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Comparative Analysis of Protein Expression Concomitant with DNA Methyltransferase 3A Depletion in a Melanoma Cell Line

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Abstract

DNA methyltransferase 3A (Dnmt3a), a de novo methyltransferase, has attracted a great deal of attention for its important role played in tumorigenesis. We have previously demonstrated that melanoma is unable to grow *in-vivo* in conditions of Dnmt3a depletion in a mouse model. In this study, we cultured the Dnmt3a depletion B16 melanoma (Dnmt3a-D) cell line to conduct a comparative analysis of protein expression con-comitant with Dnmt3a depletion in a melanoma cell line. After two-dimensional separation, by gel electro-phoresis and liquid chromatography, combined with mass spectrometry analysis (1DE-LC-MS/MS), the re-sults demonstrated that 467 proteins were up-regulated and 535 proteins were down-regulated in the Dnmt3a-D cell line compared to the negative control (NC) cell line. The Genome Ontology (GO) and KEGG pathway were used to further analyze the altered proteins. KEGG pathway analysis indicated that the MAPK signaling pathway exhibited a greater alteration in proteins, an interesting finding due to the close relation-ship with tumorigenesis. The results strongly suggested that Dnmt3a potentially controls the process of tu-morigenesis through the regulation of the proteins (JNK1, p38α, ERK1, ERK2, and BRAF) involved in tu-mor-related pathways, such as the MAPK signaling pathway and melanoma pathway.

Keywords: Dnmt3a, Melanoma Cell Line, 1DE-LC-MS/MS; MAPK Signaling Pathway, Melanoma Pathway

1. Introduction

Malignant melanoma, one of the most aggressive of all skin cancers, exhibits a high skin cancer mortality rate [1]. Upon metastasis, the disease is incurable in most affected people as melanoma does not respond to most systemic treatments and chemotherapy drugs [2].

It is well established that malignant melanoma contains at least 50 genes that exhibit differential expression as abnormal methylation changes emerge in the promoter region [3-5], and that DNA methylation patterns are established and maintained by the coordinated action of three DNA methyltransferases (Dnmts). It has been demonstrated that Dnmt1 [6,7], Dnmt3a, and Dnmt3b [8] are over-expressed in many malignant tumors [9]. Dnmt-3a plays an important role in epigenetic modification that has attracted a great deal of attention in recent years [10,11]. It has been reported that epigenetic modification is induced by hepatitis B virus X protein via interaction with de novo DNA methyltransferase-Dnmt3a [10]. Additionally, Dnmt3a has been found to maintain DNA methylation and regulate synaptic function in adult fore-brain neurons [12]. Furthermore, it has been demonstrated that Dnmt3a-dependent non-promoter DNA methylation facilitates the transcription of neurogenic genes [13]. Recently, studies of Dnmt3a have focused on its effect on proliferation and apoptosis of hepatocellular carcinoma, colorectal cancer and malignant melanoma [14-16] In a previous study we demonstrated that tumor growth inhibition was mediated by Dnmt3a depletion [17].

In this study we describe the proteomic experiment and comparative analysis of protein expression in the

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Dnmt3a depletion B16 melanoma (Dnmt3a-D) cell line. The mouse B16 melanoma cell line used in our study exhibited a specific down-regulation of Dnmt3a via stable transfection using a Dnmt3a-RNAi construct. We obtained the negative control (NC) cell line through use of an unrelated, non-target, shRNA expression vector. Proteins of the NC cell line and Dnmt3a-D cell line were initially separated by one-dimensional gel electrophoresis (1DE), and the two gel tracks were subsequently split into 20 proteome fractions, respectively, and digested by trypsin. The peptide fractions were analyzed by capillary liquid chromatography and high accuracy mass spectrometric acquisition on a LTQ-Orbitrap (Thermo Scientific Germany) in the MS/MS mode using various and complementary fragmentation modes. The results of the comparative proteomics demonstrated that Dnmt3a depletion affects a large number of proteins. The Genome Ontology and KEGG pathway were used to group these altered proteins according to respective cellular components, molecular functions, and pathway. The suppressors of skin tumour development JNK1 and p38α [18] were found to be up-regulated in the MAPK signaling pathway of the Dnmt3a-D cell line. The oncogene BRAF was down-regulated in the melanoma pathway of the Dnmt3a-D cell line. These results strongly suggested that Dnmt3a depletion potentially inhibits melanoma tumorigenesis by regulating the proteins involved in tumor-related pathways.

2. Materials and Methods

2.1. Cell Culture

The B16 cells were purchased from the American Type Culture Collection (Manassas, VA), cultured in DMEM supplemented with 10% FBS, and maintained in a humidified incubator at 37˚C and 5% CO_2. The sequence of Dnmt3a shRNA was 5′ gtgcagaaacatcgaggacTTCAAGAGAgtcctcgatgtttctg- cac 3′. A non-target shRNA with the sequence 5′gcaagtctaaccaacgcgt TTCAAGAGAacgcgttggtt - agacttgc 3′ was used as negative control (NC). The process of small hairpin RNA (shRNA) RNAi was performed as previously described [17]. At this point in the procedure we chose the B16 cells with Dnmt3a depletion (Dnmt3a-D) for further experiments.

2.2. Protein Extraction and Measurement

After harvesting the cells, the following experimental process was conducted (**Figure 1**). The cells were washed 2-3 times in ice-cold phosphate-buffered saline (PBS), lysed in 900 μL RIPA lysis buffer (Bi Yun Tian Biotechnology Research Institute, China) plus 10 μL 100 mM phenylmethanesulfonyl fluoride (PMSF) for approximately 10 - 20 min. The samples were incubated for 2 s in an ice bath and exposed to an ultrasonic power of less than 70 W, and then centrifuged for 45 min at 15,000 rpm at 4˚C. The supernatants were then collected into eppendorf tubes for the next measurement.

The total protein of the cells was measured using the BCA Protein Assay (Bi Yun Tian Biotechnology Research Institute, China) with bovine serum albumin as a standard recommended by the manufacturer. The protein was stored at –80˚C until performance of isoelectro- focusing (IEF).

2.3. 1-DE and In-Gel Tryptic Digestion

In order to conduct proteomic analysis on proteins expressed at a low level, shotgun proteomics based on 1-DE separation of total protein was evaluated in addition to the analysis of peptide mixtures produced by tryptic digestion of proteins in gel fragments by LC-MS/MS. Equal amounts of NC cell protein and Dnmt3a-D cell protein (40 μg) were prepared in an identical manner. Respective samples were separated using small analytical immobilized pH gradient (IPG) strips (7 cm, 3 - 10 pH gradient; Bio-Rad). The proteins were electro-focused by initially using a voltage of 8 V/cm for the stacking gel, and subsequently increasing the voltage to 15 V/cm for the separating gel.

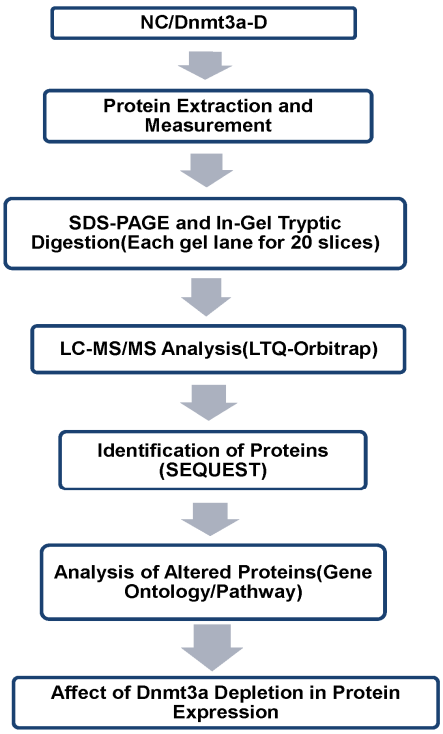

Figure 1. The experimental process of proteomic methods used in this study.

Gel lanes were excised from the SDS-PAGE gels using a razor blade and were divided into 20 slices according to the distribution of protein (**Figure 2**). The proteins were separated by 12% resolving gel. Each slice was then further divided into approximately 1 mm^3 pieces and placed into an eppendorf tube. The proteins were deoxidized, alkylated, dehydrated and digested. The peptide mixtures were extracted with frequent vortexing at 37˚C for 30 min. Samples were evaporated to dryness and stored at –20˚C until MS analysis.

2.4. LC-MS/MS Analysis

In recent years, the high performance and sensitivity of the linear quadrupole ion trap-orbitrap (LTQ-Orbitrap) mass spectrometer has interested researchers due to the capacity for top-down analysis of complete protein from tissue, body fluid, and cells [19,20].

The sample was separated using online reverse-phase nanoscale capillary liquid chromatography, and then analyzed by electrospray tandem mass spectrometry. The peptide mixtures loaded and desalted on a C18 trap column (0.5 mm diameter, 2 mm, MICHROM,USA) using a Tempo 1D nanoLC system, then separated on a reverse-phase MagicTM C18 column (100 μm diameter, 15 cm, MICHROM,USA), using a 120 min linear gradient of mobile phase A (0.875% ACN/0.125% FA/99% H_2O) at a flow rate of 500 nL/min. The eluent was analyzed on a

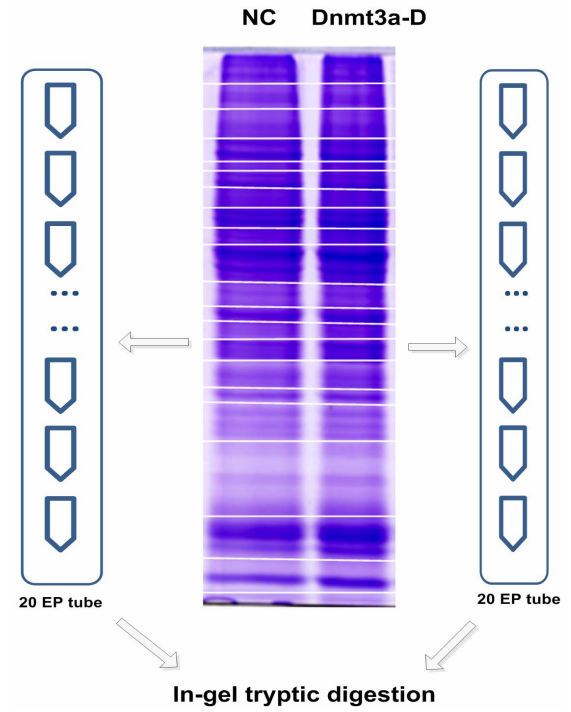

Figure 2. SDS-PAGE patterns of NC cell proteins and Dnmt3a - D cell proteins.

LTQ-orbitrap mass spectrometer (Thermo Electron, Bremen, Germany) equipped with a heated Desolvation Chamber Interface set to 200˚C and operated using XCalibur software.

The LTQ-orbitrap operated in positive ion mode to survey full scan mass spectra (from m/z 385 to 2000). The most intense ten ions were selected for tandem mass spectrometry and the lock-mass option was used as described in previously published reports [21].

2.5. Identification and Analysis of Proteins

SEQUEST (V.28 (rev.12) 1998-2007) was used to identify proteins based on MS/MS spectra with Bioworks software (Rev.3.3.1 SP1, Thermo Scientific). We searched both forward and reverse sequences against the Swissport Mouse 090303 database in order to estimate the number of identifications that were false-positive in the sample.

The parameters for the SEQUEST search were comprised of the following criteria: Enzyme, trypsin; Missed cleavage sites, 2; fragment tolerance, 1.0 Da; peptide tolerance, 50.00 ppm; Numerical results, 250; Ion and Ion Series Calculated, b ion and y ion; Peptide matches, 10; Report duplicate peptide matches, 10. Oxidation of methionine, methylation of lysine, as well as phosphorylation of serine, threonine, and tyrosine were specified as variable modifications.

We inputted the DAT files from SEQUEST to the Trans-Proteomic Pipeline (TPP) v4.2 JETSTREAM rev 1 (ISB/SPC Proteomics Tools) and searched by allocating all DAT files in the biological sample. The parameters for peptide identification probability and protein identification probability were both set at 0.95.

The results were exported and the proteins found to be altered in the Dnmt3a-D cell line as compared to the NC cell line were extracted by a program developed in-house. GO terms of altered proteins for cellular component and molecular function were searched and checked by Swiss-Prot (http://expasy.org/sprot/), NCBI (http://www.ncbi.nlm.nih.gov) and PIR (http://pir.georgetown.edu/pirwww/index.shtml). The pathways of altered proteins were established using the KEGG mapper (http://www.genome.jp/kegg/.html). Demonstration of the role of altered proteins in metabolic channels and signal transduction pathways was considered significant.

3. Results and Discussion

3.1. Cell Harvest

Growth conditions of the two cell lines were optimized in our previously reported experiment [17]. Cultured cells were harvested at a confluence level of 90% (**Fig-**

ure 3(a)).

Western blot analysis was employed to test the efficiency and specificity of the Dnmt3a-RNAi. The results demonstrated that stably transfected B16 Dnmt3a-D cells exhibited a remarkably low level of Dnmt3a expression. No change in Dnmt3a expression was observed in the control NC shRNA transfected cells. The expression of Dnmt3b was not affected in the NC or Dnmt3a-D cells, which is in concordance with our findings in our previous experiment (see **Figure 3 (b)** in [17]).

3.2. Difference of Protein Expression between NC and Dnmt3a-D Cell Lines

The NC and Dnmt3a-D cell line proteins identified were compared to determine their overlap (**Figure 3(b)**). There were 2413 proteins in common between the NC and Dnmt3a-D cell lines, and 467 were unique to the Dnmt3a-D cell line and were considered to be up-regulated proteins in the Dnmt3a-D cell line (Supplementary Materials, **Table S1**). There were 535 proteins unique to the NC cell line considered to be down-regulated proteins in the Dnmt3a-D cell line (Supplementary Materials, **Table S2**). The evidence suggests that Dnmt3a potentially either directly or indirectly regulates the expression of altered proteins.

3.3. Genome Ontology of Altered Proteins

In order to evaluate the effect of Dnmt3a depletion on protein expression and to explore the mechanism of Dnmt3a in tumorigenesis, the altered proteins were the principal targets for analysis. The genome ontology cellular localization of altered proteins was as follows: 35% of up-regulated proteins were localized to the cytoplasm, 24% to the nucleus, and 13% to the mitochondrion. The remainder of the up-regulated proteins were classified as golgi, plasma membrane, endoplasmic reticulum, cytoskeleton, extracellular, ribosome, others, and unclassified (28%). The cellular localization of down-regulated proteins was found to be similar to the cellular localization of the up-regulated proteins (**Figure 4(a)**, **(b)**). This result demonstrated that the altered proteins are primarily concentrated in the cytoplasm, nucleus, and mitochondria.

Among 467 up-regulated proteins, 161 exhibited an activity function (**Figure 4(c)**). Among the 535 down-regulated proteins, 178 exhibited an activity function (**Figure 4(d)**).

There were a large number of altered proteins that exhibited catalytic activity and transferase activity, and they played important roles in the methylation, acetylation, glycosylation, and other epigenetic modifications of

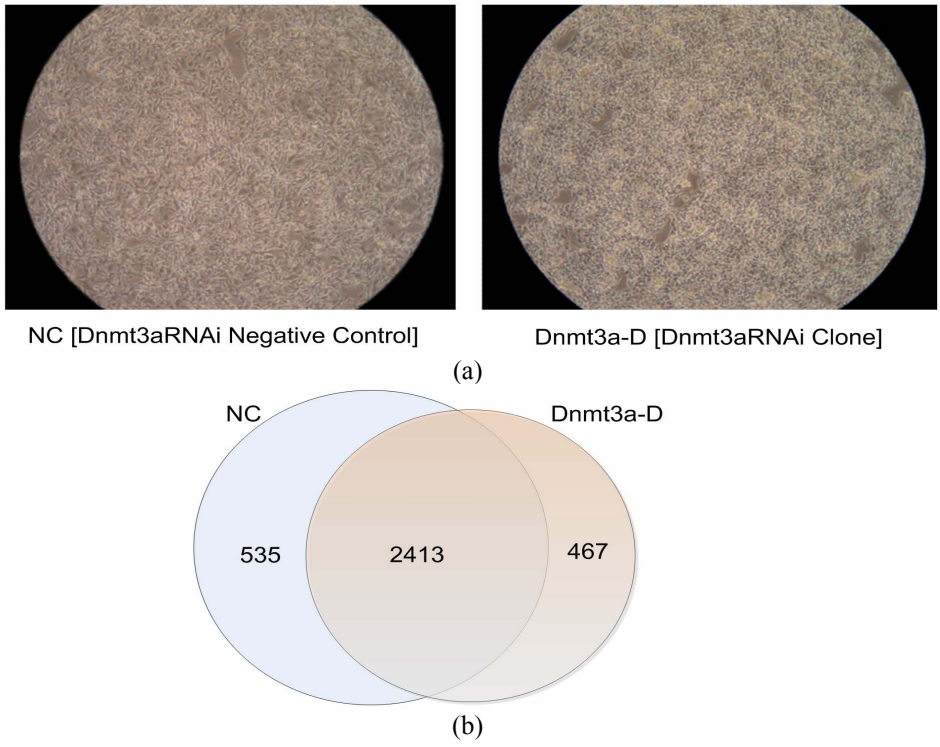

Figure 3. Cell Harvest and overlap of proteins between two cell lines. (a)The confluence of NC and Dnmt3a-D cell was more than 90% after two days under microscope. (b)The proteins of NC and Dnmt3a-D cell line identified, and overlap of proteins between the two cell lines.

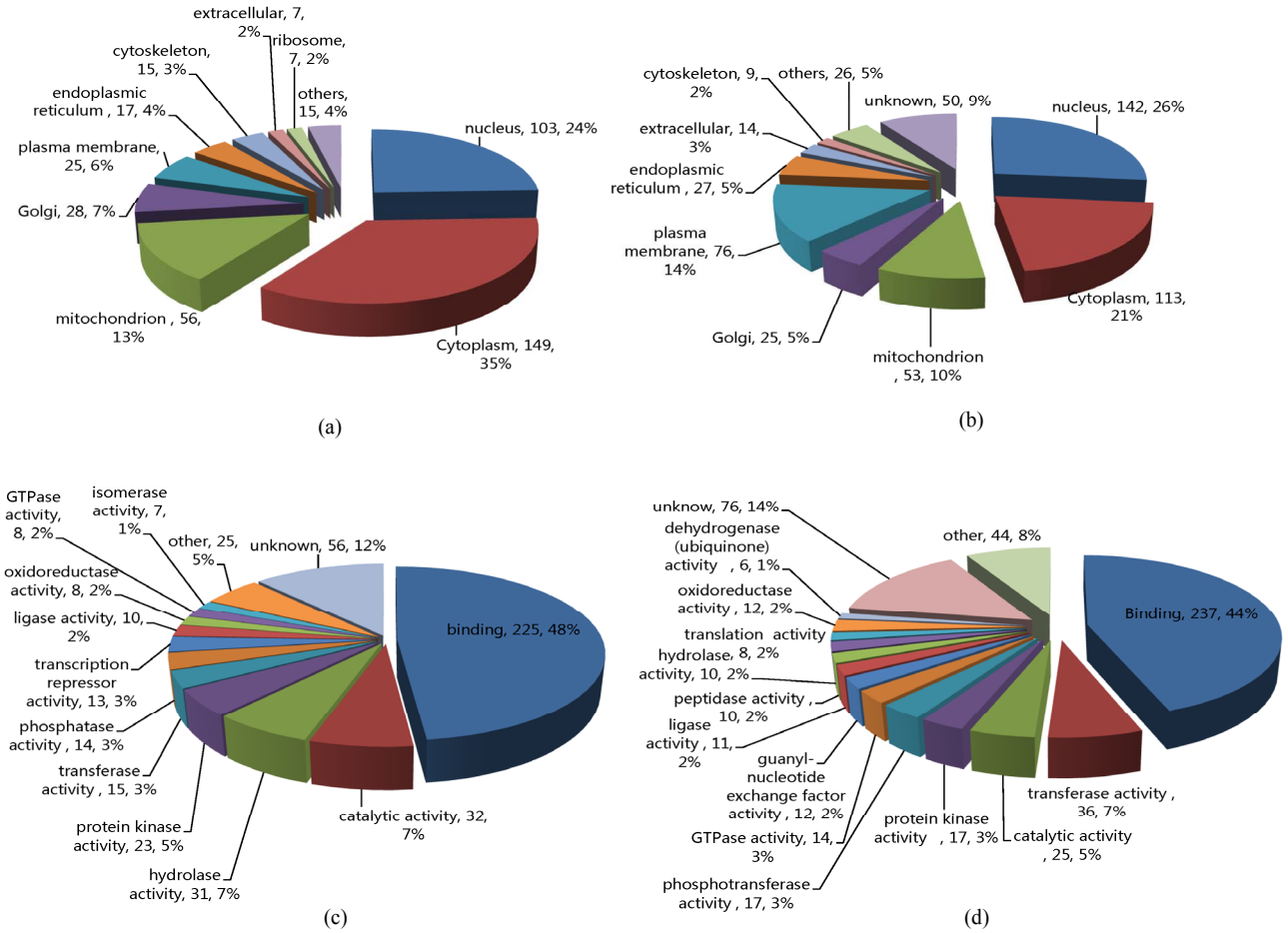

Figure. 4 Genome Ontology of altered Proteins. (A) Genome ontology cellular localization of up-regulated proteins. (B) Genome ontology cellular localization of down-regulated proteins. (C) Genome ontology molecular function of up-regulated proteins. (D) Genome ontology molecular function of down-regulated proteins.

the proteins. Another function that attracted our attention was phosphotransferase activity, which is essential for protein phosphorylation. It is well understood that protein phosphorylation is closely related to a variety of biological processes, such as DNA damage and repair [22], transcriptional regulation [23], signal transduction, and the regulation of apoptosis [24,25].

3.4. Pathway of Altered Proteins

The altered proteins were grouped according to their respective KEGG pathway (**Figure 5**). The pathways were arranged according to the number of altered proteins. The pathways that included less than 10 altered proteins were not shown. The four pathways with the largest number of altered proteins were metabolic pathways (71 proteins), endocytosis (21 proteins), mitogen activated protein kinase signaling pathway (MAPK signaling pathway, 19 proteins) and pathways in cancer (17 proteins). Among these four pathways, the MAPK signaling pathway, closely related to the cancer and melanoma pathway, and which plays a key role in melanoma tumorigenesis, attracted our attention. The locations of altered proteins in the two pathway maps were established using the KEGG mapper.

3.4.1. MAPK Signaling Pathway

The altered proteins involved in the MAPK signaling pathway are listed in **Table 1**. The locations of the altered proteins involved in the MAPK signaling pathway are marked by pink boxes (up-regulated proteins) and yellow boxes (down-regulated proteins) as shown **in Figure 6**.

The MAPKs belong to a family of highly conserved kinases that convert extracellular signals to intracellular responses. MAPKs are unique to eukaryotes and are important signal transducing enzymes regulated by a phosphorylation cascade. Two upstream protein kinases are activated in the series that leads to the activation of a MAP kinase; additional kinases may also be required

upstream of this three-kinase module. After activation, MAPKs phosphorylate specific serine and threonine residues of target substrates, including other protein kinases and many transcription factors. MAPKs are switched off by both generic phosphatases and dual-specificity phosphatases and are further regulated by scaffold proteins, which are usually specific for each of the three major mammalian MAPK pathways, including extracellular signal-regulated kinase (ERK), c-Jun N-terminal kinase (JNK), and p38 MAPK [18,26,27].

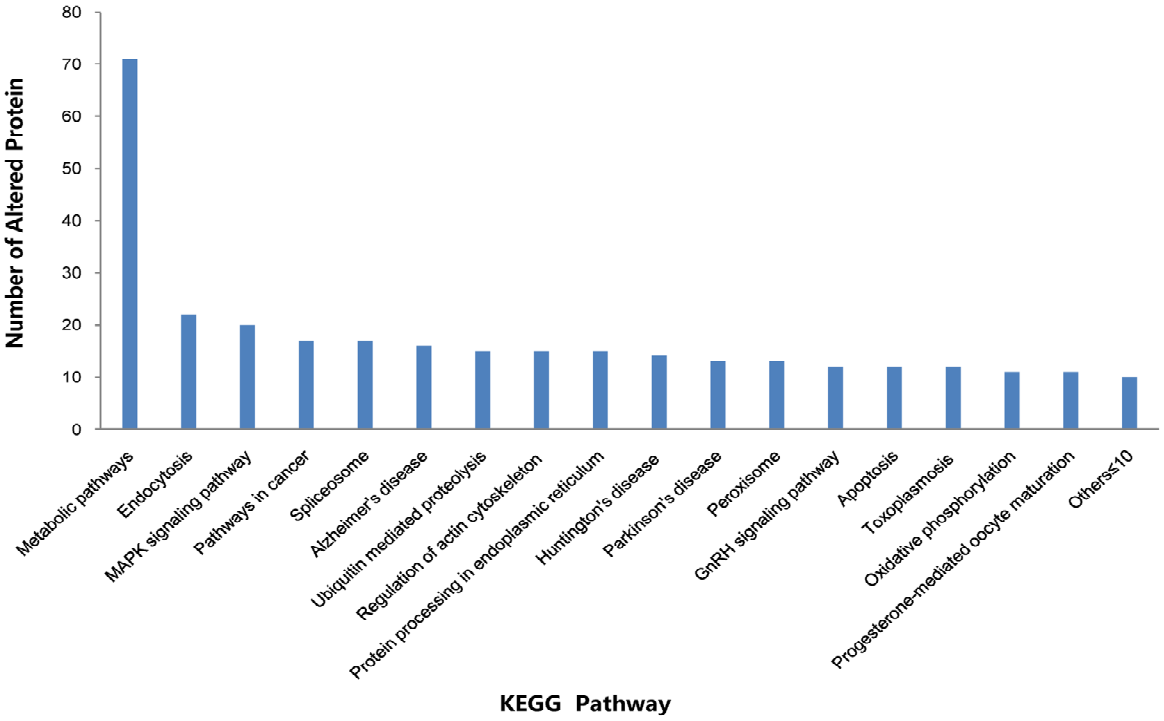

Figure 5. The altered proteins were grouped by KEGG pathway.

Table 1. The altered proteins involved in MAPK signaling pathway.

Location in Pathway	Gen Bank ID	Gene name	Synonyms	Name of Altered Protein; ↑: Up-regulated protein; ↓: Down-regulated protein
PKA	18747	Prkaca	Pkaca	cAMP-dependent protein kinase catalytic subunit alpha ↑
	18749	Prkacb	Pkacb	cAMP-dependent protein kinase catalytic subunit beta ↑
ERK	26413	Mapk1	Erk2, Mapk, Prkm1	Mitogen-activated protein kinase 1/ERK2 ↑
	26417	Mapk3	Erk1, Prkm3	Mitogen-activated protein kinase 3/ERK1 ↑
Ppp3c	19058	Ppp3r1	Cnb	Calcineurin subunit B type 1 ↑
CrkII	12929	Crkl	Crkol	Crk-like protein ↑
HGK	26921	Map4k4	Nik	Mitogen-activated protein kinase kinase kinase kinase 4 ↑
JNK	26419	Mapk8	Jnk1, Prkm8	Mitogen-activated protein kinase 8/JNK1 ↑
Cdc42Rac	12540	Cdc42	/	Cell division control protein 42 homolog precursor ↑
MKK3	26397	Map2k3	Mkk3, Prkmk3	Dual specificity mitogen-activated protein kinase kinase 3 ↑
P38	26416	Mapk14	Crk1,Csbp1,Csbp2	Mitogen-activated protein kinase 14/ p38α↑
PP2CB	19043	Ppm1b	Pp2c2, Pppm1b	Protein phosphatase 1B ↑
TAB1	66513	Tab1	Map3k7ip1	TGF-beta-activated kinase 1 and MAP3K7-binding protein 1 ↑
Rap1	109905	Rap1a	Krev-1	Ras-related protein Rap-1A precursor ↓
RafB	109880	Braf	B-raf	Serine/threonine-protein kinase B-raf ↓
cPLA2	18783	Pla2g4a	Cpla2, Pla2g4	Cytosolic phospholipase A2 ↓
CASP	12367	Casp3	Cpp32	Caspase-3 precursor ↓
ECSIT	26940	Ecsit	Sitpec	mitochondrial precursor ↓
MKK6	26399	Map2k6	Prkmk6, Sapkk3	Dual specificity mitogen-activated protein kinase kinase 6 ↓

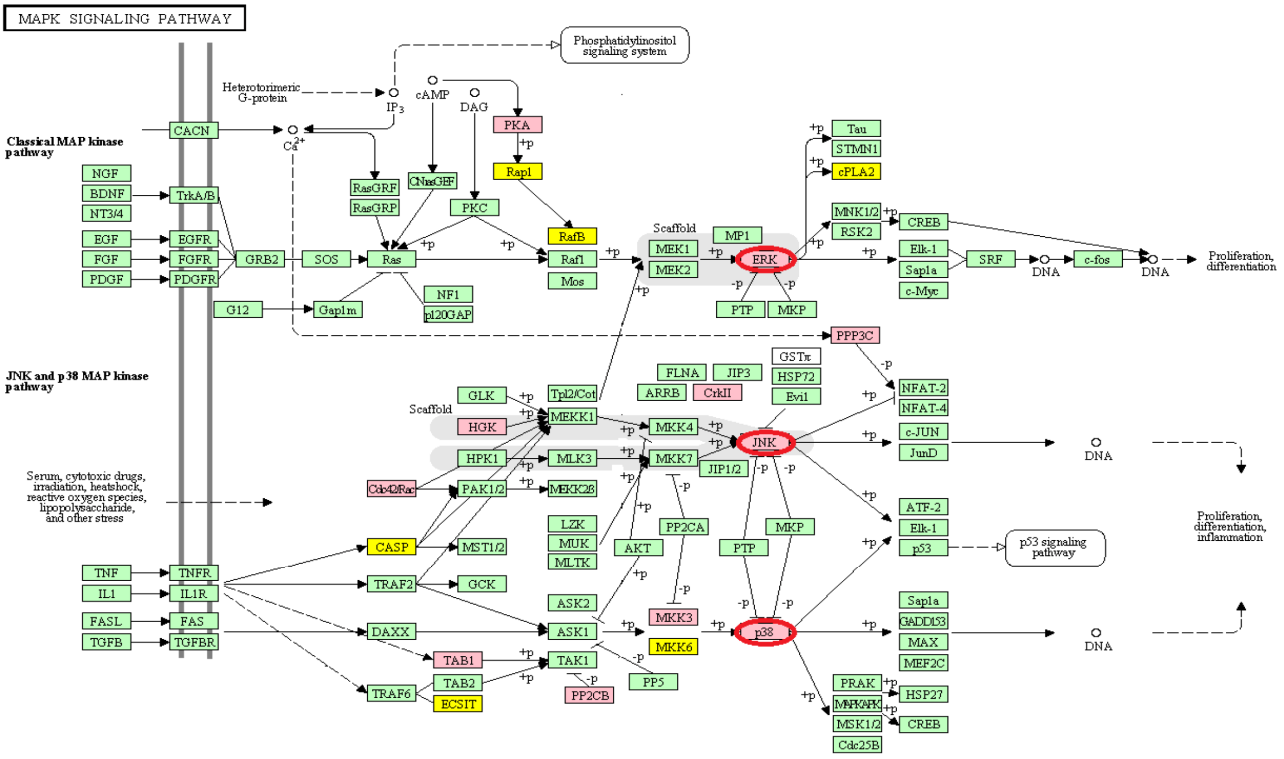

Figure 6. The location of altered proteins involved in MAPK signaling pathway from KEGG database.

In recent years, it has been demonstrated that the MAPK signaling pathway plays a key role in the cell cycle and gene expression regulation of various cells. MAP kinases are major components of the pathways that control embryogenesis, cell differentiation, cell proliferation, and cell death. Current research on the three pathways is described in detail, and offers insight into the mechanism of the pathways. Much of the review highlights research into the JNK and p38 MAPK pathways, stress activated protein kinase pathways that are also often deregulated in cancer. JNKs and p38 MAPKs are activated by environmental and genotoxic stress and are associated with tumorigenesis in humans and mice. The function of JNKs and p38 MAPKs in cancer development are complex and correlate with the wide range of cellular responses that they modulate [28,29].

3.4.2. JNK Pathway

Three genes encode the JNK proteins: MAPK8 encodes JNK1/ MAPK8, MAPK9 encodes JNK2/ MAPK9, and MAPK10 encodes JNK3/ MAPK10 [30]. Various JNKs differ substantially in their ability to interact with JUN, a well-established regulator of cell cycle progression [31]. A JNK2 deficiency results in elevated c-Jun phosphorylation and stability, whereas the absence of JNK1 reduces c-Jun phosphorylation and stability. JNK2 preferentially binds to c-Jun in unstimulated cells, thereby contributing to c-Jun degradation. In contrast, JNK1 becomes the major c-Jun interacting kinase after cell stimulation [32]. It has been recently demonstrated that the JNK pathway is linked to p53-dependent senescence via a conditional JNK1 allele [33]. The contribution of JNK1 to tumour development has also been investigated in mouse skin carcinogenesis. JNK1-knockout mice were shown to be more susceptible to tumours of the skin [34]. These results indicate that JNK1 may act as a suppressor of skin tumour development. In this study, JNK1 was found to be up-regulated in the Dnmt3a-D cell line which is unable to grow *in-vivo*, which potentially illustrates the fact that Dnmt3a depletion affects melanoma tumorigenesis by regulation of JNK1 expression.

3.4.3. p38 MAPK Pathway

The p38 MAPKs are activated by the upstream MKK3 and MKK6 kinases as shown in **Figure 6**. There are four genes that encode p38 MAPKs: MAPK14 encodes p38*α*/MAPK14; MAPK11 encodes p38*β*/MAPK11; MAPK12 encodes p38*γ*/MAPK12; and MAPK13 encodes p38*δ*/MAPK13 [35]. Among these, p38*α* was found to be up-regulated in the Dnmt3a-D cell line. Most of the published studies that have investigated p38 MAPKs refer to p38*α*, as p38*α* was highly abundant in most cell types [36]. A stress-activated protein kinase, p38*α* suppresses tumor formation by negatively regulating cell cycle pro-

gression and proliferation, or by inducing apoptosis [37-40].

There is evidence that indicates that p38*α* also may be an important regulator of differentiation programs in many cell types, including epithelial lung cells and embryonic stem cells [41,42]. Moreover, p38*α* directly phosphorylates and modulates the activity of several transcription factors involved in tissue-specific differentiation. The differentiation-inducing activity of p38*α* may be related to tumour suppression, as p38*α* activation triggers a high level of specific differentiation and lowers transformed phenotypes in renal carcinoma and colon cancer cell lines compared to cancer cell lines in which p38*α* has not been activated [43-45]. The function of p38*α* as a tumour suppressor *in-vivo* has been observed in a mouse model [18]. These results provide a reasonable explanation as to why the Dnmt3a-D cell line with p38*α* up-regulated is unable to grow *in-vivo*. Dnmt3a depletion potentially directly or indirectly regulates the expression of p38*α*.

3.4.4. ERK Pathway

ERK1 and ERK2 are ubiquitously expressed, although their relative abundance in tissues is variable. They are stimulated to a certain extent by a vast number of ligands and cellular perturbations, and there is evidence of some cell type specificity [46]. They are highly expressed in postmitotic neurons and other highly differentiated cells [47], and in these cells they are often involved in adaptive responses, such as long-term potentiation [48,49]. The receptor tyrosine kinase uses the ERK1 and ERK2 cell membrane signaling pathway [50-52]. Stimulation of these receptors by the appropriate ligand results is an increase in the catalytic activity of the receptor and subsequent autophosphorylation on tyrosine residues. Phosphorylation of these receptors results in the formation of multiprotein complexes whose organization dictates further downstream signaling events.

The ERK pathway is a major pathway involved in the control of growth signals, cell survival, and invasion. ERK acts as a central point where multiple signaling pathways coalesce to drive transcription, and it plays a critical role in the pathway downstream of Ras, Raf, and MEK. Melanomas are known to harbour activation mutations for both Ras and BRAF, suggesting that the downstream effector ERK may be playing a key role in the oncogenic behaviour of these tumours. In-vitro studies have demonstrated that melanoma cell lines and tumour tissues exhibit high constitutive ERK activity. The high constitutive ERK activity in melanoma is most likely a consequence of mutations in the upstream components of the MAPK pathway [53,54]. In this study, we found that tumour cells cannot grow normally with ERK1 and ERK2 up-regulated while upstream components B-raf are concurrently down-regulated. Accordingly, we suspected that the activity of ERK1 and ERK2 was limited by the down-regulation of upstream components B-raf. This may account for the ability of Dnmt3a to affect the growth of melanoma by regulating the activity of ERK.

3.4.5. Melanoma Pathway

The altered proteins involved in the melanoma pathway are listed in **Table 2**. The locations of the altered proteins involved in the melanoma pathway are indicated with pink boxes (up-regulated proteins) and yellow boxes (down-regulated proteins) in **Figure 7**. The figure was manually edited. BRAF plays an important role in replicative and oncogene-induced senescence, as indicated by the red oval.

Frequent somatic mutation of BRAF is described in melanoma cell lines, such as the B16 mouse melanoma cell line, and other tumors [55,56]. BRAF is a serine/threonine kinase that is commonly activated by a somatic point mutation in human cancer, and may provide new therapeutic opportunities for malignant melanoma [57]. Thus, we focused on BRAF in the melanoma pathway.

It has been reported that PTEN deficiency combined with BRAF activation induces a melanoma in-situ like phenotype without dermal invasion [58]. In our study,

Table 2. The altered proteins involved in melanoma pathway.

Location in Pathway	Gen Bank ID	Gene name	Synonyms	Name of Altered Protein; ↑: Up-regulated protein; ↓: Down-regulated protein
ERK	26413	Mapk1	Erk2, Mapk, Prkm1	Mitogen-activated protein kinase 1 ↑
	26417	Mapk3	Erk1, Prkm3	Mitogen-activated protein kinase 3 ↑
BRAF	109880	Braf	B-raf	Serine/threonine-protein kinase B-raf ↓
Raf	109880	Braf	B-raf	Serine/threonine-protein kinase B-raf ↓
CDK4/6	12571	Cdk6	Crk2	Cell division protein kinase 6 ↓

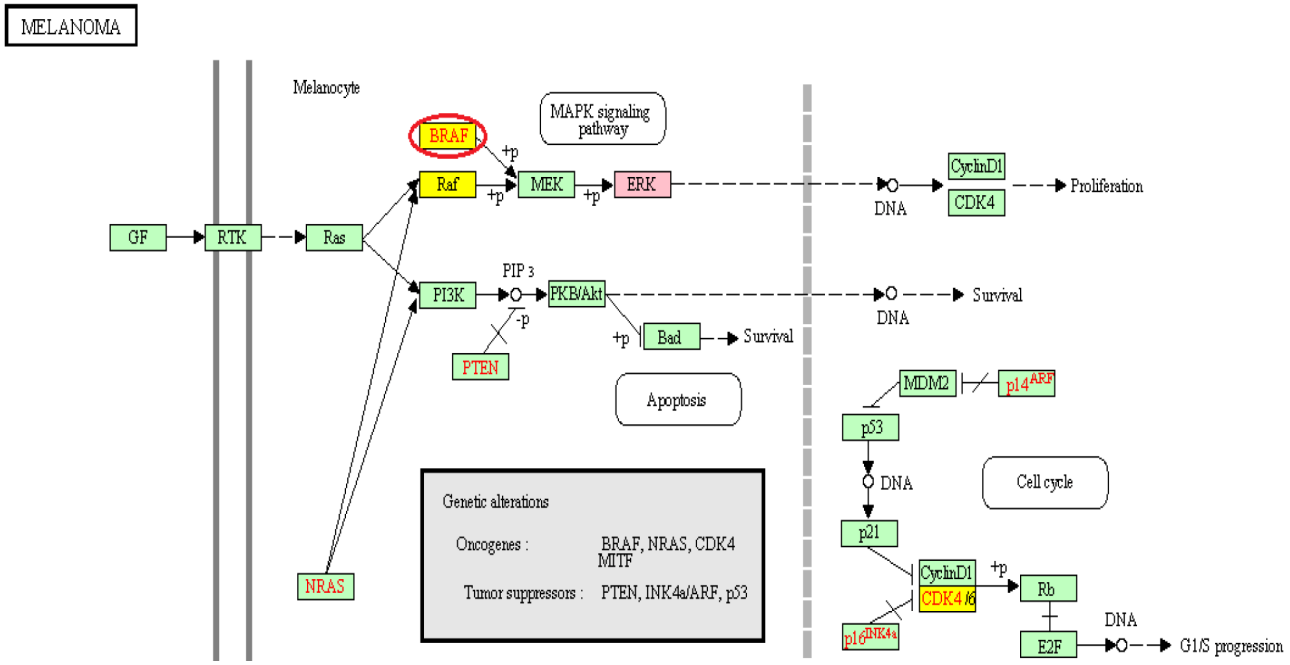

Figure 7. The location of altered proteins involved in melanoma pathway from KEGG database.

BRAF was found to be down-regulated in the melanoma pathway of the Dnmt3a-D cell line (**Figure 7**). Most likely, the down-regulated expression of BRAF resulted in the suppression of tumorigenesis. Dnmt3a depletion inhibited the growth of melanoma by directly or indirectly regulating the expression of BRAF.

4. Conclusions

This study demonstrates the varied changes in protein level, and that in the Dnmt3a-D cell line 467 proteins were up-regulated, while 535 proteins were down-regulated as compared to the NC cell line. GO analysis indicated that the altered proteins were primarily concentrated in the cytoplasm, nucleus, and mitochondrion, and that the altered proteins exhibiting activity function were primarily classified as exhibiting catalytic activity, transferase activity, and phosphotransferase activity. KEGG pathway analysis demonstrated that the MAPK signaling pathway exhibited a greater level of altered proteins, a fact that attracted our attention due to the close relationship with tumorigenesis. Taken together, our results strongly suggested that Dnmt3a depletion has a great impact on the expression of melanoma cell proteins. Additionally, Dnmt3a depletion may affect tumorigenesis through regulation of the proteins involved in tumor-related pathways, such as the MAPK signaling pathway and the melanoma pathway. These results indicated that the tumor-related pathways may be potentially valuable for the treatment of malignant melanoma in the future.

5. Acknowledgements

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Supporting Information Available

There are 467 proteins were up-regulated (Supplementary Materials, **Table S1**) and 535 proteins were down-regulated (Supplementary Materials, **Table S2**) in the Dnmt3a-D cell line as compared with the NC cell line. Supplementary materials **Table S3** including the abbreviated words and their full name.

Table S1

protein	Protein probability	num unique peps	precursor ion charge	peptide sequence
sp|Q8CGP0|H2B3B_MOUSE	0.9997	2	2	AMGIMNSFVNDIFER
sp|Q8QZT1|THIL_MOUSE	1	18	2	ASKPTLNEVVIVSAIR
sp|Q9QZQ8|H2AY_MOUSE	1	9	2	AASADSTTEGTPTDGFTVLSTK
sp|O88544|CSN4_MOUSE	1	11	2	AIQLSGTEQLEALK
sp|Q9CR16|PPID_MOUSE	1	15	2	DGSGDSHPDFPEDADIDLK
sp|Q9WVJ2|PSD13_MOUSE	1	10	2	LYENFISEFEHR
sp|P40336|VP26A_MOUSE	1	11	2	ELALPGELTQSR
sp|Q921H8|THIKA_MOUSE	1	12	2	AEELGLPILGVLR
sp|P63085|MK01_MOUSE	1	12	2	FDM[147]ELDDLPK
sp|Q9QWL7|K1C17_MOUSE	1	5	2	LLEGEDAHLTQYK
sp|Q99J62|RFC4_MOUSE	1	10	2	AITFLQSATR
sp|Q60737|CSK21_MOUSE	1	11	2	GGPNIITLADIVK
sp|Q91WK2|EIF3H_MOUSE	1	11	2	LFM[147]AQALQEYNN
sp|O54984|ARSA1_MOUSE	1	8	2	GM[147]NFSVVVFDTAPTGH
sp|Q07417|ACADS_MOUSE	1	10	2	GISAFLVPM[147]PTPGLTLGK
sp|Q99KV1|DJB11_MOUSE	1	7	2	FQDLGAAYEVLSDSEK
sp|Q9DAR7|DCPS_MOUSE	1	9	2	IVFENPDPSDGFVLIPDLK
sp|Q9R1T2|SAE1_MOUSE	1	9	2	AQNLNPM[147]VDVK
sp|Q9D0M1|KPRA_MOUSE	1	10	2	GQDIFIIQTIPR
sp|Q9JHJ0|TMOD3_MOUSE	1	7	2	DLGDYKDLDEDELLGK
sp|Q9Z2K1|K1C16_MOUSE	1	4	2	TRLEQEIATYR
sp|Q9Z1G3|VATC1_MOUSE	1	11	2	VAQYM[147]ADVLEDSKDK

sp|P70362|UFD1_MOUSE	1	7	2	FQPQSPDFLDITNPK
sp|P47811|MK14_MOUSE	1	9	2	HENVIGLLDVFTPAR
sp|Q9R0U0|FUSIP_MOUSE	1	6	2	GFAYVQFEDVR
sp|P63276|RS17_MOUSE	1	3	2	IAGYVTHLM[147]K
sp|Q9CXW2|RT22_MOUSE	1	8	2	LM[147]TQAQLEEATR
sp|Q6Y7W8|PERQ2_MOUSE	1	9	2	EVESPYEVHDYTR
sp|Q9CPX6|ATG3_MOUSE	1	5	2	LWLFGYDEQR
sp|P70318|TIAR_MOUSE	1	4	2	FEDVVNQSSPK
sp|P05132|KAPCA_MOUSE	1	9	2	ILQAVNFPFLVK
sp|Q9DBS1|TMM43_MOUSE	1	9	2	LLSDPNYGVHLPAVK
sp|P54923|ADPRH_MOUSE	1	7	3	DGETIHQQLAQM[147]GDLEAIDVAR
sp|Q9D7G0|PRPS1_MOUSE	1	6	2	IFSGSSHQDLSQK
sp|Q9ER00|STX12_MOUSE	1	4	2	ELGSLPLPLSASEQR
sp|Q9ER88|RT29_MOUSE	1	6	2	FDQPLEASTWLK
sp|Q9Z0G0|GIPC1_MOUSE	1	6	2	APPLVENEEAEPSR
sp|Q99LG2|TNPO2_MOUSE	1	4	2	ALVM[147]LLEVR
sp|Q9CQT1|EI2BL_MOUSE	1	6	2	AGAGGPGLAALVAFVR
sp|Q9WUL7|ARL3_MOUSE	1	6	2	LNVWDIGGQR
sp|P47964|RL36_MOUSE	0.9975	2	2	YPM[147]AVGLNK
sp|P26516|PSD7_MOUSE	1	5	2	TNDQM[147]VVVYLASLIR
sp|Q8K157|GALM_MOUSE	1	4	2	VSPDGEEGYPGELK
sp|P58774|TPM2_MOUSE	0.9994	1	2	ATDAEADVASLNR
sp|P61963|WDR68_MOUSE	1	3	2	DM[147]FASVGADGSVR
sp|Q64442|DHSO_MOUSE	1	4	2	AM[147]GAAQVVVTDLSASR
sp|Q99J09|MEP50_MOUSE	1	4	2	IWDLAQQVSLNSYR
sp|Q9CX34|SUGT1_MOUSE	1	6	2	DYASALETFAEGQK
sp|Q9QYA2|TOM40_MOUSE	1	6	2	FVNWQVDGEYR
sp|Q9QYJ3|DNJB1_MOUSE	1	6	2	DGSDVIYPAR
sp|P68181|KAPCB_MOUSE	0.9987	1	2	ILQAVEFPFLVR
sp|Q60766|IRGM_MOUSE	1	5	2	DLSTSVLSEVR
sp|Q64213|SF01_MOUSE	1	4	3	ILRPWQSSETR
sp|Q8R323|RFC3_MOUSE	1	7	2	AIYHLEAFVAK
sp|Q8R574|KPRB_MOUSE	1	5	2	IFVM[147]ATHGLLSSDAPR
sp|Q99JB2|STML2_MOUSE	1	4	2	AEQINQAAGEASAVLAK
sp|Q9EQ80|NIF3L_MOUSE	1	5	2	TLM[147]QVLAFLSQDR
sp|Q9JLC8|SACS_MOUSE	1	9	2	LLLVLNK
sp|O09174|AMACR_MOUSE	1	5	2	GQNILDGGAPFYTTYK
sp|O35435|PYRD_MOUSE	1	7	2	QTQLTTDGLPLGINLGK
sp|P24288|BCAT1_MOUSE	1	5	2	HLTM[147]DDLATALEGNR
sp|P70697|DCUP_MOUSE	1	5	2	LVQQM[147]LDDFGPQR
sp|Q61187|TS101_MOUSE	1	5	2	ELVNLTGTIPVR
sp|Q6PD19|CJ076_MOUSE	1	6	2	LQDGLDQYER
sp|Q91WM2|CECR5_MOUSE	1	5	2	QM[147]LVSGQGPLVENAR
sp|P18872|GNAO_MOUSE	0.9998	2	2	TTGIVETHFTFK
sp|P47941|CRKL_MOUSE	1	4	2	IHYLDTTTLIEPAPR
sp|Q8VDT9|RM50_MOUSE	1	5	2	DVLDFYNVPVQDK
sp|Q99M71|EPDR1_MOUSE	1	3	2	ALVSYDGLNQR

sp|Q9WTQ8|TIM23_MOUSE	1	3	2	NVQILNM[147]VTR
sp|Q80WQ2|VAC14_MOUSE	1	4	2	DFVAQNNTM[147]QIK
sp|Q9CQ92|FIS1_MOUSE	1	2	2	GLLQTEPQNNQAK
sp|Q9CXE7|TMED5_MOUSE	1	4	2	LEDILESINSIK
sp|Q9DC50|OCTC_MOUSE	1	5	2	AASDLQIAASTFTSFGK
sp|Q9JK48|SHLB1_MOUSE	1	4	2	LAADAGTFLSR
sp|Q8K0D0|PCTK2_MOUSE	1	4	2	LDSEGIELITK
sp|Q99J95|CDK9_MOUSE	0.9997	3	2	LADFGLAR
sp|P21278|GNA11_MOUSE	1	6	2	IATVGYLPTQQDVLR
sp|Q8BMS9|RASF2_MOUSE	1	5	2	TSVFTPAYGSVTNVR
sp|Q99JT2|MST4_MOUSE	1	3	2	LADFGVAGQLTDTQIK
sp|O70493|SNX12_MOUSE	0.9966	2	2	TNLPIFK
sp|O08915|AIP_MOUSE	1	3	2	VLELDPALAPVVSR
sp|P59708|PM14_MOUSE	1	3	2	GTAYVVYEDIFDAK
sp|P70404|IDH3G_MOUSE	1	6	2	ENTEGEYSSLEHESVAGVVESLK
sp|Q80V26|IMPA3_MOUSE	1	3	2	EM[147]LAVAVLAAER
sp|Q8BGR9|UBCP1_MOUSE	1	4	2	LDDFLELNHK
sp|Q8BTZ7|GMPPB_MOUSE	1	5	2	ALILVGGYGTR
sp|Q8N9S3|AHSA2_MOUSE	1	4	2	LQASPVALGVR
sp|Q91YM2|GRLF1_MOUSE	1	6	2	EQLTEGEEIAQEIDGR
sp|Q99JF8|PSIP1_MOUSE	1	4	2	QVDTEEAGM[147]VTAATASNVK
sp|Q9CQR4|THEM2_MOUSE	1	2	2	TLAFASVDLTNK
sp|Q9CXY9|GPI8_MOUSE	1	3	2	NVLITDFFGSVR
sp|Q9JHI5|IVD_MOUSE	1	4	2	IGQFQLM[147]QGK
sp|Q9WVL0|MAAI_MOUSE	1	2	2	VITSGFNALEK
sp|O08583|THOC4_MOUSE	1	3	2	QQLSAEELDAQLDAYNAR
sp|Q63844|MK03_MOUSE	1	3	2	FDM[147]ELDDLPK
sp|Q00899|TYY1_MOUSE	1	3	2	TLEGEFSVTM[147]WSSDEKK
sp|Q3URS9|CCD51_MOUSE	1	4	2	EDNQYLELATLEHR
sp|Q8R2U6|NUDT4_MOUSE	1	2	2	LLGIFENQDR
sp|P13011|ACOD2_MOUSE	0.9913	1	2	DDLYDPTYQDDEGPPPK
sp|O70439|STX7_MOUSE	1	2	2	TLNQLGTPQDSPELR
sp|O88543|CSN3_MOUSE	1	2	2	AM[147]DQEITVNPQFVQK
sp|P47199|QOR_MOUSE	1	3	2	VFEFGGPEVLK
sp|Q8BG94|COMD7_MOUSE	1	3	2	FGVTSGSSELEK
sp|Q8BH69|SPS1_MOUSE	1	4	2	IIEVAPQVATQNVNPTPGATS
sp|Q8CAY6|THIC_MOUSE	1	5	2	ILVTLLHTLER
sp|Q8K2Z2|PRP39_MOUSE	1	4	2	DLLTGEQFIQLR
sp|Q8R349|CDC16_MOUSE	1	4	2	YAEALDYHR
sp|Q8VCG3|WDR74_MOUSE	1	3	2	VWDLQGSEEPVFR
sp|Q921X9|PDIA5_MOUSE	1	4	2	FHISAFPTLK
sp|Q99K23|UFSP2_MOUSE	1	4	2	INAYHFPDELYK
sp|Q99LD9|EI2BB_MOUSE	1	4	2	FVAPEEVLPFTEGDILEK
sp|Q9D2R6|CCD56_MOUSE	1	3	2	FLDELEDEAK
sp|Q9D8X5|CNOT8_MOUSE	1	3	2	GGLQEVADQLDLQR
sp|Q9DCA5|BXDC2_MOUSE	1	4	2	EFLIQIFSTPR
sp|P21279|GNAQ_MOUSE	1	2	2	M[147]FVDLNPDSDK

sp|Q8VE80|THOC3_MOUSE	0.9992	2	2	YVLGM[147]QELFR
sp|Q62422|OSTF1_MOUSE	0.9989	2	2	ALYTFEPR
sp|P61294|RAB6B_MOUSE	0.9979	1	2	GSDVIIMLVGNK
sp|Q8R2E9|ERO1B_MOUSE	0.9969	1	2	TLLLSIFQDTK
sp|O09110|MP2K3_MOUSE	1	2	2	FPYESWGTPFQQLK
sp|O35658|C1QBP_MOUSE	1	2	2	AFVEFLTDEIKEEK
sp|P62488|RPB7_MOUSE	1	3	2	GEVVDAVVTQVNK
sp|Q59J78|MIMIT_MOUSE	1	3	2	ETSEELLPSPTATQVK
sp|Q60866|PTER_MOUSE	1	3	2	GGGALVENTTTGLSR
sp|Q61249|IGBP1_MOUSE	1	3	2	AAGM[147]LSQLDLFSR
sp|Q62203|SF3A2_MOUSE	1	4	2	M[147]EKPPAPPSLPAGPPGVK
sp|Q78HU3|F125A_MOUSE	1	2	2	GPLPSGFSAVNDPQDIK
sp|Q78JW9|UBFD1_MOUSE	1	4	2	IM[147]VVGSTINDVLAVNTPK
sp|Q8BFQ8|PDDC1_MOUSE	1	2	2	AIDFVDVTESNAR
sp|Q8CFE2|CD027_MOUSE	1	5	2	DSPDELPVYVGTNEAK
sp|Q8R1J3|ZCHC9_MOUSE	1	2	2	GM[147]SADYEDVLDVPK
sp|Q8VDG7|PAFA2_MOUSE	1	4	2	TVVNVFPGGLDLM[147]TLK
sp|Q8VDQ1|PTGR2_MOUSE	1	4	2	GLENM[147]GVAFQSM[147]M[147]TGG NVGK
sp|Q91VE6|MK67I_MOUSE	1	3	2	GIDYSFPSLVLPK
sp|Q91WE2|NIP30_MOUSE	1	3	2	GLDEDETNFLDEVSR
sp|Q99LC2|CSTF1_MOUSE	1	3	2	LGM[147]ENDDTAVQYAIGR
sp|Q9CQI9|MED30_MOUSE	1	2	2	IGQETVQDIVYR
sp|Q9D753|EXOS8_MOUSE	1	3	2	ATTVNIGSISTADGSALVK
sp|Q9D832|DNJB4_MOUSE	1	5	2	VIGYGLPFPK
sp|Q9DBL1|ACDSB_MOUSE	1	5	2	SGNYYVLNGSK
sp|Q9EPJ9|ARFG1_MOUSE	1	3	2	IFDDVSSGVSQLASK
sp|Q9JK38|GNA1_MOUSE	1	2	2	VLGQLTETGVVSPEQFM[147]K
sp|Q9WUN2|TBK1_MOUSE	1	5	2	LSSSQGTIESSLQDISSR
sp|Q9Z2D8|MBD3_MOUSE	1	2	2	AFM[147]VTDDDIR
sp|P18653|KS6A1_MOUSE	0.9993	1	3	DLKPENILLDEEGHIK
sp|P97820|M4K4_MOUSE	1	4	2	GQNVLLTENAEVK
sp|Q91YS8|KCC1A_MOUSE	0.9999	2	2	LIFQVLDAVK
sp|Q921E2|RAB31_MOUSE	0.9999	2	2	GSAAAVIVYDITK
sp|P0C7N9|PSMG4_MOUSE	0.9998	2	2	AAADADVSLHNFSAR
sp|P59438|HPS5_MOUSE	0.9998	4	2	LLDPLVLFEPK
sp|Q8C5Q4|GRSF1_MOUSE	0.9998	2	2	LGDEVDDVYLIR
sp|Q9Z1B5|MD2L1_MOUSE	0.9998	2	2	YGLTLLTTTDPELIK
sp|P47226|TES_MOUSE	0.9997	2	2	NVM[147]ILTNPVAAK
sp|O09117|SYPL1_MOUSE	0.9992	2	2	SAFQINLNPLK
sp|Q9D7H3|RTC1_MOUSE	0.999	3	2	AFVAGVLPLK
sp|Q91X78|ERLN1_MOUSE	0.9969	1	2	ISEIEDAAFLAR
sp|A6PWY4|WDR76_MOUSE	1	3	2	VFDSSSISSQLPLLSTIR
sp|O08579|EMD_MOUSE	1	3	2	DYNDDYYEESYLTTK
sp|O54784|DAPK3_MOUSE	1	3	2	ESLTEDEATQFLK
sp|P33611|DPOA2_MOUSE	1	3	2	QLLSPSSFSPSATPSQK
sp|P97789|XRN1_MOUSE	1	4	2	APELFSYIAK

sp|Q3U1V6|UEVLD_MOUSE	1	5	2	DGVLSPSSQAQLSSR
sp|Q64669|NQO1_MOUSE	1	3	2	ALIVLAHSEK
sp|Q78JE5|FBX22_MOUSE	1	2	2	STYVLSNLAEVVER
sp|Q810A3|TTC9C_MOUSE	1	3	2	AGVAFFHLQDYDR
sp|Q8BKX1|BAIP2_MOUSE	1	2	2	EGDLITLLVPEAR
sp|Q8BWR2|CA128_MOUSE	1	2	2	GLAYGLYLR
sp|Q8C407|YIPF4_MOUSE	1	3	2	SAASLLVGEEFK
sp|Q8CEC0|NUP88_MOUSE	1	2	2	GPSGGGVEPPLSQYQR
sp|Q8CF89|TAB1_MOUSE	1	3	2	VLLQAFDVVER
sp|Q8K194|SNR27_MOUSE	1	3	2	VDGSVNAYAINVSQK
sp|Q8K409|DPOLB_MOUSE	1	3	2	EEM[147]LQM[147]QDIVLNEIK
sp|Q8VDS4|RPR1A_MOUSE	1	2	2	SVYENDVLEQLK
sp|Q8VDS8|STX18_MOUSE	1	3	2	TAVLDFVDDYLK
sp|Q91WK1|SPRY4_MOUSE	1	3	2	VGLLLDYEAK
sp|Q91XI1|DUS3L_MOUSE	1	4	2	ISEM[147]LLGPVPPGFVFLPK
sp|Q9CR95|NECP1_MOUSE	1	3	2	ASGTGGLSLLPPPPGGK
sp|Q9CY28|GTPB8_MOUSE	1	3	2	LFDPSLEDIGR
sp|Q9CZX9|TMM85_MOUSE	1	2	2	GSGQGDSLYPVGYLDK
sp|Q9D8M4|RL7L_MOUSE	1	4	2	TVPLTDNTVIEEHLGR
sp|Q9DBX2|PHLP_MOUSE	1	3	2	EVLVLTSVR
sp|Q9ER73|ELP4_MOUSE	1	4	2	NLSDTVVGLESFIGSER
sp|Q9JLB2|MPP5_MOUSE	1	4	2	EGDEDNQPLAGLVPGK
sp|Q9R099|TBL2_MOUSE	1	3	2	APIINIGIADTGK
sp|Q9WVB0|RBPMS_MOUSE	1	3	2	ENTPSEANLQEEEVR
sp|Q6ZPF4|FMNL3_MOUSE	0.9983	1	2	AAAVSLENVLLDVK
sp|Q921Y2|IMP3_MOUSE	0.9999	2	2	VGPDVVTDPAFLVTR
sp|Q3V009|TMED1_MOUSE	0.9998	2	2	SIQM[147]LTLLR
sp|Q9CQ71|RFA3_MOUSE	0.9991	2	2	M[147]FILSDGEGK
sp|Q9CQG2|MET10_MOUSE	0.9983	2	2	APEDVILALEER
sp|O55125|NIPS1_MOUSE	0.9904	1	2	AGPNIYELR
sp|O09114|PTGDS_MOUSE	1	3	2	AQGLTEEDIVFLPQPDK
sp|P27601|GNA13_MOUSE	1	4	2	ALWEDSGIQNAYDR
sp|P42669|PURA_MOUSE	1	2	2	GPGLGSTQGQTIALPAQGLIEFR
sp|P62748|HPCL1_MOUSE	1	3	2	IYANFFPYGDASK
sp|P97493|THIOM_MOUSE	1	2	2	TTFNVQDGPDFQDR
sp|Q3U0V2|TRADD_MOUSE	1	3	2	DPALDSLAYEYER
sp|Q3UE37|UBE2Z_MOUSE	1	3	2	GHFDYQSLLM[147]R
sp|Q5SSK3|CQ042_MOUSE	1	2	2	LENLIDVPLIQYK
sp|Q62086|PON2_MOUSE	1	4	2	FQEEENSLLHLK
sp|Q8BJZ4|RT35_MOUSE	1	3	2	IPNFLHLTPVAIK
sp|Q8BKF1|RPOM_MOUSE	1	4	2	QLAELLVQAVQM[147]PR
sp|Q8BMZ5|SEN34_MOUSE	1	3	2	FGGDFLVYPGDPLR
sp|Q8BNV1|TRM2A_MOUSE	1	4	2	DDLFTSEIFK
sp|Q8BP40|PPA6_MOUSE	1	4	2	AAISQPGISEDLEK
sp|Q8BVI5|STX16_MOUSE	1	2	2	QIVQSISDLNEIFR
sp|Q8K2M0|RM38_MOUSE	1	4	2	TPPLGPM[147]PNEDIDVSNLER
sp|Q8R322|GLE1_MOUSE	1	4	2	IEAITSSGQM[147]GSFIR

sp|Q8R4Y8|RTTN_MOUSE	1	5	2	AILLYLLQGR
sp|Q8VD00|TMM97_MOUSE	1	3	2	DPLM[147]QEPPVWFK
sp|Q91VJ5|PQBP1_MOUSE	1	3	2	KDEELDPM[147]DPSSYSDAPR
sp|Q920R0|ALS2_MOUSE	1	5	2	GTSDFPLYGGGSSVQR
sp|Q921T2|TOIP1_MOUSE	1	3	2	FESLPAGSTLIFYK
sp|Q9CXR1|DHRS7_MOUSE	1	3	2	LM[147]LISM[147]ANDLK
sp|Q9CYY7|SLMO2_MOUSE	1	2	2	LNAEIEELAASAR
sp|Q9CZU4|ERAL_MOUSE	1	3	2	ETQVILLDTPGIISPVK
sp|Q9D2R8|RT33_MOUSE	1	2	2	VVSLFSEQPLAK
sp|Q9EP72|CO024_MOUSE	1	3	2	SEVPGAAAEGPGGSGVGLGDR
sp|Q9WV03|FA50A_MOUSE	1	3	2	SGPLFNFDVHDDVR
sp|Q925E7|2ABD_MOUSE	0.9951	1	2	INLWHLEITDR
sp|Q9JI46|NUDT3_MOUSE	1	2	2	LVGIFENQER
sp|Q3UA16|SPC25_MOUSE	0.9999	3	2	LQFIFTSIDPK
sp|Q6PAQ4|REXO4_MOUSE	0.9999	3	2	VSIVNQYGK
sp|Q810J8|ZFYV1_MOUSE	0.9999	3	2	FLGDASEAYLK
sp|Q8BH66|ATLA1_MOUSE	0.9999	4	2	SFLM[147]DFM[147]LR
sp|Q8JZV7|NAGA_MOUSE	0.9999	3	2	ATEDVGSGVALVAR
sp|Q9D7X8|GGCT_MOUSE	0.9999	2	2	SYLM[147]TNYESAPPSPQYK
sp|O88952|LIN7C_MOUSE	0.9999	2	2	TEEGLGFNIM[147]GGK
sp|Q9EQS3|MYCBP_MOUSE	0.9998	2	2	LVQYEPPQEEK
sp|Q9WV84|NDKM_MOUSE	0.9996	2	2	M[147]LQAPESILAEHYR
sp|Q9CQX4|PAF_MOUSE	0.9995	2	2	VLGSSTFVTNSSSSSR
sp|Q9D4J1|EFHD1_MOUSE	0.9987	1	2	VFNPYTEFPEFSR
sp|Q8R035|ICT1_MOUSE	0.9975	2	2	AGELVLTSESSR
sp|Q5BL07|PEX1_MOUSE	0.9963	1	2	YPELFANLPIR
sp|O35448|PPT2_MOUSE	0.9929	2	2	ESLRPLWEQVQGFR
sp|Q99JF5|ERG19_MOUSE	0.9913	1	2	GLQVAPVLLSDELK
sp|Q9CXA2|PRCM_MOUSE	0.9913	1	2	DLVDAASALTGAVK
sp|A2ADY9|DDI2_MOUSE	1	2	2	NPPLAEALLSGDLEK
sp|A2RSX7|CB060_MOUSE	1	2	2	DAQYLYLSGSK
sp|A3KMP2|TTC38_MOUSE	1	2	2	VLELLLPIR
sp|O35295|PURB_MOUSE	1	2	2	GGGGGGGGGPGGFQPAPR
sp|O35623|BET1_MOUSE	1	2	2	LLAEM[147]DSQFDSTTGFLGK
sp|Q03958|PFD6_MOUSE	1	2	2	ETLAQLQQEFQR
sp|Q3UGP9|LRC58_MOUSE	1	2	2	DLTYDPPTLLELAAR
sp|Q4FK66|PR38A_MOUSE	1	2	2	YVLEEAEQLEPR
sp|Q4FZF3|DDX49_MOUSE	1	2	2	ELAYQIAEQFR
sp|Q56A08|GPKOW_MOUSE	1	3	2	AVVVLSGPYR
sp|Q61823|PDCD4_MOUSE	1	3	2	DLPELALDTPR
sp|Q6P3D0|NUD16_MOUSE	1	2	2	EQLLEALQDLK
sp|Q6PCP5|MFF_MOUSE	1	3	2	IQYEM[147]EYTEGISQR
sp|Q80TH2|LAP2_MOUSE	1	4	2	IYDILGDDGPQPPSAAVK
sp|Q80UW2|FBX2_MOUSE	1	2	2	TDAGSLYELTVR
sp|Q8BGU5|CCNY_MOUSE	1	2	2	IVLGAILLASK
sp|Q8BHL8|PSMF1_MOUSE	1	2	2	VLIDPSSGLPNR
sp|Q8C163|EXOG_MOUSE	1	2	2	SPESTEPLALGAFVVPNK

sp|Q8JZM0|TFB1M_MOUSE	1	2	2	FIPGLQM[147]LSDAAPGK
sp|Q8K3J1|NDUS8_MOUSE	1	2	2	GLGM[147]TLSYLFR
sp|Q8R3Y8|I2BP1_MOUSE	1	2	2	LALPSPALEYTLGSR
sp|Q8VC70|RBMS2_MOUSE	1	3	2	GYGFVDFDSPSSAQK
sp|Q8VCN9|TBCC_MOUSE	1	2	2	QGQAALAQLQAVLTER
sp|Q8VHR5|P66B_MOUSE	1	3	2	LQQQAALSPTTAPAVSSVSK
sp|Q8WTY4|CPIN1_MOUSE	1	2	2	KPNFEVGSSSQLK
sp|Q91YY4|ATPF2_MOUSE	1	2	2	LTVEQAVLLSR
sp|Q920Q8|NS1BP_MOUSE	1	3	2	LYIVGGSDPYGQK
sp|Q922Q9|CHID1_MOUSE	1	3	2	FTQISPVWLQLK
sp|Q99K43|PRC1_MOUSE	1	2	2	EIWELIGIPEEQR
sp|Q99N94|RM09_MOUSE	1	2	2	LLSQGLAVYASPENR
sp|Q9D1C1|UBE2C_MOUSE	1	2	2	LQQELM[147]ILM[147]TSGDK
sp|Q9D920|L12R1_MOUSE	1	2	2	GLLSGQTSPTNAK
sp|Q9DCT8|CRIP2_MOUSE	1	2	2	GVNTGAVGSYIYDKD
sp|Q9JHE7|TSSC4_MOUSE	1	2	2	DAALAFLSSR
sp|Q9JJZ4|UB2J1_MOUSE	1	2	2	TALLAIIGFM[147]PTK
sp|Q9JKJ9|CP39A_MOUSE	1	4	2	TVLESISSVFGTAGK
sp|Q9JLJ0|LITAF_MOUSE	1	2	2	GM[147]NPPSYYTQPVPVPNAN
sp|Q9JMG1|EDF1_MOUSE	1	2	2	INEKPQVIADYESGR
sp|P34056|AP2A_MOUSE	1	3	2	AVAEFLNR
sp|P36993|PPM1B_MOUSE	1	3	2	GPTEQLVSPEPEVYEIVR
sp|Q9JHD1|PCAF_MOUSE	1	3	2	LFMADLQR
sp|P42230|STA5A_MOUSE	0.9999	2	2	IQAQFAQLGQLNPQER
sp|Q3UX61|ARD1B_MOUSE	0.9999	2	2	YVSLHVR
sp|Q80WC1|K2030_MOUSE	0.9999	3	2	VVPTLPEGLPVLLEK
sp|Q91YD9|WASL_MOUSE	0.9999	2	2	FYGSQVNNISHTK
sp|Q9DCS3|MECR_MOUSE	0.9999	3	2	DLGADYVLTEEELR
sp|Q02614|S30BP_MOUSE	0.9998	2	2	DPQELVASFSER
sp|Q8BSQ9|PB1_MOUSE	0.9998	3	2	VVDDEIYYFR
sp|Q9DAU1|CNPY3_MOUSE	0.9998	2	2	ELGGLGEDANAEEEEGVQK
sp|Q7TQK4|EXOS3_MOUSE	0.9996	2	2	LYPLEIVFGM[147]NGR
sp|Q8K4F5|ABHDB_MOUSE	0.9996	2	2	LNLDTLAQHLDK
sp|Q9D6Y7|MSRA_MOUSE	0.9996	3	2	VISAEEALPGR
sp|A2APY7|CT007_MOUSE	0.9994	2	2	IFQTDIAEHALK
sp|O70126|AURKB_MOUSE	0.9994	3	2	FGNVYLAR
sp|Q60759|GCDH_MOUSE	0.9994	2	2	AITGIQAFTVGK
sp|P49586|PCY1A_MOUSE	0.9992	2	2	TEGISTSDIITR
sp|Q9Z0M5|LICH_MOUSE	0.9992	2	2	LYDEIISLM[147]K
sp|Q9QYL7|ABT1_MOUSE	0.9991	2	2	NLLSAYGEVGR
sp|O88520|SHOC2_MOUSE	0.999	2	2	LVLTNNQLSTLPR
sp|Q9CR09|UFC1_MOUSE	0.999	3	3	LKEEYQSLIR
sp|Q9DCF9|SSRG_MOUSE	0.9983	2	2	QQSEEDLLLQDFSR
sp|Q8BGX2|CS052_MOUSE	0.9982	2	2	ILDVGFVGR
sp|Q9Z1R4|CF047_MOUSE	0.9978	2	2	AILDALGLR
sp|Q9DBY1|SYVN1_MOUSE	0.9977	3	2	VHTFPLFAIR
sp|Q9Z2G0|FEM1B_MOUSE	0.9977	2	2	VLTLAALLLNR

sp|P62484|ABI2_MOUSE	0.996	1	2	ALFDSYTNLER
sp|A2A4P0|DHX8_MOUSE	0.9957	1	2	FSQYFYEAPIFTIPGR
sp|Q9D735|CS043_MOUSE	0.9913	1	2	GGPGPTLSFVGK
sp|Q3UBX0|TM109_MOUSE	0.9904	1	2	ETSADILTQIGR
sp|O35972|RM23_MOUSE	1	2	2	NYLEQIYNVPVAAVR
sp|Q2TPA8|HSDL2_MOUSE	1	2	2	ADVVM[147]SM[147]ATDDFVK
sp|Q80VL1|TDRKH_MOUSE	1	2	2	DM[147]ATETDDSLASILTETK
sp|Q8C156|CND2_MOUSE	1	2	2	TIEQNLSNINVSEADGK
sp|Q8CHT0|AL4A1_MOUSE	1	3	2	TVIQAEIDAAAELIDFFR
sp|Q8K2L8|TTC15_MOUSE	1	2	2	QVLNASSVEQSFVGLK
sp|Q8R2N2|CIR1A_MOUSE	1	2	2	TDGTVEIYNLSANYFQEK
sp|Q8VE18|CQ071_MOUSE	1	2	2	AANYDFYQLLEEK
sp|Q91ZR2|SNX18_MOUSE	1	2	2	APEPGPPADGGPGAPAR
sp|Q921W4|QORL1_MOUSE	1	2	3	LSAGVFRPLLDEPIPLYEAK
sp|Q99MZ7|PECR_MOUSE	1	2	2	NQVAVVTGGGTGIGK
sp|Q9D7A8|ARMC1_MOUSE	1	2	2	AEALASAIASTK
sp|Q9DC71|RT15_MOUSE	1	3	2	TLEAQIIALTVR
sp|Q9ESP1|SDF2L_MOUSE	1	2	2	AM[147]EGIFIKPGADLSTGHDEL
sp|Q9WV85|NDK3_MOUSE	1	2	2	ALIGATDPGDAM[147]PGTIR
sp|Q3V300|KIF22_MOUSE	0.9999	3	2	ALM[147]DLLQLAR
sp|Q8BHE8|CB047_MOUSE	0.9999	2	2	QLLSASYEFQR
sp|Q8BVU5|NUDT9_MOUSE	0.9999	3	2	EFGEEALNSLQK
sp|Q8R107|PRLD1_MOUSE	0.9999	2	2	AVQEFGLAR
sp|Q9CRA5|GOLP3_MOUSE	0.9999	2	2	SDAPTGDVLLDEALK
sp|Q9D125|RT25_MOUSE	0.9999	2	2	IM[147]TVNYNTYGELGEGAR
sp|Q9D2E2|TOE1_MOUSE	0.9999	3	2	VPVVDVQSDNFK
sp|Q9DB90|CS061_MOUSE	0.9999	2	2	GGNQTSGIDFFITQER
sp|Q9WVM3|APC7_MOUSE	0.9999	2	2	AIQLNSNSVQALLLK
sp|Q9Z2E1|MBD2_MOUSE	0.9999	2	2	LQGLSASDVTEQIIK
sp|Q8K0C9|GMDS_MOUSE	0.9998	2	2	FYQASTSELYGK
sp|Q9ESW8|PGPI_MOUSE	0.9998	2	2	SAFVHVPPLGK
sp|Q62036|AZI1_MOUSE	0.9997	2	2	PAEPTDFLM[147]LFEGSTSGR
sp|Q99N87|RT05_MOUSE	0.9997	3	2	EPEPEPEVPDTK
sp|Q9CYI4|LUC7L_MOUSE	0.9997	2	2	ALLDQLM[147]GTAR
sp|Q9R1Z7|PTPS_MOUSE	0.9997	2	3	LHSPSLSDEENLR
sp|Q64437|ADH7_MOUSE	0.9997	3	2	M[147]LTYDPM[147]LLFTGR
sp|Q924W5|SMC6_MOUSE	0.9996	2	2	SAVLTALIVGLGGK
sp|Q9R0X0|MED20_MOUSE	0.9996	2	2	SLQQTVELLTK
sp|Q9D8V7|SC11C_MOUSE	0.9993	2	2	GDLLFLTNFR
sp|Q9DB40|MED27_MOUSE	0.9993	2	2	TPLYSQLLQAYK
sp|Q80W93|HYDIN_MOUSE	0.9992	3	3	QKLT[181]LLAQGQGLEPR
sp|Q91Y86|MK08_MOUSE	0.9988	3	2	NIIGLLNVFTPQK
sp|Q63810|CANB1_MOUSE	0.9977	2	3	M[147]M[147]VGNNLKDTQLQQIVDK
sp|Q91ZF0|DJC24_MOUSE	0.9973	2	2	LILLYHPDK
sp|Q8VC65|NRM_MOUSE	0.996	2	2	YFGVLQR
sp|Q99KK9|SYHM_MOUSE	0.9945	1	2	DQGGELLSLR
sp|Q9D6M3|GHC1_MOUSE	0.9933	2	2	SEGYFGM[147]YR

sp|Q8BIJ7|RUFY1_MOUSE	0.9902	2	2	GSALQLQLSQLR
sp|O89050|MKLN1_MOUSE	1	3	2	VFGGM[147]NEENM[147]TELLSSGLK
sp|P04184|KITH_MOUSE	1	2	2	KLFASQQVLQYNSAN
sp|P63271|SPT41_MOUSE	1	2	3	VSNFKPGVYAVSVTGR
sp|Q8R088|GLP3L_MOUSE	1	3	2	DLVELDPEVEGTK
sp|Q9D8T7|SLIRP_MOUSE	1	3	2	IPWTAAASELR
sp|O70325|GPX41_MOUSE	1	3	2	TDVNYTQLVDLHAR
sp|Q5SYD0|MYO1D_MOUSE	0.9963	1	2	LMYNSSNPVLK
sp|P40338|VHL_MOUSE	0.9999	3	2	SLYEDLEDYPSVR
sp|Q921G6|LRCH4_MOUSE	0.9999	2	2	SYDLSDITQADLSR
sp|Q99JN2|KLH22_MOUSE	0.9999	3	2	LFVIGGSNNDAGYR
sp|Q9D4J7|PHF6_MOUSE	0.9999	3	2	VAIDQQLTQQQLNGN
sp|P15327|PMGE_MOUSE	0.9998	3	2	HYGALIGLNR
sp|Q8K273|MMGT1_MOUSE	0.9998	3	3	NHPSFYVFNHR
sp|Q8K3C3|LZIC_MOUSE	0.9998	2	2	KVEILTALR
sp|A3KGB4|TBC8B_MOUSE	0.9998	3	2	DSLALWTFR
sp|Q60967|PAPS1_MOUSE	0.9996	2	2	M[147]VAGANFYIVGR
sp|Q8BZH4|POGZ_MOUSE	0.9996	2	2	SFLVASVLPGPDGNVNSPTR
sp|Q9CYX7|RRP15_MOUSE	0.9995	2	2	GVVQLFNAVQK
sp|P11930|NUD19_MOUSE	0.9994	2	2	LENFASLSALYR
sp|Q6P6J9|TXD15_MOUSE	0.9994	2	2	GDPM[147]VVLSVVPGAAEDQR
sp|Q9D1R1|T126B_MOUSE	0.9994	2	2	LFVTDALQSGDISK
sp|Q80TF4|KLH13_MOUSE	0.9993	3	2	NFAALLSTGEFLK
sp|Q8BJS4|UN84B_MOUSE	0.9993	2	2	ADVESQFPDWIR
sp|Q3TMH2|SCRN3_MOUSE	0.9991	2	2	SPTFEPERPVAK
sp|Q99KL7|RAB28_MOUSE	0.9991	2	2	ADIVNYNQEPLSR
sp|Q8BP48|AMPM1_MOUSE	0.9989	2	2	EVLDIAAGM[147]IK
sp|Q99M04|LIAS_MOUSE	0.9985	3	2	VGNELGFLYTASGPLVR
sp|Q9CQT5|POMP_MOUSE	0.9985	2	2	NIQGLFAPLK
sp|Q9CXZ1|NDUS4_MOUSE	0.9984	2	2	LDITTLTGVPEEHIK
sp|O08738|CASP6_MOUSE	0.9983	2	2	IEIQTLTGLFK
sp|P30280|CCND2_MOUSE	0.9983	2	2	SVEDPDQATTPTDVRDVDL
sp|Q9Z0V7|TI17B_MOUSE	0.9982	2	2	EGSPAPGYPNYQQYH
sp|Q8CFH6|SN1L2_MOUSE	0.998	2	2	IADFGFGNFFK
sp|O08914|FAAH1_MOUSE	0.9979	2	2	LQSGELSPEAVLFTYLGK
sp|P60766|CDC42_MOUSE	0.9979	2	2	TLGLFDTAGQEDYDR
sp|Q9D6H2|HSB11_MOUSE	0.9979	2	2	DGYATFLR
sp|Q9DD18|DTD1_MOUSE	0.9979	2	2	ASVTVGGEQISAIGR
sp|Q3TKY6|SDC10_MOUSE	0.9978	2	2	EDQTLALLSQFK
sp|Q9ERA0|TFCP2_MOUSE	0.9978	2	2	LFTNFSGADLLK
sp|Q3TQB2|FXRD1_MOUSE	0.9976	2	2	TIDM[147]SPFLFTR
sp|Q9D1H6|HRP20_MOUSE	0.9976	2	2	IAQEYYLELK
sp|Q9D2X5|K0892_MOUSE	0.9976	2	2	GLFSFFQGR
sp|Q9CQ02|COMD4_MOUSE	0.9971	2	2	ELLGQGIDYEK
sp|Q80UU2|RPP38_MOUSE	0.9969	1	2	VPSLNVPWLPDR
sp|Q9DBS5|KLC4_MOUSE	0.9969	1	2	DHPAVAATLNNLAVLYGK
sp|P02468|LAMC1_MOUSE	0.9966	1	2	LSAEDLVLEGAGLR

sp|Q64152|BTF3_MOUSE	0.9963	2	2	TATADDKKLQFSLK
sp|Q8BRN9|C2D1B_MOUSE	0.9963	1	2	GM[147]NLPAPPGVTPDDLDAFVR
sp|P19182|IFRD1_MOUSE	0.9961	2	2	VLYEFVLER
sp|Q91Z38|TTC1_MOUSE	0.9958	2	2	AIQLNPTYIR
sp|Q9D8T0|FAM3A_MOUSE	0.9958	2	2	IVSGAANVIGPK
sp|O09111|NDUBB_MOUSE	0.9954	2	2	EVNGLPIM[147]ESNYFDPSK
sp|Q9CYA0|CREL2_MOUSE	0.9949	2	2	YEFSEIR
sp|Q6ZQF0|TOPB1_MOUSE	0.9942	2	2	NLTVALANSSR
sp|Q8CI70|LRC20_MOUSE	0.9933	2	2	FM[147]TTFNQLR
sp|Q7TSG2|CTDP1_MOUSE	0.9931	2	2	VLTQLVLSPDAPDR
sp|Q8BRK8|AAPK2_MOUSE	0.9923	1	2	IADFGLSNM[147]M[147]SDGEFLR
sp|O35459|ECH1_MOUSE	0.9913	1	2	EVDM[147]GLAADVGTLQR
sp|P17095|HMGA1_MOUSE	0.9913	1	2	KQPPVSPGTALVGSQK
sp|Q9CQ26|STABP_MOUSE	0.9913	1	2	NEFTITHVLIPR
sp|Q9CRB2|NHP2_MOUSE	0.9913	1	2	ELLVNLNPIAQPLASR
sp|Q9D0I4|STX17_MOUSE	0.9913	1	2	VAGIAAALGGGVLGFTGGK
sp|Q8BW94|DYH3_MOUSE	0.9908	2	2	VFLEALNNNIR
sp|P70353|NFYC_MOUSE	0.9904	1	2	M[147]ISAEAPVLFAK
sp|P60762|MO4L1_MOUSE	1	2	2	VDPTVENEETFM[147]NR
sp|Q8BLY7|HPS6_MOUSE	1	2	2	LLSDLSNFTGAAR
sp|Q9DBZ1|IKIP_MOUSE	1	2	2	LLQTESSEFQGLQSK
sp|Q8C863|ITCH_MOUSE	0.9904	1	2	FIDTGFSLPFYK
sp|Q91W34|CP058_MOUSE	0.9999	2	2	ALVLETLNESR
sp|Q4VAA7|SNX33_MOUSE	0.9998	2	2	IAETYSIEM[147]GPR
sp|Q9DCT5|SDF2_MOUSE	0.9997	2	2	AM[147]EGIFM[147]KPSELLR
sp|Q9D287|SPF27_MOUSE	0.9996	2	2	EAAAALVEEETR
sp|Q9JKK1|STX6_MOUSE	0.9995	2	2	DQM[147]SASSVQALAER
sp|P97434|MPRIP_MOUSE	0.9993	2	2	LLAEETAATISAIEAMK
sp|Q3TRM4|PLPL6_MOUSE	0.9993	3	2	GDLIGVVEALTR
sp|Q9D1I5|MCEE_MOUSE	0.9988	2	3	M[147]ELLHPLGSDSPITGFLQK
sp|O55060|TPMT_MOUSE	0.9983	2	2	GALVAINPGDHDR
sp|Q64362|AKTIP_MOUSE	0.9983	2	2	IDTTSPLNPEAAVLYEK
sp|Q9Z2Q5|RM40_MOUSE	0.9983	2	2	VYTQVEFKR
sp|Q3UH68|LIMC1_MOUSE	0.9978	2	2	TSVPESIASAGTGSPSK
sp|Q8CE50|SNX30_MOUSE	0.9976	2	2	VEFDLPEYSVR
sp|Q8BQZ4|K1219_MOUSE	0.9973	2	2	EVPVIFIHPLNTGLFR
sp|Q99JY4|TRABD_MOUSE	0.9971	2	2	TVTQLVAEDGSR
sp|Q8VCR3|CF035_MOUSE	0.9966	1	2	GTM[147]ATAALPESGSSLALR
sp|Q9D892|ITPA_MOUSE	0.9931	3	2	IDLPEYQGEPDEISIQK
sp|A2RTL5|RSRC2_MOUSE	0.9913	1	2	NTAM[147]DAQEALAR
sp|O54916|REPS1_MOUSE	0.9913	1	2	LVAVAQSGFPLR
sp|Q8BKW4|ZCHC4_MOUSE	0.9913	1	2	YLSFIQLPLAQR
sp|Q8BU04|UBR7_MOUSE	0.9913	1	2	EDIQQFFEEFQSK
sp|Q9CXK8|NIP7_MOUSE	0.9913	1	2	LHVTALDYLAPYAK
sp|Q9D8Z1|ASCC1_MOUSE	0.9913	1	2	TFENFYFGSLR
sp|Q9ET47|ESPN_MOUSE	0.9913	1	2	SFNM[147]M[147]SPTGDNSELLAEIK
sp|Q9JI44|DMAP1_MOUSE	0.9913	1	2	TPEQVAEEEYLLQELR

sp|Q9WU81|SPX2_MOUSE	0.9913	1	2	EQGPEPEAISFLGALR
sp|P55302|AMRP_MOUSE	0.9913	1	2	IQEYNVLLDTLSR
sp|Q5SS80|DHR13_MOUSE	0.991	3	2	LLT[181]HLLLPR
sp|Q8BGI5|PEX26_MOUSE	0.9904	1	2	LSEAEELAVR
sp|O35144|TERF2_MOUSE	0.9977	2	2	ALSTAQDSEAAFAK
sp|Q80X71|T106B_MOUSE	0.997	2	2	GQENQLVALIPYSDQR
sp|Q8C0M9|ASGL1_MOUSE	0.9967	2	2	GLGGLILVNK
sp|Q69ZW3|EHBP1_MOUSE	0.9954	2	3	PK[142]PTSPNNLVNTVQEGETER
sp|P70428|EXT2_MOUSE	0.9914	1	2	YVDDAGVPVSSAISR
sp|P70445|4EBP2_MOUSE	0.9913	1	2	HAVGDEAQFEM[147]DI
sp|Q61827|MAFK_MOUSE	0.9913	1	2	EAGENAPVLSDDELVSM[147]SVR
sp|Q9WTK2|CDYL_MOUSE	0.9913	1	2	EVQSALSTAAADDSK
sp|P55937|GOGA3_MOUSE	0.9913	1	2	VADAAASLEQQLEQVK
sp|O35516|NOTC2_MOUSE	0.9904	1	2	EPLPPIVTFQLIPK
sp|P61205|ARF3_MOUSE	1	2	2	DAVLLVFANK
sp|Q61781|K1C14_MOUSE	1	2	2	VLDELTLAR
sp|Q9Z1K7|APC2_MOUSE	0.9993	2	2	LPVS[167]IPAPQR
sp|P09041|PGK2_MOUSE	0.9961	1	3	VSHVSTGGGASLELLEGK
sp|P62309|RUXG_MOUSE	0.9961	1	2	GNSIIMLEALER
sp|Q66JX5|FR1OP_MOUSE	0.9961	1	2	DLLVQTLENSGVLNR
sp|P62746|RHOB_MOUSE	0.9942	1	2	QVELALWDTAGQEDYDR
sp|Q9D1M7|FKB11_MOUSE	0.9942	1	2	DPLVIELGQK
sp|Q61474|MSI1H_MOUSE	0.9914	1	2	GFGFVTFMDQAGVDK

Table S2

protein	protein probability	Num unique peps	precursor ion charge	peptide sequence
sp|P68033|ACTC_MOUSE	1	9	2	AGFAGDDAPR
sp|Q64524|H2B2E_MOUSE	1	10	2	AMGIMNSFVNDIFER
sp|Q7TPR4|ACTN1_MOUSE	1	35	2	AGTQIENIEEDFR
sp|Q9WU78|PDC6I_MOUSE	1	33	2	ATLVKPTPVNVPVSQK
sp|Q62448|IF4G2_MOUSE	1	23	2	EWLTELFQQSK
sp|Q6PIC6|AT1A3_MOUSE	0.9951	4	2	GVGIISEGNETVEDIAAR
sp|P16110|LEG3_MOUSE	1	13	2	IQVLVEADHFK
sp|Q61206|PA1B2_MOUSE	1	2	2	IIVLGLLPR
sp|Q61941|NNTM_MOUSE	1	11	2	AVVLAANHFGR
sp|Q8BH74|NU107_MOUSE	1	13	2	AIYAALSGNLK
sp|Q9Z2I0|LETM1_MOUSE	1	9	2	ADDKLISEEGVDSLTVK
sp|Q921N6|DDX27_MOUSE	1	13	2	ALQEFDLALR
sp|Q6PAR5|GAPD1_MOUSE	1	12	2	AVETPPM[147]SSVNLLEGLSR
sp|Q9DBY8|NVL_MOUSE	1	13	2	AVANESGLNFISVK
sp|Q9WVL3|S12A7_MOUSE	1	13	2	DLQMFLYHLR
sp|P28271|ACOC_MOUSE	1	10	2	TSLSPGSGVVTYYLR
sp|Q9QZQ1|AFAD_MOUSE	1	12	2	LAAGDQLLSVDGR
sp|Q80TP3|UBR5_MOUSE	1	12	2	LLTATNLVTLPNSR

sp|Q8VED5|K2C79_MOUSE	0.9908	1	3	NKYEDEINKR
sp|P42859|HD_MOUSE	1	14	2	TLFGTNLASQFDGLSSNPSK
sp|P43247|MSH2_MOUSE	1	11	2	DSLIIIDELGR
sp|Q6P5H2|NEST_MOUSE	1	12	2	AGLELEQEVVGLEDPR
sp|Q64310|SURF4_MOUSE	1	9	2	GQNDLM[147]GTAEDFADQFLR
sp|Q60790|RASA3_MOUSE	1	11	2	FGDEFLGELR
sp|Q69ZN7|MYOF_MOUSE	1	9	2	ANVTVLDTQIR
sp|Q8BTI8|SRRM2_MOUSE	1	11	2	IPAASAAAM[147]NLASAR
sp|Q921G8|GCP2_MOUSE	1	11	2	ILPVAASYSTVTR
sp|Q6P2K6|P4R3A_MOUSE	1	9	2	AESDGSLLLESK
sp|Q91ZU6|BPA1_MOUSE	1	15	2	AGNDLIESSEGEEASNLQYK
sp|Q3TLH4|BA2D1_MOUSE	1	9	2	ESVTDYTTPSSSLPNTVATNNAK
sp|Q99K01|PDXD1_MOUSE	1	11	2	AVPVSNIAPAAVGR
sp|P48722|HS74L_MOUSE	1	11	2	EDINSIEIVGGATR
sp|Q07113|MPRI_MOUSE	1	8	2	LASM[147]QLDYR
sp|Q62383|SPT6H_MOUSE	1	9	2	IDTASLGDSTDSYIEVLDGSR
sp|Q6P549|SHIP2_MOUSE	1	10	2	ALQDM[147]SSTAPPAPLQPSIR
sp|Q8R0Y6|FTHFD_MOUSE	1	7	2	ANATEFGLASGVFTR
sp|Q8VHE0|SEC63_MOUSE	1	10	2	LIM[147]VLAGASEFDPQYNK
sp|Q3TZZ7|ESYT2_MOUSE	1	7	2	ALALLEDEEQAVR
sp|Q9CY27|GPSN2_MOUSE	1	8	2	LPVGTTATLYFR
sp|P53986|MOT1_MOUSE	1	4	2	AAQSPQQHSSGDPTEEESPV
sp|Q6Q899|DDX58_MOUSE	1	9	2	DNVAELEQVVYKPQK
sp|Q9DBT5|AMPD2_MOUSE	1	10	2	SAPYEFPEESPIEQLEER
sp|P46425|GSTP2_MOUSE	0.9995	1	2	AFLSSPEHVNRPINGNGK
sp|Q9EPK7|XPO7_MOUSE	1	9	2	AALSGSYVNFGVFR
sp|Q9ERA6|TFP11_MOUSE	1	7	2	AVSSNVGAYM[147]QPGAR
sp|P97386|DNLI3_MOUSE	1	7	2	HVLDALDPNAYEAFK
sp|Q8BI84|MIA3_MOUSE	1	6	2	ELEGLLEDMSIR
sp|Q9D2M8|UB2V2_MOUSE	0.9998	6	2	WTGM[147]IIGPPR
sp|Q61703|ITIH2_MOUSE	1	3	2	IQPSGGTNINEALLR
sp|Q8BH24|TM9S4_MOUSE	1	6	2	ITEEYYVHLIADNLPVATR
sp|Q91YR7|PRP6_MOUSE	1	6	2	LSQVSDSVSGQTVVDPK
sp|Q9ERG2|STRN3_MOUSE	1	6	2	AYIASAGADALAK
sp|Q9CR68|UCRI_MOUSE	0.9999	2	2	LQVTNVLSQPLTQATVK
sp|P08775|RPB1_MOUSE	1	5	2	INISQVIAVVGQQNVEGK
sp|Q61263|SOAT1_MOUSE	1	6	2	LLAAEAEELKPLFM[147]K
sp|Q8BPM2|M4K5_MOUSE	1	7	2	LISENTEGSAQAPQLPR
sp|Q99KD5|UN45A_MOUSE	1	3	2	ASFITANGVSLLK
sp|Q9D0A3|CO038_MOUSE	1	6	2	VNTGFLM[147]SSYK
sp|Q9DBC3|FTSJ2_MOUSE	1	8	2	IHAFVQDTTLSEPR
sp|O35678|MGLL_MOUSE	1	3	2	GAYLLM[147]ESSR
sp|Q8BX70|VP13C_MOUSE	1	7	2	SLDVFNIILVR
sp|Q8BYW9|AER61_MOUSE	1	5	2	AFTDYDVIHLK
sp|Q924Z4|LASS2_MOUSE	1	5	2	AGTLIM[147]ALHDASDYLLESAK

sp|Q9Z160|COG1_MOUSE	1	8	2	ALQLLYDLR
sp|O08759|UBE3A_MOUSE	1	6	2	M[147]M[147]ETFQQLITYK
sp|P22892|AP1G1_MOUSE	1	6	2	AM[147]ELSFALVNGNNIR
sp|Q52KI8|SRRM1_MOUSE	1	6	2	DSSVQEATSTSDILK
sp|Q6PGH2|HN1L_MOUSE	1	4	2	GSGIFDESTPVQTR
sp|Q80U72|LAP4_MOUSE	1	7	2	SLEELLLDANQLR
sp|Q8BVG4|DPP9_MOUSE	1	4	2	ELVQPFSSLFPK
sp|Q8R3S6|EXOC1_MOUSE	1	6	2	ALQEGDLVSSR
sp|Q9D4H1|EXOC2_MOUSE	1	6	2	ASNTADTLFQEVLGR
sp|O54988|SLK_MOUSE	1	6	2	AGNILFTLDGDIK
sp|P16056|MET_MOUSE	1	5	2	GDLTIANLGTSEGR
sp|O35382|EXOC4_MOUSE	1	5	2	FIQEIEHALGLGPAK
sp|P39053|DYN1_MOUSE	1	4	2	SSVLENFVGR
sp|P39447|ZO1_MOUSE	1	5	2	LAGGNDVGIFVAGVLEDSPAAK
sp|Q7TSC1|BAT2_MOUSE	1	5	2	AVGTPGANAGGAGPGISAM[147]SR
sp|Q8BU03|PWP2_MOUSE	1	3	2	AGQLLPVVQFLQK
sp|Q8BYH7|TBC17_MOUSE	1	5	2	IFSGGLSPGLR
sp|Q8CCB4|VPS53_MOUSE	1	6	2	M[147]VLLDLPSIGSQVVR
sp|Q8K368|FANCI_MOUSE	1	6	2	FVSDLLTALFR
sp|Q8R5L3|VPS39_MOUSE	1	8	2	AINLLPANTQINDIR
sp|Q99NH0|ANR17_MOUSE	1	6	2	NVSDYTPLSLAASGGYVNIIK
sp|Q9DC40|TELO2_MOUSE	1	6	2	LLGDLPDELLEAR
sp|Q9QX47|SON_MOUSE	1	5	2	AGIEGPLLASEVER
sp|Q9R0L6|PCM1_MOUSE	1	7	2	ALYALQDIVSR
sp|P83741|WNK1_MOUSE	1	5	2	IGDLGLATLK
sp|Q8CJG0|I2C2_MOUSE	1	5	2	YAQGADSVEPM[147]FR
sp|P17897|LYZ1_MOUSE	0.9976	2	2	STDYGIFQINSR
sp|P03911|NU4M_MOUSE	1	5	2	IILPSLM[147]LLPLTWLSSPK
sp|P45377|ALD2_MOUSE	1	4	3	AVQREDLFIVSK
sp|P97452|BOP1_MOUSE	1	4	2	VNVDPEDLIPK
sp|Q3U487|HECD3_MOUSE	1	4	2	AGLPLPAALAFVPR
sp|Q6PF93|PK3C3_MOUSE	1	5	2	DGDESSPILTSFELVK
sp|Q6PR54|RIF1_MOUSE	1	7	2	TIGDLSTLTASEIK
sp|Q8BIG7|CMTD1_MOUSE	1	2	2	PGGVLAVLR
sp|Q8BUV3|GEPH_MOUSE	1	5	2	DLVQDPSLLGGTISAYK
sp|Q8VBZ3|CLPT1_MOUSE	1	4	2	NLLTGETEADPEM[147]IK
sp|Q9D8V0|HM13_MOUSE	1	3	2	QYQLLFTQGSGENK
sp|Q9WV70|NOC2L_MOUSE	1	3	2	SIAFPELVLPTVLQLK
sp|Q99KH8|STK24_MOUSE	1	7	2	KTSYLTELIDR
sp|P01027|CO3_MOUSE	0.9999	3	2	SSVAVPYVIVPLK
sp|Q8BIV3|RNBP6_MOUSE	0.9985	2	2	EGFVEYTEQVVK
sp|O54827|AT10A_MOUSE	0.9919	2	2	ASPSPSLVIDGR
sp|O35604|NPC1_MOUSE	1	5	2	LQEETLDQQLGR
sp|O70579|PM34_MOUSE	1	4	2	LSSLDVFIIGAIAK
sp|P58021|TM9S2_MOUSE	1	5	2	RPSENLGQVLFGER

sp|Q3UDW8|HGNAT_MOUSE	1	2	2	ADPLSADYQPETR
sp|Q61464|ZN638_MOUSE	1	6	2	DVTVLSM[147]AEEQDLQQER
sp|Q6PIP5|NUDC1_MOUSE	1	6	2	LPTDVTAYDNR
sp|Q8VDF2|UHRF1_MOUSE	1	6	2	YDDYPEHGVDIVK
sp|Q91V04|TRAM1_MOUSE	1	3	2	LDFSTGNFNVLAVR
sp|Q9DBF1|AL7A1_MOUSE	1	5	2	GAPTTSLVSVAVTK
sp|Q9QY36|ARD1A_MOUSE	1	4	2	YYADGEDAYAM[147]K
sp|Q91W97|HKDC1_MOUSE	0.9956	2	2	M[147]ISGLYM[147]GELVR
sp|P31786|ACBP_MOUSE	1	5	2	TYVEKVDELKK
sp|P41216|ACSL1_MOUSE	1	2	2	LM[147]ITGAAPVSATVLTFLR
sp|P58404|STRN4_MOUSE	1	5	2	ALIASAGADALAK
sp|Q0VGY8|TANC1_MOUSE	1	7	2	ANFQEIISALPFVK
sp|Q3TCJ1|F175B_MOUSE	1	3	2	AIYQVYNALQEK
sp|Q3UVK0|ERMP1_MOUSE	1	5	2	AFINLEAAGVGGK
sp|Q5H8C4|VP13A_MOUSE	1	4	2	ALVGGAVGGLAGAASK
sp|Q60953|PML_MOUSE	1	4	2	DNSVSSFLDSTR
sp|Q6P9Q6|FKB15_MOUSE	1	5	2	EVATDGLLQGNSR
sp|Q80Y81|RNZ2_MOUSE	1	4	2	LDNIFLTR
sp|Q8C8R3|ANK2_MOUSE	1	3	2	VVTEEVTTTTTTITEK
sp|Q8K1X1|BRWD2_MOUSE	1	3	2	LLLDPDFSLLQR
sp|Q8R4G6|MGT5A_MOUSE	1	4	2	TLAVLLDNILQR
sp|Q8VDC0|SYLM_MOUSE	1	4	2	AM[147]QDALADLPEWYGIK
sp|Q91W86|VPS11_MOUSE	1	3	2	GNYPVTGLAFR
sp|Q99PG2|OGFR_MOUSE	1	3	2	QSALDYFLFAVR
sp|Q9EPU4|CPSF1_MOUSE	1	4	2	VLVDSSFGQPTTQGEVR
sp|Q9ERG0|LIMA1_MOUSE	1	5	2	SQDVGFWEGEVVR
sp|Q9ET30|TM9S3_MOUSE	1	4	2	DAFVYAIK
sp|Q9JIX8|ACINU_MOUSE	1	4	2	KVTLGDTLTR
sp|P46467|VPS4B_MOUSE	1	4	2	GILLFGPPGTGK
sp|Q922W5|P5CR1_MOUSE	0.9999	2	2	LGAQALLGAAK
sp|O35609|SCAM3_MOUSE	1	3	2	AQQEFAAGVFSNPAVR
sp|P11688|ITA5_MOUSE	1	3	2	VTAPLEAEYSGLVR
sp|P81117|NUCB2_MOUSE	1	3	2	AATADLEQYDR
sp|Q0KL02|TRIO_MOUSE	1	5	2	DNFDAFYSEVAELGR
sp|Q3TMX7|QSOX2_MOUSE	1	5	2	EGSDAVWLLDSGSVR
sp|Q3U186|SYRM_MOUSE	1	2	2	GGVTFLEDVLNEVQSR
sp|Q3UMF0|COBL1_MOUSE	1	3	2	DYQAQEPLDLTK
sp|Q6ZQ93|UBP34_MOUSE	1	10	2	SFLLLAASTLLK
sp|Q8BTY8|SCFD2_MOUSE	1	3	2	SQIAVNDVFM[147]ALR
sp|Q8BXN9|TM87A_MOUSE	1	3	2	ADEIESYLENLK
sp|Q8C0L8|COG5_MOUSE	1	3	2	GALEAYVQSVR
sp|Q8C754|VPS52_MOUSE	1	3	2	FLEQLQELDAK
sp|Q8CBQ5|P4K2B_MOUSE	1	3	2	IAAIDNGLAFPFK
sp|Q8K2C9|PTAD1_MOUSE	1	3	3	VELSDVQNPAISITDNVLHFK
sp|Q8R0A0|T2FB_MOUSE	1	4	3	VVTTNYKPVANHQYNIEYER

sp|Q8R5J9|PRAF3_MOUSE	1	2	2	TPM[147]GIILDALEQQEDNINK
sp|Q8VEL2|MTMRE_MOUSE	1	2	2	AATPSPSGAIGGLLEQFAR
sp|Q922U1|PRPF3_MOUSE	1	5	2	LFEAVEEGR
sp|Q99LB7|SARDH_MOUSE	1	3	2	DPSGGPVSLDFVK
sp|Q9CQJ6|DENR_MOUSE	1	3	2	QETGITEGQGPVGEEEEK
sp|Q9D853|METLA_MOUSE	1	3	2	SGNTVAALVFQK
sp|Q9WV68|DECR2_MOUSE	1	5	2	VAFITGGGSGIGFR
sp|Q61411|RASH_MOUSE	1	3	2	LVVVGAGGVGK
sp|Q3UV17|K22O_MOUSE	0.99	1	2	AQYEDIAQK
sp|Q8K0V4|CNOT3_MOUSE	1	3	2	M[147]LDNDSILVDAIR
sp|Q921C5|BICD2_MOUSE	1	4	2	VGLLATLQDTQK
sp|Q811J3|IREB2_MOUSE	0.9999	3	2	EGIPLIILAGK
sp|P00397|COX1_MOUSE	0.9983	2	2	M[147]IGAPDM[147]AFPR
sp|Q8BZ98|DYN3_MOUSE	0.9964	2	2	SSVLENFVGR
sp|Q9ERY9|ERG28_MOUSE	0.9955	2	2	YLEAEPVSR
sp|O08784|TCOF_MOUSE	1	3	2	AGAVTSSASLSSPALAK
sp|O35657|NEUR1_MOUSE	1	3	2	GTLLAFAEAR
sp|P03888|NU1M_MOUSE	1	3	2	GPNIVGPYGILQPFADAM[147]K
sp|P70206|PLXA1_MOUSE	1	4	2	FVDDLFETIFSTAHR
sp|Q3UMC0|SPAT5_MOUSE	1	6	2	ALANESGLNFLAIK
sp|Q5DTT3|CJ018_MOUSE	1	4	2	VIPILPALSYALLEAK
sp|Q5RJG1|NOL10_MOUSE	1	3	2	DLENLGLTHLIGSPFLR
sp|Q68FF6|GIT1_MOUSE	1	3	2	SLSSPTDNLELSAR
sp|Q80YV3|TRRAP_MOUSE	1	5	2	NFIQTILTSLIEK
sp|Q8BM72|HSP13_MOUSE	1	4	2	IFTPEELEAEVGR
sp|Q8R151|ZNFX1_MOUSE	1	5	2	INVFDFGQWPSK
sp|Q8VCR7|ABHEB_MOUSE	1	3	2	FSVLLLHGIR
sp|Q91X52|DCXR_MOUSE	1	4	2	GVPGAIVNVSSQASQR
sp|Q9D8N2|FAM45_MOUSE	1	3	2	M[147]M[147]ESYIAVLTK
sp|Q9QWT9|KIFC1_MOUSE	1	4	2	LTYLLQNSLGGSAK
sp|Q9Z2G6|SE1L1_MOUSE	1	3	2	AADM[147]GNPVGQSGLGM[147]AYLYGR
sp|P10648|GSTA2_MOUSE	1	3	2	SHGQDYLVGNR
sp|Q3B7Z2|OSBP1_MOUSE	1	4	2	IPM[147]PVNFNEPLSM[147]LQR
sp|Q8BLR2|CPNE4_MOUSE	0.9999	2	2	DIVQFVPFR
sp|P28028|BRAF1_MOUSE	0.9999	3	2	M[147]LNVTAPTPQQLQAFK
sp|Q8K4L0|DDX54_MOUSE	0.9997	3	2	AGLTEPVLIR
sp|Q6GQT1|A2MP_MOUSE	0.9992	3	2	M[147]VSGFIPLKPTVK
sp|Q8BFR1|ZCCHL_MOUSE	0.9989	2	2	FLLQEVELR
sp|O35621|PMM1_MOUSE	0.994	1	2	NGM[147]LNVSPIGR
sp|Q9CZX7|TM55A_MOUSE	0.9917	2	2	ISSVGSALPR
sp|O88487|DC1I2_MOUSE	1	3	2	EAAVSVQEESDLEK
sp|P52875|TM165_MOUSE	1	3	2	M[147]SPDEGQEELEEVQAELK
sp|P97478|COQ7_MOUSE	1	2	2	IYAGQM[147]AVLGR
sp|Q2HXL6|EDEM3_MOUSE	1	3	2	FTGATIFEEYAR
sp|Q3THK3|T2FA_MOUSE	1	3	2	IYQEEEM[147]PESGAGSEFNR

sp|Q3UHJ0|AAK1_MOUSE	1	4	2	AGQTQPNPGILPIQPALTPR
sp|Q60596|XRCC1_MOUSE	1	3	2	HFFLYGEFPGDER
sp|Q60855|RIPK1_MOUSE	1	3	2	AEYNEVLLEEGK
sp|Q80TE0|RPAP1_MOUSE	1	4	2	VSSLLLPVPK
sp|Q80U70|SUZ12_MOUSE	1	5	2	ETLTTELQTR
sp|Q811D0|DLG1_MOUSE	1	3	2	QVTPDGESDEVGVIPSK
sp|Q8BI72|CARF_MOUSE	1	4	2	GSASFVSSLLK
sp|Q8BM55|TM214_MOUSE	1	4	2	SQSVFTGNPSVWLK
sp|Q8BT07|CEP55_MOUSE	1	5	2	YSSSSLFEQLEEK
sp|Q8BZ20|PAR12_MOUSE	1	4	2	LGLSSDLVSR
sp|Q8CGU1|CACO1_MOUSE	1	3	2	AALLGEELASAAGAR
sp|Q8K0Q5|RHG18_MOUSE	1	4	2	IEEGSLETEGLLR
sp|Q8R2M2|TDIF2_MOUSE	1	3	2	LTSSSIDPGLNIK
sp|Q8VIM9|IRGQ_MOUSE	1	3	2	PLPQGDVTALFLGPPGSGK
sp|Q91VW5|GOGA4_MOUSE	1	3	2	SLLEELASQLDSR
sp|Q91WR3|ASCC2_MOUSE	1	3	2	HNIFQNDEFDVFSR
sp|Q91YK2|RRP1B_MOUSE	1	3	2	LGALPDSSSDLPVQK
sp|Q99J27|ACATN_MOUSE	1	4	2	YTAGPQPLNIFYK
sp|Q99KB8|GLO2_MOUSE	1	3	2	HVEPGNAAIQEK
sp|Q99LB2|DHRS4_MOUSE	1	4	2	LAEDGAHVVVSSR
sp|Q99M28|RNPS1_MOUSE	1	3	2	DHIMEIFSTYGK
sp|Q9D2N9|VP33A_MOUSE	1	4	2	IISAAFEER
sp|Q9DBR0|AKAP8_MOUSE	1	3	2	TVEFLQEYIINR
sp|Q9JJA2|COG8_MOUSE	1	3	2	ISQFLQVLETDLYR
sp|Q9WTR1|TRPV2_MOUSE	1	3	2	GVPEELTGLLEYLR
sp|Q9Z2V5|HDAC6_MOUSE	1	3	2	LVDALM[147]GAEIR
sp|Q64261|CDK6_MOUSE	0.9917	1	2	VQTSEEGM[147]PLSTIR
sp|P63011|RAB3A_MOUSE	1	2	2	M[147]SESLDTADPAVTGAK
sp|Q04692|SMRCD_MOUSE	0.9999	2	2	QEQLYSGLFNR
sp|Q3U308|CP084_MOUSE	0.9999	3	2	DLPSLDPLPPYVLAEAQLR
sp|Q8VHE6|DYH5_MOUSE	0.9999	7	2	RTDLNYIAAVDLK
sp|P24638|PPAL_MOUSE	0.9998	2	2	LQGGVLLAQILK
sp|Q8BZQ7|ANC2_MOUSE	0.9998	2	2	IEELFSIIR
sp|Q99KR7|PPIF_MOUSE	0.9998	3	2	HVGPGVLSM[147]AN
sp|P83510|TNIK_MOUSE	0.9993	2	2	NIATYYGAFIK
sp|P62858|RS28_MOUSE	0.9984	2	2	EGDVLTLLESER
sp|Q8R2U4|ME11A_MOUSE	0.9978	2	2	TAGLSLLAEER
sp|P45878|FKBP2_MOUSE	0.9968	2	2	LVIPSELGYGER
sp|P08032|SPTA1_MOUSE	0.9967	3	2	FLTLLAK
sp|Q8C7B8|ZSWM4_MOUSE	0.9943	2	2	LQPALTSR
sp|O35682|MYADM_MOUSE	1	2	2	TTITTTTSSSTTVGSAR
sp|O70481|UBR1_MOUSE	1	2	2	INSENAEALAQLLTLAR
sp|O88746|TOM1_MOUSE	1	4	2	SSPDLTGVVAVYEDLR
sp|P48771|CX7A2_MOUSE	1	2	2	LFQEDNGM[147]PVHLK
sp|P62313|LSM6_MOUSE	1	2	2	GNNVLYISTQK

sp|P97314|CSRP2_MOUSE	1	2	2	GFGYGQGAGALVHAQ
sp|Q00547|HMMR_MOUSE	1	3	2	DVTAQLESVQEK
sp|Q3TVI8|PBIP1_MOUSE	1	2	2	QEGLALFGVELAPVR
sp|Q3UVG3|F91A1_MOUSE	1	3	2	VQGDYFETLLYK
sp|Q60772|CDN2C_MOUSE	1	3	2	DGTGFAVIHDAAR
sp|Q64FW2|RETST_MOUSE	1	3	2	ATVQSVLLDSAGR
sp|Q6DVA0|LEMD2_MOUSE	1	3	2	ELQALGFQPGPITDTTR
sp|Q6NVE8|WDR44_MOUSE	1	2	2	LLASAGQDNIVR
sp|Q6NZN0|RBM26_MOUSE	1	3	2	VIQPLVQQPILPVVK
sp|Q80XU3|NUCKS_MOUSE	1	2	3	TPSPKEEDEEAESPPEKK
sp|Q8BFW7|LPP_MOUSE	1	3	2	M[147]LYDM[147]ENPPADDYFGR
sp|Q8BTZ5|ANR46_MOUSE	1	2	2	LLESLEEQEVK
sp|Q8BUY5|CC001_MOUSE	1	2	2	AGAVAADSPGFVEDR
sp|Q8C3I8|BRP16_MOUSE	1	3	2	DQGAYLILR
sp|Q8C9B9|DIDO1_MOUSE	1	3	2	TASPLEHILQTLFGK
sp|Q8K3X4|EAP1_MOUSE	1	2	2	YGLSAAAAAAAAAAAVEQR
sp|Q8R307|VPS18_MOUSE	1	3	2	LGALQGDPDALTLYR
sp|Q8R3P6|CO044_MOUSE	1	3	2	AALAFGFLDLLK
sp|Q8R3V5|SHLB2_MOUSE	1	2	2	LASDAGIFFTR
sp|Q8R5H6|WASF1_MOUSE	1	3	2	IENDVATILSR
sp|Q8VD04|GRAP1_MOUSE	1	4	2	TQTGDSSSVSSFSYR
sp|Q91VS7|MGST1_MOUSE	1	2	2	IYHTIAYLTPLPQPNR
sp|Q91VX9|TM168_MOUSE	1	2	2	TVDIEEADPPQLGDFTR
sp|Q91VY9|ZN622_MOUSE	1	3	3	VHSFFIPDIEYLSDLK
sp|Q922S8|KIF2C_MOUSE	1	4	2	FSLVDLAGNER
sp|Q922Y1|UBXN1_MOUSE	1	2	2	GEEPGQDQDPVQLLSGFPR
sp|Q923D5|WBP11_MOUSE	1	2	2	AVSILPLLGHGVPR
sp|Q9CQU3|RER1_MOUSE	1	2	2	LGQIYQSWLDK
sp|Q9CYK1|SYWM_MOUSE	1	3	2	YGEFFPLPK
sp|Q9D0M0|EXOS7_MOUSE	1	3	3	VYIVHGVQEDLR
sp|Q9D1C8|VPS28_MOUSE	1	2	2	AM[147]DEIQPDLR
sp|Q9DB96|NGDN_MOUSE	1	2	2	ASGASLQGHPAVLR
sp|Q9DC29|ABCB6_MOUSE	1	2	2	APDIILLDEATSALDTSNER
sp|Q9DCD2|SYF1_MOUSE	1	2	2	FYEDNGQLDDAR
sp|Q9QUJ7|ACSL4_MOUSE	1	4	2	SDQSYVISFVVPNQK
sp|Q9QWF0|CAF1A_MOUSE	1	2	2	LVGGQGPIDSFLR
sp|Q9QY06|MYO9B_MOUSE	1	3	2	TPIESLFIEATER
sp|Q9Z1T6|FYV1_MOUSE	1	3	2	DYFPEQIYWSPLLNK
sp|Q9Z2A5|ATE1_MOUSE	1	3	2	SLEDLIFQSLPENASHK
sp|Q9Z2L7|CRLF3_MOUSE	1	2	2	LIEHGVNTADDLVR
sp|O35638|STAG2_MOUSE	0.9999	2	2	M[147]YSDAFLNDSYLK
sp|P25425|PO2F1_MOUSE	1	3	2	LYGNDFSQTTISR
sp|P42232|STA5B_MOUSE	1	4	2	IQAQFAQLGQLNPQER
sp|P61620|S61A1_MOUSE	1	5	3	GM[147]EFEGAIIALFHLLATR
sp|P84075|HPCA_MOUSE	0.997	1	2	IYANFFPYGDASK

sp|P15116|CADH2_MOUSE	0.9999	3	2	LNGDFAQLNLK
sp|P70700|RPA2_MOUSE	0.9999	3	2	ISLTIVDAVISPPSVPK
sp|Q60928|GGT1_MOUSE	0.9999	2	2	FVDVSQVIR
sp|Q8CI95|OSB11_MOUSE	0.9999	3	2	SVILHLLSQLK
sp|Q91V01|PCAT3_MOUSE	0.9999	2	2	LATSLGASEQALR
sp|Q9D0P8|RAYL_MOUSE	0.9999	2	2	SQTSGISLPGVLVGTK
sp|Q9JJL8|SYSM_MOUSE	0.9999	2	2	VLIALLESNQQK
sp|Q9QZ08|NAGK_MOUSE	0.9999	2	2	LGILTHLYR
sp|Q02780|NFIA_MOUSE	0.9999	2	2	LDLVM[147]VILFK
sp|Q91W69|EPN3_MOUSE	0.9999	2	2	NIVHNYSEAEIK
sp|Q9CTG6|AT132_MOUSE	0.9996	3	2	ELSLLGLLVM[147]R
sp|Q9R0Q9|MPU1_MOUSE	0.9996	2	2	GLGLGIVAGSLLVK
sp|Q60848|HELLS_MOUSE	0.9995	2	2	LISQIQPEVNR
sp|Q91ZN5|S35B2_MOUSE	0.9994	2	2	APDEVLLAPR
sp|Q9WUU9|MCM3A_MOUSE	0.9994	3	2	LPLYLPQTLVSFPDSIK
sp|P00848|ATP6_MOUSE	0.9993	2	2	LSM[147]AIPLWAGAVITGFR
sp|Q8BTI7|ANR52_MOUSE	0.9993	2	2	DAVSPFSFSLLK
sp|Q9JHS3|MAPIP_MOUSE	0.9993	2	2	NGNQAFNEDSLK
sp|Q3TYS2|CQ062_MOUSE	0.9991	2	2	DIQDVNVEEEK
sp|O88848|ARL6_MOUSE	0.999	3	2	IPILFFANK
sp|Q80TZ9|RERE_MOUSE	0.999	2	2	VDSFFYILGYNPETR
sp|P97412|LYST_MOUSE	0.9988	5	2	DLSGLLVSAFK
sp|Q9CPP0|NPM3_MOUSE	0.9988	2	2	DHDNQEIAVPVANLR
sp|Q8BFS6|CSTP1_MOUSE	0.9986	2	2	LTEQAVEAINK
sp|Q8R1S0|COQ6_MOUSE	0.9981	2	2	ILLLEAGPK
sp|Q8VHN7|GPR98_MOUSE	0.998	4	2	FAEPCVLR
sp|Q9R0M6|RAB9A_MOUSE	0.9976	2	2	EPESFPFVILGNK
sp|Q8BYU6|TOIP2_MOUSE	0.9957	5	2	FESLPAGSTLIFYK
sp|Q9WTL7|LYPA2_MOUSE	0.9956	2	2	FGALTAEK
sp|Q9Z2R6|U119A_MOUSE	0.9949	1	2	QPIGPEDVLGLQR
sp|Q9CQT2|RBM7_MOUSE	0.9919	2	2	TLFVGNLETK
sp|Q9CY57|CA077_MOUSE	0.9917	1	2	EQLDNQLDAYM[147]SK
sp|P03930|ATP8_MOUSE	1	2	2	VSSQTFPLAPSPK
sp|P24610|PAX3_MOUSE	1	3	2	TTFTAEQLEELER
sp|P70302|STIM1_MOUSE	1	3	2	YAEEELEQVR
sp|P70677|CASP3_MOUSE	1	4	2	LEFM[147]HILTR
sp|Q09143|CTR1_MOUSE	1	2	2	VIYAM[147]AEDGLLFK
sp|Q3UA37|QRIC1_MOUSE	1	3	2	EIQEAIAVANATTM[147]H
sp|Q3UGY8|BIG3_MOUSE	1	4	2	NLIDTLSTPLTGR
sp|Q3UW53|NIBAN_MOUSE	1	4	2	VLTSEEEYSLLSDK
sp|Q64430|ATP7A_MOUSE	1	5	2	QIEAVGFPAFIK
sp|Q8BHY8|SNX14_MOUSE	1	3	2	LVSLITLLR
sp|Q8BTG3|T11L1_MOUSE	1	3	2	AIFSVLDLM[147]K
sp|Q8C5W3|TBCEL_MOUSE	1	3	2	YYVDVPQEEVPFR
sp|Q8CIM8|INT4_MOUSE	1	3	2	FLQEVDFFQR

sp|Q91VZ6|SMAP1_MOUSE	1	3	2	LLYEANLPENFR
sp|Q9JLV1|BAG3_MOUSE	1	3	2	ELLALDSVDPEGR
sp|Q9QYC7|VKGC_MOUSE	1	3	2	DGLTGELGYLNPGVFTQSR
sp|Q9QYH6|MAGD1_MOUSE	1	3	2	ATEAVLWEALR
sp|Q9R0I7|YLPM1_MOUSE	1	3	2	VFSSEQGLGESSALSQSIIAAK
sp|P61028|RAB8B_MOUSE	0.9993	2	2	SSTNVEEAFFTLAR
sp|Q8JZR6|S4A8_MOUSE	0.9984	2	2	FLFILLGPVGK
sp|Q9CQK7|RWDD1_MOUSE	1	4	3	AKFDAELLEIKK
sp|P10922|H10_MOUSE	0.9999	2	2	YSDM[147]IVAAIQAEK
sp|Q3UUQ7|PGAP1_MOUSE	0.9998	3	2	AFFDLIDADTK
sp|Q8CHC4|SYNJ1_MOUSE	0.9998	3	2	VLDAYGLLGVLR
sp|Q8K370|ACD10_MOUSE	0.9998	4	2	LSLQPSEAIFLDDLGSNLK
sp|Q8BGZ2|F168A_MOUSE	0.9997	2	2	SIPSAIYPAPVAAPR
sp|Q922H1|ANM3_MOUSE	0.9997	3	2	QTVFLLEKPFPVK
sp|P58854|GCP3_MOUSE	0.9996	3	2	YLLLGQGDFIR
sp|Q9CQZ6|NDUB3_MOUSE	0.9996	3	2	M[147]ELPDYR
sp|P47713|PA24A_MOUSE	0.9995	3	2	DVPVVAILGSGGGFR
sp|Q99JP7|GGT7_MOUSE	0.9995	3	2	LPEDEPAPAAPLR
sp|O55242|OPRS1_MOUSE	0.9994	2	2	QYAGLDHELAFSR
sp|Q8K5B2|MCFD2_MOUSE	0.9994	2	2	DDDKNNDGYIDYAEFAK
sp|Q5U430|UBR3_MOUSE	0.9992	3	2	LDPDYFISSVFER
sp|Q9QZH6|ECSIT_MOUSE	0.9992	3	2	IFVHYPR
sp|Q9Z0J0|NPC2_MOUSE	0.9991	2	2	LPVKNEYPSIK
sp|Q6P8H8|ALG8_MOUSE	0.999	2	2	AILLAILPM[147]SLLSVEK
sp|Q8K4M5|COMD1_MOUSE	0.999	2	2	LSEVEESINR
sp|Q9CQB5|CISD2_MOUSE	0.9987	3	2	QLPVPDSITGFAR
sp|Q03173|ENAH_MOUSE	0.9986	2	2	VEDGSFPGGGNTGSVSLASSK
sp|Q9EPN1|NBEA_MOUSE	0.9984	3	2	EISNFEYLM[147]FLNTIAGR
sp|Q9R0Q4|MO4L2_MOUSE	0.9983	2	2	EYAVNEVVGGIK
sp|Q8VCI5|PEX19_MOUSE	0.9975	2	2	ELAEEEPHLVEQFQK
sp|Q80U78|PUM1_MOUSE	0.9973	1	2	SASSASSLFSPSSTLFSSSR
sp|Q6ZPE2|MTMR5_MOUSE	0.9964	2	2	GLLALLFPLR
sp|Q8CHT3|INT5_MOUSE	0.9957	2	2	EQPLLFELLK
sp|Q91XL9|OSBL1_MOUSE	0.9917	1	2	ITM[147]PVIFNEPLSFLQR
sp|Q80UG2|PLXA4_MOUSE	0.9911	1	2	FVDDLFETIFSTAHR
sp|A2AAJ9|OBSCN_MOUSE	0.9904	3	2	EDENFVCIR
sp|P97857|ATS1_MOUSE	0.99	1	2	GIGYFFVLQPK
sp|O89017|LGMN_MOUSE	1	2	2	DYTGEDVTPENFLAVLR
sp|Q3UFM5|NOM1_MOUSE	1	3	2	ELITEAQTQASGAGNK
sp|Q5PRF0|HTR5A_MOUSE	1	2	2	VLILEQLLNSIK
sp|Q5SUC9|SCO1_MOUSE	1	2	2	LVGLTGTKEEIDGVAR
sp|Q64282|IFIT1_MOUSE	1	3	2	ISEQVQFLDIK
sp|Q91WG2|RABE2_MOUSE	1	2	2	LQAELETSEQVQR
sp|Q99MU3|DSRAD_MOUSE	1	3	2	YLNTNPVGGLLEYAR
sp|Q9CR88|RT14_MOUSE	1	2	2	HLADHGLLSGVQR

sp|Q9D187|FA96B_MOUSE	1	2	2	SGERPVTAGEEDEEVPDSIDAR
sp|Q9Z0R9|FADS2_MOUSE	1	3	2	ALIDIVSSLK
sp|Q61771|KIF3B_MOUSE	1	2	2	HLIIENFIPLEEK
sp|O08601|MTP_MOUSE	0.9999	3	2	SGFTTANQVLGVSSK
sp|O35350|CAN1_MOUSE	0.9999	2	2	APSDLYQIILK
sp|O88879|APAF_MOUSE	0.9999	2	2	GSPLVVSLIGALLR
sp|Q3SXD3|HDDC2_MOUSE	0.9999	2	2	LQDFYDSTAGK
sp|Q3U5F4|YRDC_MOUSE	0.9999	2	2	LPESEPVEAASPER
sp|Q80XQ2|TBCD5_MOUSE	0.9999	2	2	TFPEM[147]QFFQQENVR
sp|Q8BKX6|SMG1_MOUSE	0.9999	4	2	AQDTFQTIEGIIR
sp|Q9CQ75|NDUA2_MOUSE	0.9999	2	2	TVSLNNLSADEVTR
sp|Q9DBA9|TF2H1_MOUSE	0.9999	2	2	M[147]LQEDPVLFQLYK
sp|Q9EQG9|C43BP_MOUSE	0.9999	2	2	DVLYLSAIR
sp|Q3TEL6|RN157_MOUSE	0.9999	2	2	VSYLLQEIYGIENK
sp|Q66T02|PKHG5_MOUSE	0.9998	3	2	SLGEVLLPVFER
sp|Q8R080|GTSE1_MOUSE	0.9998	2	2	VPQFSVGESPGGVTPK
sp|Q8VHL1|SETD7_MOUSE	0.9998	2	2	VYVADSLISSAGEGLFSK
sp|Q99LH1|NOG2_MOUSE	0.9998	2	2	VIDSSDVVVQVLDAR
sp|Q05793|PGBM_MOUSE	0.9997	5	2	VIPYFTQTPYSFLPLPTIK
sp|Q3UGP8|AG10B_MOUSE	0.9997	2	2	YFILPYIIYR
sp|Q9D4H2|GCC1_MOUSE	0.9997	2	2	TQLATLTSSLATVTQEK
sp|Q9Z1X9|CC45L_MOUSE	0.9997	2	2	LQEFLADM[147]GLPLK
sp|Q6IQX7|CHSS2_MOUSE	0.9996	2	2	LTVLLPLAAAER
sp|Q6PEV3|WIPF2_MOUSE	0.9996	2	2	GSSGGYGPGAAALQPK
sp|Q6XUX1|RIPK5_MOUSE	0.9996	2	3	SPLYGQLVDLGYLSSSHR
sp|Q6ZWZ2|UB2R2_MOUSE	0.9996	2	2	FPIDYPYSPPTFR
sp|P40201|CHD1_MOUSE	0.9927	2	2	M[147]LDILAEYLK
sp|Q5SWT3|S2535_MOUSE	0.9994	2	2	LGTYGLAESR
sp|Q91ZR1|RAB4B_MOUSE	0.9994	2	2	M[147]GSGIQYGDISLR
sp|P46414|CDN1B_MOUSE	0.9993	2	2	NLFGPVNHEELTR
sp|Q3U5Q7|CMPK2_MOUSE	0.9993	2	2	AFYSLGNYLVASEIAK
sp|Q9CQ86|CQ037_MOUSE	0.9993	2	2	EEYPGIEIESR
sp|P62311|LSM3_MOUSE	0.9992	2	2	GDGVVLVAPPLR
sp|Q5BLK4|ZCHC6_MOUSE	0.9992	2	2	NTEPVGQLWLGLLR
sp|Q8R550|SH3K1_MOUSE	0.9992	2	2	M[147]EPAVSSQAAIEELK
sp|P54116|STOM_MOUSE	0.9991	2	2	EASM[147]VITESPAALQLR
sp|Q501J2|F173A_MOUSE	0.9991	2	2	LQAELPVGAR
sp|Q3UDR8|YIPF3_MOUSE	0.999	2	2	DIPAVLPAAR
sp|Q9EPQ7|STAR5_MOUSE	0.999	2	2	SM[147]AEFYPNLQK
sp|Q9CYZ6|CS060_MOUSE	0.9989	2	2	DAPIATLVQR
sp|P28741|KIF3A_MOUSE	0.9988	2	2	SAKPETVIDSLLQ
sp|Q9CYA6|ZCHC8_MOUSE	0.9988	2	2	LVNYPGFNISTPR
sp|Q9R1S3|PIGN_MOUSE	0.9988	2	2	EATLPFLFTPFK
sp|Q9R207|NBN_MOUSE	0.9988	2	2	LLPAAGAAPGEPYR
sp|Q9JKX4|AATF_MOUSE	0.9987	2	2	ALLTTNQLPQPDVFPVFK

sp|Q5KU39|VPS41_MOUSE	0.9986	4	2	IVLLM[147]DFDSEK
sp|P0C1Q2|PDE11_MOUSE	0.9985	2	2	DISNDLDLTSLSYK
sp|Q76KJ5|RPA34_MOUSE	0.9985	2	2	EATLLASSSEAGGR
sp|Q9D850|TMM68_MOUSE	0.9985	2	2	TFLGDPIPYDPK
sp|Q9R0D8|WDR54_MOUSE	0.9985	2	2	TISALDLAPEVGK
sp|Q8K2F8|LS14A_MOUSE	0.9981	2	2	YEGILYTIDTENSTVALAK
sp|Q9CPV5|PMF1_MOUSE	0.9981	2	2	NQELADAVLAGR
sp|Q9DCI9|RM32_MOUSE	0.998	2	2	QQIGAQEGGPFR
sp|Q9CQ18|RNH2C_MOUSE	0.9978	2	2	HDADGLQASFR
sp|Q9D8Y1|T126A_MOUSE	0.9978	2	2	ILNVTQAR
sp|Q9WTK3|GPAA1_MOUSE	0.9976	2	2	YGVEALTLR
sp|P70444|BID_MOUSE	0.9975	2	2	IEPDSESQEEIIHNIAR
sp|Q07139|ECT2_MOUSE	0.9974	2	2	LPSVALLLNDLK
sp|Q8BMD6|CN101_MOUSE	0.9974	3	2	LPGTGIDPEVLLSEAIR
sp|Q9D600|PSF2_MOUSE	0.9974	2	2	TNLQPSESTQSQDF
sp|Q8BTJ4|ENPP4_MOUSE	0.9973	2	2	EVDDLIGDIVLK
sp|Q8QZX2|CD015_MOUSE	0.9973	2	2	TNPM[147]VFLSQFPLGK
sp|Q924L1|LTMD1_MOUSE	0.9972	2	2	LGIGQLTAQEVK
sp|Q7TSZ8|NACC1_MOUSE	0.9971	2	2	FSTPDLALNR
sp|Q61207|SAP_MOUSE	0.997	2	2	TVVTEAGNLLK
sp|Q9D023|BR44_MOUSE	0.9969	3	2	YSLVIIPK
sp|Q8K1A6|C2D1A_MOUSE	0.9967	2	2	SFDPVLEALSR
sp|Q9CPR1|RWDD4_MOUSE	0.9966	2	2	SIYEGDNSFR
sp|Q3TBW2|RM10_MOUSE	0.996	2	2	VFPSQVLKPFLENSK
sp|Q8BK75|CC075_MOUSE	0.9958	2	2	GQLVFLEGLK
sp|P50096|IMDH1_MOUSE	0.9954	1	2	NLIDAGVDGLR
sp|P63139|NFYB_MOUSE	0.9951	2	2	EQDIYLPIANVAR
sp|Q9R059|FHL3_MOUSE	0.9949	2	2	TLTQGGVTYR
sp|Q3ULF4|SPG7_MOUSE	0.9944	2	2	EGGFSAFNQLK
sp|Q80UZ2|SDA1_MOUSE	0.9943	1	2	DLLVQYATGK
sp|Q8VE19|MIO_MOUSE	0.9932	2	2	NLAIFDLR
sp|Q9JKK8|ATR_MOUSE	0.9931	3	2	FLDLIPQDTLAVASFR
sp|Q8CIG3|AOF1_MOUSE	0.9927	2	2	VLVTVPLAILQR
sp|Q3TDD9|KLRAQ_MOUSE	0.9917	2	2	EGLAQQVQQSLEK
sp|Q6PCM2|INT6_MOUSE	0.9917	1	2	NLQAEGLTTLGQSLR
sp|Q8K2F0|BRD3_MOUSE	0.9917	1	2	EYPDAQGFAADIR
sp|Q8R0J7|VP37B_MOUSE	0.9917	1	2	SLAEGNLLYQPQLDAQK
sp|Q9QUG2|POLK_MOUSE	0.9912	2	2	ASTVPAAISTAEEIFAIAK
sp|Q68EF0|RAB3I_MOUSE	0.9908	1	2	IDVLQAEVAALK
sp|Q7TPM1|BAT2L_MOUSE	0.99	1	2	LLSFSPEEFPTLK
sp|O35379|MRP1_MOUSE	1	2	2	LYAWELAFQDK
sp|P70399|TP53B_MOUSE	1	3	2	VITDVYYVDGTEVER
sp|Q4FZC9|SYNE3_MOUSE	1	2	2	AATLLEQVTSSVR
sp|Q6P8M1|TATD1_MOUSE	1	2	2	HQDDLQDVIER
sp|Q8BK03|FA73B_MOUSE	1	2	2	PAAAYEEALQLVK

sp|Q8BW10|NOB1_MOUSE	1	2	2	TDVFAPDYIAGVSPFAENDISSR
sp|Q99K74|MED24_MOUSE	1	2	2	VESLVALLNNSSEM[147]K
sp|Q9CQF4|CF203_MOUSE	1	2	2	SEQEEELESEPGVAK
sp|Q9Z2A7|DGAT1_MOUSE	1	2	2	LQDSLFSSDSGFSNYR
sp|P59016|VP33B_MOUSE	0.9999	2	2	AGLLTEQAPGDTLTAVESK
sp|Q5DU25|IQEC2_MOUSE	0.9999	2	2	LIEAFSQR
sp|Q8VDD9|PHIP_MOUSE	0.9999	2	3	YHDM[147]PDVIDFLVLR
sp|A2AR02|PPIG_MOUSE	0.9998	2	2	DFM[147]VQGGDFSEGNGR
sp|Q8C3X8|LMF2_MOUSE	0.9998	2	2	LFGSVEHLQLANSYGLFR
sp|P70188|KIFA3_MOUSE	0.9997	2	2	SLNANTDITSLAR
sp|Q9ER69|FL2D_MOUSE	0.9997	2	2	STM[147]VDPAINLFFLK
sp|Q9QZ73|DCNL1_MOUSE	0.9997	2	2	QFM[147]IFTQSSEK
sp|P58501|GCFC_MOUSE	0.9996	2	2	TLQELSIDGLLNR
sp|P22366|MYD88_MOUSE	0.9991	2	2	FALSLSPGVQQK
sp|P97480|EYA3_MOUSE	0.999	2	2	SNVGGLLSPQR
sp|Q0P678|ZCH18_MOUSE	0.999	2	3	ASQQAAAPQPAVPGQPQQGSFVAHK
sp|Q9CX00|K0174_MOUSE	0.999	2	2	ELDSGLAESVSTLIWAAPR
sp|Q61037|TSC2_MOUSE	0.9987	3	2	LGYLPYSLLFR
sp|P46938|YAP1_MOUSE	0.9985	2	2	GDSETDLEALFNAVM[147]NPK
sp|P62046|LRCH1_MOUSE	0.9985	2	2	NLESIDPQFTIR
sp|P97473|TRBP2_MOUSE	0.9985	2	2	TPISLLQEYGTR
sp|Q5PSV9|MDC1_MOUSE	0.9985	3	2	LGLPLLSPEFLLTGVLK
sp|Q9JKL4|CC060_MOUSE	0.9985	2	2	IEIVVVGTGNK
sp|P97300|NPTN_MOUSE	0.9984	2	3	KRPDEVPDDDEPAGPM[147]K
sp|Q99KY4|GAK_MOUSE	0.9984	2	2	IAVM[147]SFPAEGVESAIK
sp|P59672|ANS1A_MOUSE	0.9981	3	2	LLLNGFDDVR
sp|Q8VDR9|DOCK6_MOUSE	0.9979	2	2	VAELYLPLLSLAR
sp|Q80VQ1|LRRC1_MOUSE	0.9967	1	2	SLEELLLDANQLR
sp|Q9CXF7|CHD1L_MOUSE	0.9963	2	2	GIPTYIYYFPR
sp|Q9D820|U566_MOUSE	0.9962	2	2	FVLDSAFLEGGHEK
sp|Q8K2J4|CCD14_MOUSE	0.9952	3	2	NVSQTAEK
sp|P49769|PSN1_MOUSE	0.9937	2	2	NETLFPALIYSST
sp|Q3V1H1|CKAP2_MOUSE	0.9924	2	2	IEPITSPIENIISIYEK
sp|P70236|MP2K6_MOUSE	0.9923	2	2	ADDLEPIVELGR
sp|O35375|NRP2_MOUSE	0.9917	1	2	IFQANNDATEVVLNK
sp|P50427|STS_MOUSE	0.9917	1	2	VLAALDELGLAR
sp|P84089|ERH_MOUSE	0.9917	1	2	ADTQTYQPYNK
sp|Q5DTK1|CHSS3_MOUSE	0.9917	1	2	DNTVQGQQVYYPIIFSQYDPK
sp|Q8K4R9|DLGP5_MOUSE	0.9917	1	2	ANEILVQQGLESLTDR
sp|Q91YU8|SSF1_MOUSE	0.9917	1	2	TEEELQAILAAK
sp|Q9CQ39|MED21_MOUSE	0.9917	1	2	IQSALADIAQSQLK
sp|Q9Z0R4|ITSN1_MOUSE	0.9917	1	2	LQEIDVFNNQLK
sp|Q8VCF0|MAVS_MOUSE	0.9914	2	2	DTLWGLFNNLQR
sp|Q6TEK5|VKORL_MOUSE	0.9908	1	2	GFGLLGSIFGK
sp|Q9JIA7|SPHK2_MOUSE	0.9908	1	2	LLILVNPFGGR

sp|Q99LC9|PEX6_MOUSE	0.9902	3	2	LVFVGASEDR
sp|Q3U1G5|I20L2_MOUSE	0.9985	2	2	IDLLGEFQSALPK
sp|Q8BXA1|GOLI4_MOUSE	0.9981	2	2	DAGFQALEEQNQVEPR
sp|P70158|ASM3A_MOUSE	0.998	2	2	NGNPLNSVFVAPAVTPVK
sp|Q61624|ZN148_MOUSE	0.9979	2	2	LPQGLQYALNVPISVK
sp|Q9QXE7|TBLX_MOUSE	0.9979	2	2	HQEPVYSVAFSPDGK
sp|P59997|JHD1A_MOUSE	0.9974	2	2	ILLEELASSDPK
sp|Q8BRG8|TM209_MOUSE	0.9918	2	2	YTVAPTSLVVSPGQQALLGLK
sp|Q3URD3|SLMAP_MOUSE	0.9917	1	2	IEALQADNDFTNER
sp|Q62388|ATM_MOUSE	0.9917	1	2	SVATSSIVGYILGLGDR
sp|Q7TMW6|NARFL_MOUSE	0.9917	1	2	APDTEGSELLQQLER
sp|Q80YR4|ZN598_MOUSE	0.9917	1	2	TPGLAPTPQAYLVPENFR
sp|Q8K3K8|OPTN_MOUSE	0.9917	1	2	ADLLGIVSELQLK
sp|Q9CPS7|PNO1_MOUSE	0.9917	1	2	RPVFPPLSGDQLLTGK
sp|P70261|PALD_MOUSE	0.9908	1	2	ALGNILAYLSDAK
sp|Q8BW49|TTC12_MOUSE	0.9908	1	2	ANTAIGILTDLALEER
sp|Q91W92|BORG5_MOUSE	0.9908	1	2	LTADM[147]ISPPLGDFR
sp|Q9Z0P7|SUFU_MOUSE	0.9908	1	2	VSILPDVVFDSPLH
sp|P62737|ACTA_MOUSE	1	5	2	AVFPSIVGR
sp|P12246|SAMP_MOUSE	0.9965	1	2	APPSIVLGQEQDNYGGGFQR
sp|P62835|RAP1A_MOUSE	0.9952	1	2	INVNEIFYDLVR
sp|Q80Y17|L2GL1_MOUSE	0.9948	1	2	APVVAIAVLDGR

Table S3

All the abbreviated words and their full name	
1DE-LC-MS/MS	dimensional gel electrophoresis- liquid chromatography-mass spectrometry
ACN	Acetonitrile
BSA	Bovine Albumin Standards
DMEM	Dulbecco's Modified Eagle Media
Dnmt3a	DNA methyltransferase 3A
Dnmt3a-D	Dnmt3a depletion B16 melanoma
ERK	extracellular signal-regulated kinase
FBS	Fetal bovine serum
GO	Genome Ontology
IEF	isoelectro- focusing
IPG	immobilized pH gradient
IPI	International Protein Index
JNK	c-Jun N-terminal kinase
KEGG	Kyoto Encyclopedia of Genes and Genomes
LTQ-Orbitrap	Linear ion trap Orbitrap
MAPK	mitogen activated protein kinase signaling pathway
NC	negative control cell line
PBS	phosphate-buffered saline
PMSF	phenylmethanesulfonyl fluoride
TPP	Trans-Proteomic Pipeline

