kDa protein (Fragment)	HSPA8	1	0	0
K	325	Tri	43.43	Heat shock cognate 71 kDa protein	HSPA8	2	1	1
K	405	Mono	17.15	60 kDa heat shock protein, mitochondrial	HSPD1	1	0	0
R	6	Di	16.22	Isoleucine--tRNA ligase, mitochondrial	IARS2	1	0	0

K	98	Tri	24.59	Peptidyl-tRNA hydrolase ICT1, mitochondrial (Fragment)	ICT1	7	7	2
K	437	Mono	13.73	Inosine-5'-monophosphate dehydrogenase	IMPDH1	2	0	1
K	435	Mono	13.73	Inosine-5'-monophosphate dehydrogenase	IMPDH1	2	0	1
K	437	Di	13.73	Inosine-5'-monophosphate dehydrogenase	IMPDH1	2	0	1
K	435	Di	13.73	Inosine-5'-monophosphate dehydrogenase	IMPDH1	2	0	1
R	85	Mono	35.74	Importin-8 (Fragment)	IPO8	2	0	0
K	324	Mono	23.36	ITGA10 protein	ITGA10	5	0	1
K	238	Mono	16.39	Integral membrane protein 2A	ITM2A	0	0	1
R	230	Di	16.39	Integral membrane protein 2A	ITM2A	0	0	1
K	794	Mono	28.58	Protein IWS1 homolog	IWS1	0	1	0
R	88	Mono	11.51	Jun dimerization protein 2 (Fragment)	JDP2	2	0	0
R	90	Mono	11.51	Jun dimerization protein 2 (Fragment)	JDP2	2	0	0
R	90	Di	11.51	Jun dimerization protein 2 (Fragment)	JDP2	2	0	0
R	88	Di	11.51	Jun dimerization protein 2 (Fragment)	JDP2	2	0	0
K	357	Tri	19.29	Potassium channel subfamily K member 13	KCNK13	0	0	2
R	658	Mono	33.25	Lysine-specific demethylase 3B	KDM3B	0	0	1
R	383	Di	19.29	Lysine-specific demethylase 5A (Fragment)	KDM5A	0	0	2
R	320	Di	31.09	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	1	0	0
R	325	Di	40.06	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	2	0	1
R	346	Di	35.17	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	2	5	0
R	348	Di	30.4	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	3	0	6
K	164	Di	15.68	Pumilio domain-containing protein KIAA0020	KIAA0020	4	1	0
R	25	Mono	24.89	PCNA-associated factor	KIAA0101	0	1	0
R	443	Di	26.83	Uncharacterized protein KIAA1522	KIAA1522	1	0	0
R	758	Di	12.67	WD repeat-containing protein KIAA1875	KIAA1875	3	0	0
R	197	Mono	28.55	Krueppel-like factor 10	KLF10	0	0	1
K	1350	Mono	13.98	Histone-lysine N-methyltransferase MLL (Fragment)	KMT2A	0	1	0
K	1712	Mono	19.34	Histone-lysine N-methyltransferase 2D	KMT2D	0	0	2
K	1711	Mono	19.34	Histone-lysine N-methyltransferase 2D	KMT2D	0	0	2
R	1709	Mono	19.34	Histone-lysine N-methyltransferase 2D	KMT2D	0	0	2
K	1982	Tri	22.86	Laminin subunit alpha-2	LAMA2	1	0	0
K	319	Mono	29.26	L-lactate dehydrogenase B chain	LDHB	0	1	0
K	279	Mono	42.69	L-lactate dehydrogenase B chain	LDHB	0	1	0
K	308	Mono	54.71	L-lactate dehydrogenase B chain	LDHB	0	3	0
K	264	Mono	27.74	L-lactate dehydrogenase	LDHC	0	5	0
K	84	Mono	16.81	Lutropin-choriogonadotropic hormone receptor	LHCGR	0	1	0
K	13	Di	27.24	Protein Lines homolog (Fragment)	LINS	0	1	0
R	4	Mono	28.77	Lipase member I (Fragment)	LIPI	0	0	2
R	236	Di	15.81	Lysyl oxidase homolog 3	LOXL3	8	0	0
K	93	Tri	16.81	Leucine-rich repeat-containing protein 40	LRRC40	0	1	0
K	34	Mono	13.19	Mastermind-like domain-containing protein 1 (Fragment)	MAMLD1	2	0	0
R	428	Mono	31.24	Alpha-mannosidase 2	MAN2A1	7	0	0
R	1170	Mono	24.89	Mitogen-activated protein kinase-binding protein 1	MAPKBP1	0	1	0

K	391	Tri	16.57	Matrin-3	MATR3	0	0	1
R	435	Mono	28.34	DNA replication licensing factor MCM6	MCM6	0	0	1
R	221	Di	16.9	Calcium uniporter protein, mitochondrial	MCU	0	0	2
R	211	Mono	22.84	Methionine aminopeptidase 1D, mitochondrial	METAP1D	0	1	0
K	115	Mono	29.37	Protein-methionine sulfoxide oxidase MICAL1 (Fragment)	MICAL1	3	0	0
R	116	Mono	29.37	Protein-methionine sulfoxide oxidase MICAL1 (Fragment)	MICAL1	3	0	0
R	116	Di	29.37	Protein-methionine sulfoxide oxidase MICAL1 (Fragment)	MICAL1	3	0	0
K	115	Di	29.37	Protein-methionine sulfoxide oxidase MICAL1 (Fragment)	MICAL1	3	0	0
K	115	Tri	29.37	Protein-methionine sulfoxide oxidase MICAL1 (Fragment)	MICAL1	3	0	0
R	205	Mono	16.9	Modulator of apoptosis 1	MOAP1	0	0	2
R	91	Mono	25.72	Mov10, Moloney leukemia virus 10, homolog (Mouse), isoform CRA_a	MOV10	8	4	0
K	277	Tri	10.94	28S ribosomal protein S2, mitochondrial	MRPS2	0	1	0
R	141	Mono	20.65	Myelin expression factor 2	MYEF2	2	2	4
R	163	Mono	28.5	Myosin-10 (Fragment)	MYH10	1	0	0
K	578	Mono	31.72	Myosin-10	MYH10	0	1	0
K	106	Mono	29.45	Myosin-10 (Fragment)	MYH10	0	1	0
R	108	Mono	29.45	Myosin-10 (Fragment)	MYH10	0	1	0
R	146	Di	12.83	N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae), isoform CRA_a	NAA20	0	0	1
K	150	Tri	12.83	N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae), isoform CRA_a	NAA20	0	0	1
K	63	Di	34.86	Nucleosome assembly protein 1-like 4 (Fragment)	NAP1L4	2	0	0
K	235	Mono	31.18	Nucleolin (Fragment)	NCL	0	1	0
K	109	Mono	26.65	Nucleolin (Fragment)	NCL	0	1	0
K	108	Mono	26.65	Nucleolin (Fragment)	NCL	0	1	0
K	490	Di	11.85	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 2	NDST2	0	1	0
K	1183	Tri	12.5	Neurofibromin truncated (Fragment)	NF1	1	3	3
R	64	Di	11.37	NHS-like protein 2	NHSL2	1	0	0
R	344	Mono	14.63	Nucleolar MIF4G domain-containing protein 1	NOM1	0	0	1
K	16	Mono	30.46	Nucleophosmin (Fragment)	NPM1	1	2	0
K	16	Tri	34.42	Nucleophosmin (Fragment)	NPM1	1	0	0
K	54	Tri	34.9	Nucleophosmin	NPM1	1	0	0
K	88	Mono	51.85	GTPase NRas	NRAS	0	0	1
K	99	Di	25.05	Neuregulin-1 (Fragment)	NRG1	0	1	0
R	396	Di	15.44	5'-nucleotidase domain-containing protein 2	NT5DC2	1	0	3
R	50	Mono	15.12	Otogelin-like protein (Fragment)	OTOGL	8	0	0
R	448	Di	82.97	Polyadenylate-binding protein 1	PABPC1	5	4	3
K	361	Mono	31.71	Polyadenylate-binding protein 1-like	PABPC1L	1	1	0
K	361	Di	31.71	Poly(A) binding protein, cytoplasmic 4 (Inducible form), isoform CRA_e	PABPC4	1	1	0
R	489	Di	70.11	Poly(A) binding protein, cytoplasmic 4 (Inducible form), isoform CRA_e	PABPC4	3	0	4
R	17	Di	104.86	Polyadenylate-binding protein 2	PABPN1	4	4	11
R	23	Di	80.58	Polyadenylate-binding protein 2	PABPN1	1	2	0
K	110	Mono	30.4	Protein DJ-1	PARK7	0	1	0
R	346	Di	73.37	Poly(rC)-binding protein 1	PCBP1	0	6	8
R	54	Mono	16.81	Ig lambda chain V-II region VIL	PE=1	0	1	0

K	64	Mono	76.95	Uncharacterized protein (Fragment)	PE=2	9	15	18
K	64	Di	28.1	Uncharacterized protein (Fragment)	PE=2	0	0	1
K	37	Mono	19.34	Putative Rab-43-like protein ENSP00000330714	PE=5	0	0	1
K	278	Tri	27.91	Period circadian protein homolog 2	PER2	1	1	0
K	392	Mono	13.98	Phosphatase and actin regulator 4	PHACTR4	0	1	0
K	170	Mono	25.95	D-3-phosphoglycerate dehydrogenase	PHGDH	0	1	0
K	67	Mono	11	Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma (Fragment)	PIP4K2C	0	0	1
K	710	Di	15.33	Phospholipase D1	PLD1	0	4	0
R	75	Mono	14.41	Polymerase delta-interacting protein 3	POLDIP3	3	0	0
K	72	Mono	14.41	Polymerase delta-interacting protein 3	POLDIP3	3	0	0
K	171	Mono	24.76	Peptidyl-prolyl cis-trans isomerase B	PPIB	1	0	0
K	100	Mono	24.76	Peptidyl-prolyl cis-trans isomerase	PPIH	1	0	0
R	341	Mono	25.67	Probable protein phosphatase 1N (Fragment)	PPM1N	0	1	2
K	288	Mono	52.99	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B gamma isoform	PPP2R2C	2	3	0
R	196	Mono	15.15	PRAME family member 23	PRAMEF23	0	0	1
R	193	Mono	15.15	PRAME family member 23	PRAMEF23	0	0	1
K	396	Mono	29.93	5'-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1	1	0	0
R	283	Mono	10.87	cAMP-dependent protein kinase catalytic subunit PRKX	PRKX	0	1	0
R	81	Di	15.44	Protamine-3	PRM3	1	0	3
K	339	Mono	29.28	Protein S (Alpha), isoform CRA_b	PROS1	0	0	1
K	342	Mono	29.28	Protein S (Alpha), isoform CRA_b	PROS1	0	0	1
K	342	Di	29.28	Protein S (Alpha), isoform CRA_b	PROS1	0	0	1
K	339	Di	29.28	Protein S (Alpha), isoform CRA_b	PROS1	0	0	1
K	342	Tri	29.28	Protein S (Alpha), isoform CRA_b	PROS1	0	0	1
K	339	Tri	29.28	Protein S (Alpha), isoform CRA_b	PROS1	0	0	1
K	69	Tri	35.88	Pre-mRNA-processing-splicing factor 8 (Fragment)	PRPF8	5	3	0
R	1164	Di	34.4	Protein PRRC2A	PRRC2A	0	1	0
K	126	Mono	32.65	Trypsin-1	PRSS1	1	0	0
R	72	Di	15.81	Proteasome subunit beta type (Fragment)	PSMA4	8	0	0
R	68	Mono	24.62	Proteasome subunit beta type-11	PSMB11	0	0	1
R	43	Mono	11.49	26S protease regulatory subunit 6A (Fragment)	PSMC3	1	6	0
R	991	Di	22.84	Receptor-type tyrosine-protein phosphatase U	PTPRU	0	1	0
R	1339	Mono	13.4	Peroxidasin-like protein	PXDNL	4	0	0
K	107	Mono	56.08	Pyrroline-5-carboxylate reductase 2	PYCR2	1	0	0
K	106	Mono	56.08	Pyrroline-5-carboxylate reductase 2	PYCR2	1	0	0
R	166	Mono	26.5	R3H domain-containing protein 1	R3HDM1	0	1	1
K	13	Mono	19.34	Ras-related protein Rab-30 (Fragment)	RAB30	0	0	1
K	72	Mono	19.34	Ras-related protein Rab-3B	RAB3B	0	0	1
K	875	Mono	18.51	Ankycorbin	RAI14	1	1	3
K	873	Mono	18.51	Ankycorbin	RAI14	1	1	3
K	873	Di	18.51	Ankycorbin	RAI14	1	1	3
K	875	Di	18.51	Ankycorbin	RAI14	1	1	3
K	34	Di	56.74	RNA-binding protein Raly (Fragment)	RALY	0	0	2

K	34	Di	56.74	RNA-binding Raly-like protein	RALYL	0	0	2
R	34	Mono	32.46	Ras-like protein family member 10A	RASL10A	0	0	1
K	136	Mono	36.25	Pre-mRNA-splicing factor RBM22	RBM22	0	0	3
R	105	Di	77.22	Putative RNA-binding protein 3	RBM3	10	9	12
R	602	Mono	25.97	RNA-binding protein 44	RBM44	0	0	1
R	234	Di	28.89	RNA-binding motif protein, X chromosome, N-terminally processed	RBMX	1	0	0
R	37	Di	34.93	RNA-binding motif protein, X chromosome, N-terminally processed	RBMX	0	0	1
R	50	Di	31.14	RNA-binding motif protein, X chromosome, N-terminally processed	RBMX	0	0	2
R	113	Di	31.65	RNA binding motif protein, X-linked-like-1	RBMXL1	0	0	2
K	120	Mono	13.98	Protein RCC2	RCC2	0	1	0
K	977	Mono	59.23	RanBP2-like and GRIP domain-containing protein 3	RGPD3	0	0	1
R	84	Mono	34.33	Inactive rhomboid protein 1 (Fragment)	RHBDF1	0	1	2
R	6	Di	40.66	Ribonuclease kappa (Fragment)	RNASEK	1	0	0
K	611	Di	29.69	RING finger protein 17	RNF17	1	7	3
K	414	Di	12.83	E3 ubiquitin-protein ligase RNF216	RNF216	0	0	1
K	413	Di	12.83	E3 ubiquitin-protein ligase RNF216	RNF216	0	0	1
R	56	Di	10.89	Retinitis pigmentosa 1-like 1 protein	RP1L1	0	0	1
K	40	Mono	27.34	60S ribosomal protein L12	RPL12	0	1	0
K	69	Mono	29.5	60S ribosomal protein L24	RPL24	0	1	0
K	2	Mono	29.96	60S ribosomal protein L24	RPL24	0	0	1
R	26	Mono	50.02	60S ribosomal protein L26-like 1 (Fragment)	RPL26L1	2	4	7
K	67	Mono	26.95	60S ribosomal protein L27 (Fragment)	RPL27	0	1	0
K	149	Mono	26.3	60S ribosomal protein L29	RPL29	0	1	0
K	5	Mono	74.54	60S ribosomal protein L29	RPL29	0	0	10
K	5	Di	28.83	60S ribosomal protein L29	RPL29	0	0	1
K	9	Mono	45.9	40S ribosomal protein S16 (Fragment)	RPS16	0	4	0
K	26	Mono	45.9	40S ribosomal protein S16	RPS16	0	4	0
R	58	Mono	34.15	40S ribosomal protein S4, Y isoform 1 (Fragment)	RPS4Y1	2	2	0
K	22	Di	12.5	40S ribosomal protein S9	RPS9	1	3	3
K	42	Mono	15.24	Ras-related protein R-Ras	RRAS	1	0	0
K	27	Mono	15.24	Ras-related protein R-Ras2	RRAS2	1	0	0
K	559	Di	15.32	Remodeling and spacing factor 1 (Fragment)	RSF1	0	0	3
K	6	Di	24.56	Ribosomal L1 domain-containing protein 1 (Fragment)	RSL1D1	1	0	0
K	410	Mono	31.81	Protein strawberry notch homolog 2	SBNO2	0	1	0
R	324	Mono	26.53	Amiloride-sensitive sodium channel subunit beta	SCNN1B	2	0	0
R	244	Di	52.02	Splicing factor 3B subunit 2 (Fragment)	SF3B2	0	0	2
R	246	Di	43.89	Splicing factor 3B subunit 2 (Fragment)	SF3B2	0	0	1
R	221	Di	43.89	Splicing factor 3B subunit 2 (Fragment)	SF3B2	0	0	1
R	9	Di	66.02	Splicing factor, proline- and glutamine-rich	SFPQ	0	0	4
R	693	Di	31.22	Splicing factor, proline- and glutamine-rich	SFPQ	1	0	0
R	283	Di	11.74	E3 ubiquitin-protein ligase SH3RF1 (Fragment)	SH3RF1	1	0	0
R	284	Di	11.74	E3 ubiquitin-protein ligase SH3RF1 (Fragment)	SH3RF1	1	0	0
K	675	Tri	45.81	Single-minded homolog 1	SIM1	1	0	0

R	15	Di	24.58	Isoform 4 of SLAIN motif-containing protein 1	SLAIN1	1	0	0
K	1061	Mono	15.67	Solute carrier family 12 (Sodium/potassium/chloride transporters), member 2, isoform CRA_a	SLC12A2	2	1	0
K	23	Mono	56.36	ADP/ATP translocase 1	SLC25A4	17	3	44
K	52	Di	69.72	ADP/ATP translocase 2	SLC25A5	4	0	0
K	52	Tri	49.67	ADP/ATP translocase 2	SLC25A5	19	1	24
K	52	Tri	52.63	ADP/ATP translocase 3 (Fragment)	SLC25A6	4	0	21
K	116	Di	24.47	Transporter	SLC6A7	0	1	0
R	77	Mono	10.87	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1	0	1	0
K	643	Di	26.28	Structural maintenance of chromosomes protein 2	SMC2	1	0	0
K	158	Di	25.15	Structural maintenance of chromosomes protein 6 (Fragment)	SMC6	0	1	0
R	152	Di	25.63	Structural maintenance of chromosomes protein 6 (Fragment)	SMC6	0	2	2
R	839	Di	32.09	Protein SMG8	SMG8	0	1	0
R	1162	Mono	13.01	Sushi, nidogen and EGF-like domain-containing protein 1	SNED1	1	0	0
R	4	Di	37.1	Small nuclear ribonucleoprotein E	SNRPE	2	1	2
R	1443	Mono	29.37	Sperm-associated antigen 17	SPAG17	3	0	0
K	1444	Mono	29.37	Sperm-associated antigen 17	SPAG17	3	0	0
K	1444	Di	29.37	Sperm-associated antigen 17	SPAG17	3	0	0
R	1443	Di	29.37	Sperm-associated antigen 17	SPAG17	3	0	0
K	1444	Tri	29.37	Sperm-associated antigen 17	SPAG17	3	0	0
R	571	Mono	24.89	Spermatogenesis-associated protein 31A4 (Fragment)	SPATA31A4	0	1	0
R	160	Mono	13.94	Kunitz-type protease inhibitor 1	SPINT1	3	0	0
R	739	Mono	25.28	Spectrin alpha chain, erythrocytic 1	SPTA1	1	0	0
R	109	Di	60.89	Serine/arginine-rich-splicing factor 1	SRSF1	0	0	2
R	111	Di	43.76	Serine/arginine-rich-splicing factor 1	SRSF1	0	0	1
K	28	Mono	26.75	Lactosylceramide alpha-2,3-sialyltransferase (Fragment)	ST3GAL5	1	13	8
R	30	Mono	26.75	Lactosylceramide alpha-2,3-sialyltransferase (Fragment)	ST3GAL5	1	13	8
K	205	Di	11.89	Alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3-N-acetyl-galactosaminide alpha-2,6-sialyltransferase	ST6GALNAC4	0	0	2
K	204	Di	11.89	Alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3-N-acetyl-galactosaminide alpha-2,6-sialyltransferase	ST6GALNAC4	0	0	2
K	205	Tri	11.89	Alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3-N-acetyl-galactosaminide alpha-2,6-sialyltransferase	ST6GALNAC4	0	0	2
K	204	Tri	11.89	Alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3-N-acetyl-galactosaminide alpha-2,6-sialyltransferase	ST6GALNAC4	0	0	2
K	365	Mono	16.83	Serine/threonine-protein kinase 31	STK31	0	0	1
K	370	Di	16.83	Serine/threonine-protein kinase 31	STK31	0	0	1
K	2	Tri	25.8	Serine-threonine kinase receptor-associated protein (Fragment)	STRAP	0	1	0
K	349	Di	25.29	Striatin-interacting protein 1	STRIP1	0	0	2
R	2	Mono	33.61	Extracellular sulfatase Sulf-1 (Fragment)	SULF1	1	2	7
R	211	Di	15.81	Synaptogyrin-3 (Fragment)	SYNGR3	8	0	0
R	184	Mono	27.44	TATA-binding protein-associated factor 2N (Fragment)	TAF15	0	0	1
R	192	Di	51.62	TATA-binding protein-associated factor 2N (Fragment)	TAF15	0	0	1
R	184	Di	39.82	TATA-binding protein-associated factor 2N (Fragment)	TAF15	0	0	1
R	483	Di	83.81	TATA-binding protein-associated factor 2N	TAF15	9	0	4
R	182	Di	63.07	TATA-binding protein-associated factor 2N (Fragment)	TAF15	3	0	5
R	203	Di	48.43	TATA-binding protein-associated factor 2N (Fragment)	TAF15	5	0	0
K	85	Mono	13.15	Isoform 4 of TBC1 domain family member 4	TBC1D4	1	1	2

R	87	Mono	13.15	Isoform 4 of TBC1 domain family member 4	TBC1D4	1	1	2
R	87	Di	13.15	Isoform 4 of TBC1 domain family member 4	TBC1D4	1	1	2
K	85	Di	13.15	Isoform 4 of TBC1 domain family member 4	TBC1D4	1	1	2
K	85	Tri	13.15	Isoform 4 of TBC1 domain family member 4	TBC1D4	1	1	2
R	23	Di	12.66	T-cell leukemia/lymphoma protein 1A (Fragment)	TCL1A	0	1	0
R	385	Di	49.54	Protein TFG	TFG	0	3	0
R	825	Di	27.57	Thyroid hormone receptor-associated protein 3	THRAP3	1	0	0
K	202	Di	80.12	Thyroid hormone receptor-associated protein 3	THRAP3	0	0	6
R	188	Di	32.67	Thrombospondin type-1 domain-containing protein 4	THSD4	2	0	0
K	26	Mono	10.82	Tigger transposable element-derived protein 4	TIGD4	0	0	1
K	575	Tri	30.12	Transketolase	TKT	2	0	1
R	217	Mono	11.74	Transmembrane protein 51	TMEM51	1	0	0
K	214	Mono	11.74	Transmembrane protein 51	TMEM51	1	0	0
R	217	Di	11.74	Transmembrane protein 51	TMEM51	1	0	0
K	214	Di	11.74	Transmembrane protein 51	TMEM51	1	0	0
K	214	Tri	11.74	Transmembrane protein 51	TMEM51	1	0	0
R	7	Di	34.44	Tropomodulin 2 (Neuronal), isoform CRA_a	TMOD2	0	0	2
K	329	Di	27.92	Transmembrane protease serine 5	TMPRSS5	2	0	0
K	329	Tri	27.04	Transmembrane protease serine 5	TMPRSS5	1	0	0
R	939	Mono	18.02	Transmembrane and TPR repeat-containing protein 1	TMTC1	1	0	0
R	71	Mono	27.94	Mitochondrial import receptor subunit TOM70	TOMM70A	0	0	1
K	321	Mono	43.1	Isoform 3 of DNA topoisomerase 2-alpha	TOP2A	0	0	1
K	321	Mono	43.1	DNA topoisomerase 2-alpha	TOP2A	0	0	1
K	256	Mono	55.99	Triosephosphate isomerase	TPI1	2	0	0
K	106	Mono	31.32	Triosephosphate isomerase	TPI1	1	0	0
K	256	Tri	38.15	Triosephosphate isomerase	TPI1	1	0	0
R	61	Di	48.55	Transformer-2 protein homolog beta (Fragment)	TRA2B	2	0	1
K	257	Mono	34.88	TRAF3-interacting protein 1	TRAF3IP1	0	0	1
K	252	Di	34.88	TRAF3-interacting protein 1	TRAF3IP1	0	0	1
K	576	Mono	26.48	Heat shock protein 75 kDa, mitochondrial	TRAP1	1	0	0
R	203	Mono	25.05	Transcription intermediary factor 1-alpha	TRIM24	0	0	1
R	1537	Mono	33.61	Triple functional domain protein (Fragment)	TRIO	1	2	7
K	567	Tri	16.2	Triple functional domain protein (Fragment)	TRIO	0	0	5
R	25	Mono	35.43	tRNA (adenine(58)-N(1))-methyltransferase, mitochondrial (Fragment)	TRMT61B	0	1	1
R	704	Di	27.17	Tau-tubulin kinase 1	TTBK1	4	2	0
K	234	Mono	17.96	Tetratricopeptide repeat protein 13	TTC13	0	1	0
K	60	Mono	13.38	Tetratricopeptide repeat protein 16	TTC16	1	0	0
K	130	Mono	34.06	Tubulin alpha-1C chain	TUBA1C	0	1	0
R	460	Mono	25.25	Tubulin alpha-1C chain	TUBA1C	26	49	95
R	79	Mono	44.66	Tubulin alpha-3C/D chain	TUBA3C	2	4	2
K	148	Mono	30.96	Tubulin alpha-4A chain	TUBA4A	0	2	0
K	265	Mono	28.9	Tubulin alpha-4A chain	TUBA4A	0	1	0
K	149	Di	30.96	Tubulin alpha-4A chain	TUBA4A	0	2	0

K	136	Mono	23.57	Tubulin alpha-8 chain (Fragment)	TUBA8	2	8	1
R	28	Mono	65.05	Tubulin beta chain	TUBB	7	7	0
K	19	Mono	39.58	Tubulin beta chain	TUBB	0	2	0
R	46	Mono	65.05	Tubulin beta chain	TUBB	7	7	0
R	84	Mono	26.44	HCG1983504, isoform CRA_f	TUBB3	0	2	0
R	90	Mono	26.44	HCG1983504, isoform CRA_f	TUBB3	0	2	0
K	102	Mono	50.75	HCG1983504, isoform CRA_f	TUBB3	0	3	0
K	19	Mono	39.58	Tubulin beta-3 chain	TUBB3	0	2	0
K	102	Tri	37.86	HCG1983504, isoform CRA_f	TUBB3	0	1	0
K	19	Mono	39.58	Tubulin beta-4A chain	TUBB4A	0	2	0
R	318	Mono	44.48	Tubulin beta-4A chain	TUBB4A	2	2	2
K	19	Mono	39.58	Tubulin beta-4A chain	TUBB4A	0	2	0
X	1	Mono	55.27	Tubulin beta-6 chain (Fragment)	TUBB6	0	2	0
R	390	Mono	29.02	Tubulin beta-6 chain	TUBB6	2	0	0
X	1	Di	55.27	Tubulin beta-6 chain (Fragment)	TUBB6	0	2	0
R	308	Mono	49.12	Tubulin beta-8 chain	TUBB8	5	9	1
R	356	Di	15.81	Thioredoxin reductase 1, cytoplasmic	TXNRD1	8	0	0
R	537	Di	15.81	Thioredoxin reductase 3 (Fragment)	TXNRD3	8	0	0
K	39	Mono	60.12	Splicing factor U2AF 35 kDa subunit	U2AF1	3	1	0
K	39	Mono	51.15	Isoform 2 of Splicing factor U2AF 35 kDa subunit	U2AF1	3	2	0
K	80	Tri	12.5	Ubiquitin carboxyl-terminal hydrolase 8	USP8	1	3	3
K	15	Mono	26.47	Utrophin (Fragment)	UTRN	1	0	0
R	297	Mono	15.81	Vasorin	VASN	8	0	0
K	315	Tri	29.13	Transitional endoplasmic reticulum ATPase	VCP	3	0	0
K	238	Mono	56.57	Voltage-dependent anion-selective channel protein 2	VDAC2	6	0	5
K	223	Tri	12.11	Vimentin	VIM	0	1	0
R	42	Di	29.61	Vacuolar protein sorting-associated protein 13A (Fragment)	VPS13A	1	0	0
K	50	Tri	29.61	Vacuolar protein sorting-associated protein 13A (Fragment)	VPS13A	1	0	0
R	2619	Mono	33.61	Vacuolar protein sorting-associated protein 13C	VPS13C	1	2	7
K	461	Di	28.96	WD repeat domain 19, isoform CRA_a	WDR19	0	2	0
K	460	Di	28.96	WD repeat domain 19, isoform CRA_a	WDR19	0	2	0
K	460	Tri	28.96	WD repeat domain 19, isoform CRA_a	WDR19	0	2	0
K	461	Tri	28.96	WD repeat domain 19, isoform CRA_a	WDR19	0	2	0
K	367	Tri	15.06	WD repeat-containing protein 25	WDR25	0	0	1
R	7	Mono	30.85	WD repeat-containing protein 52 (Fragment)	WDR52	0	0	1
R	65	Mono	25.86	WAP four-disulfide core domain protein 1	WFDC1	0	0	1
K	212	Mono	81.49	14-3-3 protein theta	YWHAQ	0	2	1
R	30	Di	27.93	Zonadhesin	ZAN	5	2	1
R	81	Mono	27.66	Zinc finger C2HC domain-containing protein 1A (Fragment)	ZC2HC1A	0	1	0
R	32	Mono	27.52	Zinc finger protein 36, C3H1 type-like 1 (Fragment)	ZFP36L1	0	0	2
K	193	Mono	11.49	Zinc fingers and homeoboxes protein 3	ZHX3	1	6	0
K	197	Mono	11.49	Zinc fingers and homeoboxes protein 3	ZHX3	1	6	0
K	7	Tri	11.05	Zinc finger protein 106 (Fragment)	ZNF106	0	0	1

K	36	Di	11.37	Neurotrophin receptor-interacting factor homolog (Fragment)	ZNF274	1	0	0
K	238	Di	25.72	DBIRD complex subunit ZNF326	ZNF326	0	0	1
R	175	Di	79.98	DBIRD complex subunit ZNF326	ZNF326	4	0	2
R	235	Di	59.03	DBIRD complex subunit ZNF326	ZNF326	4	0	0
K	89	Mono	18.48	Zinc finger protein 707 (Fragment)	ZNF707	0	0	1
K	207	Mono	21.7	Zinc finger protein 721	ZNF721	0	0	3
K	336	Mono	21.7	Putative zinc finger protein 724	ZNF724P	0	0	3
R	8	Di	36.93	Zinc finger protein 785 (Fragment)	ZNF785	6	2	0
R	7	Di	36.93	Zinc finger protein 785 (Fragment)	ZNF785	6	2	0
K	549	Mono	21.7	Zinc finger protein 813	ZNF813	0	0	3
R	378	Mono	11.2	Zinc finger protein 99	ZNF99	0	0	1

Appendix 5: List of methylation sites identified by MS/MS in tryptic, chymotryptic and Glu-C digested samples.

Sites identified at the 1% peptide FDR confidence level for the different digested samples. The numbers on the right of the table indicate peptide hits for each site in each sample.

K/R	Site	Type	Mascot Score	Protein Name	Gene Name	Trypsin	Chymotrypsin	Glu-c
R	11	Mono	25.88	Very long-chain-specific acyl-CoA dehydrogenase, mitochondrial (Fragment)	ACADVL	1	0	0
R	7	Mono	25.77	Long-chain-fatty-acid--CoA ligase 1 (Fragment)	ACSL1	1	0	0
K	129	Mono	57.13	Actin, alpha skeletal muscle	ACTA1	21	0	0
K	240	Mono	25.3	Actin, alpha skeletal muscle	ACTA1	1	0	0
K	293	Di	25.31	Actin, aortic smooth muscle	ACTA2	1	0	0
R	63	Mono	19.38	Beta-actin-like protein 2	ACTBL2	1	0	0
R	196	Mono	33.11	Actin, cytoplasmic 2, N-terminally processed (Fragment)	ACTG1	0	0	2
R	740	Mono	52.97	Alpha-actinin-3	ACTN3	3	0	0
R	278	Mono	23.4	A disintegrin and metalloproteinase with thrombospondin motifs 10	ADAMTS10	1	0	0
R	829	Mono	29.37	ADAMTS-like protein 4	ADAMTSL4	2	0	0
K	578	Tri	27.15	Actin filament-associated protein 1	AFAP1	1	0	0
R	70	Mono	39.71	Aldo-keto reductase family 1 member B10	AKR1B10	3	0	0
K	108	Mono	51.12	Fructose-bisphosphate aldolase	ALDOC	1	0	0
K	111	Mono	51.12	Fructose-bisphosphate aldolase	ALDOC	1	0	0
K	108	Di	51.12	Fructose-bisphosphate aldolase	ALDOC	1	0	0
K	111	Di	51.12	Fructose-bisphosphate aldolase	ALDOC	1	0	0
K	111	Tri	51.12	Fructose-bisphosphate aldolase	ALDOC	1	0	0
K	108	Tri	51.12	Fructose-bisphosphate aldolase	ALDOC	1	0	0
X	1	Di	19.47	ALS2 C-terminal-like protein (Fragment)	ALS2CL	1	0	0
R	57	Di	37.93	THO complex subunit 4	ALYREF	7	0	0
R	204	Di	64.62	THO complex subunit 4	ALYREF	18	0	0
R	211	Di	71.83	THO complex subunit 4	ALYREF	24	0	0
R	70	Di	89.5	THO complex subunit 4	ALYREF	29	0	0
R	45	Di	86.84	THO complex subunit 4	ALYREF	33	0	0
K	235	Mono	27.68	Ankyrin repeat domain-containing protein 32	ANKRD32	0	0	4
K	457	Mono	64.44	AP-2 complex subunit beta	AP2B1	2	0	0
K	456	Mono	64.44	AP-2 complex subunit beta	AP2B1	2	0	0
K	281	Mono	26.54	Apoptosis-resistant E3 ubiquitin protein ligase 1	AREL1	0	0	8
K	95	Tri	30.4	ATP synthase lipid-binding protein, mitochondrial	ATP5G1	0	7	0
K	170	Tri	26.25	V-type proton ATPase subunit C 1	ATP6V1C1	1	0	0
K	158	Mono	34.17	Probable phospholipid-transporting ATPase IA	ATP8A1	1	0	0
R	8	Di	35.35	Advillin	AVIL	3	0	0
R	85	Di	35.78	Bcl-2-associated transcription factor 1	BCLAF1	0	3	0
K	266	Mono	23.4	Golgin-45	BLZF1	0	0	1
R	68	Di	31.33	Nucleosome-remodeling factor subunit BPTF (Fragment)	BPTF	1	0	0
R	2066	Di	25.89	Nucleosome-remodeling factor subunit BPTF	BPTF	2	0	0
R	517	Di	20.9	BRCA1-associated ATM activator 1	BRAT1	0	0	1

R	60	Di	26.51	Bromodomain-containing protein 9	BRD9	0	0	1
R	302	Mono	25.63	Bromodomain and WD repeat-containing protein 1 (Fragment)	BRWD1	0	0	1
R	100	Di	33.12	Bromodomain and WD repeat-containing protein 1 (Fragment)	BRWD1	4	0	0
K	401	Mono	25.53	Uncharacterized protein C10orf71	C10orf71	1	0	0
R	14	Di	73.17	Isoform 2 of UPF0696 protein C11orf68	C11orf68	14	0	0
R	172	Mono	20.74	Uncharacterized protein C17orf74	C17orf74	0	3	0
K	7	Mono	19.57	Uncharacterized protein C21orf59	C21orf59	1	0	0
R	334	Mono	26.25	C2 domain-containing protein 3 (Fragment)	C2CD3	1	0	0
R	168	Di	30.62	Voltage-dependent L-type calcium channel subunit alpha-1S	CACNA1S	1	0	0
K	163	Mono	25.66	Calmodulin	CALM2	1	0	0
R	174	Mono	25.66	Calmodulin	CALM2	1	0	0
R	174	Di	25.66	Calmodulin	CALM2	1	0	0
K	163	Di	25.66	Calmodulin	CALM2	1	0	0
K	163	Tri	33.82	Calmodulin	CALM2	3	0	0
R	1010	Di	42.72	Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	1	0	0
R	1013	Di	42.72	Calmodulin-regulated spectrin-associated protein 3	CAMSAP3	1	0	0
R	15	Mono	27.47	Cullin-associated NEDD8-dissociated protein 2 (Fragment)	CAND2	2	0	0
R	23	Di	27.58	Probable cysteine--tRNA ligase, mitochondrial	CARS2	0	3	0
K	143	Mono	45.81	Chromobox protein homolog 3	CBX3	1	0	0
K	31	Mono	18.43	Chromobox protein homolog 7	CBX7	4	0	0
R	5	Mono	42.1	Coiled-coil domain-containing protein 137 (Fragment)	CCDC137	1	0	0
R	5	Di	37.58	Coiled-coil domain-containing protein 137 (Fragment)	CCDC137	1	0	0
R	6	Di	37.58	Coiled-coil domain-containing protein 137 (Fragment)	CCDC137	1	0	0
K	130	Mono	33.93	Coiled-coil domain-containing protein 172	CCDC172	2	0	0
R	125	Di	33.93	Coiled-coil domain-containing protein 172	CCDC172	2	0	0
K	9	Mono	44.44	T-complex protein 1 subunit delta	CCT4	1	0	0
R	6	Mono	27.4	Serine/threonine-protein kinase MRCK alpha	CDC42BPA	1	0	0
K	76	Tri	29.13	Cell division cycle 5-like protein	CDC5L	2	0	0
K	3	Di	20.33	Centromere protein K	CENPK	0	0	1
R	1027	Mono	26.54	Centrosome-associated protein CEP250	CEP250	0	0	8
K	13	Mono	81.04	Cofilin-1 (Fragment)	CFL1	1	0	0
R	201	Di	32.61	Chromosome transmission fidelity protein 8 homolog isoform 2	CHTF8	0	4	0
R	58	Di	39.81	Chromatin target of PRMT1 protein	CHTOP	3	0	0
R	148	Di	29.31	Chromatin target of PRMT1 protein	CHTOP	2	0	0
K	3	Mono	42.64	Clathrin heavy chain 1 (Fragment)	CLTC	2	0	0
K	3	Tri	42.64	Clathrin heavy chain 1 (Fragment)	CLTC	2	0	0
R	27	Di	41.83	Cellular nucleic acid-binding protein	CNBP	3	0	0
R	25	Di	41.83	Cellular nucleic acid-binding protein	CNBP	3	0	0
K	31	Mono	31.04	Cysteine-rich protein 2	CRIP2	1	0	0
K	31	Mono	31.04	Cysteine-rich protein 3	CRIP3	1	0	0
R	617	Mono	18.86	Rootletin (Fragment)	CROCC	11	0	0
K	251	Tri	26.41	Chymotrypsinogen B	CTRB1	0	2	0
K	243	Mono	19.48	Pre-mRNA-splicing factor CWC22 homolog	CWC22	22	0	0

K	577	Mono	26.15	Dachshund homolog 1	DACH1	1	0	0
R	428	Mono	40.77	Probable ATP-dependent RNA helicase DDX17	DDX17	8	0	0
R	423	Di	37.88	Probable ATP-dependent RNA helicase DDX5	DDX5	2	0	0
K	7	Mono	25.58	DEP domain-containing protein 5 (Fragment)	DEPDC5	1	0	0
R	3	Di	25.58	DEP domain-containing protein 5 (Fragment)	DEPDC5	1	0	0
R	1227	Di	31.03	ATP-dependent RNA helicase A	DHX9	0	1	0
R	1265	Di	43.29	ATP-dependent RNA helicase A	DHX9	0	5	0
R	796	Mono	26.3	Endoribonuclease Dicer	DICER1	1	0	0
K	1096	Mono	28.07	Disco-interacting protein 2 homolog A	DIP2A	1	0	0
R	1214	Mono	29.33	Dynein heavy chain 8, axonemal	DNAH8	0	1	0
K	1215	Mono	29.33	Dynein heavy chain 8, axonemal	DNAH8	0	1	0
R	1214	Di	29.33	Dynein heavy chain 8, axonemal	DNAH8	0	1	0
K	1215	Di	29.33	Dynein heavy chain 8, axonemal	DNAH8	0	1	0
K	1209	Mono	29.18	Dynein heavy chain 9, axonemal	DNAH9	2	0	0
K	223	Mono	29.96	DnaJ homolog subfamily A member 2	DNAJA2	1	0	0
R	14	Mono	30.05	Protein DPCD (Fragment)	DPCD	16	0	0
R	114	Di	22.92	Desmocollin-1	DSC1	2	0	0
K	25	Mono	38.19	Endothelial differentiation-related factor 1	EDF1	1	0	0
K	79	Mono	27.51	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	3	0	0
R	166	Mono	46.88	Elongation factor 1-alpha 1	EEF1A1	4	0	0
K	318	Mono	37.82	Elongation factor 1-alpha 1	EEF1A1	19	0	0
K	165	Mono	59.81	Elongation factor 1-alpha 1	EEF1A1	66	0	0
K	84	Mono	27.51	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	3	0	0
K	36	Mono	29.75	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	1	0	0
K	55	Di	61.11	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	22	0	0
K	36	Di	41.42	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	12	0	0
K	165	Di	59.36	Elongation factor 1-alpha 1	EEF1A1	83	0	0
K	84	Di	27.51	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	3	0	0
K	318	Di	43.44	Elongation factor 1-alpha 1	EEF1A1	94	0	0
K	79	Di	27.51	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	3	0	0
R	166	Di	46.88	Elongation factor 1-alpha 1	EEF1A1	4	0	0
K	84	Tri	27.51	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	3	0	0
K	318	Tri	50.08	Elongation factor 1-alpha 1	EEF1A1	188	0	0
K	36	Tri	50.9	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	10	0	0
K	165	Tri	60.14	Elongation factor 1-alpha 1	EEF1A1	52	0	0
K	79	Tri	60.94	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	42	0	0
K	165	Mono	34.52	Elongation factor 1-alpha 2	EEF1A2	1	0	0
K	84	Mono	27.51	Elongation factor 1-alpha 2	EEF1A2	3	0	0
K	79	Mono	27.51	Elongation factor 1-alpha 2	EEF1A2	3	0	0
R	166	Mono	33.14	Elongation factor 1-alpha 2	EEF1A2	3	0	0
K	318	Di	39.31	Elongation factor 1-alpha 2	EEF1A2	8	0	0
K	79	Di	27.51	Elongation factor 1-alpha 2	EEF1A2	3	0	0
K	165	Di	52.89	Elongation factor 1-alpha 2	EEF1A2	12	0	0

K	84	Di	27.51	Elongation factor 1-alpha 2	EEF1A2	3	0	0
K	318	Tri	39.21	Elongation factor 1-alpha 2	EEF1A2	20	0	0
K	42	Mono	27.07	Elongation factor 2	EEF2	1	0	0
K	525	Mono	26.18	Elongation factor 2	EEF2	2	0	0
K	407	Mono	43.44	Elongation factor 2	EEF2	17	0	0
K	407	Di	25.69	Elongation factor 2	EEF2	1	0	0
K	525	Tri	34.59	Elongation factor 2	EEF2	19	0	0
R	103	Di	34.25	Eukaryotic translation initiation factor 3 subunit D (Fragment)	EIF3D	3	0	0
R	8	Di	38.44	Eukaryotic translation initiation factor 4 gamma 1 (Fragment)	EIF4G1	6	0	0
R	19	Mono	34.23	Eukaryotic translation initiation factor 4H	EIF4H	2	0	0
R	22	Mono	34.23	Eukaryotic translation initiation factor 4H	EIF4H	2	0	0
R	19	Di	57.36	Eukaryotic translation initiation factor 4H	EIF4H	8	0	0
R	97	Mono	25.3	Eukaryotic translation initiation factor 5A-2	EIF5A2	1	0	0
K	105	Mono	41.19	Enolase (Fragment)	ENO1	0	0	3
K	103	Mono	41.19	Enolase (Fragment)	ENO1	0	0	3
K	103	Mono	38.63	Gamma-enolase	ENO2	0	0	3
K	105	Mono	38.63	Gamma-enolase	ENO2	0	0	3
K	120	Di	38.63	Gamma-enolase	ENO2	0	0	3
K	103	Mono	38.63	Beta-enolase (Fragment)	ENO3	0	0	3
K	105	Mono	38.63	Beta-enolase (Fragment)	ENO3	0	0	3
K	120	Di	38.63	Beta-enolase (Fragment)	ENO3	0	0	3
K	454	Di	25.81	Epidermal growth factor receptor kinase substrate 8-like protein 3	EPS8L3	0	1	0
R	269	Mono	23.35	TFIIH basal transcription factor complex helicase XPD subunit (Fragment)	ERCC2	3	0	0
K	6	Mono	23.08	Endoplasmic reticulum-Golgi intermediate compartment protein 3	ERGIC3	1	0	0
R	468	Di	32.85	RNA-binding protein EWS	EWSR1	1	0	0
R	433	Di	97.35	RNA-binding protein EWS	EWSR1	2	0	0
R	577	Di	91.69	RNA-binding protein EWS	EWSR1	43	0	0
K	9	Di	26.77	Protein FAM127B	FAM127B	5	0	0
R	88	Di	36.95	Myelin-associated neurite-outgrowth inhibitor	FAM168B	0	6	0
K	471	Mono	19.19	Protein FAM184A	FAM184A	0	0	6
K	131	Di	32.89	Protein FAM25D/E	FAM25D	2	0	0
R	41	Di	26.78	Protein FAM3C (Fragment)	FAM3C	0	1	0
K	87	Mono	26.9	Protein FAM47E	FAM47E	0	2	0
K	5	Mono	35.33	Protein FAM50A	FAM50A	1	0	0
K	299	Di	27.66	Isoform 2 of Protein FAM53B	FAM53B	0	1	0
R	384	Di	37.01	Isoform 2 of Protein FAM98B	FAM98B	0	3	0
R	6	Mono	26.43	40S ribosomal protein S30 (Fragment)	FAU	0	3	0
K	273	Tri	28.35	Fructose-1,6-bisphosphatase isozyme 2	FBP2	1	0	0
R	483	Di	18.48	F-box only protein 15	FBXO15	0	0	1
R	278	Di	43.7	Ras GTPase-activating protein-binding protein 1	G3BP1	0	1	0
R	253	Di	71.7	Ras GTPase-activating protein-binding protein 1	G3BP1	7	0	0
R	468	Di	45.83	Ras GTPase-activating protein-binding protein 2	G3BP2	7	0	0
K	54	Di	25.15	Gamma-aminobutyric acid receptor subunit rho-2	GABRR2	1	0	0

R	309	Mono	27.4	Galactose-3-O-sulfotransferase 2	GAL3ST2	1	0	0
R	13	Di	43.51	H/ACA ribonucleoprotein complex subunit 1	GAR1	0	5	0
R	30	Di	45.59	H/ACA ribonucleoprotein complex subunit 1	GAR1	0	9	0
K	195	Di	23.07	Ganglioside-induced differentiation-associated protein 1	GDAP1	2	0	0
K	60	Di	22.92	Ganglioside-induced differentiation-associated protein 2	GDAP2	2	0	0
R	149	Di	36.41	PERQ amino acid-rich with GYF domain-containing protein 2 (Fragment)	GIGYF2	0	0	1
K	62	Tri	36.48	PDZ domain-containing protein GIPC1 (Fragment)	GIPC1	0	0	2
K	17	Di	42.98	Guanine nucleotide-binding protein G(olf) subunit alpha (Fragment)	GNAL	3	0	0
R	472	Di	27.85	G-protein coupled receptor-associated sorting protein 1	GPRASP1	0	0	2
R	143	Di	44.03	G protein pathway suppressor 2 (Fragment)	GPS2	0	4	0
K	82	Tri	32.01	Histone H2A (Fragment)	H2AFJ	1	0	0
K	80	Mono	68.69	Histone H3	H3F3A	98	0	0
K	80	Di	38.33	Histone H3	H3F3A	8	0	0
K	28	Di	54.03	Histone H3	H3F3A	3	0	0
K	10	Di	55.3	Histone H3	H3F3A	1	0	0
K	37	Di	33.1	Histone H3	H3F3A	3	0	0
R	70	Di	47.59	Intracellular hyaluronan-binding protein 4	HABP4	1	0	0
R	656	Di	48.03	HCG2044799	hCG_2044799	15	0	0
R	469	Di	25.99	Hypermethylated in cancer 1 protein	HIC1	0	0	1
K	118	Mono	36.74	Histone H1.3	HIST1H1D	4	0	0
K	119	Tri	32.01	Histone H2A type 1-B/E	HIST1H2AB	1	0	0
K	38	Mono	55.58	Histone H3.1	HIST1H3A	1	0	0
K	37	Mono	55.58	Histone H3.1	HIST1H3A	1	0	0
K	28	Mono	64.95	Histone H3.1	HIST1H3A	18	0	0
K	28	Di	78.37	Histone H3.1	HIST1H3A	32	0	0
K	37	Di	42.29	Histone H3.1	HIST1H3A	3	0	0
K	38	Di	32.44	Histone H3.1	HIST1H3A	3	0	0
K	28	Tri	46.37	Histone H3.1	HIST1H3A	4	0	0
R	24	Di	29.7	Histone H4	HIST1H4A	1	0	0
R	89	Mono	37.61	Histone H2A type 2-B	HIST2H2AB	46	0	0
K	58	Mono	43.32	Histone H2B	HIST2H2BF	3	0	0
R	169	Mono	29.95	HLA class I histocompatibility antigen, B-48 alpha chain	HLA-B	1	0	0
R	291	Di	98.48	Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	22	0	0
R	215	Mono	52.46	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	9	0	0
R	31	Mono	76.27	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	20	0	0
R	213	Mono	65.52	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	4	0	0
K	112	Mono	33.17	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	1	0	0
R	206	Mono	31.87	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	2	0	0
R	225	Di	68.27	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	13	0	0
R	225	Di	50.19	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	5	0	0
R	145	Di	44.41	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	1	0	0
R	116	Di	77.73	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	0	5	0
R	215	Di	74.96	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	4	0	0

R	218	Di	43.5	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	0	15	0
R	213	Di	77	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	81	0	0
R	206	Di	95.46	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	18	0	0
R	194	Mono	65.52	Heterogeneous nuclear ribonucleoprotein A1-like 2	HNRNPA1L2	4	0	0
R	196	Mono	52.46	Heterogeneous nuclear ribonucleoprotein A1-like 2	HNRNPA1L2	9	0	0
R	196	Di	70.64	Heterogeneous nuclear ribonucleoprotein A1-like 2	HNRNPA1L2	45	0	0
R	194	Di	77	Heterogeneous nuclear ribonucleoprotein A1-like 2	HNRNPA1L2	81	0	0
R	213	Mono	28.88	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	1	0	0
R	203	Mono	33.98	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	1	0	0
R	266	Di	72.26	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	0	5	0
R	203	Di	32.46	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	1	0	0
R	52	Mono	88.52	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	19	0	0
R	239	Di	52.64	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	0	6	0
R	52	Di	76.27	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	20	0	0
R	246	Di	51.44	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	1	0	0
R	24	Di	58.04	Heterogeneous nuclear ribonucleoprotein A3 (Fragment)	HNRNPA3	6	0	0
R	22	Di	58.04	Heterogeneous nuclear ribonucleoprotein A3 (Fragment)	HNRNPA3	6	0	0
R	286	Di	79.67	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	0	12	0
R	34	Di	37.87	Heterogeneous nuclear ribonucleoprotein A3 (Fragment)	HNRNPA3	0	6	0
R	226	Di	31.05	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	0	11	0
R	245	Mono	38.15	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	1	0	0
R	248	Mono	38.15	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	1	0	0
R	245	Di	74.71	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	3	0	0
R	248	Di	74.71	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	3	0	0
R	226	Mono	25.4	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	1	0	0
K	67	Mono	38.79	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	2	0	0
R	220	Mono	25.4	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	1	0	0
R	220	Di	25.4	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	1	0	0
R	293	Di	25.57	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	1	0	0
R	226	Di	25.4	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	1	0	0
R	224	Di	33.4	Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	0	6	0
R	129	Di	29.83	Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	0	2	0
R	296	Di	35.48	Heterogeneous nuclear ribonucleoprotein K	HNRNPK	8	0	0
K	99	Mono	27	Heterogeneous nuclear ribonucleoprotein R	HNRNPR	1	0	0
R	739	Di	40.18	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	8	0	0
R	733	Di	40.18	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	8	0	0
R	727	Di	28.07	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	1	0	0
R	556	Di	63.78	Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	0	17	0
K	161	Mono	63.6	Heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	2	0	0
K	162	Mono	59.17	Heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	8	0	0
R	408	Di	48.85	Heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	10	0	0
K	378	Di	57.75	Putative heat shock protein HSP 90-beta-3	HSP90AB3P	3	0	0
K	470	Mono	26.51	Heat shock 70 kDa protein 1A/1B	HSPA1A	0	0	1

K	459	Mono	22.82	Heat shock 70 kDa protein 1A/1B	HSPA1A	0	0	1
R	378	Mono	46.99	Heat shock 70 kDa protein 1A/1B	HSPA1A	0	0	72
K	470	Di	35.51	Heat shock 70 kDa protein 1A/1B	HSPA1A	0	0	5
K	470	Tri	30.58	Heat shock 70 kDa protein 1A/1B	HSPA1A	0	0	5
K	25	Tri	96.64	Heat shock 70 kDa protein 1A/1B	HSPA1A	0	0	128
R	460	Mono	42.41	Heat shock 70 kDa protein 1-like	HSPA1L	0	0	1
K	563	Mono	26.51	Heat shock 70 kDa protein 1-like	HSPA1L	0	0	1
K	563	Di	35.51	Heat shock 70 kDa protein 1-like	HSPA1L	0	0	5
K	563	Tri	30.58	Heat shock 70 kDa protein 1-like	HSPA1L	0	0	5
K	612	Mono	35.28	Heat shock-related 70 kDa protein 2	HSPA2	2	0	0
R	492	Mono	41.41	78 kDa glucose-regulated protein	HSPA5	0	0	15
K	154	Di	30.04	78 kDa glucose-regulated protein	HSPA5	2	0	0
K	585	Tri	54.42	78 kDa glucose-regulated protein	HSPA5	8	0	0
R	233	Mono	41.41	Heat shock cognate 71 kDa protein	HSPA8	0	0	15
K	3	Di	50.93	Heat shock cognate 71 kDa protein (Fragment)	HSPA8	0	0	128
R	218	Mono	34.93	Stress-70 protein, mitochondrial	HSPA9	0	3	0
K	1220	Mono	25.83	Intraflagellar transport protein 140 homolog	IFT140	0	1	0
R	16	Mono	25.89	Zinc finger protein Eos	IKZF4	1	0	0
K	538	Tri	27.31	Isoform 4 of Interleukin-1 receptor accessory protein	IL1RAP	1	0	0
R	16	Di	32.1	Interleukin enhancer-binding factor 2	ILF2	0	1	0
K	100	Mono	26.98	Inosine-5'-monophosphate dehydrogenase 1 (Fragment)	IMPDH1	0	0	1
R	439	Mono	28.69	Type I inositol 3,4-bisphosphate 4-phosphatase	INPP4A	1	0	0
R	99	Mono	27.17	IQ domain-containing protein E (Fragment)	IQCE	1	0	0
R	98	Mono	27.17	IQ domain-containing protein E (Fragment)	IQCE	1	0	0
R	99	Di	27.17	IQ domain-containing protein E (Fragment)	IQCE	1	0	0
R	98	Di	27.17	IQ domain-containing protein E (Fragment)	IQCE	1	0	0
K	324	Mono	23.36	ITGA10 protein	ITGA10	1	0	0
R	223	Di	41.8	Junctophilin-2	JPH2	0	3	0
K	229	Tri	28.35	Junctophilin-2	JPH2	1	0	0
K	6	Tri	22.97	Lysine--tRNA ligase (Fragment)	KARS	4	0	0
R	325	Di	29.48	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	4	0	0
R	346	Di	34.07	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	11	0	0
R	310	Di	36.94	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	3	0	0
R	348	Di	34.07	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	11	0	0
R	1803	Di	26.22	Protein virilizer homolog	KIAA1429	1	0	0
R	1805	Di	26.22	Protein virilizer homolog	KIAA1429	1	0	0
K	23	Tri	39.98	DNA/RNA-binding protein KIN17	KIN	4	0	0
R	306	Mono	27.91	Isoform 3 of Krueppel-like factor 12	KLF12	1	0	0
K	273	Tri	31.95	Keratin, type II cytoskeletal 75	KRT75	0	0	1
R	59	Di	50.74	La-related protein 4B (Fragment)	LARP4B	1	0	0
R	61	Di	50.74	La-related protein 4B (Fragment)	LARP4B	1	0	0
K	264	Mono	20.6	L-lactate dehydrogenase	LDHC	6	0	0
R	99	Mono	28.82	L-lactate dehydrogenase C chain	LDHC	1	0	0

R	68	Mono	20.74	Galectin-9	LGALS9	0	3	0
K	124	Mono	25.53	Leukemia inhibitory factor receptor	LIFR	0	0	1
R	208	Mono	26	Lamin-B1	LMNB1	0	0	1
K	209	Mono	26	Lamin-B1	LMNB1	0	0	1
R	428	Mono	27.47	Alpha-mannosidase 2	MAN2A1	5	0	0
R	1220	Di	29.25	Microtubule-associated protein 1B	MAP1B	1	0	0
R	51	Mono	25.32	Putative methyl-CpG-binding domain protein 3-like 4	MBD3L4	1	0	0
R	45	Mono	25.32	Putative methyl-CpG-binding domain protein 3-like 4	MBD3L4	1	0	0
R	211	Mono	23.35	Methionine aminopeptidase 1D, mitochondrial	METAP1D	3	0	0
K	317	Mono	33.39	Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase A	MGAT4A	0	0	1
R	6	Di	27.37	Multiple myeloma tumor-associated protein 2	MMTAG2	1	0	0
R	71	Mono	32.79	MOB kinase activator 3A (Fragment)	MOB3A	0	2	0
R	91	Mono	18.86	Mov10, Moloney leukemia virus 10, homolog (Mouse), isoform CRA_a	MOV10	11	0	0
R	37	Di	60.34	M-phase-specific PLK1-interacting protein	MPLKIP	8	0	0
R	71	Mono	26.98	39S ribosomal protein L30, mitochondrial	MRPL30	3	0	0
K	79	Mono	29.18	39S ribosomal protein L4, mitochondrial (Fragment)	MRPL4	2	0	0
R	161	Mono	19.24	Metastasis associated 1 family, member 3, isoform CRA_a	MTA3	1	0	0
R	3	Di	30.4	Monofunctional C1-tetrahydrofolate synthase, mitochondrial (Fragment)	MTHFD1L	0	5	0
K	19	Mono	21.04	Myotrophin	MTPN	0	0	1
R	141	Mono	19.63	Myelin expression factor 2	MYEF2	3	0	0
R	1325	Di	28.08	Myosin-14	MYH14	0	0	1
R	1787	Di	27.82	Myosin-14	MYH14	0	0	1
R	477	Mono	26.67	Unconventional myosin-Ia	MYO1A	1	0	0
R	593	Mono	33.64	Alpha-N-acetylglucosaminidase	NAGLU	0	8	0
K	884	Mono	32.14	N-acetyltransferase 10	NAT10	0	1	0
R	20	Di	31.85	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	1	0	0
K	50	Tri	38.87	Serine/threonine-protein kinase Nek3	NEK3	3	0	0
R	904	Di	26.83	Nidogen-1	NID1	0	0	1
R	629	Mono	29.44	Caspase recruitment domain family, member 4, isoform CRA_c	NOD1	0	1	0
K	88	Mono	29.48	GTPase NRas	NRAS	1	0	0
R	1928	Mono	25.4	Nuclear pore complex protein Nup205	NUP205	0	2	0
R	137	Mono	26.67	P protein (Fragment)	OCA2	1	0	0
R	38	Di	26.98	Dynamin-like 120 kDa protein, mitochondrial (Fragment)	OPA1	3	0	0
R	448	Di	94.91	Polyadenylate-binding protein 1	PABPC1	27	0	0
R	2	Di	36.23	Polyadenylate-binding protein 1 (Fragment)	PABPC1	1	0	0
R	387	Di	40.6	Polyadenylate-binding protein 1	PABPC1	1	0	0
R	398	Di	31.64	Polyadenylate-binding protein 1	PABPC1	0	7	0
R	489	Di	59.33	Poly(A) binding protein, cytoplasmic 4 (Inducible form), isoform CRA_e	PABPC4	8	0	0
R	501	Di	39.52	Poly(A) binding protein, cytoplasmic 4 (Inducible form), isoform CRA_e	PABPC4	0	3	0
R	23	Mono	80.57	Polyadenylate-binding protein 2	PABPN1	1	0	0
R	17	Mono	111.71	Polyadenylate-binding protein 2	PABPN1	12	0	0
R	17	Di	114.19	Polyadenylate-binding protein 2	PABPN1	21	0	0
R	141	Di	35.78	Polyadenylate-binding protein 2	PABPN1	2	0	0

R	23	Di	54.23	Polyadenylate-binding protein 2	PABPN1	2	0	0
R	951	Di	28.11	Pre-mRNA cleavage complex 2 protein Pcf11 (Fragment)	PCF11	0	1	0
R	89	Mono	50.87	Protein-L-isoaspartate O-methyltransferase	PCMT1	3	0	0
K	7	Mono	25.92	Phosducin-like protein	PDCL	1	0	0
K	485	Mono	25.95	Protein disulfide-isomerase A4	PDIA4	0	1	0
K	484	Mono	25.95	Protein disulfide-isomerase A4	PDIA4	0	1	0
K	485	Di	28.07	Protein disulfide-isomerase A4	PDIA4	0	3	0
K	484	Di	28.07	Protein disulfide-isomerase A4	PDIA4	0	3	0
R	42	Di	35.65	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	PDPR	1	0	0
K	64	Mono	94.63	Uncharacterized protein (Fragment)	PE=2	7	0	0
K	64	Di	35.1	Uncharacterized protein (Fragment)	PE=2	3	0	0
K	62	Tri	29.47	Uncharacterized protein	PE=2	0	0	1
K	37	Mono	25.09	Putative Rab-43-like protein ENSP00000330714	PE=5	2	0	0
R	7	Di	52.96	Peflin	PEF1	0	4	0
X	1	Tri	93.68	Proline-, glutamic acid- and leucine-rich protein 1 (Fragment)	PELP1	7	0	0
R	248	Di	35.89	Phosphatidylinositol-binding clathrin assembly protein (Fragment)	PICALM	0	4	0
K	1203	Mono	30.34	Membrane-associated phosphatidylinositol transfer protein 1	PITPNM1	4	0	0
K	97	Mono	29.89	Serine/threonine-protein kinase D1 (Fragment)	PKD1	0	1	0
K	403	Mono	29.34	PNMA-like protein 1	PNMAL1	1	0	0
K	1045	Mono	36.06	DNA-directed RNA polymerase	POLR2B	1	0	0
R	196	Mono	94.25	cAMP-dependent protein kinase type II-beta regulatory subunit	PRKAR2B	3	0	0
K	176	Mono	94.25	cAMP-dependent protein kinase type II-beta regulatory subunit	PRKAR2B	3	0	0
K	69	Tri	46.82	Pre-mRNA-processing-splicing factor 8 (Fragment)	PRPF8	17	0	0
R	1164	Di	36.71	Protein PRRC2A	PRRC2A	2	0	0
K	12	Mono	43.4	Proline-rich transmembrane protein 2 (Fragment)	PRRT2	0	0	2
K	562	Mono	30.5	PH and SEC7 domain-containing protein 2	PSD2	0	3	0
R	252	Di	31.97	Pregnancy-specific beta-1-glycoprotein 8	PSG8	0	2	0
R	2	Mono	18.87	26S protease regulatory subunit 10B (Fragment)	PSMC6	0	1	0
K	15	Mono	44.02	Thymosin alpha-1	PTMA	1	0	0
R	991	Di	23.35	Receptor-type tyrosine-protein phosphatase U	PTPRU	3	0	0
R	139	Di	27.88	Protein quaking (Fragment)	QKI	0	3	0
R	166	Mono	25.67	R3H domain-containing protein 1	R3HDM1	1	0	0
K	13	Mono	25.09	Ras-related protein Rab-30 (Fragment)	RAB30	2	0	0
R	127	Di	26.64	Ras-related protein Rab-34, isoform NARR	RAB34	1	0	0
R	125	Di	26.64	Ras-related protein Rab-34, isoform NARR	RAB34	1	0	0
R	24	Di	37.91	Ras-related protein Rab-34, isoform NARR	RAB34	1	0	0
K	72	Mono	25.09	Ras-related protein Rab-3B	RAB3B	2	0	0
K	3142	Mono	43.97	E3 SUMO-protein ligase RanBP2	RANBP2	0	1	0
K	136	Mono	52.95	Pre-mRNA-splicing factor RBM22	RBM22	2	0	0
R	105	Di	82.14	Putative RNA-binding protein 3	RBM3	40	0	0
R	324	Di	50.03	RNA-binding protein 33 (Fragment)	RBM33	0	9	0
R	602	Mono	26.62	RNA-binding protein 44	RBM44	1	0	0
R	37	Mono	56.18	RNA-binding motif protein, X chromosome, N-terminally processed	RBMX	3	0	0

R	52	Di	51.41	RNA-binding motif protein, X chromosome, N-terminally processed	RBMX	2	0	0
R	234	Di	31.73	RNA-binding motif protein, X chromosome, N-terminally processed	RBMX	3	0	0
R	37	Di	44.51	RNA-binding motif protein, X chromosome, N-terminally processed	RBMX	3	0	0
R	50	Di	55.67	RNA-binding motif protein, X chromosome, N-terminally processed	RBMX	5	0	0
R	185	Mono	26.02	RNA binding motif protein, X-linked-like-1	RBMXL1	1	0	0
R	113	Di	31.31	RNA binding motif protein, X-linked-like-1	RBMXL1	1	0	0
K	81	Mono	51.87	Reticulocalbin-1	RCN1	2	0	0
X	1	Mono	26.11	Reticulocalbin-1 (Fragment)	RCN1	1	0	0
K	9	Tri	26.11	Reticulocalbin-1 (Fragment)	RCN1	1	0	0
R	1119	Di	38.6	Arginine-glutamic acid dipeptide (RE) repeats, isoform CRA_b	RERE	0	0	3
K	86	Mono	19.65	Replication factor C subunit 1 (Fragment)	RFC1	0	0	1
K	293	Tri	27.75	Isoform 2 of Replication factor C subunit 3	RFC3	0	0	1
R	265	Mono	30.4	Inactive rhomboid protein 1	RHBDF1	0	5	0
R	84	Mono	29.37	Inactive rhomboid protein 1 (Fragment)	RHBDF1	2	0	0
K	7	Mono	23.33	Rho-related GTP-binding protein RhoB	RHOB	5	0	0
K	42	Mono	37.17	60S ribosomal protein L10-like	RPL10L	1	0	0
R	26	Mono	32.79	60S ribosomal protein L26-like 1 (Fragment)	RPL26L1	2	0	0
R	137	Mono	30.16	40S ribosomal protein S15	RPS15	1	0	0
R	22	Di	89.3	40S ribosomal protein S2	RPS2	0	100	0
R	58	Mono	34.22	40S ribosomal protein S4, Y isoform 1 (Fragment)	RPS4Y1	4	0	0
K	310	Di	31.82	Visual pigment-like receptor peropsin	RRH	1	0	0
K	882	Mono	20.33	RRP12-like protein	RRP12	0	0	1
K	6	Di	22.92	Ribosomal L1 domain-containing protein 1 (Fragment)	RSL1D1	2	0	0
R	660	Di	28.92	Scaffold attachment factor B1	SAFB	2	0	0
R	422	Di	47.71	Steroidogenic factor 1	SF1	4	0	0
R	425	Di	47.71	Steroidogenic factor 1	SF1	4	0	0
R	243	Di	29.67	Splicing factor 3B subunit 2 (Fragment)	SF3B2	1	0	0
R	244	Di	53.28	Splicing factor 3B subunit 2 (Fragment)	SF3B2	9	0	0
R	246	Di	53.28	Splicing factor 3B subunit 2 (Fragment)	SF3B2	9	0	0
R	221	Di	29.71	Splicing factor 3B subunit 2 (Fragment)	SF3B2	2	0	0
R	245	Di	29.67	Splicing factor 3B subunit 2 (Fragment)	SF3B2	1	0	0
R	390	Di	65.93	Splicing factor 3B subunit 4	SF3B4	0	26	0
R	693	Mono	53.97	Splicing factor, proline- and glutamine-rich	SFPQ	2	0	0
R	2	Mono	38.01	Splicing factor, proline- and glutamine-rich (Fragment)	SFPQ	2	0	0
R	695	Mono	49.03	Splicing factor, proline- and glutamine-rich	SFPQ	0	0	1
R	2	Di	20.33	Splicing factor, proline- and glutamine-rich (Fragment)	SFPQ	0	0	1
R	9	Di	67.1	Splicing factor, proline- and glutamine-rich	SFPQ	9	0	0
K	675	Tri	45.06	Single-minded homolog 1	SIM1	2	0	0
K	23	Mono	54.23	ADP/ATP translocase 1	SLC25A4	56	0	0
K	52	Mono	42.57	ADP/ATP translocase 2	SLC25A5	3	0	0
K	52	Di	68.56	ADP/ATP translocase 2	SLC25A5	7	0	0
K	52	Tri	48.37	ADP/ATP translocase 2	SLC25A5	50	0	0
K	52	Di	63.46	ADP/ATP translocase 3 (Fragment)	SLC25A6	3	0	0

K	52	Tri	60.04	ADP/ATP translocase 3 (Fragment)	SLC25A6	20	0	0
R	38	Mono	21.47	Structure-specific endonuclease subunit SLX1 (Fragment)	SLX1B	0	3	0
R	60	Di	32.11	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMARCD2	0	5	0
R	43	Di	25.37	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2 (Fragment)	SMARCD2	0	1	0
R	449	Di	30.28	Histone-lysine N-methyltransferase SMYD1	SMYD1	0	2	0
K	447	Tri	30.28	Histone-lysine N-methyltransferase SMYD1	SMYD1	0	2	0
R	4	Di	27.54	Small nuclear ribonucleoprotein E	SNRPE	3	0	0
R	240	Di	32.84	Small nuclear ribonucleoprotein-associated protein	SNRPN	4	0	0
R	43	Di	34.85	Sorting nexin-3	SNX3	0	0	1
R	358	Di	28.51	Protein SOGA2	SOGA2	0	0	21
R	713	Di	34.29	Son of sevenless homolog 1	SOS1	0	0	2
R	3121	Di	30.43	Msx2-interacting protein	SPEN	0	0	3
K	1981	Tri	29.88	Spectrin beta chain, non-erythrocytic 1	SPTBN1	2	0	0
R	1232	Di	27.79	Helicase SRCAP	SRCAP	0	1	0
R	814	Di	25.55	Serrate RNA effector molecule homolog	SRRT	0	1	0
R	97	Di	25.51	Serine/arginine-rich-splicing factor 1	SRSF1	1	0	0
R	109	Di	41.8	Serine/arginine-rich-splicing factor 1	SRSF1	1	0	0
K	336	Di	26.52	Serine/threonine-protein kinase 32C	STK32C	0	1	0
K	349	Di	30.62	Striatin-interacting protein 1	STRIP1	1	0	0
R	62	Di	69.7	Heterogeneous nuclear ribonucleoprotein Q (Fragment)	SYNCRIP	10	0	0
K	509	Mono	29.01	Nesprin-1	SYNE1	0	0	1
K	2350	Mono	29.92	Nesprin-2	SYNE2	0	0	1
R	124	Di	27.68	TATA-binding protein-associated factor 2N (Fragment)	TAF15	0	2	0
R	80	Di	28.69	TATA-binding protein-associated factor 2N (Fragment)	TAF15	0	2	0
R	150	Di	26.9	TATA-binding protein-associated factor 2N (Fragment)	TAF15	0	1	0
R	483	Di	72.15	TATA-binding protein-associated factor 2N	TAF15	5	0	0
R	182	Di	79.22	TATA-binding protein-associated factor 2N (Fragment)	TAF15	11	0	0
R	157	Di	43.52	TATA-binding protein-associated factor 2N (Fragment)	TAF15	0	9	0
R	23	Di	31.93	T-cell leukemia/lymphoma protein 1A (Fragment)	TCL1A	1	0	0
R	304	Mono	25.04	Isoform 4 of Transcription factor AP-2-alpha	TFAP2A	1	0	0
R	385	Di	45.61	Protein TFG	TFG	5	0	0
R	101	Di	33.98	Thyroid hormone receptor-associated protein 3	THRAP3	0	1	0
R	188	Di	28.31	Thrombospondin type-1 domain-containing protein 4	THSD4	3	0	0
K	575	Tri	29.18	Transketolase	TKT	2	0	0
R	29	Di	25.83	Transmembrane protein 214	TMEM214	1	0	0
R	181	Mono	25.77	182 kDa tankyrase-1-binding protein	TNKS1BP1	0	1	0
K	140	Di	28.93	Transportin-1	TNPO1	0	0	8
K	143	Tri	25.39	Two pore calcium channel protein 2	TPCN2	0	1	0
K	257	Mono	43.24	TRAF3-interacting protein 1	TRAF3IP1	6	0	0
K	252	Di	43.24	TRAF3-interacting protein 1	TRAF3IP1	6	0	0
X	1	Mono	18.34	Trem-like transcript 4 protein (Fragment)	TREML4	0	1	0
R	25	Mono	34.32	tRNA (adenine(58)-N(1))-methyltransferase, mitochondrial (Fragment)	TRMT61B	1	0	0
K	991	Mono	27.89	Tetratricopeptide repeat protein 28	TTC28	0	0	1

K	170	Tri	30.24	Transcription termination factor 2	TTF2	1	0	0
R	79	Mono	43.27	Tubulin alpha-3C/D chain	TUBA3C	2	0	0
R	46	Mono	52.78	Tubulin beta chain	TUBB	9	0	0
R	28	Mono	52.78	Tubulin beta chain	TUBB	9	0	0
R	84	Mono	44.03	HCG1983504, isoform CRA_f	TUBB3	19	0	0
R	90	Mono	19.83	HCG1983504, isoform CRA_f	TUBB3	1	0	0
R	318	Mono	44.62	Tubulin beta-4A chain	TUBB4A	4	0	0
R	390	Mono	32.97	Tubulin beta-6 chain	TUBB6	1	0	0
X	1	Mono	52.54	Tubulin beta-6 chain (Fragment)	TUBB6	3	0	0
X	1	Di	51.7	Tubulin beta-6 chain (Fragment)	TUBB6	6	0	0
R	308	Mono	51.25	Tubulin beta-8 chain	TUBB8	8	0	0
K	330	Mono	44.3	Alpha-taxilin	TXLNA	3	0	0
X	1	Mono	27.52	Thioredoxin domain-containing protein 11 (Fragment)	TXNDC11	3	0	0
K	39	Mono	32.65	Splicing factor U2AF 35 kDa subunit	U2AF1	1	0	0
R	236	Di	38.19	Ubiquilin-1	UBQLN1	0	0	1
R	41	Mono	30.25	UDP-glucuronosyltransferase 3A2 (Fragment)	UGT3A2	0	1	0
R	161	Mono	29.24	Protein unc-119 homolog A (Fragment)	UNC119	0	8	0
K	346	Mono	21.04	Utrophin	UTRN	0	0	1
K	238	Mono	39.36	Voltage-dependent anion-selective channel protein 2	VDAC2	18	0	0
R	42	Di	25.88	Vacuolar protein sorting-associated protein 13A (Fragment)	VPS13A	1	0	0
K	50	Tri	25.88	Vacuolar protein sorting-associated protein 13A (Fragment)	VPS13A	1	0	0
R	768	Mono	26.05	WD repeat-containing protein 3	WDR3	0	0	2
K	229	Di	27.3	Isoform 2 of pre-mRNA 3' end processing protein WDR33	WDR33	0	1	0
R	7	Mono	27.23	WD repeat-containing protein 52 (Fragment)	WDR52	2	0	0
K	209	Mono	42.52	X-ray repair cross-complementing protein 5	XRCC5	2	0	0
R	816	Di	25.75	5'-3' exoribonuclease 2	XRN2	0	1	0
K	28	Mono	42.02	14-3-3 protein epsilon (Fragment)	YWHAE	1	0	0
K	12	Mono	26.9	Probable ribonuclease ZC3H12D	ZC3H12D	0	2	0
K	457	Mono	25.86	Zinc finger protein 286A	ZNF286A	1	0	0
K	454	Mono	25.86	Zinc finger protein 286A	ZNF286A	1	0	0
K	453	Mono	25.86	Zinc finger protein 286A	ZNF286A	1	0	0
R	175	Di	69.04	DBIRD complex subunit ZNF326	ZNF326	4	0	0
K	41	Mono	31.55	Zinc finger protein 563 (Fragment)	ZNF563	0	0	1
R	34	Mono	26.67	Zinc finger protein 772	ZNF772	1	0	0
R	8	Di	39.1	Zinc finger protein 785 (Fragment)	ZNF785	5	0	0
R	7	Di	39.1	Zinc finger protein 785 (Fragment)	ZNF785	5	0	0

Appendix 6: List of methylation sites identified by MS/MS in a tryptically digested whole cell lysate compared to cytosolic and nuclear fractions digested with trypsin, chymotrypsin, and Glu-C.

Sites identified at the 1% peptide FDR confidence level for the samples. The numbers on the right of the table indicate peptide hits for each site in each sample.

K/R	Site	Type	Mascot Score	Protein Name	Gene Name	Cytosol	Nucleus	Whole Cell Lysate
K	35	Tri	23.68	Isoform 2 of Kynurenine/alpha-aminoadipate aminotransferase, mitochondrial	AADAT	0	0	1
K	51	Mono	26.49	Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	0	0	3
K	349	Tri	20.81	Probable inactive 1-aminocyclopropane-1-carboxylate synthase-like protein 2	ACCSL	0	1	0
K	129	Mono	66.51	Actin, alpha skeletal muscle	ACTA1	0	1	6
K	293	Di	46.21	Actin, aortic smooth muscle	ACTA2	2	3	8
K	292	Mono	48.89	Beta-actin-like protein 2	ACTBL2	1	4	5
K	235	Mono	24.1	Actin-like protein 6B	ACTL6B	0	1	0
K	236	Mono	24.1	Actin-like protein 6B	ACTL6B	0	1	0
R	740	Mono	52.3	Alpha-actinin-3	ACTN3	1	0	1
R	3	Mono	14.61	Serine/threonine-protein kinase receptor R3 (Fragment)	ACVRL1	0	1	0
R	829	Mono	29.97	ADAMTS-like protein 4	ADAMTSL4	0	0	1
R	251	Mono	26.33	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 1	AGAP1	0	0	1
X	1	Mono	16.09	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3 (Fragment)	AGAP3	0	0	1
R	165	Mono	24.39	Ethanolamine-phosphate phospho-lyase	AGXT2L1	0	1	0
R	2	Mono	12.44	Adenosylhomocysteinase (Fragment)	AHCYL2	0	0	1
R	70	Mono	30.58	Aldo-keto reductase family 1 member B10	AKR1B10	1	0	0
K	77	Mono	25.09	Serum albumin (Fragment)	ALB	1	0	0
K	443	Mono	65.23	Serum albumin	ALB	3	0	8
K	4063	Mono	52.06	Alstrom syndrome protein 1	ALMS1	0	0	1
R	204	Di	32.39	THO complex subunit 4	ALYREF	0	1	0
R	211	Di	82.41	THO complex subunit 4	ALYREF	0	2	4
R	70	Di	40.01	THO complex subunit 4	ALYREF	0	2	1
R	45	Di	51.34	THO complex subunit 4	ALYREF	2	2	5
R	416	Mono	14.79	Anoctamin-7	ANO7	1	0	0
R	63	Mono	67.62	Putative annexin A2-like protein	ANXA2P2	0	2	4
R	17	Mono	28.14	Brefeldin A-inhibited guanine nucleotide-exchange protein 1	ARFGEF1	0	0	1
R	604	Mono	24.2	Rho guanine nucleotide exchange factor 15	ARHGEF15	0	0	1
R	604	Di	24.2	Rho guanine nucleotide exchange factor 15	ARHGEF15	0	0	1
K	606	Di	24.2	Rho guanine nucleotide exchange factor 15	ARHGEF15	0	0	1
K	606	Tri	24.2	Rho guanine nucleotide exchange factor 15	ARHGEF15	0	0	1
K	739	Mono	27.14	Rho guanine nucleotide exchange factor 33	ARHGEF33	0	0	5
R	98	Di	20.25	Beta-arrestin-1 (Fragment)	ARRB1	0	0	1
R	368	Mono	25.52	Autophagy-related protein 2 homolog A (Fragment)	ATG2A	0	0	1
K	371	Mono	25.52	Autophagy-related protein 2 homolog A (Fragment)	ATG2A	0	0	1
R	196	Mono	14.71	Sodium/potassium-transporting ATPase subunit alpha-2	ATP1A2	0	0	4

R	206	Mono	14.71	Sodium/potassium-transporting ATPase subunit alpha-4	ATP1A4	0	0	4
R	1159	Di	24	Isoform WA of Plasma membrane calcium-transporting ATPase 2	ATP2B2	1	0	0
R	209	Mono	14.71	Potassium-transporting ATPase alpha chain 1	ATP4A	0	0	4
R	304	Mono	22.29	Isoform 2 of BRCA2 and CDKN1A-interacting protein	BCCIP	0	0	2
R	27	Di	57.63	Bcl-2-associated transcription factor 1	BCLAF1	0	1	0
R	85	Di	35.89	Bcl-2-associated transcription factor 1	BCLAF1	0	1	0
K	504	Tri	29.9	Peregrin	BRPF1	0	0	3
R	14	Di	39.9	Isoform 2 of UPF0696 protein C11orf68	C11orf68	0	0	3
K	14	Di	24.48	Uncharacterized protein C12orf40	C12orf40	0	0	1
R	4	Di	23.73	Autophagy-related protein 101 (Fragment)	C12orf44	0	1	0
K	4	Di	15.27	Uncharacterized protein C1orf198 (Fragment)	C1orf198	0	0	2
K	7	Mono	26.46	Uncharacterized protein C21orf59	C21orf59	0	0	1
R	148	Mono	18.52	Chromosome 9 open reading frame 18, isoform CRA_a	C9orf18	2	0	0
R	144	Mono	18.52	Chromosome 9 open reading frame 18, isoform CRA_a	C9orf18	2	0	0
K	163	Tri	41.41	Calmodulin	CALM2	0	0	6
K	116	Mono	32.27	Calmodulin-like protein 3	CALML3	0	0	1
R	15	Mono	25.56	Cullin-associated NEDD8-dissociated protein 2 (Fragment)	CAND2	0	0	1
R	513	Mono	14.79	Calpain-13	CAPN13	1	0	0
K	31	Mono	13.37	Chromobox protein homolog 7	CBX7	0	1	2
R	76	Di	28.08	Protein chibby homolog 1 (Fragment)	CBY1	0	0	1
K	71	Di	19.68	Coiled-coil domain-containing protein 134	CCDC134	0	1	0
K	10	Tri	25.37	Coiled-coil domain-containing protein 171 (Fragment)	CCDC171	0	0	1
R	739	Di	25.49	Isoform 4 of B-cell receptor CD22	CD22	0	0	1
K	76	Tri	25.12	Cell division cycle 5-like protein	CDC5L	0	0	1
R	18	Mono	18.52	Centrosomal protein of 76 kDa (Fragment)	CEP76	2	0	0
R	21	Mono	18.52	Centrosomal protein of 76 kDa (Fragment)	CEP76	2	0	0
K	73	Mono	23.73	Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	0	0	1
R	44	Mono	34.83	Chromodomain-helicase-DNA-binding protein 3 (Fragment)	CHD3	0	1	0
R	679	Mono	34.83	Chromodomain-helicase-DNA-binding protein 5 (Fragment)	CHD5	0	1	0
X	1	Tri	15.22	Probable ATP-dependent RNA helicase DDX11 (Fragment)	CHL1	0	1	0
R	63	Di	25.69	Cold-inducible RNA-binding protein	CIRBP	0	1	0
K	156	Tri	29.57	Creatine kinase B-type (Fragment)	CKB	0	0	2
K	3	Mono	32.94	Clathrin heavy chain 1 (Fragment)	CLTC	0	0	1
R	34	Mono	28.84	Isoform 2 of Cellular nucleic acid-binding protein	CNBP	0	0	1
R	25	Di	26.78	Cellular nucleic acid-binding protein	CNBP	0	0	1
R	354	Mono	28.62	Coronin-1B	CORO1B	0	1	4
R	453	Di	28.08	Rootletin (Fragment)	CROCC	0	0	1
R	495	Di	47.29	Cleavage stimulation factor subunit 2	CSTF2	0	1	0
K	19	Mono	13.52	Copper homeostasis protein cutC homolog	CUTC	0	0	1
K	243	Mono	12.91	Pre-mRNA-splicing factor CWC22 homolog	CWC22	1	1	5
R	62	Mono	14.79	Cysteine and histidine-rich protein 1	CYHR1	1	0	0
R	370	Mono	12.36	Cholesterol 24-hydroxylase	CYP46A1	0	0	1
R	191	Di	12.78	Disheveled-associated activator of morphogenesis 2	DAAM2	0	0	1

R	382	Di	20.25	Death-associated protein kinase 3	DAPK3	0	0	1
R	607	Mono	33.61	Probable ATP-dependent RNA helicase DDX17	DDX17	0	1	0
R	428	Mono	27.93	Probable ATP-dependent RNA helicase DDX17	DDX17	0	1	0
K	283	Mono	57.19	ATP-dependent RNA helicase DDX50	DDX50	0	0	2
R	1227	Di	32.69	ATP-dependent RNA helicase A	DHX9	0	3	0
R	1207	Di	59.12	ATP-dependent RNA helicase A	DHX9	0	14	0
R	1265	Di	37.81	ATP-dependent RNA helicase A	DHX9	0	2	0
R	304	Mono	12.37	Protein kintoun	DNAAF2	0	0	1
K	223	Mono	28.71	DnaJ homolog subfamily A member 2	DNAJA2	0	0	2
K	371	Di	17	Isoform 2 of DnaJ homolog subfamily B member 12	DNAJB12	1	0	0
R	141	Di	13.2	DNA (cytosine-5)-methyltransferase 3-like (Fragment)	DNMT3L	0	0	1
R	16	Mono	35.52	Histone-lysine N-methyltransferase, H3 lysine-79-specific (Fragment)	DOT1L	0	0	1
R	14	Mono	30.97	Protein DPCD (Fragment)	DPCD	0	2	10
K	4	Mono	24	Cytoplasmic dynein 1 intermediate chain 1	DYNC1I1	0	0	1
K	79	Mono	44.54	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	0	0	1
R	166	Mono	50.24	Elongation factor 1-alpha 1	EEF1A1	0	0	2
K	55	Mono	35.65	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	0	0	2
K	84	Mono	44.54	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	0	0	1
K	318	Mono	38.48	Elongation factor 1-alpha 1	EEF1A1	0	0	4
K	165	Mono	68.72	Elongation factor 1-alpha 1	EEF1A1	11	0	45
K	55	Di	65.03	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	0	0	18
K	36	Di	34.23	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	3	0	6
K	165	Di	76.16	Elongation factor 1-alpha 1	EEF1A1	14	2	65
K	84	Di	44.54	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	0	0	1
K	318	Di	39.04	Elongation factor 1-alpha 1	EEF1A1	21	0	60
K	79	Di	44.54	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	0	0	1
R	166	Di	50.24	Elongation factor 1-alpha 1	EEF1A1	0	0	2
K	84	Tri	44.54	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	0	0	1
K	318	Tri	61.72	Elongation factor 1-alpha 1	EEF1A1	71	3	225
K	36	Tri	46.74	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	20	0	106
K	165	Tri	54.54	Elongation factor 1-alpha 1	EEF1A1	7	1	26
K	79	Tri	57.95	Elongation factor 1-alpha 1 (Fragment)	EEF1A1	0	0	82
R	166	Mono	17.81	Elongation factor 1-alpha 2	EEF1A2	0	0	1
K	165	Mono	28.24	Elongation factor 1-alpha 2	EEF1A2	0	0	1
K	84	Mono	44.54	Elongation factor 1-alpha 2	EEF1A2	0	0	1
K	79	Mono	44.54	Elongation factor 1-alpha 2	EEF1A2	0	0	1
K	79	Di	44.54	Elongation factor 1-alpha 2	EEF1A2	0	0	1
K	84	Di	44.54	Elongation factor 1-alpha 2	EEF1A2	0	0	1
K	318	Tri	34.18	Elongation factor 1-alpha 2	EEF1A2	0	0	2
K	407	Mono	32.65	Elongation factor 2	EEF2	2	0	11
K	525	Di	29.48	Elongation factor 2	EEF2	0	0	1
K	525	Tri	30.75	Elongation factor 2	EEF2	10	0	11
X	1	Mono	14.85	EF-hand calcium-binding domain-containing protein 5 (Fragment)	EFCAB5	1	0	0

R	19	Di	24.41	Eukaryotic translation initiation factor 4H	EIF4H	0	0	1
R	97	Mono	25.46	Eukaryotic translation initiation factor 5A-2	EIF5A2	0	1	1
R	9	Mono	51.43	Enolase	ENO2	0	0	1
R	15	Mono	51.43	Enolase	ENO2	0	0	1
R	9	Mono	16.28	Isoform 2 of Eomesodermin homolog	EOMES	0	0	1
R	8	Mono	16.28	Isoform 2 of Eomesodermin homolog	EOMES	0	0	1
R	806	Di	24.12	Serine/threonine-protein kinase/endoribonuclease IRE1	ERN1	0	1	0
K	799	Tri	24.12	Serine/threonine-protein kinase/endoribonuclease IRE1	ERN1	0	1	0
R	234	Di	14.18	HERV-FRD_6p24.1 provirus ancestral Env polyprotein	ERVFRD-1	1	0	0
R	605	Mono	25.58	Extended synaptotagmin-2	ESYT2	0	1	0
R	577	Di	36.87	RNA-binding protein EWS	EWSR1	0	0	2
K	276	Mono	26.68	Exosome complex component RRP42	EXOSC7	0	0	1
K	9	Mono	25.9	Protein FAM127B	FAM127B	9	15	52
K	9	Di	27.59	Protein FAM127B	FAM127B	0	1	1
R	60	Di	14.58	Protein FAM217B	FAM217B	0	1	0
K	281	Mono	24.68	Protein FAM49A	FAM49A	0	0	1
K	466	Mono	12.71	Protein fem-1 homolog C	FEM1C	0	0	1
R	31	Mono	12.71	Forkhead-associated domain-containing protein 1 (Fragment)	FHAD1	0	1	0
R	183	Mono	18.52	Peptidyl-prolyl cis-trans isomerase	FKBP6	2	0	0
R	186	Mono	18.52	Peptidyl-prolyl cis-trans isomerase	FKBP6	2	0	0
K	156	Mono	26.29	Forkhead box protein G1	FOXG1	0	1	0
K	157	Mono	26.29	Forkhead box protein G1	FOXG1	0	1	0
K	156	Di	26.29	Forkhead box protein G1	FOXG1	0	1	0
K	157	Di	26.29	Forkhead box protein G1	FOXG1	0	1	0
R	408	Mono	58.08	RNA-binding protein FUS	FUS	0	1	0
R	408	Di	77.69	RNA-binding protein FUS	FUS	0	2	0
R	216	Di	35.16	RNA-binding protein FUS	FUS	0	0	1
R	218	Di	35.16	RNA-binding protein FUS	FUS	0	0	1
R	99	Mono	12.98	G0/G1 switch protein 2	G0S2	0	0	1
R	424	Mono	13.52	Gamma-aminobutyric acid receptor subunit alpha-1	GABRA1	0	0	1
R	421	Mono	13.52	Gamma-aminobutyric acid receptor subunit alpha-1	GABRA1	0	0	1
R	424	Di	13.52	Gamma-aminobutyric acid receptor subunit alpha-1	GABRA1	0	0	1
R	421	Di	13.52	Gamma-aminobutyric acid receptor subunit alpha-1	GABRA1	0	0	1
R	306	Mono	25.15	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific	GAPDHS	0	0	1
R	253	Di	15.03	Erythroid transcription factor	GATA1	0	0	1
R	471	Mono	24.39	D-glucuronyl C5-epimerase	GLCE	1	0	0
R	326	Mono	13.52	Glutamate receptor 1	GRIA1	0	0	1
R	327	Mono	13.52	Glutamate receptor 1	GRIA1	0	0	1
R	326	Di	13.52	Glutamate receptor 1	GRIA1	0	0	1
R	327	Di	13.52	Glutamate receptor 1	GRIA1	0	0	1
R	324	Mono	13.52	Glutamate receptor 4	GRIA4	0	0	1
R	325	Mono	13.52	Glutamate receptor 4	GRIA4	0	0	1
R	325	Di	13.52	Glutamate receptor 4	GRIA4	0	0	1

R	324	Di	13.52	Glutamate receptor 4	GRIA4	0	0	1
R	291	Mono	24.17	Metabotropic glutamate receptor 5	GRM5	0	0	1
K	80	Mono	69.6	Histone H3	H3F3A	0	8	30
R	656	Di	32.58	HCG2044799	hCG_2044799	0	1	2
R	101	Mono	12.37	HD domain-containing protein 2	HDDC2	0	0	1
K	107	Di	12.37	HD domain-containing protein 2	HDDC2	0	0	1
R	11	Mono	23.75	Probable E3 ubiquitin-protein ligase HECTD2	HECTD2	0	0	1
R	12	Mono	23.75	Probable E3 ubiquitin-protein ligase HECTD2	HECTD2	0	0	1
R	89	Mono	36.82	Histone H2A type 2-B	HIST2H2AB	2	9	36
R	291	Di	77.31	Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	0	2	3
R	215	Mono	30.44	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	0	0	1
R	319	Mono	25.27	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	0	1	0
R	318	Mono	25.27	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	0	1	0
R	213	Mono	30.44	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	0	0	1
R	284	Mono	29.96	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	0	0	1
R	232	Mono	29.54	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	0	1	0
R	206	Mono	57.9	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	0	1	3
R	31	Mono	95.05	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	0	106	9
R	218	Mono	56.38	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	0	2	0
K	112	Mono	55.03	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	0	2	0
R	225	Di	47.16	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	0	1	1
R	225	Di	24.32	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	0	1	0
R	215	Di	71.73	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	4	47	88
R	218	Di	47.86	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	0	3	0
R	213	Di	78	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	HNRNPA1	3	52	34
R	206	Di	65.07	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	0	1	0
R	196	Di	71.73	Heterogeneous nuclear ribonucleoprotein A1-like 2	HNRNPA1L2	4	47	88
R	194	Di	78	Heterogeneous nuclear ribonucleoprotein A1-like 2	HNRNPA1L2	3	52	34
R	213	Mono	47.22	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	0	2	2
K	113	Mono	18.57	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	0	10	0
K	112	Mono	18.57	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	0	10	0
R	266	Mono	71.5	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	0	1	0
R	203	Mono	42	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	0	0	2
R	325	Mono	30.24	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	0	1	0
R	266	Di	91.65	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	0	2	0
K	104	Di	18.57	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	0	10	0
R	52	Mono	101.64	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	3	151	33
R	239	Di	44.66	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	0	1	0
R	52	Di	95.05	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	0	106	9
R	246	Di	28.74	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	0	1	0
R	286	Di	64.4	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	0	1	0
R	34	Di	34.79	Heterogeneous nuclear ribonucleoprotein A3 (Fragment)	HNRNPA3	0	1	0
R	226	Di	44.66	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	0	1	0

R	245	Di	56.57	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	0	2	0
R	248	Di	65.64	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	0	2	0
R	226	Mono	32.5	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	0	0	2
R	220	Mono	33.07	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	0	0	1
R	220	Di	32.5	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	0	0	2
R	293	Di	25.45	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	0	0	1
R	226	Di	32.5	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	0	0	2
K	87	Mono	20.81	Heterogeneous nuclear ribonucleoprotein F	HNRNPF	0	1	0
K	124	Mono	25.21	Heterogeneous nuclear ribonucleoprotein H (Fragment)	HNRNPH1	0	1	0
R	224	Di	37.27	Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	1	14	0
R	217	Di	34.03	Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	0	2	0
K	29	Mono	25.21	Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	0	1	0
R	215	Mono	65.29	Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	0	1	0
R	129	Di	32.32	Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	0	1	0
R	215	Di	30.17	Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	0	1	0
K	99	Mono	47.07	Heterogeneous nuclear ribonucleoprotein R	HNRNPR	0	0	2
R	372	Di	23.92	Heterogeneous nuclear ribonucleoprotein R	HNRNPR	0	1	0
R	442	Mono	32.94	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	0	2	0
R	739	Di	68.17	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	0	1	0
R	733	Di	43.83	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	0	4	2
K	161	Mono	64.64	Heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	0	1	0
K	162	Mono	55.93	Heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	0	2	3
R	408	Di	32.13	Heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	0	2	2
R	695	Mono	14.79	Protein Hook homolog 2	HOOK2	1	0	0
R	185	Mono	13.69	Histidine-rich glycoprotein	HRG	0	1	0
R	182	Mono	13.69	Histidine-rich glycoprotein	HRG	0	1	0
R	202	Di	53.32	Putative heat shock protein HSP 90-alpha A2	HSP90AA2	0	0	1
K	30	Mono	51.53	Endoplasmin (Fragment)	HSP90B1	0	0	1
R	325	Mono	24.33	Heat shock 70 kDa protein 1A/1B	HSPA1A	0	0	1
K	459	Mono	19.5	Heat shock 70 kDa protein 1A/1B	HSPA1A	3	0	0
R	378	Mono	42.22	Heat shock 70 kDa protein 1A/1B	HSPA1A	14	0	0
K	470	Tri	53.31	Heat shock 70 kDa protein 1A/1B	HSPA1A	0	0	1
K	25	Tri	39.91	Heat shock 70 kDa protein 1A/1B	HSPA1A	0	5	0
K	461	Mono	31.64	Heat shock-related 70 kDa protein 2	HSPA2	0	0	3
R	472	Mono	31.64	Heat shock-related 70 kDa protein 2	HSPA2	0	0	3
R	492	Mono	27.8	78 kDa glucose-regulated protein	HSPA5	2	0	0
K	154	Di	46.84	78 kDa glucose-regulated protein	HSPA5	1	0	9
K	585	Tri	52.81	78 kDa glucose-regulated protein	HSPA5	0	0	3
K	330	Mono	39.65	Heat shock 70 kDa protein 6	HSPA6	4	4	177
R	233	Mono	31.64	Heat shock cognate 71 kDa protein	HSPA8	0	0	3
K	3	Di	31.79	Heat shock cognate 71 kDa protein (Fragment)	HSPA8	0	5	0
K	325	Tri	26.88	Heat shock cognate 71 kDa protein	HSPA8	0	0	2
R	218	Mono	38.16	Stress-70 protein, mitochondrial	HSPA9	5	0	0

R	401	Mono	35.11	5-hydroxytryptamine receptor 3A	HTR3A	0	1	0
K	98	Tri	24.17	Peptidyl-tRNA hydrolase ICT1, mitochondrial (Fragment)	ICT1	21	0	60
R	1535	Mono	26.02	Cation-independent mannose-6-phosphate receptor	IGF2R	0	1	0
R	321	Mono	45.69	Inosine-5'-monophosphate dehydrogenase	IMPDH1	1	0	0
K	324	Mono	17.27	ITGA10 protein	ITGA10	0	0	1
X	1	Di	16.06	Histone acetyltransferase KAT5 (Fragment)	KAT5	0	1	0
R	337	Mono	14.3	Potassium voltage-gated channel subfamily G member 4	KCNG4	0	4	5
R	564	Mono	25.26	Potassium voltage-gated channel subfamily H member 1	KCNH1	0	0	2
K	561	Tri	25.26	Potassium voltage-gated channel subfamily H member 1	KCNH1	0	0	2
R	114	Mono	14.88	BTB/POZ domain-containing protein KCTD8	KCTD8	1	0	6
K	385	Tri	33.06	Mitochondrial ribonuclease P protein 3	KIAA0391	0	3	0
R	1184	Di	46.87	Uncharacterized protein KIAA0556	KIAA0556	1	0	0
K	259	Mono	20.61	Uncharacterized protein KIAA1211-like (Fragment)	KIAA1211L	0	0	1
K	398	Mono	13.42	Uncharacterized protein KIAA1671	KIAA1671	0	0	1
K	1142	Mono	23.78	Kinesin-like protein KIF14	KIF14	1	0	0
K	1151	Mono	23.78	Kinesin-like protein KIF14	KIF14	1	0	0
K	1146	Mono	23.78	Kinesin-like protein KIF14	KIF14	1	0	0
K	1142	Di	23.78	Kinesin-like protein KIF14	KIF14	1	0	0
K	1146	Di	23.78	Kinesin-like protein KIF14	KIF14	1	0	0
R	306	Mono	19.49	Isoform 3 of Krueppel-like factor 12	KLF12	0	0	1
R	204	Di	26.02	Kelch-like protein 21	KLHL21	0	1	0
K	17	Mono	24.49	Kallikrein-11 (Fragment)	KLK11	1	0	0
K	7	Di	24.49	Kallikrein-11 (Fragment)	KLK11	1	0	0
R	24	Mono	34.21	Kallikrein-2 (Fragment)	KLK2	16	28	0
R	431	Mono	30.5	Keratin, type I cytoskeletal 27	KRT27	0	0	1
K	158	Tri	36.39	Probable leucine--tRNA ligase, mitochondrial	LARS2	0	5	0
K	264	Mono	20.03	L-lactate dehydrogenase	LDHC	4	0	9
K	599	Mono	24.6	LIM and calponin homology domains-containing protein 1	LIMCH1	1	0	0
R	596	Di	24.6	LIM and calponin homology domains-containing protein 1	LIMCH1	1	0	0
K	13	Di	26.59	Protein Lines homolog (Fragment)	LINS	0	1	0
R	16	Di	14.79	Protein LOC100506518	LOC100506518	1	0	0
K	163	Mono	13.42	Leucine-rich repeat-containing protein 45 (Fragment)	LRRC45	0	0	1
R	3193	Mono	30.63	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	MACF1	0	0	1
R	100	Mono	14.61	Alpha-mannosidase 2x (Fragment)	MAN2A2	0	1	0
R	124	Mono	12.44	DNA replication licensing factor MCM6	MCM6	0	0	1
K	193	Di	23.81	Calcium uptake protein 1, mitochondrial (Fragment)	MICU1	0	1	0
R	3246	Mono	12.44	Antigen KI-67	MKI67	0	0	1
R	27	Mono	12.71	MORN repeat-containing protein 3	MORN3	0	1	0
K	108	Mono	15.38	28S ribosomal protein S25, mitochondrial	MRPS25	0	0	1
R	20	Di	28.15	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	0	0	2
R	42	Di	36.43	Neurofilament medium polypeptide	NEFM	0	2	0
R	379	Mono	36.43	Isoform 2 of Serine/threonine-protein kinase Nek2	NEK2	1	0	0
K	50	Tri	39.32	Serine/threonine-protein kinase Nek3	NEK3	2	0	1

K	523	Tri	31.04	Merlin	NF2	0	1	0
R	64	Di	12.71	NHS-like protein 2	NHSL2	0	0	1
R	516	Di	32.73	Ninein-like protein	NINL	0	0	1
K	520	Tri	32.73	Ninein-like protein	NINL	0	0	1
R	184	Mono	18.52	NACHT, LRR and PYD domains-containing protein 7	NLRP7	2	0	0
R	181	Mono	18.52	NACHT, LRR and PYD domains-containing protein 7	NLRP7	2	0	0
K	732	Tri	16.66	Nucleolar MIF4G domain-containing protein 1	NOM1	0	2	0
K	198	Mono	40.94	Non-POU domain-containing octamer-binding protein (Fragment)	NONO	0	1	1
R	1498	Mono	26.61	Notch 4 intracellular domain	NOTCH4	0	0	1
R	367	Mono	23.89	Nucleobindin-1	NUCB1	0	0	1
K	9	Mono	38.2	Olfactory receptor 4A15	OR4A15	0	0	3
R	448	Di	48.19	Polyadenylate-binding protein 1	PABPC1	1	0	3
R	374	Di	31.47	Polyadenylate-binding protein 1	PABPC1	1	0	0
R	398	Di	41.38	Polyadenylate-binding protein 1	PABPC1	1	0	0
K	361	Mono	39.39	Polyadenylate-binding protein 1-like	PABPC1L	2	0	8
K	104	Mono	39.49	Polyadenylate-binding protein 3	PABPC3	0	0	5
K	361	Di	39.39	Poly(A) binding protein, cytoplasmic 4 (Inducible form), isoform CRA_e	PABPC4	2	0	8
R	501	Di	24.87	Poly(A) binding protein, cytoplasmic 4 (Inducible form), isoform CRA_e	PABPC4	1	0	0
R	23	Mono	68.77	Polyadenylate-binding protein 2	PABPN1	0	2	2
R	17	Mono	93.7	Polyadenylate-binding protein 2	PABPN1	0	0	3
R	17	Di	83.23	Polyadenylate-binding protein 2	PABPN1	0	2	8
R	23	Di	71.39	Polyadenylate-binding protein 2	PABPN1	0	3	3
K	288	Di	21.91	Poly (ADP-ribose) polymerase family, member 9, isoform CRA_b	PARP9	0	0	1
K	141	Mono	13.78	Protocadherin beta-3	PCDHB3	0	1	0
R	89	Mono	35.1	Protein-L-isoaspartate O-methyltransferase	PCMT1	1	0	0
R	164	Di	25.21	PEST proteolytic signal-containing nuclear protein	PCNP	0	0	1
K	154	Di	25.02	PDZ domain-containing protein 9	PDZD9	0	0	9
K	153	Tri	25.02	PDZ domain-containing protein 9	PDZD9	0	0	9
R	54	Mono	35.36	Ig lambda chain V-II region VIL	PE=1	1	0	1
K	64	Mono	73.42	Uncharacterized protein (Fragment)	PE=2	8	1	16
K	7	Mono	15.38	Uncharacterized protein (Fragment)	PE=3	0	0	1
R	1111	Mono	14.79	Uncharacterized protein (Fragment)	PE=4	1	0	0
K	3	Mono	49.05	Uncharacterized protein (Fragment)	PE=4	0	0	1
R	819	Di	28.08	p53-induced protein with a death domain	PIDD	0	0	1
K	1203	Mono	31.32	Membrane-associated phosphatidylinositol transfer protein 1	PITPNM1	0	0	1
R	1077	Mono	14.74	Plexin-B3	PLXNB3	0	0	1
K	633	Di	12.98	PNMA-like protein 2	PNMAL2	0	0	1
R	110	Di	14.79	Patatin-like phospholipase domain-containing protein 4 (Fragment)	PNPLA4	1	0	0
R	927	Mono	30.54	DNA polymerase	POLA1	10	0	11
K	929	Di	29.48	DNA polymerase	POLA1	0	0	1
K	929	Tri	30.54	DNA polymerase	POLA1	10	0	11
K	1045	Mono	33.49	DNA-directed RNA polymerase	POLR2B	0	0	1
K	1078	Tri	24.1	DNA-directed RNA polymerase III subunit RPC1	POLR3A	0	1	0

K	238	Di	38.08	Putative beta-actin-like protein 3	POTEKP	0	10	0
R	62	Mono	14.79	Liprin-alpha-2 (Fragment)	PPFIA2	1	0	0
R	341	Mono	31.53	Probable protein phosphatase 1N (Fragment)	PPM1N	0	0	1
K	5	Mono	12.63	Protein phosphatase 1 regulatory subunit 12C (Fragment)	PPP1R12C	0	1	0
K	288	Mono	52.5	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B gamma isoform	PPP2R2C	1	0	1
K	150	Mono	15.22	Histone-lysine N-methyltransferase PRDM9	PRDM9	0	1	0
K	69	Tri	51.25	Pre-mRNA-processing-splicing factor 8 (Fragment)	PRPF8	0	1	5
R	68	Di	28.49	Proline-rich protein 19	PRR19	1	0	0
R	318	Mono	13.52	Protein PRRC1	PRRC1	0	0	1
R	317	Mono	13.52	Protein PRRC1	PRRC1	0	0	1
R	317	Di	13.52	Protein PRRC1	PRRC1	0	0	1
R	318	Di	13.52	Protein PRRC1	PRRC1	0	0	1
K	562	Mono	27.25	PH and SEC7 domain-containing protein 2	PSD2	0	1	0
R	230	Mono	12.24	26S protease regulatory subunit 6A (Fragment)	PSMC3	1	0	0
R	99	Di	27.59	26S proteasome non-ATPase regulatory subunit 1 (Fragment)	PSMD1	0	0	1
K	10	Mono	25.69	Proteasome assembly chaperone 3	PSMG3	0	0	1
R	139	Di	30.38	Protein quaking (Fragment)	QKI	0	2	0
R	166	Mono	26.34	R3H domain-containing protein 1	R3HDM1	0	4	0
R	69	Mono	31.73	Ras-related protein Rab-7b	RAB7B	0	0	5
K	34	Di	66.32	RNA-binding protein Raly (Fragment)	RALY	0	0	1
K	34	Di	66.32	RNA-binding Raly-like protein	RALYL	0	0	1
K	136	Mono	46.78	Pre-mRNA-splicing factor RBM22	RBM22	0	0	2
K	180	Di	13.42	Pre-mRNA-splicing factor RBM22	RBM22	0	0	1
R	105	Di	84.09	Putative RNA-binding protein 3	RBM3	5	17	28
R	602	Mono	36.32	RNA-binding protein 44	RBM44	0	1	0
R	50	Di	44.2	RNA-binding motif protein, X chromosome, N-terminally processed	RBMX	0	1	1
K	1101	Mono	12.61	ATP-dependent DNA helicase Q4	RECQL4	0	0	1
R	84	Mono	29.97	Inactive rhomboid protein 1 (Fragment)	RHBDF1	0	0	1
R	6	Di	28.5	Rapamycin-insensitive companion of mTOR (Fragment)	RICTOR	1	0	0
R	434	Mono	33.71	Isoform RIN1-delta of Ras and Rab interactor 1	RIN1	1	0	0
K	611	Di	27.38	RING finger protein 17	RNF17	0	0	4
K	20	Tri	16.66	RING finger protein 222	RNF222	0	2	0
R	64	Di	24.09	E3 ubiquitin-protein ligase RNF6	RNF6	0	0	1
R	409	Mono	16.79	Protein fantom	RPGRIP1L	5	0	40
K	411	Mono	16.79	Protein fantom	RPGRIP1L	5	0	40
K	411	Di	16.79	Protein fantom	RPGRIP1L	5	0	40
R	409	Di	16.79	Protein fantom	RPGRIP1L	5	0	40
K	411	Tri	16.79	Protein fantom	RPGRIP1L	5	0	40
R	26	Mono	41.18	60S ribosomal protein L26-like 1 (Fragment)	RPL26L1	0	0	4
R	27	Mono	12.66	60S ribosomal protein L26-like 1 (Fragment)	RPL26L1	0	0	1
K	266	Mono	49.28	60S acidic ribosomal protein P0-like	RPLP0P6	0	0	2
R	22	Di	100.33	40S ribosomal protein S2	RPS2	21	5	0
R	339	Di	24.2	RNA pseudouridylate synthase domain-containing protein 2	RPUSD2	0	0	1

K	331	Mono	25.77	Serine/threonine-protein kinase SBK1	SBK1	0	0	1
K	440	Di	27.27	S phase cyclin A-associated protein in the endoplasmic reticulum (Fragment)	SCAPER	1	0	0
R	40	Mono	18.81	Selenocysteine lyase (Fragment)	SCLY	0	0	1
K	198	Mono	25.82	Alpha-1-antitrypsin	SERPINA1	0	0	2
R	202	Mono	25.82	Alpha-1-antitrypsin	SERPINA1	0	0	2
K	198	Di	25.82	Alpha-1-antitrypsin	SERPINA1	0	0	2
R	202	Di	25.82	Alpha-1-antitrypsin	SERPINA1	0	0	2
R	485	Di	33.79	Splicing factor 3B subunit 2	SF3B2	0	0	1
R	390	Di	61.57	Splicing factor 3B subunit 4	SF3B4	1	10	0
R	779	Mono	29.34	Scm-like with four MBT domains protein 2	SFMBT2	0	9	1
R	777	Mono	29.34	Scm-like with four MBT domains protein 2	SFMBT2	0	9	1
R	779	Di	29.34	Scm-like with four MBT domains protein 2	SFMBT2	0	9	1
R	777	Di	29.34	Scm-like with four MBT domains protein 2	SFMBT2	0	9	1
R	9	Di	26.78	Splicing factor, proline- and glutamine-rich	SFPQ	0	1	0
K	675	Tri	46.18	Single-minded homolog 1	SIM1	0	0	2
R	897	Di	27.98	Signal-induced proliferation-associated protein 1	SIPA1	0	0	1
K	894	Tri	27.98	Signal-induced proliferation-associated protein 1	SIPA1	0	0	1
K	1206	Di	21.9	Signal-induced proliferation-associated 1-like protein 2	SIPA1L2	0	0	1
K	1201	Di	21.9	Signal-induced proliferation-associated 1-like protein 2	SIPA1L2	0	0	1
K	1201	Tri	21.9	Signal-induced proliferation-associated 1-like protein 2	SIPA1L2	0	0	1
K	1206	Tri	21.9	Signal-induced proliferation-associated 1-like protein 2	SIPA1L2	0	0	1
R	70	Mono	15.14	Solute carrier family 12 member 6	SLC12A6	0	1	0
K	634	Di	16.59	Solute carrier family 12 member 6	SLC12A6	0	1	0
K	338	Mono	26.6	Monocarboxylate transporter 2	SLC16A7	0	0	1
K	23	Mono	70.37	ADP/ATP translocase 1	SLC25A4	12	5	116
K	49	Tri	25.72	ADP/ATP translocase 1	SLC25A4	0	0	1
R	56	Mono	18.16	Mitochondrial coenzyme A transporter SLC25A42	SLC25A42	0	0	1
K	49	Tri	25.72	ADP/ATP translocase 2	SLC25A5	0	0	1
K	52	Tri	43.82	ADP/ATP translocase 2	SLC25A5	2	1	10
K	52	Tri	37.95	ADP/ATP translocase 3 (Fragment)	SLC25A6	0	1	6
R	60	Di	37.3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMARCD2	0	3	0
K	570	Mono	36.35	Structural maintenance of chromosomes protein 2	SMC2	0	0	6
R	566	Mono	27.3	Structural maintenance of chromosomes protein 2	SMC2	0	0	1
R	566	Di	36.35	Structural maintenance of chromosomes protein 2	SMC2	0	0	6
K	245	Di	15.22	Structural maintenance of chromosomes protein 3	SMC3	0	1	0
K	158	Di	25.96	Structural maintenance of chromosomes protein 6 (Fragment)	SMC6	2	1	1
R	152	Di	25.96	Structural maintenance of chromosomes protein 6 (Fragment)	SMC6	2	1	1
K	2	Tri	12.51	Isoform A of Smoothelin	SMTN	0	0	21
R	33	Di	29.12	Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	0	3	2
R	29	Di	29.12	Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	0	3	2
R	4	Di	41.52	Small nuclear ribonucleoprotein E	SNRPE	1	1	0
R	53	Mono	24.8	Sorting nexin-12	SNX12	1	0	0
X	1	Tri	16.66	Kinetochore protein Spc24 (Fragment)	SPC24	0	2	0

R	2190	Di	25.4	Spatacsin	SPG11	0	1	0
R	209	Di	24.66	Sphingosine kinase 1	SPHK1	0	0	1
R	718	Mono	12.44	Spondin-1	SPON1	0	0	1
K	113	Mono	30.08	Spectrin alpha chain, erythrocytic 1	SPTA1	0	2	0
K	113	Tri	31.04	Spectrin alpha chain, erythrocytic 1	SPTA1	0	1	0
R	1232	Di	27.98	Helicase SRCAP	SRCAP	0	1	0
R	814	Di	41.27	Serrate RNA effector molecule homolog	SRRT	0	1	0
R	79	Mono	19.27	Serine/arginine-rich splicing factor 12	SRSF12	0	1	0
K	60	Mono	13.66	Serine/arginine-rich-splicing factor 5	SRSF5	1	0	0
R	32	Mono	23.69	Serine/arginine-rich splicing factor 8	SRSF8	0	0	1
R	31	Mono	23.69	Serine/arginine-rich splicing factor 8	SRSF8	0	0	1
K	121	Di	13.44	Beta-galactoside alpha-2,6-sialyltransferase 1 (Fragment)	ST6GAL1	1	0	0
K	2	Tri	28.51	Serine-threonine kinase receptor-associated protein (Fragment)	STRAP	0	2	9
K	233	Tri	24.39	Striatin-3	STRN3	0	0	1
R	618	Mono	14.1	Synaptopodin-2 (Fragment)	SYNPO2	0	1	0
R	622	Di	14.1	Synaptopodin-2 (Fragment)	SYNPO2	0	1	0
R	106	Mono	30.64	TATA-binding protein-associated factor 2N (Fragment)	TAF15	0	1	0
R	115	Mono	43.73	TATA-binding protein-associated factor 2N (Fragment)	TAF15	0	1	0
R	87	Mono	64.81	TATA-binding protein-associated factor 2N (Fragment)	TAF15	0	1	0
R	192	Di	43.36	TATA-binding protein-associated factor 2N (Fragment)	TAF15	0	1	0
R	51	Mono	12.33	Transcription initiation factor TFIID subunit 3	TAF3	1	0	0
R	47	Mono	12.33	Transcription initiation factor TFIID subunit 3	TAF3	1	0	0
R	102	Mono	13.24	Transcription initiation factor TFIID subunit 6 (Fragment)	TAF6	0	0	1
R	87	Mono	14.61	Chromosome 3 open reading frame 31, isoform CRA_e	TAMM41	0	1	0
R	23	Di	14.99	T-cell leukemia/lymphoma protein 1A (Fragment)	TCL1A	0	1	0
R	513	Mono	33.94	Thyroid hormone receptor-associated protein 3	THRAP3	0	3	0
R	101	Di	38.94	Thyroid hormone receptor-associated protein 3	THRAP3	0	4	0
K	202	Di	82.91	Thyroid hormone receptor-associated protein 3	THRAP3	0	2	1
R	91	Mono	24.17	Transmembrane protein 194A	TMEM194A	21	0	60
K	329	Di	30.23	Transmembrane protease serine 5	TMPRSS5	0	0	2
R	227	Mono	14.79	Tankyrase-1	TNKS	1	0	0
R	7	Mono	16.44	DNA topoisomerase 3-alpha (Fragment)	TOP3A	1	0	0
R	5	Mono	16.44	DNA topoisomerase 3-alpha (Fragment)	TOP3A	1	0	0
K	82	Mono	15.22	Tumor protein p63-regulated gene 1 protein (Fragment)	TPRG1	0	1	0
R	706	Mono	27.37	Trafficking kinesin-binding protein 1	TRAK1	0	3	0
K	37	Mono	24.39	Trafficking protein particle complex subunit 5	TRAPPC5	1	0	0
R	8	Mono	29.37	Tripartite motif-containing protein 65 (Fragment)	TRIM65	1	0	0
R	25	Mono	39.51	tRNA (adenine(58)-N(1))-methyltransferase, mitochondrial (Fragment)	TRMT61B	0	0	2
K	688	Di	24.39	Transcription termination factor 1	TTF1	0	0	1
R	79	Mono	72.95	Tubulin alpha-3C/D chain	TUBA3C	1	1	2
K	136	Mono	19.74	Tubulin alpha-8 chain (Fragment)	TUBA8	1	0	2
R	28	Mono	62.03	Tubulin beta chain	TUBB	0	0	9
R	46	Mono	62.03	Tubulin beta chain	TUBB	0	0	9

R	84	Mono	43.56	HCG1983504, isoform CRA_f	TUBB3	0	0	7
R	90	Mono	15.22	HCG1983504, isoform CRA_f	TUBB3	0	0	1
R	318	Mono	15.48	Tubulin beta-4A chain	TUBB4A	0	0	2
X	1	Mono	55.96	Tubulin beta-6 chain (Fragment)	TUBB6	2	1	3
R	390	Mono	38.23	Tubulin beta-6 chain	TUBB6	0	0	2
X	1	Di	55.96	Tubulin beta-6 chain (Fragment)	TUBB6	2	1	3
R	308	Mono	51.24	Tubulin beta-8 chain	TUBB8	0	0	5
R	458	Di	14.79	Speckle targeted PIP5K1A-regulated poly(A) polymerase	TUT1	1	0	0
K	330	Mono	40.88	Alpha-taxilin	TXLNA	0	0	1
K	39	Mono	38.55	Splicing factor U2AF 35 kDa subunit	U2AF1	0	0	1
R	54	Mono	37.91	Protein UBBP4 (Fragment)	UBBP4	0	1	0
R	130	Mono	44.4	Protein UBBP4	UBBP4	0	1	0
K	101	Mono	28.99	Ubiquitin-conjugating enzyme E2 D1	UBE2D1	1	0	0
K	101	Mono	28.99	Ubiquitin-conjugating enzyme E2 D4	UBE2D4	1	0	0
R	1222	Mono	12.37	Regulator of nonsense transcripts 2	UPF2	1	0	0
K	85	Mono	56.83	Vesicle-associated membrane protein 1	VAMP1	1	0	0
K	238	Mono	32.25	Voltage-dependent anion-selective channel protein 2	VDAC2	3	1	20
R	42	Di	26.33	Vacuolar protein sorting-associated protein 13A (Fragment)	VPS13A	0	0	2
K	50	Tri	26.33	Vacuolar protein sorting-associated protein 13A (Fragment)	VPS13A	0	0	2
X	1	Di	28.12	WD repeat and HMG-box DNA-binding protein 1 (Fragment)	WDHD1	0	0	1
K	229	Di	35.21	Isoform 2 of pre-mRNA 3' end processing protein WDR33	WDR33	4	1	0
K	23	Di	27.62	Protein WWC2	WWC2	0	0	1
K	138	Mono	28.86	WW domain-containing oxidoreductase	WWOX	0	0	1
R	114	Mono	24.78	WW domain-containing transcription regulator protein 1 (Fragment)	WWTR1	0	1	0
K	737	Mono	24.39	Exportin-T	XPOT	1	0	0
K	732	Mono	24.39	Exportin-T	XPOT	1	0	0
K	209	Mono	43.38	X-ray repair cross-complementing protein 5	XRCC5	0	0	1
K	9	Tri	51.91	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa), isoform CRA_b	XRCC6	0	0	1
K	97	Mono	16.79	Protein YIPF1	YIPF1	5	0	40
K	96	Mono	16.79	Protein YIPF1	YIPF1	5	0	40
K	96	Di	16.79	Protein YIPF1	YIPF1	5	0	40
K	97	Di	16.79	Protein YIPF1	YIPF1	5	0	40
K	97	Tri	16.79	Protein YIPF1	YIPF1	5	0	40
K	212	Mono	101.73	14-3-3 protein theta	YWHAQ	0	0	1
R	358	Mono	16.28	Zinc finger and BTB domain-containing protein 8B	ZBTB8B	0	0	1
R	361	Mono	16.28	Zinc finger and BTB domain-containing protein 8B	ZBTB8B	0	0	1
K	36	Di	12.71	Neurotrophin receptor-interacting factor homolog (Fragment)	ZNF274	0	0	1
R	235	Mono	37.43	DBIRD complex subunit ZNF326	ZNF326	0	1	0
K	238	Mono	37.43	DBIRD complex subunit ZNF326	ZNF326	0	1	0
R	175	Di	48.74	DBIRD complex subunit ZNF326	ZNF326	0	1	1
K	72	Mono	31.81	Zinc finger protein 440 (Fragment)	ZNF440	0	1	0
K	664	Di	39.03	Zinc finger protein 512B	ZNF512B	0	9	0
R	2	Mono	13.26	Putative zinc finger protein 730 (Fragment)	ZNF730	0	1	0

R	38	Mono	25.74	Zinc finger protein 789	ZNF789	0	1	0
R	5	Di	13.69	Zinc finger and SCAN domain-containing protein 18 (Fragment)	ZSCAN18	0	1	0
R	4	Di	13.69	Zinc finger and SCAN domain-containing protein 18 (Fragment)	ZSCAN18	0	1	0

Appendix 7: Curriculum vitae for Alexandra Star.

Curriculum Vitae for Alexandra Star

SUMMARY OF SKILLS AND QUALIFICATIONS

- M.Sc. in Biochemistry
- 3 years of laboratory research
- Software skills: Microsoft Office, Microsoft Excel, Microsoft PowerPoint
- Problem solving, critical thinking, and continuous learning

EDUCATION

September 2013-December 2015	**M.Sc. Biochemistry**. University of Ottawa, Ottawa, Canada Thesis title: "Enrichment and identification of methylation at the proteome level."
September 2014	**Radiation Safety Training.** University of Ottawa, Ottawa, Canada
September 2013	**WHIMIS, Lab Safety Training, and Principles of Biosafety Training.** University of Ottawa, Ottawa, Canada
September 2009-April 2013	**B.Sc. (Hon) with Specialization in Biochemistry**. University of Ottawa, Ottawa, Canada Thesis title: "Comparative analyses of the cellular responses to urban particles using differential in-gel electrophoresis (DIGE)."
September 2005-June 2009	**All Saints Catholic High School**. Ottawa, Canada

SKILLS PROFILE

Knowledge of laboratory equipment, procedures and data analysis for biochemistry, cell culture, molecular biology, and proteomics:

- Proteomics Skills: extracting and purifying protein from cells, 2D-gel electrophoresis, Differential In-gel Electrophoresis (DIGE), preparing samples for MALDI-TOF/TOF MS analysis, in-solution digestion, FASP, methylation enrichment, and preparing samples for ESI LC-MS/MS analysis
- Molecular Biology Skills: bacterial transformation, DNA prep, and analysis of DNA sequencing results
- Cell Culture Skills: aseptic technique, cell transfections, and exposing cells to particulate matter

- Biochemistry Skills: western blotting, protein immunoprecipitation, and subcellular fractionation
- Software and Bioinformatic Tool Skills: DECODON Delta 2D for differential protein expression analysis, Mascot and MaxQuant for database searching for mass spectrometry data analysis, Ingenuity Pathway Analysis and Database for Annotation, Visualization and Integrated Discovery (DAVID) for data analysis, Microsoft Word, PowerPoint, Excel and EndNote for data analysis, document writing, preparing presentations, Chromas and Gene Construction Kit for analysis of DNA sequencing results, and PubMed and Scopus for literature searching
- Communication Skills: presenting scientific data, and teaching undergraduate students
- Critical thinking, problem solving, and analytical skills

WORK EXPERIENCE

September 2013-December 2015	**MSc Student, University of Ottawa** My work involved enriching and identifying methylation on lysine and arginine using a novel enrichment technique coupled with mass spectrometry.
January 2015-April 2015	**Teaching Assistant, University of Ottawa** I was responsible for in-lab instruction and demonstration of biological and chemical principles and experiments. I was also responsible for marking lab reports and for proctoring and correcting final exams.
September 2012-May 2013	**Undergraduate Research Assistant, Health Canada** I used DIGE to compare A549 cells upon exposure to the EHC-93 urban air particulate matter.
July 2008-September 2012	**Supervisor at the Dekok Family Berry Farm** As supervisor I was responsible for assigning duties to other workers, handling money, cashier work, customer service, general maintenance and irrigation management.

LIST OF SCHOLARSHIPS AND AWARDS

- BMI Travel Award – Value $900.00 – October 2014
- FGPS Travel Award – Value $650.00 – September 2014
- Entrance scholarship to University of Ottawa 2009-2010.

PUBLICATIONS AND PRESENTATIONS

Referred Review Article

- Mayne, J., Ning, Z., Zhang, X., Starr, AE., Chen, R., Deeke, S., Chiang, CK., Xu, B., Wen, M., Cheng, K., Seebun, D., **Star, A.**, Moore, JI., Figeys, D. (2015). Bottom-Up Proteomics (2013-2015): Keeping up in the Era of Systems Biology. Anal Chem. 2015.

Conference Poster Presentations

- **Star, A.**, Ning, Z., Mayne, J., Couture, J-F., and Figeys, D. (May 2015) Enrichment and identification of lysine methylation at the proteome level. Ottawa Institute for Systems Biology (OISB) Symposium, Mont-Tremblant, Quebec, Canada
- **Star, A.**, Ning, Z., Cramet, M., Mayne, J., Couture, J-F., and Figeys, D. (October 2014) Elucidating the roles of lysine methyltransferases using a novel enrichment technique. Human Proteome Organization (HUPO) 2014 Conference, Madrid, Spain

Seminar Presentation

- **Star, A.**, Ning, Z., Mayne, J., Couture, J-F., and Figeys, D. (March 2015) Enrichment and identification of lysine methylation at the proteome level. Seminar presented at University of Ottawa Seminar Day, Ottawa, Ontario, Canada. March 10th 2015.

Poster Presentations

- **Star, A.**, Ning, Z., Cramet, M., Mayne, J., Couture, J-F., and Figeys, D. (May 2014) Elucidating the roles of lysine methyltransferases based on their non-histone protein targets using a novel technique. Poster presented at University of Ottawa Poster Day, Ottawa, Ontario, Canada (M.Sc. work)
- **Star, A.**, Vuong, N., and Vincent, R. (April 2009) Cellular responses to urban particles. Poster presented at University of Ottawa Poster Day, Ottawa, Ontario, Canada (Undergraduate work)

VOLUNTEER WORK EXPERIENCE

January 2014-Present — **League president of the West Carleton Women's Ball Hockey League (WCWBHL)**

I am responsible for organizing the yearly meeting, organizing information for insurance with CARHA, organizing team captains and dealing with issues that turn up during the season. I also act as a liaison between league, manager of arena, and referees.

September 2009-April 2010	**Hockey Assistant Coach with KGHA** I assisted in running the practices and assisted on the bench during games for a hockey team.
September 2008-June 2009	**Group Leader** Organized a high school singing group (Vertical Limit) in my last school year at All Saints Catholic High School.
September 2005-June 2009	**Peer Helper at All Saints Catholic High School** As a peer helper our responsibilities included going to grade 7 and 8 classes to introduce the students to high school life, and assisting with parent-teacher interviews and other school functions.

REFERENCES

Available upon request