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Melanocyte development in the mouse tail epidermis requires the Adamts9 metalloproteinase

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SUMMARY

The mouse tail has an important role in the study of melanogenesis, because mouse tail skin can be used to model human skin pigmentation. To better understand the development of melanocytes in the mouse tail, we cloned two dominant ENU-generated mutations of the *Adamts9* gene, *Und3* and *Und4*, which cause an unpigmented ring of epidermis in the middle of the tail, but do not alter pigmentation in the rest of the mouse. *Adamts9* encodes a widely expressed zinc metalloprotease with thrombospondin type 1 repeats with few known substrates. Melanocytes are lost in the *Adamts9* mutant tail epidermis at a relatively late stage of development, around E18.5. Studies of our *Adamts9* conditional allele suggest that there is a melanocyte cell autonomous requirement for *Adamts9*. In addition, we used a proteomics approach, TAILS N-terminomics, to identify new Adamts9 candidate substrates in the extracellular matrix of the skin. The tail phenotype of *Adamts9* mutants is strikingly similar to the unpigmented trunk belt in *Adamts20* mutants, which suggests a particular requirement for Adamts family activity at certain positions along the anterior-posterior axis.

SIGNIFICANCE

This work extends our understanding of the shared functional role of the *Adamts9* and *Adamts20* metalloproteinases in late melanocyte development and illustrates the specialization of these two genes in the trunk and the tail.

Keywords: Melanoblast development, Adamts, metalloproteinase, skin pigmentation, tail.

Running title: Mouse tail melanocytes require Adamts9

INTRODUCTION

Due to the high level of conservation in the pigmentary systems of mice and humans, the modeling of skin pigmentation in the mouse has great potential (Fitch et al., 2003; Van Raamsdonk et al., 2004). The epidermis of the mouse tail is organized into rows of scales, with exactly 3 hair follicles and around 100 inter-follicular melanocytes per scale. Although human skin is not organized into scales, the function of melanocytes is conserved between the species; melanocytes are located at the basal layer of the epidermis and transfer melanosomes to surrounding keratinocytes. The underlying dermis is also populated by melanocytes in the mouse tail, although this is not a typical site for melanocytes in humans. We previously found that the inter-follicular epidermal melanocytes of the mouse tail responded to germline mutations in Neurofibromin *(Nf1)*, recapitulating the *cafe au lait* macules and generalized skin hyper-pigmentation of human neurofibromatosis type 1 (Deo et al., 2012; Deo et al., 2013). In addition, expression of the oncogenic version of the heterotrimeric G protein alpha subunit, *GNAQ*, caused dermal melanocytosis in the mouse tail, while sparing the epidermis, analogous to the effects of oncogenic *GNAQ* mutations in humans (Huang et al., 2015; Van Raamsdonk et al., 2009; Van Raamsdonk et al., 2010). These findings support the usefulness of the mouse tail for modeling skin pigmentation disorders.

To better understand the biology of these inter-follicular melanocytes, we searched for mouse mutants with defects in tail skin pigmentation among a large cohort of mice generated during large scale ENU-mutagenesis screening. We noted two mutants (*Undetermined-3* and *Undetermined-4*) that had a very similar and specific phenotype, which consisted of a white ring in the middle of the tail, with normal pigmentation at the tip and base, as well as in the rest of the body. Already present at weaning age, this ring phenotype was indistinguishable between *Und3* and *Und4* mice, and no other mouse mutant with a similar phenotype has been reported. Thus, we suspected that a novel gene was involved in regulating skin pigmentation in the mouse tail in these two mutants and the identification of this gene would prove interesting.

In this paper, we report that *Adamts9* is mutant in both *Und3* and *Und4* mice. Strikingly, this tail ring phenotype is directly analogous to the "belt" phenotype present in mutants of the closely related *Adamts20* gene (Silver et al., 2008; Somerville et al., 2003). Although an additive affect between *Adamts9* and *Adamts20* has been previously reported in the trunk, no role for either gene was suspected in the tail, which develops later during development and through a different process involving a multipotent mesenchyme called the tailbud (Beck, 2015). Collectively, the ADAMTS protease family is known to cleave the core protein of most proteoglycans, which alters extracellular

matrix organization and function and leads to shedding of the O-linked carbohydrate core protein domain from assembled matrix or cell membranes. In doing so, glycosaminoglycan-bound growth factors can also be mobilized, thereby indirectly influencing cell function (Kelwick et al., 2015). In addition to analyzing the *Und3* and *Und4* alleles, which are splice site mutations, we determined when *Adamts9* is required for tail skin pigmentation during development and created a conditional allele to test the cell autonomous effects of *Adamts9* in melanocytes and keratinocytes. Finally, we identified new *in vivo* candidate substrates for Adamts9 in the skin using a proteomics approach, Terminal Amino Isotopic Labeling of Substrates (TAILS).

MATERIALS AND METHODS

Mice

All experiments involving mice were conducted under the approval of the Animal Care Committee at the University of British Columbia. The *Und3* and *Und4* alleles were recovered from a dominant ENU-mutagenesis screen of C3HeB/FeJ mice conducted at the Helmholtz Zentrum München in Germany (Hrabe de Angelis et al., 2000). They were continually maintained on the C3HeB/FeJ genetic background. *EIIa-cre* (*Tg(EIIa-Cre)C5379Lmgd*), *K14-cre (Tg(KRT14-cre)1Amc/J*), and *Mitf-cre (Tg(Mitf-cre)7114Gsb)* transgenic mice were backcrossed to the C3HeB/FeJ background for at least six generations before use (Alizadeh et al., 2008; Dassule et al., 2000; Lakso et al., 1996). *Dct-LacZ* (*Tg(Dct-LacZ)A12Jkn*) and *Rosa26-Tomato* (*Gt(ROSA)26Sortm14(CAG-tdTomato)Hze/J)* mice were on a mixed C3HeB/FeJ;C57Bl/6J background (Mackenzie et al., 1997; Madisen et al., 2009).

Adamts9^{flox} allele

The conditional *Adamts9^{flox}* allele was generated at inGenious Targeting Laboratory (Ronkonkoma, New York, USA). *Adamts9* was subcloned from the C57BL/6 BAC clone, RP23: 363L15, and used to build a construct that was electroporated into BA1 (C57Bl/6 x 129/SvEv hybrid) embryonic stem cells. Correctly targeted cells were microinjected into C57BL/6 blastocysts. Resulting chimeric mice were mated to C57BL/6 FLP mice to remove the Neo cassette and establish germline transmission. The *Adamts9^{flox}* allele was then backcrossed to C3HeB/FeJ for four generations before further use and thereafter maintained on the C3HeB/FeJ background.

Genotyping

DNA was purified from tissue samples using DNeasy columns (Qiagen) and amplified using PCR. The *Adamts9^{Und3}* and *Adamts9^{Und4}* alleles were genotyped by sequencing the amplicons produced by

the Und3-35L,5'-GAAACTGGAAAAGCCAGCAG, Und3-35R,5'-GAAGCCGCTAAAGGTGAGTG, Und4-3L,5'-TGTCCTGCAAACATGGAGAA, and Und4-3R,5'-TTTCTGTTGGCTGAGTCGTG. To genotype the *Adamts9*^{flox} allele, we used NEDL1,5'-CAGGGGAGGTTCTTAGCCTAGT and NDEL2,5'-CCAATAAGCTAGCATCATTCTGTTG. Primers MADA3,5'-CCTGTTACCTCTCAGATCGCTCTC and NDEL2 span the deleted region and only can produce a product from the recombined allele. Cre lines were genotyped as previously described (Alizadeh et al., 2008; Dassule et al., 2000; Lakso et al., 1996)

Skin histology

For X-gal staining, tail skin was excised and the tail bones removed. Skin was stained overnight in X-gal solution at room temperature and the next day the dermis and epidermis were separated and photographed with a stereomicroscope. For detection of Tomato positive cells, tail skin was similarly dissected, the dermis and epidermis were separated, and the epidermal sheet was placed on a slide under a cover slip with PBS and scanned using a 3DHistech fluorescent slide scanner. For the TUNEL assay, epidermal sheets were then fixed overnight in 10% formalin at 4°C in the dark and the TUNEL assay was performed the next morning using the TACS® 2 TdT Fluorescein Kit (Trevigen) with the Cytonin option for permeabilization. Sheets were placed in Vectasheild under a coverslip and then scanned for fluorescein and rescanned for Tomato signal simultaneously.

To separate the dermis from the epidermis, tissue samples were incubated in 2M sodium bromide for 5 min at room temperature (for P0 samples) increasing to 2 hours at 37°C (for P42 samples). Forceps were used to separate the epidermal and dermal sheets.

To assess the amount of skin hypo-pigmentation, the average pixel intensity of group photographed epidermal and dermal sheets was calculated using ImageJ software (National Institutes of Health, Bethesda, MD, USA).

For Adamts9 immunohistochemistry, tail skin was fixed in 4% paraformaldehyde for 20 minutes, incubated in a sucrose gradient, and embedded in Tissue-Tek OCT. 10 micron sections were treated with hydrogen peroxide, blocked, and incubated with primary antibody: RP4-Adamts9 diluted 1:35 overnight at 4°C (Triple Point Biologics). The ABC elite kit (Vector) was used for DAB substrate staining. For Mitf/Tomato immunofluorescence, P0 tail skin was fixed in 10% neutral buffered formalin overnight at 4°C, washed and incubated in a sucrose gradient, and embedded in Tissue-Tek OCT. 10 micron sections were washed with PBS, blocked in 1.5% serum for 5 hours, incubated with

anti-Mitf antibody (HPA003259, Sigma) overnight at 4°C, washed with PBS, and incubated with 488 donkey anti-rabbit antibody in PBS + 0.3% Triton X-100 and 5% donkey serum for 1 hour at room temperature. Slides were washed again and viewed with a DMI 600B inverted fluorescent microscope.

TAILS proteomics

In brief, soluble and insoluble protein fractions of four biological replicates of mouse skin were blocked by reductive demethylation using isotopically labeled formaldehyde. +/+ (labeled with heavy formaldehyde) and *Adamts9*^{Und4}/+ (labeled with light formaldehyde) proteomes were combined for TAILS analyses (auf dem Keller et al., 2013). After tryptic digestion, internal tryptic peptides were removed from the N-terminome by a high molecular weight polyaldehyde polymer (HPG-ALD; available through flintbox, http://flintbox.com/public/project/1948/) under reductive conditions. The resulting N-terminome was analyzed by LC-MS/MS on a LTQ-Orbitrap Velos as described in Supplementary Methods.

Statistical Analysis

Data was analyzed by students *t* test for statistical significance. Error bars represent the standard error of the mean.

RESULTS

***Und3* and *Und4* cause a white tail ring phenotype**

To identify genes necessary for caudal melanocyte development, we studied *Und3/+* and *Und4/+* mice, which were recovered during a dominant ENU-mutagenesis screen of C3HeB/FeJ mice (Hrabe de Angelis et al., 2000). *Und3/+* and *Und4/+* mice exhibited a ring of unpigmented skin in the middle of the tail, but were pigmented normally in the rest of the body (**Figure 1A-B**). The most frequently affected area of the tail was located three-quarters of the way from the base to the tip (**Figure 1C**). Progeny with tail rings were observed less frequently than expected in our maintenance crosses on the original C3HeB/FeJ genetic background, and following the molecular identification of the mutations (below), the penetrance of any tail hypo-pigmentation phenotype at weaning age was calculated to be 83% and 71% for the *Und3*/+ and *Und4*/+ genotypes, respectively (**Figure 1D**). There is variable expressivity in the amount of tail hypo-pigmentation, with only 66% and 50% of *Und3*/+ and *Und4*/+ mice exhibiting a full tail ring that encircles the dorsum and ventrum. Unlike C57BL/6J mice, which can have white tail tips, the tails of C3HeB/FeJ mice were fully pigmented (Hirobe, 1991). For example, in our study, only 1 out of 65 C3HeB/FeJ mice exhibited any tail hypo-pigmentation. Within

the hypo-pigmented areas of the adult *Und3/+* and *Und4/+* tails, the epidermis is affected, but the dermis is pigmented normally (**Figure 1E-F**).

Splice site mutations in *Adamts9* in *Und3* and *Und4* mutants

To identify the mutation responsible for the *Und4* phenotype, we employed an outcross-backcross mapping strategy. We crossed *Und4*/+ females with white tail rings to Cast/EiJ males. The resulting F1 progeny with tail rings were collected and backcrossed to C3HeB/FeJ mice. Ten of the resulting N1 progeny that exhibited tail rings were selected for an initial genome scan using SSLP makers polymorphic between the C3HeB/FeJ and Cast/EiJ alleles. We searched for regions of the genome that were homozygous for the C3HeB/FeJ allele in all of the progeny with tail rings. In this way, linkage was detected on Chromosome 6. Subsequently, 100 additional *Und4* N1 mapping progeny with tail rings were genotyped with a denser array of SSLP markers on Chromosome 6, resulting in a 1.3 megabase physical interval for the *Und4* mutation, as defined by the minimal region of C3HeB/FeJ homozygosity in all N1 mice with tail rings (**Figure 2A**).

According to the mouse Ensembl genome database (GRCm38), the 1.3 Mb *Und4* physical interval contains 11 predicted or known genes, including *Adamts9*. We sequenced all 40 *Adamts9* exons in *Und3*/+ and *Und4*/+ DNA (according to Ensembl transcript ENSMUST00000113438). Compared to the C3HeB/FeJ genetic background, on which the *Und3* and *Und4* alleles arose, a donor splice site mutation was found in intron 35-36 in *Und3* and in intron 3-4 in *Und4* (**Figure 2B-C**).

The canonical donor splice site in mammals consists of an almost invariant 5'-GT-3' with the next base usually an A or G (Burset et al., 2000). Using a wider context around the splice site, the Human Splicing Finder prediction program assigns strong donor sites a consensus value (CV) of greater than 80 (Desmet et al., 2009). Using this analysis, the donor sites at wildtype exon 35 and exon 3 were calculated to have a CV of 97.66 and 78.88, respectively. These values fell to 70.83 and 73.85 in the *Und3* and *Und4* alleles. In addition, sequencing of RT-PCR products generated from primers flanking the exon 35-36 or exon 3-4 junctions in *Und3*/+ or *Und4*/+ tail skin RNA revealed incorrectly spliced transcripts (**Figure 3A-C**). In the case of *Und4*, the incorrectly spliced transcript could be inferred to come specifically from the *Und4* allele, because it contained a mutant base (T), and not the wildtype base (A), at position 3 of intron 3-4 (**Figure 3C**). This incorrectly spliced transcript could not include the entire intron, because intron 3-4 is greater than 23 kb in length. Splicing must have occurred within intron 3-4 at a cryptic splice site fairly close to the normal exon-intron junction to produce this slightly larger PCR product. Other transcripts may be present in the mutant that would not be detected by this

particular assay, such as a longer read into intron 3-4 or exon 3 skipping. All of these mistakes could lead to gibberish being included in the protein as a result of read through into the intron and/or a frameshift of the reading frame upon return to an exon. We conclude that splicing is impaired by the *Und3* and *Und4* mutations.

To determine the effect of homozygosity of the *Und4* mutation, we intercrossed F1 animals. At weaning age, none of the resulting F2 progeny had inherited two copies of *Und4* based upon the identified mapping boundaries (66 animals genotyped; $p=3x10^{-9}$). This indicates that *Und4* is homozygous lethal, which is consistent with previously described loss-of-function mutations in *Adamts9* (Dubail et al., 2014; Silver et al., 2008).

An engineered knockout allele of *Adamts9* also causes a tail ring phenotype

A tail ring phenotype had not been previously reported in *Adamts9* mutant mice. However, previous mutant alleles of *Adamts9* were studied on the C57Bl/6 background, which is subject to spurious tail hypo-pigmentation that would complicate identification of a incompletely penetrant phenotype. To address this, we engineered an *Adamts9* mutant allele and crossed it to the C3HeB/FeJ genetic background. In this allele (hereafter referred to as "*Adamts9*^{flox}"), exons 4, 5, and 6 of *Adamts9* are deleted upon Cre mediated recombination (**Figure 4A-B**). The deletion of these exons is expected to remove amino acids 227 to 390, which includes part of the peptidase M12B domain.

Mice carrying the *Adamts9*^{flox} allele were crossed to a ubiquitously expressed Cre line, *EIIa-cre*, and then the resulting *Adamts9*^{flox}/+; *EIIa-cre*/+ mice were backcrossed to wildtype C3HeB/FeJ mice to produce mice carrying a germline recombined *Adamts9* allele without Cre (hereafter referred to as "*Adamts9*^{KO}/+"). 5 out of 7 *Adamts9*^{KO}/+ mice exhibited tail rings, while all control littermates were normal (**Figure 4C**). Thus, haploinsufficiency of *Adamts9* definitively causes a tail ring phenotype. We next crossed the *Adamts9*^{KO}/+ mice to *Adamts9*^{Und3}/+ mice for a complementation test. No *Adamts9*^{KO}/*Adamts9*^{Und3} progeny were recovered at wean (53 animals genotyped; $p=1x10^{-7}$), further demonstrating loss-of-function of *Adamts9* in the *Und3* allele. Using immunohistochemistry, we detected Adamts9 protein throughout the skin of normal mice (**Figure 4D**). We conclude that haploinsufficiency of *Adamts9* on the C3HeB/FeJ genetic background causes an incompletely penetrant tail ring phenotype.

The *Adamts9* tail ring phenotype initiates at around postnatal day 0

To study how *Adamts9* regulates melanoblast development in the tail, we crossed *Adamts9*^{Und4}/+ to *Dct-LacZ*/+ in timed matings (**Figure 5**). *Dct-LacZ* is expressed in melanoblasts as early as E9 of development (Mackenzie et al., 1997). At E16.5, we found that melanoblasts extended throughout the tail, with a concentration at the tip. There were similar numbers in *Adamts9*^{Und4}/+ and +/+ embryos (**Figure 5A**). However, two days later (E18.5/P0), 67% of wildtype mice (*n*=9) were affected by an area of reduced melanoblast density, while 100% of *Adamts9*^{Und4}/+ mice contained areas with no melanoblasts at all (*n*=3) (**Figure 5B**). By P2, the number of affected wildtype mice had dropped to 18% (*n*=11), compared to 88% of mutant mice (*n*=8). At P8, all wildtype mice were fully populated, yet 66% of *Adamts9*^{Und4}/+ mice continued to exhibit areas completely lacking melanoblasts (*n*=6 and *n*=3, respectively). At each of these time points, LacZ-positive melanoblasts were observed throughout the dermis in both +/+ and *Adamts9*^{Und4}/+ mice, hence the reduction was specifically in the epidermis. We note that *Dct-LacZ* stains some nerves in the tail dermis, but these can be distinguished from melanoblasts based on cellular morphology. Identical findings were present in *Adamts9*^{Und3}/+ mice (**Figure 5B** and data not shown). Thus, we conclude that the tail ring phenotype arises during the postnatal period around P0, following a relatively normal establishment of melanoblasts throughout the anterior-posterior axis during embryogenesis.

To determine if there was any change to the size of the tail ring after P8, when the phenotype becomes visible because of a lack of melanin production in the ring, we photographed 5 *Adamts9*^{Und4}/+ pups every other day and measured the distance between 5 marks tattoo-inked along each tail. We found that between P8 and P19, the tail grows relatively evenly along its length; however, there was a trend of slightly less growth towards the tip (**Figure 6A**). The boundaries affected by hypo-pigmentation remained stable over this time period in all 5 mice. At P28, the affected epidermis of *Adamts9*^{Und4}/+ ; *Dct-LacZ*/+ mice continued to have no LacZ-positive cells in the scales or hair (**Figure 6B-C**). Some scales at the edges of the affected skin were lightly pigmented and contained less dendritic melanocytes (**Figure 6B**). We noted pigmented scales directly adjacent to unpigmented scales in the boundary region of *Adamts9*^{Und4}/+ mice, which suggests restriction of melanocyte movement within scales.

Assessment of a melanocyte cell autonomous requirement for *Adamts9*

The generation of the conditional *Adamts9* allele (above) allowed us to investigate whether the requirement for *Adamts9* in melanocyte development is cell autonomous. The pigmentation defect in *Adamts9* mutants is confined to the epidermis. The most abundant cell type in the epidermis is the keratinocytes. To make a conditional knockout in keratinocytes, we used *K14-cre* (Dassule et al.,

2000). The *Keratin 14* (*K14*) promoter has been particularly useful in targeting the expression of transgenes to the mitotically active basal layer of mouse epidermis, which produces the stratified epithelium (Vasioukhin et al., 1999). To make a tissue specific conditional knockout in melanocytes, we used *Mitf-cre*. *Mitf-cre* is a 185 kb BAC transgene that has cre inserted into the first exon of the melanocyte specific *Microphthalmia* transcript, produced at the M promoter (Alizadeh et al., 2008). It has previously been used to successfully drive pigmentation phenotypes in hair follicle and skin melanocytes (Alizadeh et al., 2008; Deo et al., 2012; Huang et al., 2015; Urtatiz et al., 2018). Both of these Cre lines were kept on the C3HeB/FeJ genetic background.

We crossed *Adamts9*^{flox}/+ mice to *K14-cre*/+ mice and *Adamts9*^{flox}/+ mice to *Mitf-cre*/+ mice. We found that all *K14-cre*/+; *Adamts9*^{flox}/+ mice possessed normally pigmented tails (*n*=6), while one *Mitf-cre*/+; *Adamts9*^{flox}/+ mouse exhibited a small tail ring (*n*=9) (**Figure 6D-E**). No tail hypo-pigmentation was observed in mice of the control genotypes from these crosses (*n*=41). We then intercrossed mice to produce *Mitf-cre*/+; *K14-cre*/+; *Adamts9*^{flox}/+ animals, and found that they were pigmented normally (*n*=3). Hence, neither conditional knockout (*K14-cre* or *Mitf-cre*) fully recapitulated the germline knockout phenotype of the *Adamts9*^{flox} allele. To determine whether this could be due to low cre efficiency, we assessed the activity of cre in *K14-cre* and *Mitf-cre* P0 tails using the *Rosa26-floxed stop-Tomato* ("*R26-Tomato*") fluorescent reporter (Madisen et al., 2010). We found that *K14-cre* led to wide spread expression of Tomato in the epidermis (**Figure 6F**). Melanoblasts staining positive for an Mitf antibody did not express Tomato signal (arrows, **Figure 6F**). Therefore, the efficiency of *K14-cre* appears to be very high and K14 and Mitf expression are mutually exclusive, as expected. To determine the efficiency of *Mitf-cre*, we compared tomato signal with Mitf antibody signal in *Mitf-cre/+; R26-Tomato/+* tail epidermis. *Mitf-cre* induced tomato expression in numerous hair follicle melanoblasts that co-expressed Mitf protein (**Figure 6H**). The efficiency of *Mitf-cre* throughout the epidermis was calculated to be 74% (the fraction of Mitf-positive melanoblasts that were also positive for Tomato) (**Figure 6G-H**). The low penetrance of the tail ring phenotype in *Mitf-cre/+; Adamts9*^{flox}/+ mice may be related to the 74% efficiency of *Mitf-cre*, particularly considering that the tail ring phenotype is not fully penetrant even in *Adamts9*^{KO}/+ mice.

We next examined the Tomato-positive melanoblasts in *Mitf-cre/+; Adamts9*^{flox}/+; *R26-Tomato/+* mutants. These melanoblasts are presumed to have recombined the *Adamts9*^{flox} allele at the same time as the *R26-Tomato* allele and therefore may have a cell autonomous phenotype detectable on the cellular level. *Rosa26* and *Adamts9* are located within 20 Mb of each other on chromosome 6, so we crossed *Mitf-cre/+; R26-Tomato*/+ males to *Adamts9*^{flox}/+ females in timed matings. We collected the

resulting litters at P0 and identified the progeny that carried both *Mitf-cre* and *R26-Tomato* by examining a piece of trunk skin for Tomato signal. We produced epidermal sheets from the tails of the Tomato positive mice and generated a composite image of each whole mounted epidermal sheet using a 3DHistech fluorescent slide scanner. We found Tomato-positive melanoblasts with an abnormal morphology in the *Adamts9*^{flox}/+ samples (*n*=5) (**Figure 7B**), that were not present in wildtype controls (*n*=3)(**Figure 7A**). These melanoblasts were undergoing fragmentation indicating cell death (**Figure 7B,** example cells #3-5). In the segment from the 8 mm mark to 12 mm mark along the tails of a matched pair of littermates, we determined that 21% of the Tomato-positive melanoblasts in the *Adamts9*^{flox}/+ sample were abnormal (*n*=112 cells in total) (**Figure 7B**), compared to 0.6% in the +/+ sample (*n*=346 cells in total) (**Figure 7A**). There were also Tomato-positive melanoblasts that appeared to be in the process of cell division or to have recently completed it (see **Figure 7C-D** for examples). These were quantified, but no obvious difference was found between the *Adamts9*^{flox}/+ and +/+ samples (6% vs. 7%, respectively.) In addition, we performed the TUNEL assay to detect double stranded breaks in DNA, also in whole mount format. We found 1 to 3 Tomato/TUNEL-double positive melanoblasts in each *Adamts9*^{flox}/+ sample, but none in wildtype controls. These cells were not yet undergoing fragmentation and probably represent an earlier stage in the process of cell death (**Figure 7E**, note cell undergoing fragmentation directly beneath the TUNEL-positive cell). Taken together, this data suggests that there is a cell autonomous requirement for *Adamts9* in melanoblasts located in the tail epidermis and that a deficiency of *Adamts9* contributes to reduced melanoblast survival. This explains the formation of the tail ring following normal colonization of the tail by melanoblasts at E16. Because numerous Tomato-positive melanoblasts are dying within the *Adamts9*^{flox}/+ epidermis at P0, the ring phenotype is not simply a failure of melanoblasts to cross from the dermis into the epidermis.

As part of a separate study, we sorted Tomato-positive melanocytes from epidermis of *Mitf-cre/+; R26-Tomato/+* tails at P14 and P28 for transcriptome analysis (*full analysis in manuscript in preparation*). From within this dataset, we present here a comparison of the relative expression levels of the 19 *Adamts* family members (**Figure 7F**). The most abundantly expressed *Adamts* gene was *Adamts1*, followed by *Adamts20*. At P14, *Adamts9* was the 6th most abundantly expressed *Adamts* gene, but its expression decreased by P28. *Adamts2, 3, 8, 13, 15, 16, 18,* and *19* were not detectable at either time point.

Proteomic analysis of *Und4* tail skin

Substrates for the Adamts family are difficult to identify using biochemical approaches as these proteinases are large multi-domain, heavily disulfide cross-linked, enzymes up to 220 kDa, thus posing challenges for their recombinant expression with all ancillary domains present (Cerda-Costa and Gomis-Ruth, 2014; Kelwick et al., 2015). This has hampered biochemical investigation of Adamts proteases as these domains include substrate binding exosite domains, and thus are integral to proteolytic and extracellular matrix degradative functions. Hence, in the absence of recombinant protease to screen or validate substrates for Adamts9, we used an unbiased N-terminomics approach known as Terminal Amino Isotopic Labeling of Substrates (TAILS) that has been well established to identify protease cleavage sites and substrates *in vivo* (auf dem Keller et al., 2013; Kleifeld et al., 2010; Kleifeld et al., 2011). Thus, we proteomically quantified the relative abundance of neo N-Termini generated at cleavage sites in one week old +/+ versus *Adamts9*^{Und4}/+ tail skin. 1,777 proteins were identified in total in skin from the base of the tail, including dermis and epidermis (false discovery rate FDR ≤ 1%) (**Supplementary Table 1A**; full details of all peptides identified in preTAILS and TAILS analyses are presented in **Supplementary Table 1 A-G**). 68 peptides occurred with greater frequency in +/+ versus *Adamts9*^{Und4}/+ samples following TAILS (**Supplementary Table 1F-a**). Of these, 21 were from extracellular matrix and basement membrane proteins, including biglycan and basement membrane specific heparan sulfate core protein (HSPG), which conform to the proteoglycan substrate specificity profile of Adamts proteases (Apte, 2009). In addition, fibronectin, tenascin, fibrilin-1, and periostin were identified with several cleavage sites found. These initial data identifying potential new candidates for Adamts9 cleavage targets requires follow-up in future proteo-genomic and biochemical studies once methods for expression of recombinant Adamts9 can be established.

DISCUSSION

The modeling of the genetics of skin pigmentation in mice has generally lagged behind understanding of coat color because, for many years, mouse geneticists focused on trunk skin, which is unpigmented. While the tail and its scale organization appears to be dissimilar to human skin, the melanocytes there actively produce melanin and distribute it to surrounding keratinocytes. Alterations in pathways corresponding to those implicated in human skin pigmentation disorders and melanoma have also disrupted pigmentation of the mouse tail skin (Deo et al., 2012; Huang et al., 2015; Kohler et al., 2017; Urtatiz et al., 2018). A number of mouse mutations increase tail skin pigmentation without affecting coat color, and among several large scale ENU-mutagenesis screens, now finished, saturation of this phenotype had not yet been reached (Fitch et al., 2003; Hrabe de Angelis et al., 2000; Van Raamsdonk et al., 2004); hence, many skin specific pigmentation genes remain to be identified. *Und3* and *Und4*,

studied in this paper, are the first examples of mutants with a specific pattern of tail skin hypo-pigmentation. We found that both of these mutations are splice site alterations within *Adamts9*, which encodes a widely expressed zinc secreted metalloprotease with thrombospondin type 1 repeats.

Because *Und3* and *Und4* affect the development of melanocytes in the tail, it is necessary to consider how tail development differs from the development of the trunk. The caudal end of the vertebrate body, including all of the tail, is created by the tailbud, a multipotent mesenchyme from which all three germ layers are derived (Beck, 2015; Gofflot et al., 1997; Griffith et al., 1992; Shum et al., 2010). In mice, the tailbud is formed from the remnants of the node and the primitive streak at E12.5. The tailbud generates the notochord, secondary neural tube, muscles and vertebrae. The secondary neural tube is formed from tailbud mesenchyme that undergoes a mesenchymal to epithelial transformation, with cells oriented around a central lumen. The lumen gradually grows larger with the accumulation of additional cells into the tube. It is not known whether melanoblasts in the tail originate from the tailbud or the secondary neural tube or migrate into the tail from the trunk; however, we found that melanoblasts are present throughout the tail by E16.5.

While a tail spotting phenotype had not been noticed previously in *Adamts9* mutant mice, a role for *Adamts9* in melanocyte development in the trunk was already known (Silver et al., 2008). Because *Adamts9* and *Adamts20* shared high sequence homology, an *Adamts9*; *Adamts20* double mutant mouse was made to determine whether the two genes have overlapping functions. Loss of function mutations in *Adamts20* alone cause the recessive *Belted* phenotype in mice, a ring of unpigmented hair extending all the way around the middle of the trunk with normal pigmentation in the rest of the body (Rao et al., 2003). The additional loss of one knockout allele of *Adamts9* in combination with homozygosity of the $Adamts20^{Bt\text{-}9J}$ allele increased the size of the trunk ring by 25% at birth, immediately after which the double mutants died (Silver et al., 2008). This suggested that *Adamts9* plays a role in melanocyte development in the trunk, however, *Adamts9* plays a more important role in the tail, because the loss of only one copy of *Adamts9* affects tail pigmentation, but not trunk pigmentation. Furthermore, mutations of *Adamts20* have been made on a C3H genetic background and no tail spotting has been reported. We conclude that *Adamts9* is specialized for the tail, whereas *Adamts20* is specialized for the trunk. The distinct mechanism of development of the tail from the tailbud provides a plausible explanation for the necessity of this duplication in gene function.

Between E12.5 and E14.5, melanoblasts in the trunk that are migrating from the dorsum finally reach all areas of the ventrum. Silver et al reported that in *Adamts20* homozygous mutants, there were a

normal number of melanoblasts in the trunk until E12.5. Melanoblasts were lost first in the ventrum and then in the dorsum between E14.5 and E16.5 (Silver et al., 2008). We found that *Adamts9*^{Und}/+ embryos possessed a normal number of melanoblasts in the tail at E16.5, but developed a significant loss between P0 and P2. Therefore, in both cases, deficiency of *Adamts* genes induces a late loss of melanoblasts. Rao *et al* (Rao et al., 2003) had previously hypothesized a late role for *Adamts20* in the trunk, based in part upon the observation that the unpigmented area on the back was larger than the unpigmented area on the belly in *Adamts20* mutant mice.

It is striking that the *Adamts20* and *Adamts9* mutations primarily affect the middles of two anterior-posterior axes, one in the trunk and one in the tail. Ring or belt phenotypes that eliminate pigmentation all the way around the dorsal-ventral axis are rare. Most coat spotting mutations affect the belly only, which happens to be the last area reached during migration in the trunk (Baxter et al., 2004). The MGI database lists *Dock7*^{Mnlt}, *Kit*, *Mitf*$^{Mi\text{-}crc}$, *Aebp2*$^{Gt(Bc0681)Wtsi}$, *Mcoln3*$^{Va\text{-}J}$, and 15 uncharacterized *Rgsc* Riken mutants with an annotated white tail tip phenotype, but no tail rings. The ENU- mutagenesis screen at the Helmholtz Zentrum München produced no other mouse mutants with tail rings and yet got two independent hits in *Adamts9*. These observations are consistent with a late, specific role for the Adamts protease family in melanoblast development and indicate that they are necessary during the period when the anterior-posterior axes of the trunk and tail are elongating. Why they are needed most in the middle of these anterior-posterior axes remains mysterious. It could be that this portion of the axis grows particularly rapidly at some stage or perhaps has a different extracellular matrix composition less favorable for supporting melanoblast survival.

Adamts20 loss was previously found to increase melanoblast apoptosis, coincident with the disappearance of melanoblasts in *Belted* mice (Silver et al., 2008). Similarly, we observed that conditional *Adamts9* haploinsufficiency driven by *Mitf-cre* in melanoblasts resulted in an abnormal morphology consistent with cell death at P0. From these data, we propose that there is a cell autonomous requirement for *Adamts9* in melanoblasts. Importantly, death occurred after the melanoblasts reached the epidermis, further suggesting that melanoblast migration is not affected in *Adamts9* mutants. A cell autonomous requirement would be surprising because Adamts9 protein expression was detected throughout the tail skin and Adamts9 is a secreted protein. One possibility is that the immediate microenvironment around a melanoblast is altered by its secretion of Adamts9. By releasing glycosaminoglycan-bound growth factors anchored in the extracellular matrix that in turn stimulate melanoblast growth and survival by modulating cell behaviour, Adamts9 may do more than just degrade the extracellular matrix. Indeed, the candidate substrates we identified by TAILS

proteomics (see Supplementary Information) include 21 new extracellular matrix and basement membrane proteins, such as basement membrane-specific heparan sulfate core protein and biglycan, that conform to the reported proteoglycan substrate specificity profile of Adamts proteases (Apte, 2009). Alternatively, there could be an intracellular role for Adamts9 within melanocytes. An intracellular role for the *Adamts9* homolog, *Gon-1*, in protein trafficking in the endoplasmic reticulum was reported in *C. elegans*, and some of the candidate substrates that we identified by TAILS are expected to be intracellular (Yoshina et al., 2012).

In summary, the work described here highlights the important role of *Adamts9* in regulating melanoblast survival in the epidermis, which is necessary for normal skin pigmentation. *Adamts9* plays a late role in supporting melanocyte development after the initial phase of melanoblast specification and migration to the epidermis are completed.

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COMPETING INTERESTS

No competing interests to declare.

REFERENCES

Alizadeh, A., Fitch, K. R., Niswender, C. M., Mcknight, G. S., and Barsh, G. S. (2008). Melanocyte-lineage expression of Cre recombinase using Mitf regulatory elements. Pigment Cell Melanoma Res *21***,** 63-9.

Apte, S. S. (2009). A disintegrin-like and metalloprotease (reprolysin-type) with thrombospondin type 1 motif (ADAMTS) superfamily: functions and mechanisms. J Biol Chem *284***,** 31493-7.

Auf Dem Keller, U., Prudova, A., Eckhard, U., Fingleton, B., and Overall, C. M. (2013). Systems-level analysis of proteolytic events in increased vascular permeability and complement activation in skin inflammation. Sci Signal *6***,** rs2.

Baxter, L. L., Hou, L., Loftus, S. K., and Pavan, W. J. (2004). Spotlight on spotted mice: a review of white spotting mouse mutants and associated human pigmentation disorders. Pigment Cell Res *17***,** 215-24.

Beck, C. W. (2015). Development of the vertebrate tailbud. Wiley Interdiscip Rev Dev Biol *4***,** 33-44.

Burset, M., Seledtsov, I. A., and Solovyev, V. V. (2000). Analysis of canonical and non-canonical splice sites in mammalian genomes. Nucleic Acids Res *28***,** 4364-75.

Cerda-Costa, N., and Gomis-Ruth, F. X. (2014). Architecture and function of metallopeptidase catalytic domains. Protein Sci *23***,** 123-44.

Dassule, H. R., Lewis, P., Bei, M., Maas, R., and Mcmahon, A. P. (2000). Sonic hedgehog regulates growth and morphogenesis of the tooth. Development *127***,** 4775-85.

Deo, M., Huang, J. L., Fuchs, H., De Angelis, M. H., and Van Raamsdonk, C. D. (2012). Differential effects of neurofibromin gene dosage on melanocyte development. J Invest Dermatol *133***,** 49-58.

Deo, M., Huang, J. L., and Van Raamsdonk, C. D. (2013). Genetic interactions between neurofibromin and endothelin receptor B in mice. PLoS One *8***,** e59931.

Desmet, F. O., Hamroun, D., Lalande, M., Collod-Beroud, G., Claustres, M., and Beroud, C. (2009). Human Splicing Finder: an online bioinformatics tool to predict splicing signals. Nucleic Acids Res *37***,** e67.

Dubail, J., Aramaki-Hattori, N., Bader, H. L., Nelson, C. M., Katebi, N., Matuska, B., Olsen, B. R., and Apte, S. S. (2014). A new Adamts9 conditional mouse allele identifies its non-redundant role in interdigital web regression. Genesis *52***,** 702-12.

Fitch, K. R., Mcgowan, K. A., Van Raamsdonk, C. D., Fuchs, H., Lee, D., Puech, A., Herault, Y., Threadgill, D. W., Hrabe De Angelis, M., and Barsh, G. S. (2003). Genetics of dark skin in mice. Genes Dev *17***,** 214-28.

Gofflot, F., Hall, M., and Morriss-Kay, G. M. (1997). Genetic patterning of the developing mouse tail at the time of posterior neuropore closure. Dev Dyn *210***,** 431-45.

Griffith, C. M., Wiley, M. J., and Sanders, E. J. (1992). The vertebrate tail bud: three germ layers from one tissue. Anat Embryol (Berl) *185***,** 101-13.

Hirobe, T. (1991). Developmental interactions in the pigmentary system of the tip of the mouse tail: effects of coat-color genes on the expression of a tail-spotting gene. J Exp Zool *258***,** 353-8.

Hrabe De Angelis, M. H., Flaswinkel, H., Fuchs, H., Rathkolb, B., Soewarto, D., Marschall, S., Heffner, S., Pargent, W., Wuensch, K., Jung, M., et al. (2000). Genome-wide, large-scale production of mutant mice by ENU mutagenesis. Nat Genet *25***,** 444-7.

Huang, J. L., Urtatiz, O., and Van Raamsdonk, C. D. (2015). Oncogenic G Protein GNAQ Induces Uveal Melanoma and Intravasation in Mice. Cancer Res *75***,** 3384-97.

Kelwick, R., Desanlis, I., Wheeler, G. N., and Edwards, D. R. (2015). The ADAMTS (A Disintegrin and Metalloproteinase with Thrombospondin motifs) family. Genome Biol *16***,** 113.

Kleifeld, O., Doucet, A., Auf Dem Keller, U., Prudova, A., Schilling, O., Kainthan, R. K., Starr, A. E., Foster, L. J., Kizhakkedathu, J. N., and Overall, C. M. (2010). Isotopic labeling of terminal amines in complex samples identifies protein N-termini and protease cleavage products. Nat Biotechnol *28***,** 281-8.

Kleifeld, O., Doucet, A., Prudova, A., Auf Dem Keller, U., Gioia, M., Kizhakkedathu, J. N., and Overall, C. M. (2011). Identifying and quantifying proteolytic events and the natural N terminome by terminal amine isotopic labeling of substrates. Nat Protoc *6***,** 1578-611.

Kohler, C., Nittner, D., Rambow, F., Radaelli, E., Stanchi, F., Vandamme, N., Baggiolini, A., Sommer, L., Berx, G., Van Den Oord, J. J., et al. (2017). Mouse Cutaneous Melanoma Induced by Mutant BRaf Arises from Expansion and Dedifferentiation of Mature Pigmented Melanocytes. Cell Stem Cell *21***,** 679-693 e6.

Lakso, M., Pichel, J. G., Gorman, J. R., Sauer, B., Okamoto, Y., Lee, E., Alt, F. W., and Westphal, H. (1996). Efficient in vivo manipulation of mouse genomic sequences at the zygote stage. Proc Natl Acad Sci U S A *93***,** 5860-5.

Mackenzie, M. A., Jordan, S. A., Budd, P. S., and Jackson, I. J. (1997). Activation of the receptor tyrosine kinase Kit is required for the proliferation of melanoblasts in the mouse embryo. Dev Biol *192***,** 99-107.

Madisen, L., Zwingman, T. A., Sunkin, S. M., Oh, S. W., Zariwala, H. A., Gu, H., Ng, L. L., Palmiter, R. D., Hawrylycz, M. J., Jones, A. R., et al. (2009). A robust and high-throughput Cre reporting and characterization system for the whole mouse brain. Nat Neurosci *13***,** 133-40.

Madisen, L., Zwingman, T. A., Sunkin, S. M., Oh, S. W., Zariwala, H. A., Gu, H., Ng, L. L., Palmiter, R. D., Hawrylycz, M. J., Jones, A. R., et al. (2010). A robust and high-throughput Cre reporting and characterization system for the whole mouse brain. Nat Neurosci *13***,** 133-40.

Rao, C., Foernzler, D., Loftus, S. K., Liu, S., Mcpherson, J. D., Jungers, K. A., Apte, S. S., Pavan, W. J., and Beier, D. R. (2003). A defect in a novel ADAMTS family member is the cause of the belted white-spotting mutation. Development *130***,** 4665-72.

Shum, A. S., Tang, L. S., Copp, A. J., and Roelink, H. (2010). Lack of motor neuron differentiation is an intrinsic property of the mouse secondary neural tube. Dev Dyn *239***,** 3192-203.

Silver, D. L., Hou, L., Somerville, R., Young, M. E., Apte, S. S., and Pavan, W. J. (2008). The secreted metalloprotease ADAMTS20 is required for melanoblast survival. PLoS Genet *4***,** e1000003.

Somerville, R. P., Longpre, J. M., Jungers, K. A., Engle, J. M., Ross, M., Evanko, S., Wight, T. N., Leduc, R., and Apte, S. S. (2003). Characterization of ADAMTS-9 and ADAMTS-20 as a distinct ADAMTS subfamily related to Caenorhabditis elegans GON-1. J Biol Chem *278***,** 9503-13.

Urtatiz, O., Samani, A. M. V., Kopp, J. L., and Van Raamsdonk, C. D. (2018). Rapid melanoma induction in mice expressing oncogenic Braf(V600E) using Mitf-cre. Pigment Cell Melanoma Res.

Van Raamsdonk, C. D., Bezrookove, V., Green, G., Bauer, J., Gaugler, L., O'brien, J. M., Simpson, E. M., Barsh, G. S., and Bastian, B. C. (2009). Frequent somatic mutations of GNAQ in uveal melanoma and blue naevi. Nature *457***,** 599-602.

Van Raamsdonk, C. D., Fitch, K. R., Fuchs, H., De Angelis, M. H., and Barsh, G. S. (2004). Effects of G-protein mutations on skin color. Nat Genet *36***,** 961-8.

Van Raamsdonk, C. D., Griewank, K. G., Crosby, M. B., Garrido, M. C., Vemula, S., Wiesner, T., Obenauf, A. C., Wackernagel, W., Green, G., Bouvier, N., et al. (2010). Mutations in GNA11 in uveal melanoma. N Engl J Med *363***,** 2191-9.

Vasioukhin, V., Degenstein, L., Wise, B., and Fuchs, E. (1999). The magical touch: genome targeting in epidermal stem cells induced by tamoxifen application to mouse skin. Proc Natl Acad Sci U S A *96***,** 8551-6.

Yoshina, S., Sakaki, K., Yonezumi-Hayashi, A., Gengyo-Ando, K., Inoue, H., Iino, Y., and Mitani, S. (2012). Identification of a novel ADAMTS9/GON-1 function for protein transport from the ER to the Golgi. Mol Biol Cell *23***,** 1728-41.

FIGURE LEGENDS

Figure 1. **White tail ring phenotype in *Und3* and *Und4***

A-B) *Und3*/+ (A) and *Und4*/+ (B) four week old mice. The first mouse in each group of mutants exhibits a mild white patch phenotype; the rest are fully ringed. **C**) Graph showing the affected portion of the tail in *Und3*/+ and *Und4*/+ mice. **D**) Percent of *Und3/*+ and *Und4/*+ mice with normal pigmentation, a mild white patch phenotype, or a full tail ring on the C3HeB/FeJ background. **E**) Epidermal (top) and dermal (bottom) sheets of mice from affected tail region. The epidermal and dermal sheets are from the same piece of tail and include the border between affected and unaffected epidermis. **F**) Quantification of the average relative pixel intensity of group photographed samples. Skin was sampled from within the hypo-pigmented area.

Figure 2. Splice site mutations in *Adamts9* in *Und3* and *Und4*

A) A map of the physical interval of *Und4* on chromosome 6, according to the Ensembl genome database GRCm38. The recombination fractions are shown below each marker. **B-C**) Base substitutions found in *Und3*/+ (B) and *Und4*/+ (C) genomic DNA, compared to C3HeB/FeJ.

Figure 3. Intron retention in *Adamts9*^{Und} transcripts

A) Schematic showing experimental design for RT-PCR. **B**) Additional bands (stars) result from RT-PCR using RNA from *Und3*/+ and *Und4*/+ neonatal mouse tail skin. **C**) Sequencing traces from *Und3*/+ and *Und4*/+ RT-PCR products in B. The double peaks correspond to the intronic sequence overlaid on the sequence of the next exon.

Figure 4. Conditional allele of *Adamts9*

A) The protein structure of Adamts9, amino acid number shown at top. The locations of the *Und* affected exon junctions are indicated by stars. The *Adamts9* ^{flox} allele targets amino acids 227 to 390. **B)** Creation of the *Adamts9* floxed allele. A, ApaI; X, XbaI; triangles, loxP. **C)** *Adamts9*^{KO}/+ mice exhibit tail rings, while controls are pigmented normally. **D)** Immunohistochemistry against the Adamts9 propeptide in neonatal mouse tail skin.

Figure 5. Melanoblast deficiency in *Adamts9*^{Und} mutants

A) X-gal stained whole mount *Dct-LacZ*/+ E16.5 tails, +/+ (left) and *Und4*/+ (right). **B**) X-gal stained epidermal (left column) and dermal (right column) sheets from the same representative tails at P0 and P2. At P0, the representative +/+ epidermis exhibits an area of decreased melanoblast density that overlaps the area completely lacking melanoblasts in the representative *Und4*/+ mutant (circled with dashed line). At P2, the representative +/+ epidermis is uniformly populated, while the *Und4*/+ and *Und3*/+ mutants exhibit one or more areas devoid of melanoblasts. The dermis of wildtype and mutants (shown to the right of each epidermis) contains LacZ-positive cells throughout. Nerves in the dermis are also LacZ-positive.

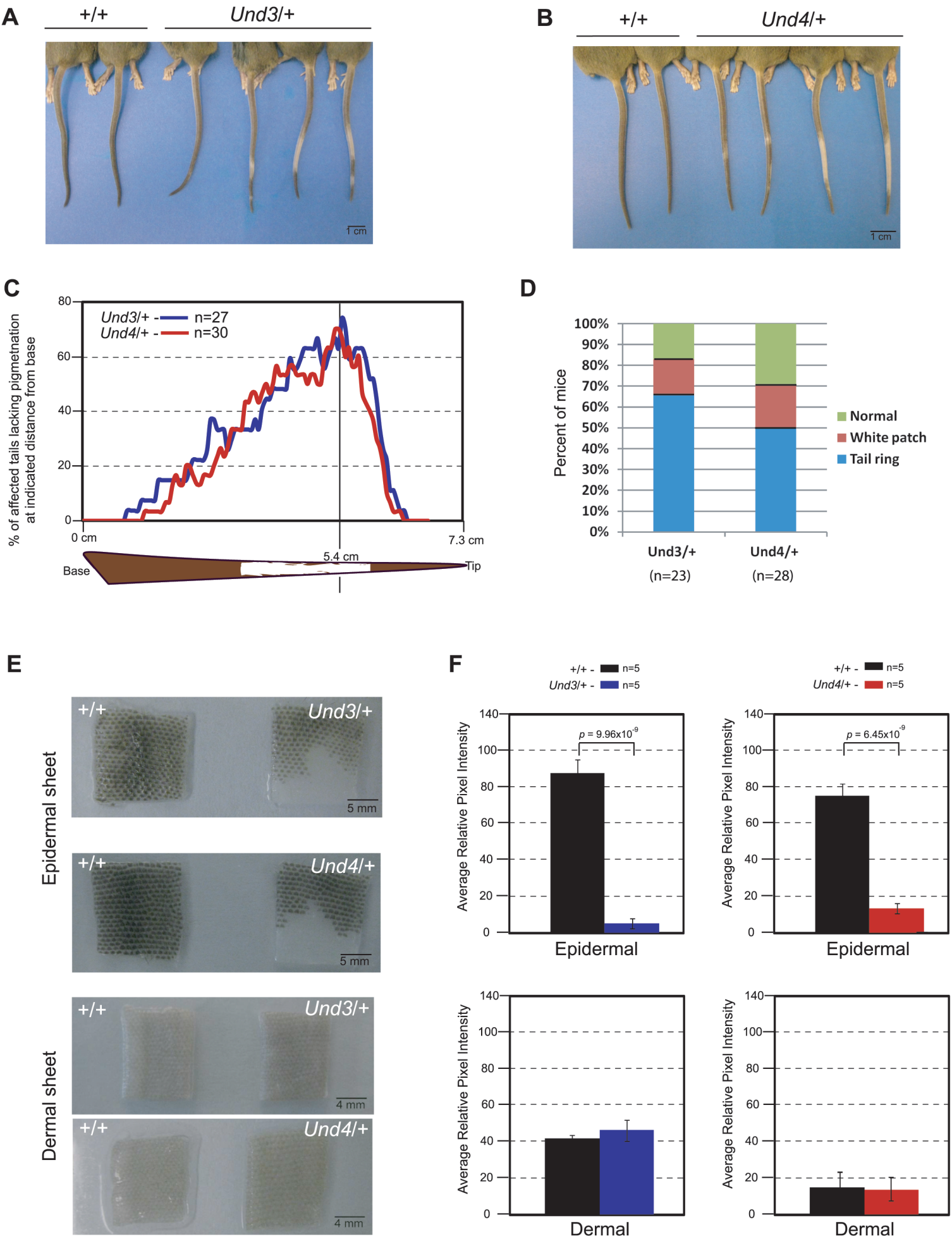
Figure 6. Conditional haploinsufficiency of *Adamts9* in melanocytes or keratinocytes

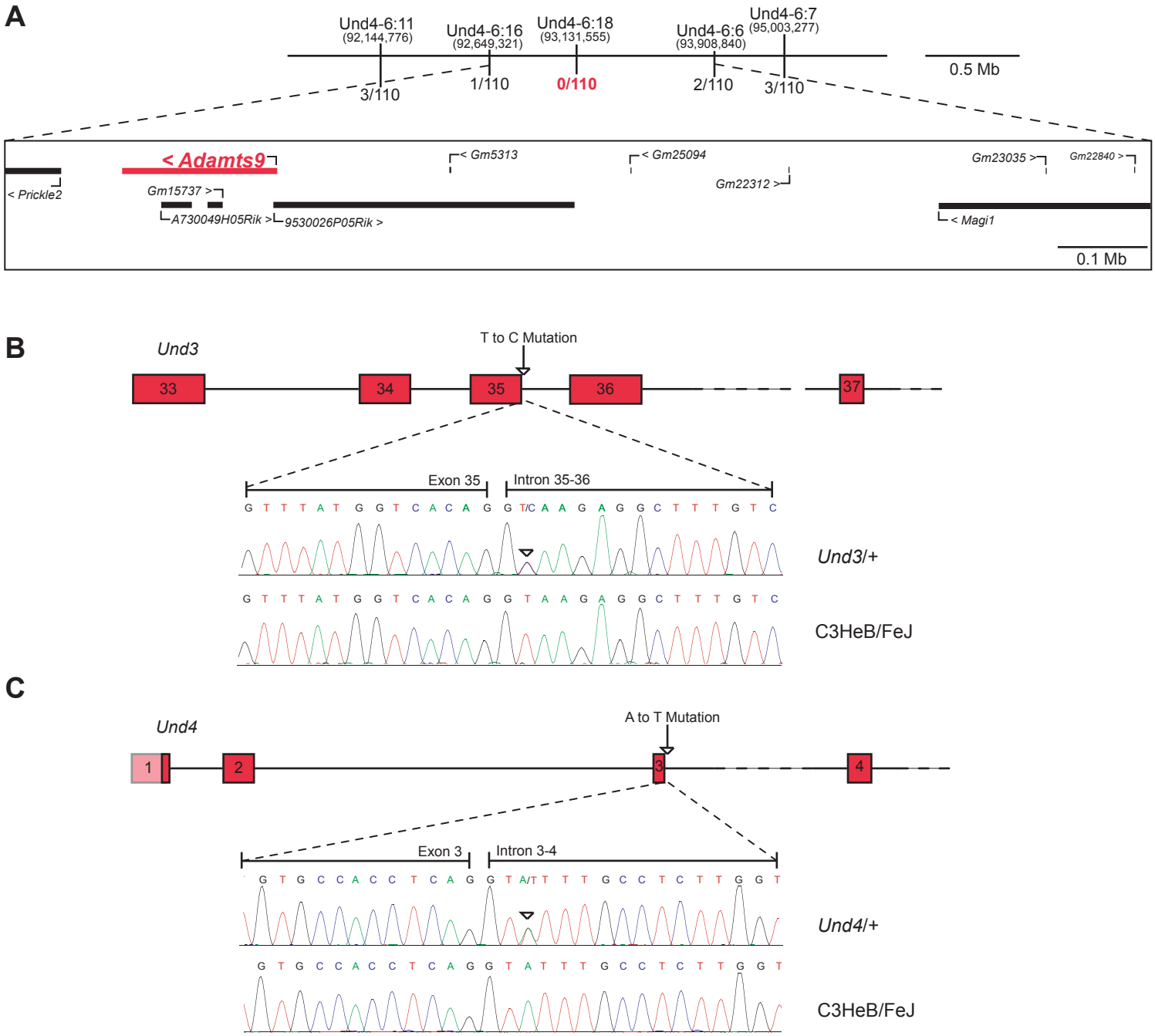
A) Percent growth of six segments along the tail between P10 and P19, averaged from 5 *Und4*/+ pups. **B**) X-gal stained whole mount *Dct-LacZ*/+; *Und4*/+ P28 epidermal sheets, from the base of the tail (position 1) and from the area around the boundary between the affected and unaffected skin (positions 2 and 3). Arrows indicate LacZ-positive melanocytes. **C**) X-gal stained hairs plucked from the pigmented (left) and unpigmented (right) areas of a *Und4*/+ tail. LacZ-positive melanocytes are present in the pigmented hair bulb (black arrow). **D-E)** Tails from the progeny of *Adamts9*^{flox}/+ mice crossed to either *K14-cre/*+ mice (D) or *Mitf-cre/*+ mice (E). Open arrowhead in E indicates a small tail ring in one out of nine *Mitf-cre/*+; *Adamts9*^{flox}/+ mice produced. Mice are 4 weeks of age. **F**) Anti-Mitf antibody staining (green) in PO *K14-cre/+; R26-Tomato/*+ tail skin. Tomato signal is shown in red. Arrows indicate Mitf-positive, Tomato-negative cells. **G)** Quantification of cells in *Mitf-cre/+; R26-Tomato/*+ tail skin that were either positive for the Mitf antibody signal only, positive for Tomato signal only, or positive for both signals. 74% of Mitf ab positive cells also expressed Tomato, while 84% of Tomato positive cells were also positive for Mitf protein. That not all Tomato positive cells were positive for Mitf ab could be due to a failure of antibody staining or to cells that currently express low levels of Mitf protein. **H)** Anti-Mitf antibody staining in PO *Mitf-cre/+; R26-Tomato/*+ tail skin. Double positive Mitf/Tomato melanoblasts were located in characteristic locations in hair follicles ("hf" - traced with dashed line). Scale bars represent 40 μm.

Figure 7. Cell death in *Adamts9* haploinsufficient melanocytes at P0

A-B) Tomato signal (red) in tail epidermal sheets from P0 *Mitf-cre*/+; +/+; *R26-Tomato*/+ (A) or *Mitf-cre*/+; *Adamts9*^{flox}/+; *R26-Tomato*/+ (B) littermates. Example melanoblasts 1 and 2 are a normal spherical shape, while example melanoblasts 3-5 are undergoing fragmentation. Scale bars represent 50 μm (boxed fields) or 20 μm (individual cells). **C-D**) Representative Tomato positive proliferative

melanoblasts. Left, melanoblast in the process of division along the midline; Right, melanoblasts within 3 μm of each other, presumed to have recently divided. Scale bar represents 20 μm. **E**) A TUNEL positive (green) melanoblast is indicated by an arrow in an *Mitf-cre*/+; *Adamts9*^{flox}/+; *R26-Tomato*/+ whole mount epidermal sheet. Tomato signal (red) is weaker in the TUNEL-positive melanoblast than in the normal shaped melanoblast located just above it. A melanoblast undergoing fragmentation is below. Scale bar represents 20 μm. **F)** Relative expression of *Adamts* family members in FACS sorted *Mitf-cre*/+; *R26-Tomato*/+ P14 and P28 epidermal tail melanocytes analyzed by RNAseq.


A
+/+
Und3/+
1 cm
B
+/+
Und4/+
1 cm
C
% of affected tails lacking pigmetnation at indicated distance from base
Und3/+ - n=27
Und4/+ - n=30
0 cm
5.4 cm
7.3 cm
Base
Tip
D
Percent of mice
Normal
White patch
Tail ring
Und3/+ (n=23)
Und4/+ (n=28)
E
Epidermal sheet
Dermal sheet
+/+
Und3/+
Und4/+
5 mm
4 mm
F
+/+ - n=5
Und3/+ - n=5
Und4/+ - n=5
Average Relative Pixel Intensity
p = 9.96x10-9
p = 6.45x10-9
Epidermal
Dermal


A
Und4-6:11
(92,144,776)
Und4-6:16
(92,649,321)
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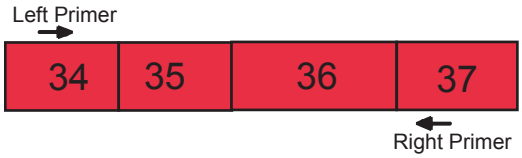
(93,131,555)
Und4-6:6
(93,908,840)
Und4-6:7
(95,003,277)
3/110
1/110
0/110
2/110
3/110
0.5 Mb
< Prickle2
< Adamts9
Gm15737 >
A730049H05Rik >
9530026P05Rik >
< Gm5313
< Gm25094
Gm22312 >
Gm23035 >
Gm22840 >
< Magi1
0.1 Mb
B
Und3
T to C Mutation
33
34
35
36
37
Exon 35
Intron 35-36
Und3/+
C3HeB/FeJ
C
Und4
A to T Mutation
1
2
3
4
Exon 3
Intron 3-4
Und4/+
C3HeB/FeJ

A

Und3 assay

Expected amplicon size: 299 bp



Und4 assay

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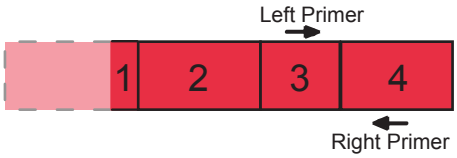
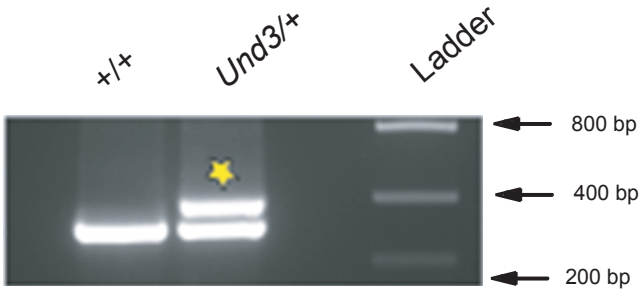
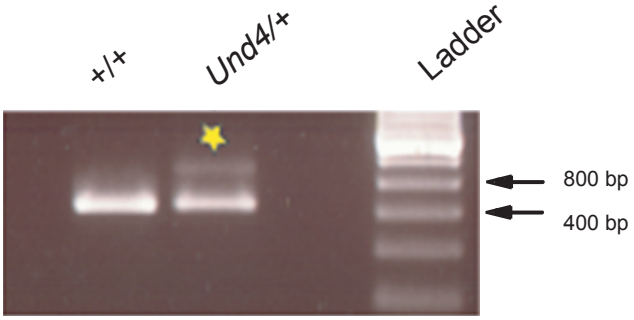


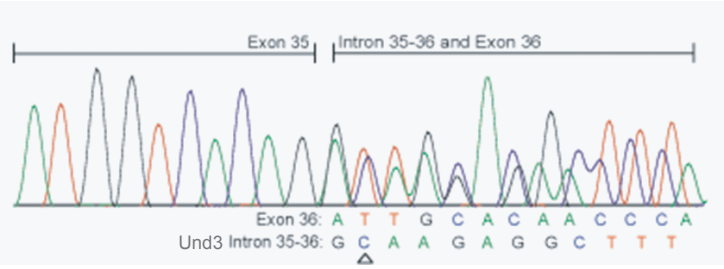
B



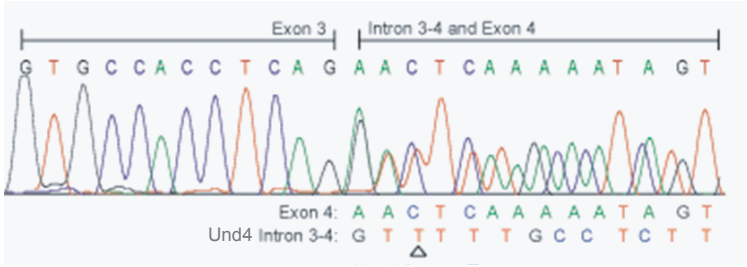


C

Und3/+

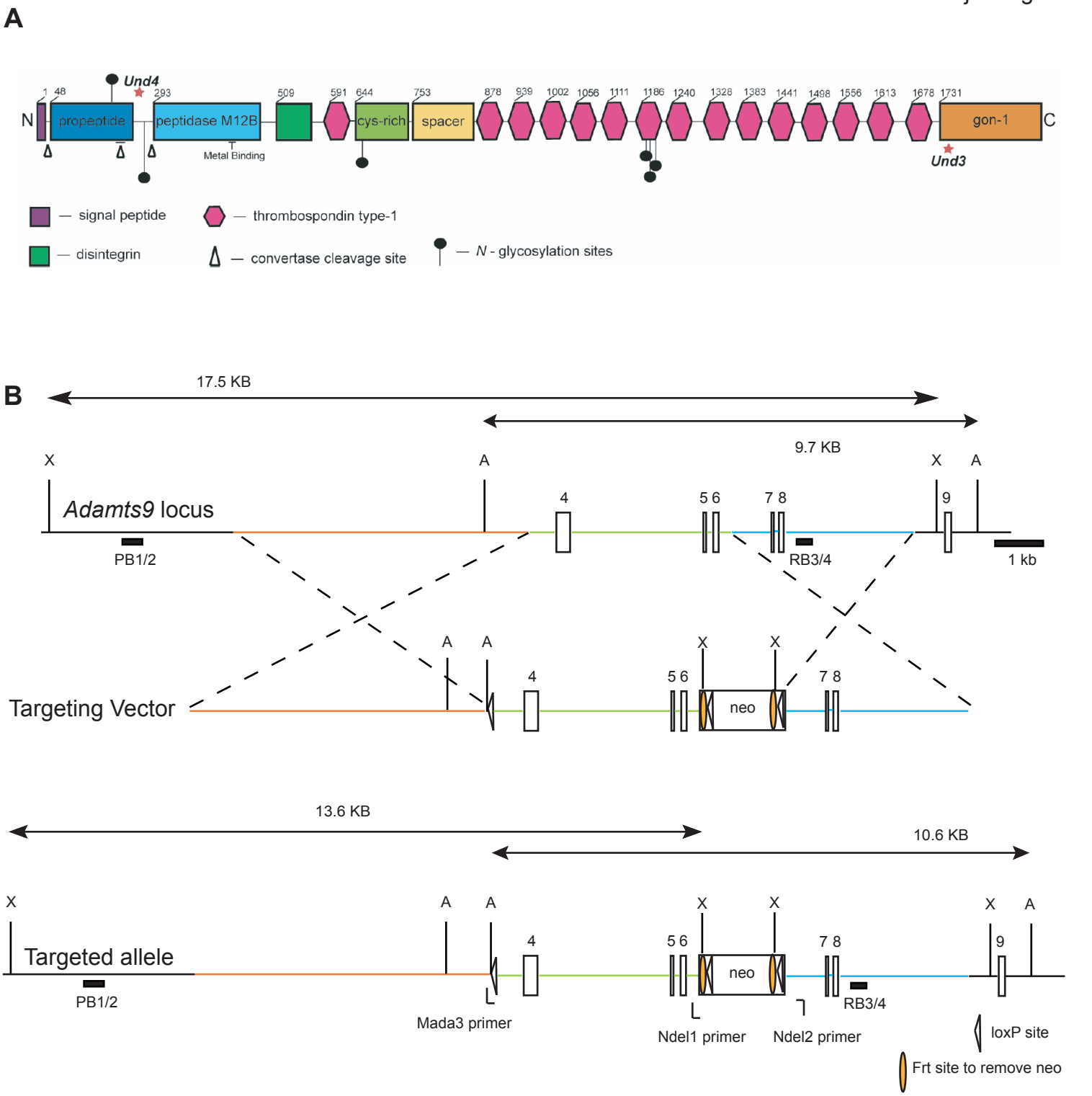


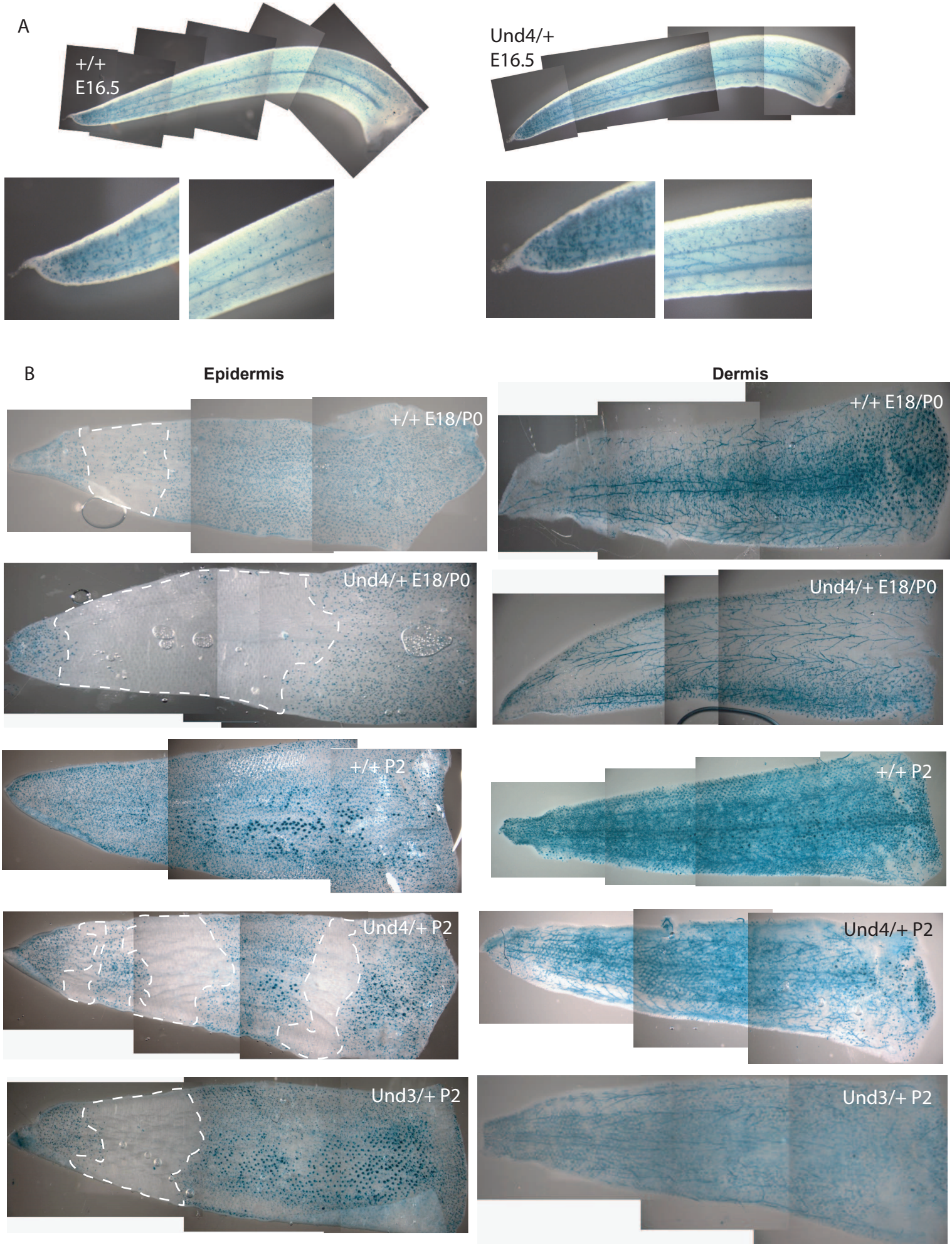
Und4/+



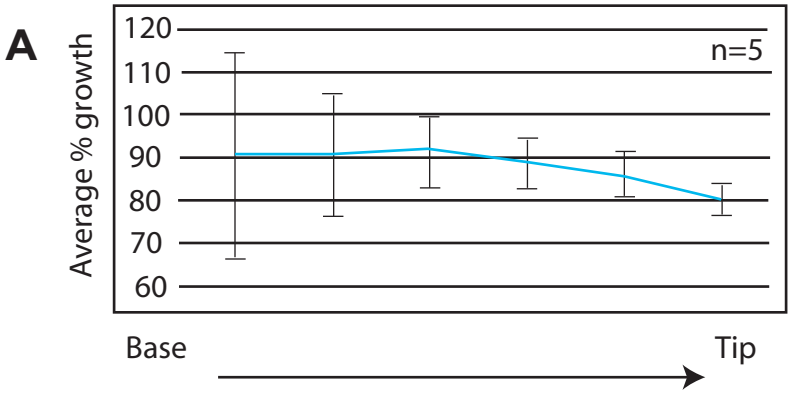
Und3 mutation in intron = T to C

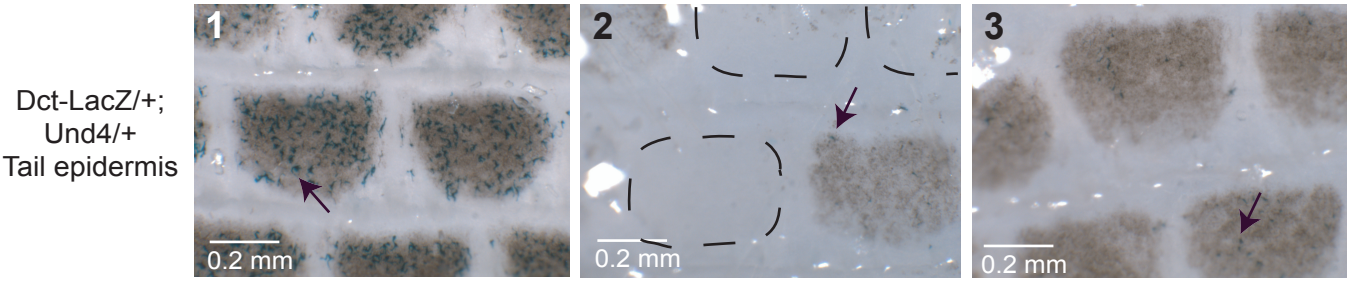
Und4 mutation in intron = A to T

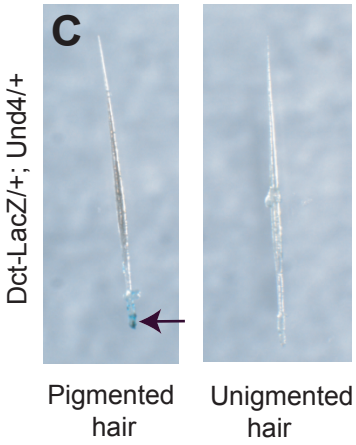

A
N
C
Und4
Und3
propeptide
peptidase M12B
Metal Binding
cys-rich
spacer
gon-1
signal peptide
thrombospondin type-1
disintegrin
convertase cleavage site
N - glycosylation sites
B
17.5 KB
9.7 KB
Adamts9 locus
PB1/2
RB3/4
1 kb
Targeting Vector
neo
13.6 KB
10.6 KB
Targeted allele
Mada3 primer
NdeI1 primer
NdeI2 primer
loxP site
Frt site to remove neo
C
Adamts9 Flox/+
Ella-cre/+
Adamts9 KO /+
D
anti-Adamts9 IHC
no primary antibody
50 μm
50 μm

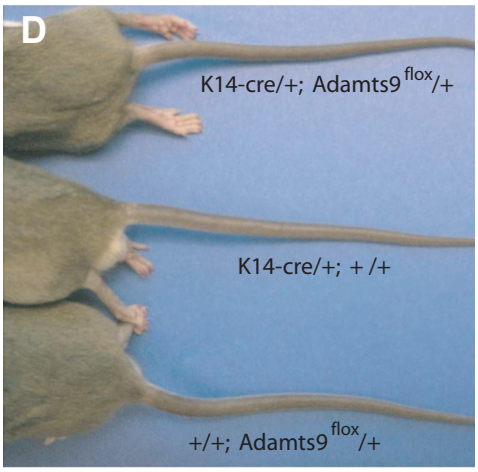

A
+/+
E16.5
Und4/+
E16.5
B
Epidermis
Dermis
+/+ E18/P0
+/+ E18/P0
Und4/+ E18/P0
Und4/+ E18/P0
+/+ P2
+/+ P2
Und4/+ P2
Und4/+ P2
Und3/+ P2
Und3/+ P2

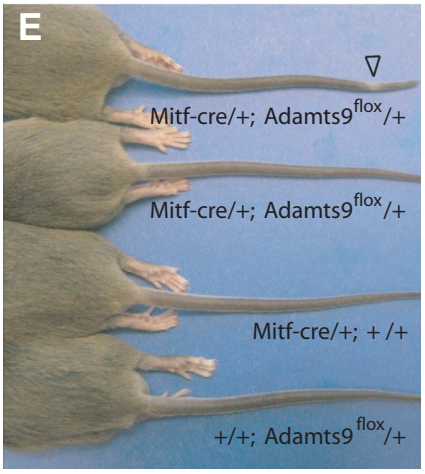
Tharmarajah Figure 6

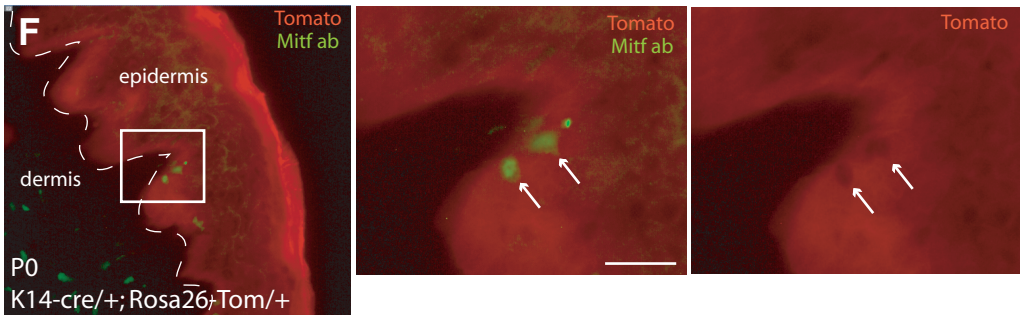


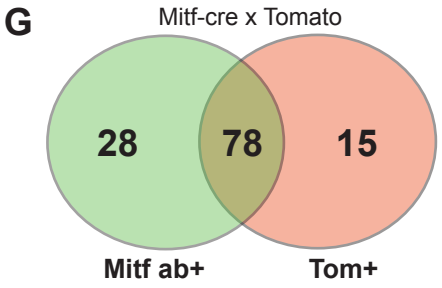


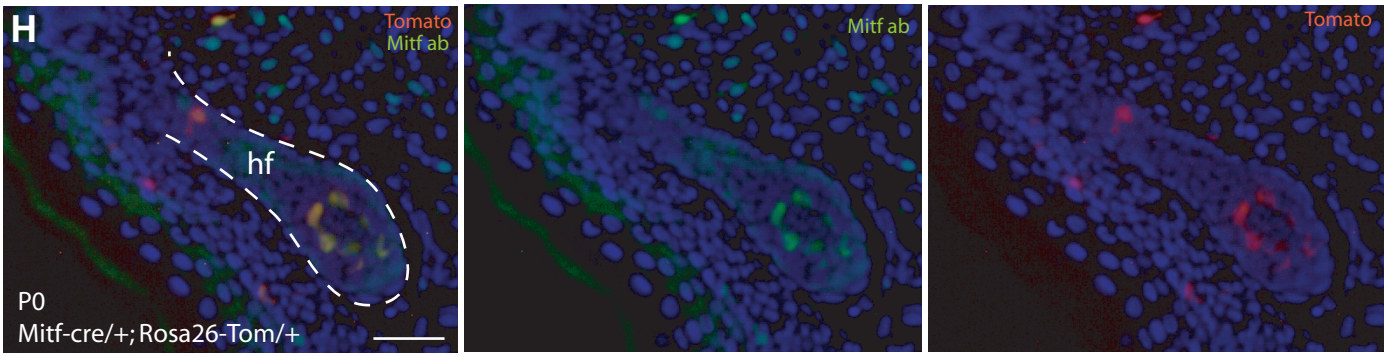


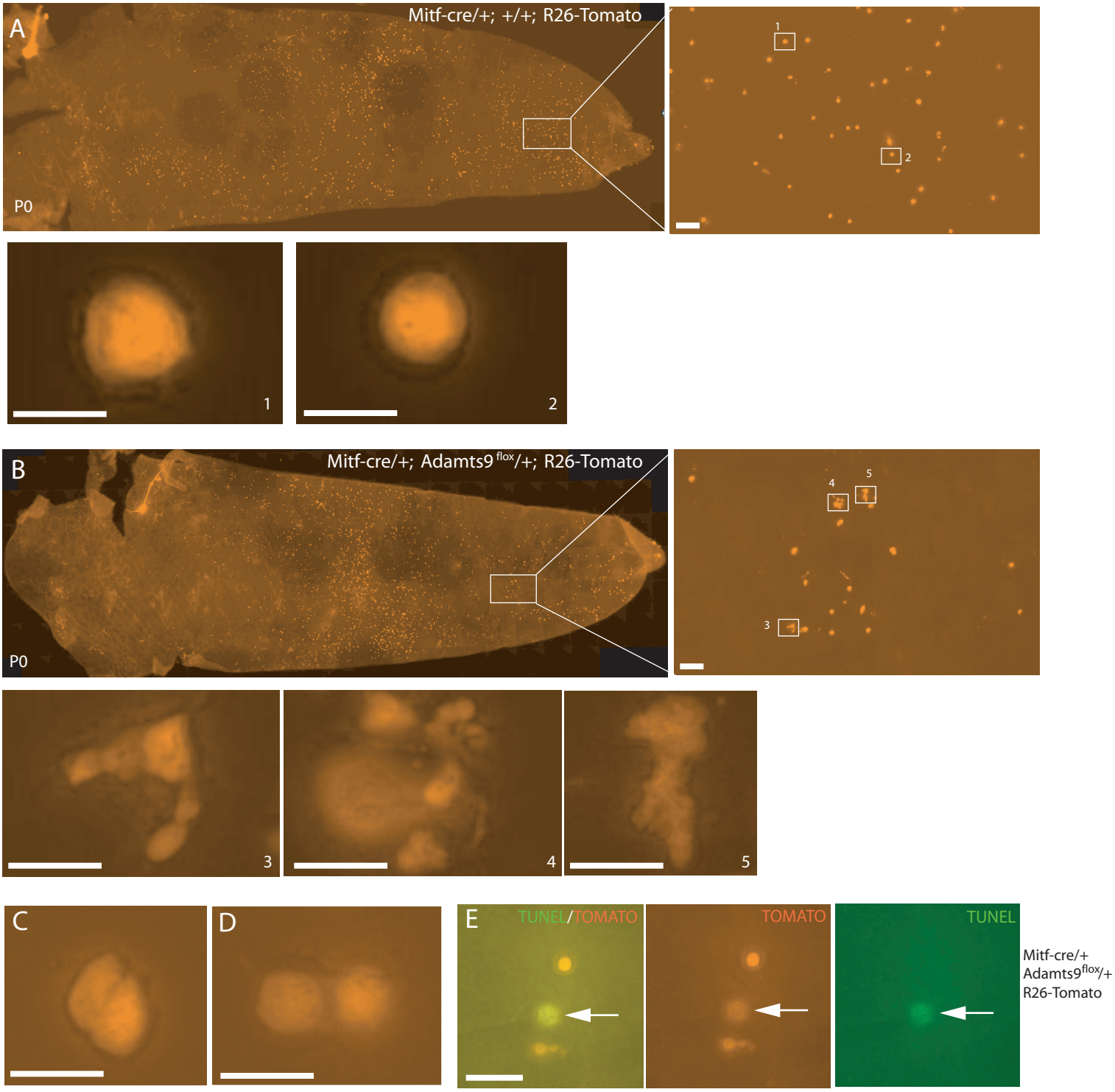


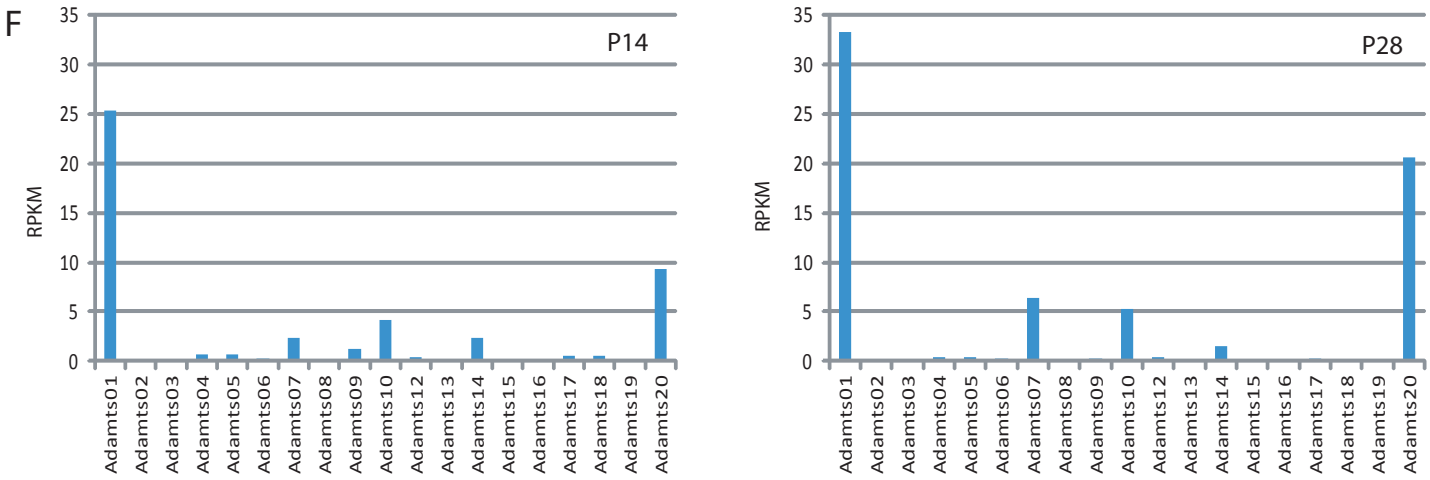









A
Mitf-cre/+; +/+; R26-Tomato
P0
1
2
B
Mitf-cre/+; Adamts9 flox/+; R26-Tomato
P0
3
4
5
C
D
E
TUNEL/TOMATO
TOMATO
TUNEL
Mitf-cre/+
Adamts9flox/+
R26-Tomato


F
P14
P28
RPKM
0
5
10
15
20
25
30
35
Adamts01
Adamts02
Adamts03
Adamts04
Adamts05
Adamts06
Adamts07
Adamts08
Adamts09
Adamts10
Adamts12
Adamts13
Adamts14
Adamts15
Adamts16
Adamts17
Adamts18
Adamts19
Adamts20

Supplementary Materials for:

Melanocyte development in the mouse tail epidermis requires the Adamts9 metalloproteinase

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cvr@mail.ubc.ca
Phone:604-827-4224
Fax:604-822-5348

Supplementary Results

BoxPlot analysis of the ratio of the frequency of occurrence of each peptide in +/+ versus *Adamts9*^{Und4}/+ samples was used to identify significant ($p \leq 5\%$) outliers from the mean ratio of all peptides identified by TAILS (**Supplementary Tables 1F-a, 1G-a)** and shotgun (preTAILS) (**Supplementary Tables 1F-b, 1G-b)** mass spectrometry analyses. Note that some proteins were represented by more than one peptide in Supplementary Tables 1F and 1G. These can be distinguished by comparing the provided peptide sequences. For peptides with a higher occurrence in +/+ versus *Adamts9*^{Und4}/+ samples, the ratios ranged from 1.6 to 14.1, with an average fold change of 3.7. For peptides with a lower occurrence in +/+ than *Adamts9*^{Und4}/+ samples, the ratios ranged from 0.53 to 0.001, corresponding to a 2.7 to 874-fold difference. The average fold change was 77. A direct substrate of Adamts9 would be expected to appear in the group of peptides found more often in +/+ versus *Adamts9*^{Und4}/+ samples (*i.e.* **Supplementary Table 1F-a**), but a reduction in Adamts9 could also generally perturb the proteomic web leading to compensatory expression of other proteases. We note that some proteins appear in both Supplementary Tables 1F and 1G, represented by different peptides, increasing protein identification confidence. Candidate extracellular matrix substrates (direct or indirect), including proteoglycan core proteins found previously for other Adamts proteases, are highlighted in orange in Table 1F-a (Apte, 2009). Thus, these form reasonable candidates for future validation and functional analyses.

Supplementary Methods

Total soluble and insoluble proteome was extracted from pigmented skin (dermis and epidermis) from the proximal first quarter of the tails of P7.5 *Adamts9*^{Und4}/+ and +/+ littermates and quantified by Bradford assay. 2 *Adamts9*^{Und4}/+ and 2 +/+ littermates were analyzed in 2 paired replicates. The data from these replicates was pooled together in Supplementary Tables 1A-G. TAILS was performed as described in detail previously (Kleifeld et al., 2010; Kleifeld et al., 2011). In brief, soluble and insoluble protein fractions of four biological replicates were denatured and cysteine side chains were reduced and alkylated. Free primary amines, including those generated by endogenous protease activity, were blocked by reductive demethylation using isotypically labeled formaldehyde. +/+ (labeled with heavy formaldehyde) and *Adamts9*^{Und4}/+ (labeled with light formaldehyde) proteomes were combined to form duplex samples. Proteins were then digested with trypsin to generate peptides suitable for mass spectrometry. Trypsin generated peptides with free reactive primary amines were subsequently removed by binding to a hyperbranched polyglycerol aldehyde derivatized polymer. The remaining peptides were desalted using C18 STAGE tips prior to LC0MS/MS analysis on a LTQ-Orbitrap Velos coupled to an Agilent 1290 Series HPLC. The resulting MS data files were processed using MaxQuant software (v. 1.5.1.2). The integrated search engine Andromeda was used to search MS/MS spectra against murine UniProtKB FASTA database

(October 2013 release).

Supplementary References

Apte, S. S. (2009). A disintegrin-like and metalloprotease (reprolysin-type) with thrombospondin type 1 motif (ADAMTS) superfamily: functions and mechanisms. J Biol Chem *284***,** 31493-7.

Kleifeld, O., Doucet, A., Auf Dem Keller, U., Prudova, A., Schilling, O., Kainthan, R. K., Starr, A. E., Foster, L. J., Kizhakkedathu, J. N., and Overall, C. M. (2010). Isotopic labeling of terminal amines in complex samples identifies protein N-termini and protease cleavage products. Nat Biotechnol *28***,** 281-8.

Kleifeld, O., Doucet, A., Prudova, A., Auf Dem Keller, U., Gioia, M., Kizhakkedathu, J. N., and Overall, C. M. (2011). Identifying and quantifying proteolytic events and the natural N terminome by terminal amine isotopic labeling of substrates. Nat Protoc *6***,** 1578-611.

Supplementary Table 1

A	List of all proteins identified by proteomics in tail skin of Adamts9-Und4/+ and +/+ mice.
B	Peptides identified by shotgun proteomics prior to TAILS (preTAILS) with an unlabeled N-terminus (i.e. free, acetylated, or after pyro-Glu formation).
C	Peptides identified by shotgun proteomics prior to TAILS (preTAILS) with a labeled N-terminus (i.e. dimethylated with heavy (+/+) or light (Adamts9-Und4/+) formaldehyde).
D	Peptides identified by TAILS with an unlabeled N-terminus (i.e. free, acetylated, or after pyro-Glu formation).
E	Peptides identified by TAILS with a labeled N-terminus (i.e. dimethylated with heavy (+/+) or light (Adamts9-Und4/+) formaldehyde).
Fa	Outlier peptides identified by TAILS with a higher occurrence in +/+ than Adamts9-Und4/+ mice.
Fb	Outlier peptides identified by shotgun proteomics prior to TAILS (preTAILS) with a higher occurrence in +/+ than Adamts9-Und4/+ mice.
Ga	Outlier peptides identified by TAILS procedure with a lower occurrence in +/+ than Adamts9-Und4/+.
Gb	Outlier peptides identified by shotgun proteomics prior to TAILS (preTAILS) with a lower occurrence in +/+ than Adamts9-Und4/+.

ST1A **Supplementary Table 1A:** **List of all proteins identified by proteomics in tail skin of Adamts9-Und4/+ and +/+ mice.**

Abbreviations: aa - amino acids; Da - Dalton.

Index	UniProt ID	Entry name	Protein names	Organism	Gene names	Protein existence	Length (# aa)	Mass (Da)	Gene ontology (biological process)	Gene ontology (molecular function)	Gene ontology (cellular component)
1	Q9QXS1	PLEC_MOUSE	Plectin (PCN) (PLTN	Mus musculus (Mouse)	Plec	Evidence at protein level	4691	534188	hemidesmosome assemb	ankyrin binding [GO:0030	brush border [GO:00059
2	E9Q557	DESP_MOUSE	Desmoplakin (DP)	Mus musculus (Mouse)	Dsp	Evidence at protein level	2883	332912	adherens junction organi	protein binding, bridging	basolateral plasma memb
3	P02535	K1C10_MOUSE	Keratin, type I cyto	Mus musculus (Mouse)	Krt10	Evidence at protein level	570	57770	cellular response to calci	cytoskeletal protein bindi	keratin filament [GO:004
4	Q61897	KT33B_MOUSE	Keratin, type I cuti	Mus musculus (Mouse)	Krt33b	Evidence at protein level	404	45864		structural molecule activi	extracellular exosome [G
5	Q61781	K1C14_MOUSE	Keratin, type I cyto	Mus musculus (Mouse)	Krt14	Evidence at protein level	484	52867	aging [GO:0007568]; epit	keratin filament binding [	basal part of cell [GO:004
6	Q60847	COCA1_MOUSE	Collagen alpha-1(X	Mus musculus (Mouse)	Col12a1	Evidence at transcript level	3120	340214	cell adhesion [GO:0007155]; endodermal cell differ		collagen trimer [GO:0005
7	P63260	ACTG_MOUSE	Actin, cytoplasmic	Mus musculus (Mouse)	Actg1	Evidence at protein level	375	41793	membrane organization [	ATP binding [GO:000552	actin cytoskeleton [GO:0
8	P20152	VIME_MOUSE	Vimentin	Mus musculus (Mouse)	Vim	Evidence at protein level	466	53688	astrocyte development [G	double-stranded RNA bin	cell leading edge [GO:003
9	P04104	K2C1_MOUSE	Keratin, type II cyto	Mus musculus (Mouse)	Krt1	Evidence at protein level	637	65606	complement activation, l	carbohydrate binding [GO	blood microparticle [GO:0
10	Q3TTY5	K22E_MOUSE	Keratin, type II cyto	Mus musculus (Mouse)	Krt2	Evidence at protein level	707	70923	epidermis development [	cytoskeletal protein bindi	extracellular exosome [G
11	Q8VDD5	MYH9_MOUSE	Myosin-9 (Cellular	Mus musculus (Mouse)	Myh9	Evidence at protein level	1960	226372	actin cytoskeleton reorga	actin binding [GO:000377	actin cytoskeleton [GO:0
12	Q01853	TERA_MOUSE	Transitional endopl	Mus musculus (Mouse)	Vcp	Evidence at protein level	806	89322	activation of cysteine-typ	ADP binding [GO:004353	cytosol [GO:0005829]; De
13	P99024	TBB5_MOUSE	Tubulin beta-5 chai	Mus musculus (Mouse)	Tubb5	Evidence at protein level	444	49671	cellular process [GO:000	GTPase activity [GO:0003	cell body [GO:0044297];
14	P48678	LMNA_MOUSE	Prelamin-A/C [Clea	Mus musculus (Mouse)	Lmna	Evidence at protein level	665	74238	cellular response to hypo	structural molecule activi	extracellular matrix [GO:0
15	Q9D646	KRT34_MOUSE	Keratin, type I cuti	Mus musculus (Mouse)	Krt34	Evidence at transcript level	392	44560		structural molecule activi	extracellular exosome [G
16	P68373	TBA1C_MOUSE	Tubulin alpha-1C ch	Mus musculus (Mouse)	Tuba1c	Evidence at protein level	449	49909	microtubule-based proce	GTPase activity [GO:0003	cytoplasmic microtubule
17	P10126	EF1A1_MOUSE	Elongation factor 1	Mus musculus (Mouse)	Eef1a1	Evidence at protein level	462	50114	cellular response to epide	GTPase activity [GO:0003	cortical actin cytoskeleto
18	Q03265	ATPA_MOUSE	ATP synthase subu	Mus musculus (Mouse)	Atp5a1	Evidence at protein level	553	59753	ATP synthesis coupled pro	ATP binding [GO:000552	COP9 signalosome [GO:0
19	P07724	ALBU_MOUSE	Serum albumin	Mus musculus (Mouse)	Alb	Evidence at protein level	608	68693	cellular response to starv	chaperone binding [GO:0	blood microparticle [GO:0
20	Q9R0H5	K2C71_MOUSE	Keratin, type II cyto	Mus musculus (Mouse)	Krt71	Evidence at protein level	524	57383	hair follicle morphogenes	structural molecule activi	cytoplasm [GO:0005737]
21	P07356	ANXA2_MOUSE	Annexin A2 (Annex	Mus musculus (Mouse)	Anxa2	Evidence at protein level	339	38676	angiogenesis [GO:000152	cadherin binding involved	basement membrane [GO
22	P58252	EF2_MOUSE	Elongation factor 2	Mus musculus (Mouse)	Eef2	Evidence at protein level	858	95314	aging [GO:0007568]; cell	5S rRNA binding [GO:000	aggresome [GO:0016235
23	P16546	SPTN1_MOUSE	Spectrin alpha chai	Mus musculus (Mouse)	Sptan1	Evidence at protein level	2472	284597	actin filament capping [G	cadherin binding involved	cell-cell adherens junctio
24	P63017	HSP7C_MOUSE	Heat shock cognate	Mus musculus (Mouse)	Hspa8	Evidence at protein level	646	70871	ATP metabolic process [G	ATPase activity [GO:0016	blood microparticle [GO:0
25	Q9R269	PEPL_MOUSE	Periplakin	Mus musculus (Mouse)	Ppl	Evidence at protein level	1755	204004	keratinization [GO:00314	cadherin binding involved	cell-cell adherens junctio
26	Q9JHU4	DYHC1_MOUSE	Cytoplasmic dynein	Mus musculus (Mouse)	Dync1h1	Evidence at protein level	4644	532045	cilium movement [GO:00	ATP binding [GO:000552	centrosome [GO:000581
27	Q8BGZ7	K2C75_MOUSE	Keratin, type II cyto	Mus musculus (Mouse)	Krt75	Evidence at protein level	551	59741	hematopoietic progenitor	structural molecule activi	extracellular exosome [G
28	P84244	H33_MOUSE	Histone H3.3	Mus musculus (Mouse)	H3f3a; H3f3b	Evidence at protein level	136	15328	brain development [GO:0	histone binding [GO:0042	Barr body [GO:0001740];
29	P17742	PPIA_MOUSE	Peptidyl-prolyl cis-t	Mus musculus (Mouse)	Ppia	Evidence at protein level	164	17971	lipid particle organization	peptidyl-prolyl cis-trans i	cytosol [GO:0005829]; ex
30	P97350	PKP1_MOUSE	Plakophilin-1	Mus musculus (Mouse)	Pkp1	Evidence at protein level	728	80896	intermediate filament bu	lamin binding [GO:00055	desmosome [GO:003005
31	O70456	1433S_MOUSE	14-3-3 protein sign	Mus musculus (Mouse)	Sfn	Evidence at protein level	248	27706	establishment of skin bar	cadherin binding involved	cell-cell adherens junctio
32	P19096	FAS_MOUSE	Fatty acid synthase	Mus musculus (Mouse)	Fasn	Evidence at protein level	2504	272428	acetyl-CoA metabolic pro	[acyl-carrier-protein] S-ac	cell-cell adherens junctio
33	P56480	ATPB_MOUSE	ATP synthase subu	Mus musculus (Mouse)	Atp5b	Evidence at protein level	529	56300	angiogenesis [GO:000152	ATP binding [GO:000552	cell surface [GO:0009986
34	Q62261	SPTB2_MOUSE	Spectrin beta chain	Mus musculus (Mouse)	Sptbn1	Evidence at protein level	2363	274223	actin filament capping [G	ankyrin binding [GO:0030	axolemma [GO:0030673]
35	P57780	ACTN4_MOUSE	Alpha-actinin-4 (No	Mus musculus (Mouse)	Actn4	Evidence at protein level	912	104977	actin filament bundle ass	actin filament binding [G	brush border [GO:00059
36	Q8BG05	ROA3_MOUSE	Heterogeneous nuc	Mus musculus (Mouse)	Hnrnpa3	Evidence at protein level	379	39652	mRNA processing [GO:00	mRNA binding [GO:00037	catalytic step 2 spliceoso
37	P52480	KPYM_MOUSE	Pyruvate kinase PK	Mus musculus (Mouse)	Pkm	Evidence at protein level	531	57845	cellular response to insuli	ATP binding [GO:000552	cell-cell adherens junctio
38	P14602	HSPB1_MOUSE	Heat shock protein	Mus musculus (Mouse)	Hspb1	Evidence at protein level	209	23014	anterograde axonal prote	identical protein binding	axon cytoplasm [GO:190
39	Q61414	K1C15_MOUSE	Keratin, type I cyto	Mus musculus (Mouse)	Krt15	Evidence at protein level	452	49138		scaffold protein binding [	extracellular exosome [G
40	P11499	HS90B_MOUSE	Heat shock protein	Mus musculus (Mouse)	Hsp90ab1	Evidence at protein level	724	83281	cellular response to drug	ATP binding [GO:000552	apical plasma membrane
41	Q922U2	K2C5_MOUSE	Keratin, type II cyto	Mus musculus (Mouse)	Krt5	Evidence at protein level	580	61767		scaffold protein binding [	cytoplasm [GO:0005737]
42	Q02788	CO6A2_MOUSE	Collagen alpha-2(V	Mus musculus (Mouse)	Col6a2	Evidence at protein level	1034	110334	cell adhesion [GO:0007155];	protein heterotrimeriz	collagen trimer [GO:0005
43	Q9QZU5	KR151_MOUSE	Keratin-associated	Mus musculus (Mouse)	Krtap15-1	Evidence at transcript level	150	16242			intermediate filament [G
44	Q922T6	KRT85_MOUSE	Keratin, type II cuti	Mus musculus (Mouse)	Krt85	Evidence at protein level	507	55759		structural molecule activi	keratin filament [GO:004
45	Q9QWL7	K1C17_MOUSE	Keratin, type I cyto	Mus musculus (Mouse)	Krt17	Evidence at protein level	433	48162	hair follicle morphogenes	MHC class II protein bind	cell periphery [GO:00719
46	Q497I4	KRT35_MOUSE	Keratin, type I cuti	Mus musculus (Mouse)	Krt35	Evidence at protein level	455	50530		structural molecule activi	extracellular exosome [G
47	Q9DBJ1	PGAM1_MOUSE	Phosphoglycerate r	Mus musculus (Mouse)	Pgam1	Evidence at protein level	254	28832	gluconeogenesis [GO:000	2,3-bisphosphoglycerate-	cytoplasm [GO:0005737]
48	P62908	RS3_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps3	Evidence at protein level	243	26674	apoptotic process [GO:00	damaged DNA binding [G	cytoplasm [GO:0005737]
49	Q00612	G6PD1_MOUSE	Glucose-6-phospha	Mus musculus (Mouse)	G6pdx	Evidence at protein level	515	59263	angiotensin-mediated vas	glucose-6-phosphate deh	cytoplasm [GO:0005737]
50	Q02257	PLAK_MOUSE	Junction plakoglobi	Mus musculus (Mouse)	Jup	Evidence at protein level	745	81801	adherens junction assem	alpha-catenin binding [GO	actin cytoskeleton [GO:0
51	Q01768	NDKB_MOUSE	Nucleoside diphosp	Mus musculus (Mouse)	Nme2	Evidence at protein level	152	17363	cellular response to fatty	ATP binding [GO:000552	cell periphery [GO:00719
52	Q68FD5	CLH1_MOUSE	Clathrin heavy chai	Mus musculus (Mouse)	Cltc	Evidence at protein level	1675	191557	autophagy [GO:0006914]	clathrin light chain bindin	clathrin-coated vesicle [G
53	Q61495	DSG1A_MOUSE	Desmoglein-1-alph	Mus musculus (Mouse)	Dsg1a	Evidence at transcript level	1057	114597	homophilic cell adhesion	calcium ion binding [GO:0	cytoplasmic side of plasm
54	Q05816	FABP5_MOUSE	Fatty acid-binding p	Mus musculus (Mouse)	Fabp5	Evidence at protein level	135	15137	glucose metabolic proces	fatty acid binding [GO:00	cytoplasm [GO:0005737]
55	Q9Z2X1	HNRPF_MOUSE	Heterogeneous nuc	Mus musculus (Mouse)	Hnrnpf	Evidence at protein level	415	45730	mRNA processing [GO:00	nucleotide binding [GO:0	catalytic step 2 spliceoso
56	Q8R0W0	EPIPL_MOUSE	Epiplakin	Mus musculus (Mouse)	Eppk1	Evidence at protein level	6548	724646	cytoskeleton organizatior	intermediate filament bir	apicolateral plasma mem
57	P61979	HNRPK_MOUSE	Heterogeneous nuc	Mus musculus (Mouse)	Hnrnpk	Evidence at protein level	463	50976	mRNA processing [GO:00	cadherin binding involved	catalytic step 2 spliceoso
58	P40142	TKT_MOUSE	Transketolase (TK)	Mus musculus (Mouse)	Tkt	Evidence at protein level	623	67630	glyceraldehyde-3-phosph	cofactor binding [GO:004	extracellular exosome [G
59	Q921I1	TRFE_MOUSE	Serotransferrin (Tra	Mus musculus (Mouse)	Tf	Evidence at protein level	697	76724	actin filament organizatic	ferric iron binding [GO:00	apical plasma membrane
60	Q08189	TGM3_MOUSE	Protein-glutamine g	Mus musculus (Mouse)	Tgm3	Evidence at protein level	693	77309	cell envelope organizatior	calcium ion binding [GO:0	cornified envelope [GO:0
61	P16045	LEG1_MOUSE	Galectin-1 (Gal-1) (	Mus musculus (Mouse)	Lgals1	Evidence at protein level	135	14866	apoptotic process [GO:00	carbohydrate binding [GO	cell surface [GO:0009986
62	Q9Z320	K1C27_MOUSE	Keratin, type I cyto	Mus musculus (Mouse)	Krt27	Evidence at protein level	448	49105	hair follicle morphogenes	structural molecule activi	cytoplasm [GO:0005737]
63	P97861	KRT86_MOUSE	Keratin, type II cuti	Mus musculus (Mouse)	Krt86	Evidence at transcript level	486	53251		structural molecule activi	extracellular exosome [G
64	P11088	FILA_MOUSE	Filaggrin (Fragment	Mus musculus (Mouse)	Flg	Evidence at transcript level	336	35678	epidermis development [	keratin filament binding [	cornified envelope [GO:0
65	P14733	LMNB1_MOUSE	Lamin-B1	Mus musculus (Mouse)	Lmnb1	Evidence at protein level	588	66786	positive regulation of cyc	JUN kinase binding [GO:0	lamin filament [GO:0005
66	P80314	TCPB_MOUSE	T-complex protein	Mus musculus (Mouse)	Cct2	Evidence at protein level	535	57477	'de novo' protein folding	ATP binding [GO:000552	cell body [GO:0044297];
67	Q6IMF0	KRT87_MOUSE	Keratin, type II cuti	Mus musculus (Mouse)	Krt87	Evidence at transcript level	495	54629		structural molecule activi	keratin filament [GO:004
68	Q62168	K1H2_MOUSE	Keratin, type I cuti	Mus musculus (Mouse)	Krt32	Evidence at protein level	407	46422		structural molecule activi	extracellular exosome [G
69	Q61656	DDX5_MOUSE	Probable ATP-depe	Mus musculus (Mouse)	Ddx5	Evidence at protein level	614	69290	alternative mRNA splicing	androgen receptor bindin	catalytic step 2 spliceoso
70	Q04857	CO6A1_MOUSE	Collagen alpha-1(V	Mus musculus (Mouse)	Col6a1	Evidence at protein level	1025	108489	cell adhesion [GO:00071	platelet-derived growth f	collagen trimer [GO:0005
71	Q62009	POSTN_MOUSE	Periostin (PN) (Ost	Mus musculus (Mouse)	Postn	Evidence at protein level	838	93144	bone regeneration [GO:1	heparin binding [GO:000	extracellular matrix [GO:0
72	Q9CZD3	GARS_MOUSE	Glycine--tRNA ligas	Mus musculus (Mouse)	Gars	Evidence at protein level	729	81878	diadenosine tetraphosph	ATP binding [GO:000552	axon [GO:0030424]; cyto
73	P70296	PEBP1_MOUSE	Phosphatidylethan	Mus musculus (Mouse)	Pebp1	Evidence at protein level	187	20830	aging [GO:0007568]; eati	ATP binding [GO:000552	apical part of cell [GO:00
74	Q9D8N0	EF1G_MOUSE	Elongation factor 1	Mus musculus (Mouse)	Eef1g	Evidence at protein level	437	50061	response to virus [GO:00	cadherin binding involved	cell-cell adherens junctio
75	Q02053	UBA1_MOUSE	Ubiquitin-like modi	Mus musculus (Mouse)	Uba1	Evidence at protein level	1058	117809	cellular response to DNA	ATP binding [GO:000552	cytoplasm [GO:0005737]
76	P60843	IF4A1_MOUSE	Eukaryotic initiatio	Mus musculus (Mouse)	Eif4a1	Evidence at protein level	406	46154	regulation of gene expres	ATP binding [GO:000552	cytoplasm [GO:0005737]
77	P20029	GRP78_MOUSE	78 kDa glucose-reg	Mus musculus (Mouse)	Hspa5	Evidence at protein level	655	72422	activation of signaling pro	ATPase activity [GO:0016	cell-cell adherens junctio
78	Q91VI7	RINI_MOUSE	Ribonuclease inhibi	Mus musculus (Mouse)	Rnh1	Evidence at protein level	456	49816	regulation of angiogenesi	ribonuclease inhibitor act	angiogenin-PRI complex [
79	Q8VEK3	HNRPU_MOUSE	Heterogeneous nuc	Mus musculus (Mouse)	Hnrnpu	Evidence at protein level	800	87918	cardiac muscle cell devel	ATP binding [GO:000552	catalytic step 2 spliceoso
80	Q80X19	COEA1_MOUSE	Collagen alpha-1(X	Mus musculus (Mouse)	Col14a1	Evidence at protein level	1797	193013	cell adhesion [GO:00071	RNA binding [GO:000372	collagen trimer [GO:0005
81	Q9D7P9	SPB12_MOUSE	Serpin B12	Mus musculus (Mouse)	Serpinb12	Evidence at transcript level	423	47835	hematopoietic progenitor	serine-type endopeptidas	cytoplasm [GO:0005737]
82	P23116	EIF3A_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif3a	Evidence at protein level	1344	161936	formation of cytoplasmic	mRNA binding [GO:00037	cytosol [GO:0005829]; eu
83	P17563	SBP1_MOUSE	Selenium-binding p	Mus musculus (Mouse)	Selenbp1	Evidence at protein level	472	52514	brown fat cell differentiat	selenium binding [GO:00	cytosol [GO:0005829]; ex
84	Q9CPY7	AMPL_MOUSE	Cytosol aminopept	Mus musculus (Mouse)	Lap3	Evidence at protein level	519	56141		aminopeptidase activity [	cytosol [GO:0005829]; ex
85	Q9D8E6	RL4_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl4	Evidence at protein level	419	47154	translation [GO:0006412]	RNA binding [GO:000372	cytoplasm [GO:0005737]
86	O88569	ROA2_MOUSE	Heterogeneous nuc	Mus musculus (Mouse)	Hnrnpa2b1	Evidence at protein level	353	37403	miRNA transport [GO:199	miRNA binding [GO:0035	catalytic step 2 spliceoso
87	Q9ERE2	KRT81_MOUSE	Keratin, type II cuti	Mus musculus (Mouse)	Krt81	Evidence at transcript level	481	52863		structural molecule activi	extracellular space [GO:0
88	P17182	ENOA_MOUSE	Alpha-enolase (EC	Mus musculus (Mouse)	Eno1	Evidence at protein level	434	47141	glycolytic process [GO:00	cadherin binding involved	cell-cell adherens junctio
89	P14824	ANXA6_MOUSE	Annexin A6 (67 kDa	Mus musculus (Mouse)	Anxa6	Evidence at protein level	673	75885	apoptotic signaling pathw	calcium-dependent phos	cytosol [GO:0005829]; ex
90	P29341	PABP1_MOUSE	Polyadenylate-bind	Mus musculus (Mouse)	Pabpc1	Evidence at protein level	636	70671	gene silencing by RNA [G	mRNA 3'-UTR binding [GO	catalytic step 2 spliceoso
91	P10107	ANXA1_MOUSE	Annexin A1 (Annex	Mus musculus (Mouse)	Anxa1	Evidence at protein level	346	38734	actin cytoskeleton reorga	annealing helicase activit	apical plasma membrane
92	P18760	COF1_MOUSE	Cofilin-1 (Cofilin, n	Mus musculus (Mouse)	Cfl1	Evidence at protein level	166	18560	actin filament depolymer	actin filament binding [G	cell-cell junction [GO:000
93	Q8K0Y2	KT33A_MOUSE	Keratin, type I cuti	Mus musculus (Mouse)	Krt33a	Evidence at protein level	404	46137		structural molecule activi	extracellular exosome [G
94	P60710	ACTB_MOUSE	Actin, cytoplasmic	Mus musculus (Mouse)	Actb	Evidence at protein level	375	41737	ATP-dependent chromati	ATP binding [GO:000552	blood microparticle [GO:0
95	P27773	PDIA3_MOUSE	Protein disulfide-iso	Mus musculus (Mouse)	Pdia3	Evidence at protein level	505	56678	antigen processing and pr	protein disulfide isomera	cell surface [GO:0009986
96	P24452	CAPG_MOUSE	Macrophage-cappi	Mus musculus (Mouse)	Capg	Evidence at protein level	352	39240	barbed-end actin filamen	cadherin binding involved	cell-cell adherens junctio
97	P57776	EF1D_MOUSE	Elongation factor 1	Mus musculus (Mouse)	Eef1d	Evidence at protein level	281	31293	cellular response to ionizi	activating transcription fa	cell-cell adherens junctio
98	Q01149	CO1A2_MOUSE	Collagen alpha-2(I)	Mus musculus (Mouse)	Col1a2	Evidence at protein level	1372	129557	blood vessel developmen	extracellular matrix struc	collagen trimer [GO:0005
99	Q8CF02	FM25C_MOUSE	Protein FAM25C	Mus musculus (Mouse)	Fam25c	Evidence at protein level	89	9235			
100	P51881	ADT2_MOUSE	ADP/ATP transloca	Mus musculus (Mouse)	Slc25a5	Evidence at protein level	298	32931	chromosome segregation	ATP:ADP antiporter activi	extracellular exosome [G
101	P14206	RSSA_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rpsa	Evidence at protein level	295	32838	endonucleolytic cleavage	laminin binding [GO:0043	90S preribosome [GO:00
102	P19253	RL13A_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl13a	Evidence at protein level	203	23464	cellular response to interf	mRNA binding [GO:00037	cytoplasm [GO:0005737]
103	P56399	UBP5_MOUSE	Ubiquitin carboxyl-	Mus musculus (Mouse)	Usp5	Evidence at protein level	858	95833	positive regulation of pro	thiol-dependent ubiquitin-specific protease activity	
104	P25206	MCM3_MOUSE	DNA replication lic	Mus musculus (Mouse)	Mcm3	Evidence at protein level	812	91546	cell cycle [GO:0007049];	ATP binding [GO:000552	centrosome [GO:000581
105	P26041	MOES_MOUSE	Moesin (Membran	Mus musculus (Mouse)	Msn	Evidence at protein level	577	67767	cellular response to testo	cell adhesion molecule bi	apical part of cell [GO:00
106	P48036	ANXA5_MOUSE	Annexin A5 (Ancho	Mus musculus (Mouse)	Anxa5	Evidence at protein level	319	35752	blood coagulation [GO:00	calcium-dependent phos	endothelial microparticle
107	Q9Z1Q9	SYVC_MOUSE	Valine--tRNA ligase	Mus musculus (Mouse)	Vars	Evidence at protein level	1263	140215	valyl-tRNA aminoacylatio	aminoacyl-tRNA editing a	mitochondrion [GO:0005
108	P08249	MDHM_MOUSE	Malate dehydroger	Mus musculus (Mouse)	Mdh2	Evidence at protein level	338	35611	carbohydrate metabolic p	L-malate dehydrogenase	extracellular exosome [G
109	O35129	PHB2_MOUSE	Prohibitin-2 (B-cell	Mus musculus (Mouse)	Phb2	Evidence at protein level	299	33296	mammary gland alveolus	amide binding [GO:00332	cell periphery [GO:00719
110	Q8BGQ7	SYAC_MOUSE	Alanine--tRNA ligas	Mus musculus (Mouse)	Aars	Evidence at protein level	968	106909	alanyl-tRNA aminoacylati	alanine-tRNA ligase activi	cytosol [GO:0005829]; ex
111	Q9JII6	AK1A1_MOUSE	Alcohol dehydroge	Mus musculus (Mouse)	Akr1a1	Evidence at protein level	325	36587	aldehyde catabolic proce	alcohol dehydrogenase (N	apical plasma membrane
112	P16858	G3P_MOUSE	Glyceraldehyde-3-p	Mus musculus (Mouse)	Gapdh	Evidence at protein level	333	35810	cellular response to interf	enzyme binding [GO:001	cytoplasm [GO:0005737]

113	P08113	ENPL_MOUSE	Endoplasmin (94 kI	Mus musculus (Mouse)	Hsp90b1	Evidence at protein level	802	92476	actin rod assembly [GO:0	ATP binding [GO:000552	cytosol [GO:0005829]; er
114	P10605	CATB_MOUSE	Cathepsin B (EC 3.4	Mus musculus (Mouse)	Ctsb	Evidence at protein level	339	37280	cellular response to thyro	collagen binding [GO:000	extracellular exosome [G
115	Q8BHN3	GANAB_MOUSE	Neutral alpha-gluca	Mus musculus (Mouse)	Ganab	Evidence at protein level	944	106911	carbohydrate metabolic p	carbohydrate binding [GC	endoplasmic reticulum [C
116	Q925H3	KRA65_MOUSE	Keratin-associated	Mus musculus (Mouse)	Krtap6-5	Evidence at transcript level	78	7945			intermediate filament [G
117	Q64674	SPEE_MOUSE	Spermidine synthas	Mus musculus (Mouse)	Srm	Evidence at protein level	302	33995	spermidine biosynthetic p	identical protein binding [GO:0042802]; protein hor	
118	Q6NXH9	K2C73_MOUSE	Keratin, type II cyto	Mus musculus (Mouse)	Krt73	Evidence at protein level	539	58911		structural molecule activi	extracellular exosome [G
119	Q05793	PGBM_MOUSE	Basement membra	Mus musculus (Mouse)	Hspg2	Evidence at protein level	3707	398294	angiogenesis [GO:000152	calcium ion binding [GO:(	basal lamina [GO:000560
120	Q9QY23	PKP3_MOUSE	Plakophilin-3	Mus musculus (Mouse)	Pkp3	Evidence at protein level	797	87333	desmosome assembly [G	alpha-catenin binding [GC	cell-cell adherens junctio
121	P11276	FINC_MOUSE	Fibronectin (FN) [C	Mus musculus (Mouse)	Fn1	Evidence at protein level	2477	272538	acute-phase response [G	heparin binding [GO:0008	apical plasma membrane
122	P38647	GRP75_MOUSE	Stress-70 protein, r	Mus musculus (Mouse)	Hspa9	Evidence at protein level	679	73461	erythrocyte differentiatio	ATP binding [GO:000552	cytoplasm [GO:0005737]
123	Q9Z1N5	DX39B_MOUSE	Spliceosome RNA h	Mus musculus (Mouse)	Ddx39b	Evidence at protein level	428	49035	cellular response to DNA	ATPase activity [GO:0016	cytoplasm [GO:0005737]
124	P05064	ALDOA_MOUSE	Fructose-bisphosph	Mus musculus (Mouse)	Aldoa	Evidence at protein level	364	39356	ATP biosynthetic process	cadherin binding involved	actin cytoskeleton [GO:0
125	P05202	AATM_MOUSE	Aspartate aminotra	Mus musculus (Mouse)	Got2	Evidence at protein level	430	47411	2-oxoglutarate metabolic	amino acid binding [GO:0	cell surface [GO:0009986
126	O70133	DHX9_MOUSE	ATP-dependent RN	Mus musculus (Mouse)	Dhx9	Evidence at protein level	1380	149475	cellular response to heat	ATP binding [GO:000552	centrosome [GO:000581
127	Q00623	APOA1_MOUSE	Apolipoprotein A-I	Mus musculus (Mouse)	Apoa1	Evidence at protein level	264	30616	adrenal gland developme	apolipoprotein A-I recept	blood microparticle [GO:(
128	Q99KI0	ACON_MOUSE	Aconitate hydratas	Mus musculus (Mouse)	Aco2	Evidence at protein level	780	85464	citrate metabolic process	3 iron, 4 sulfur cluster bir	mitochondrion [GO:0005
129	O35737	HNRH1_MOUSE	Heterogeneous nu	Mus musculus (Mouse)	Hnrnph1	Evidence at protein level	449	49199	mRNA processing [GO:00	nucleotide binding [GO:0	catalytic step 2 spliceoso
130	Q64727	VINC_MOUSE	Vinculin (Metavinc	Mus musculus (Mouse)	Vcl	Evidence at protein level	1066	116717	adherens junction assem	alpha-catenin binding [GC	actin cytoskeleton [GO:0
131	P09103	PDIA1_MOUSE	Protein disulfide-is	Mus musculus (Mouse)	P4hb	Evidence at protein level	509	57058	cell redox homeostasis [G	integrin binding [GO:000	endoplasmic reticulum [C
132	P53996	CNBP_MOUSE	Cellular nucleic acic	Mus musculus (Mouse)	Cnbp	Evidence at protein level	178	19592	positive regulation of cell	RNA binding [GO:000372	cytosol [GO:0005829]; er
133	P62334	PRS10_MOUSE	26S protease regul	Mus musculus (Mouse)	Psmc6	Evidence at protein level	389	44173	positive regulation of incl	ATP binding [GO:000552	cytosolic proteasome con
134	Q8JZQ9	EIF3B_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif3b	Evidence at protein level	803	91370	IRES-dependent viral tran	nucleotide binding [GO:0	eukaryotic translation ini
135	Q8BTM8	FLNA_MOUSE	Filamin-A (FLN-A) (	Mus musculus (Mouse)	Flna	Evidence at protein level	2647	281222	actin crosslink formation	actin binding [GO:000377	actin cytoskeleton [GO:0
136	Q6ZWV3	RL10_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl10	Evidence at protein level	214	24604	liver regeneration [GO:00	RNA binding [GO:000372	cytoplasm [GO:0005737]
137	Q8CGC7	SYEP_MOUSE	Bifunctional glutam	Mus musculus (Mouse)	Eprs	Evidence at protein level	1512	170079	cellular response to interf	ATP binding [GO:000552	aminoacyl-tRNA syntheta
138	Q8K4L4	POF1B_MOUSE	Protein POF1B	Mus musculus (Mouse)	Pof1b	Evidence at transcript level	587	67785			bicellular tight junction [C
139	P17225	PTBP1_MOUSE	Polypyrimidine trac	Mus musculus (Mouse)	Ptbp1	Evidence at protein level	527	56478	IRES-dependent viral tran	nucleotide binding [GO:0	extracellular exosome [G
140	P49312	ROA1_MOUSE	Heterogeneous nu	Mus musculus (Mouse)	Hnrnpa1	Evidence at protein level	320	34196	alternative mRNA splicing	nucleotide binding [GO:0	cytoplasm [GO:0005737]
141	Q99KK7	DPP3_MOUSE	Dipeptidyl peptidas	Mus musculus (Mouse)	Dpp3	Evidence at protein level	738	82898	proteolysis [GO:0006508	dipeptidyl-peptidase acti	cytoplasm [GO:0005737]
142	Q9CZM2	RL15_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl15	Evidence at transcript level	204	24146	cytoplasmic translation [(	cadherin binding involved	A band [GO:0031672]; ce
143	Q8BG32	PSD11_MOUSE	26S proteasome nc	Mus musculus (Mouse)	Psmd11	Evidence at protein level	422	47437	proteasome assembly [G	structural molecule activi	extracellular exosome [G
144	Q3THS6	METK2_MOUSE	S-adenosylmethion	Mus musculus (Mouse)	Mat2a	Evidence at protein level	395	43689	one-carbon metabolic pr	ATP binding [GO:000552	cytosol [GO:0005829]; m
145	P62242	RS8_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps8	Evidence at protein level	208	24205	maturation of SSU-rRNA	RNA binding [GO:000372	cytosol [GO:0005829]; cy
146	P62270	RS18_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps18	Evidence at protein level	152	17719	ribosome biogenesis [GO	RNA binding [GO:000372	cytosol [GO:0005829]; cy
147	Q6P253	DMKN_MOUSE	Dermokine (Epiden	Mus musculus (Mouse)	Dmkn	Evidence at transcript level	517	51661	cell differentiation [GO:0030154]; cornified envelop		extracellular exosome [G
148	Q8CGP6	H2A1H_MOUSE	Histone H2A type 1	Mus musculus (Mouse)	Hist1h2ah	Evidence at protein level	128	13950	chromatin silencing [GO:(	DNA binding [GO:000367	extracellular exosome [G
149	P21107	TPM3_MOUSE	Tropomyosin alpha	Mus musculus (Mouse)	Tpm3	Evidence at protein level	285	32994	actin filament organizatic	actin filament binding [GC	actin cytoskeleton [GO:0
150	P70372	ELAV1_MOUSE	ELAV-like protein 1	Mus musculus (Mouse)	Elavl1	Evidence at protein level	326	36169	3'-UTR-mediated mRNA s	AU-rich element binding [	cytoplasm [GO:0005737]
151	Q3UPL0	SC31A_MOUSE	Protein transport p	Mus musculus (Mouse)	Sec31a	Evidence at protein level	1230	133569	protein transport [GO:00	calcium-dependent prote	cytoplasm [GO:0005737]
152	Q8VIJ6	SFPQ_MOUSE	Splicing factor, prol	Mus musculus (Mouse)	Sfpq	Evidence at protein level	699	75442	alternative mRNA splicing	chromatin binding [GO:0(	chromatin [GO:0000785]
153	P46471	PRS7_MOUSE	26S protease regul	Mus musculus (Mouse)	Psmc2	Evidence at protein level	433	48648	osteoblast differentiation	ATPase activity [GO:0016	cytosol [GO:0005829]; cy
154	P50516	VATA_MOUSE	V-type proton ATP	Mus musculus (Mouse)	Atp6v1a	Evidence at protein level	617	68326	ATP hydrolysis coupled pr	ATP binding [GO:000552	apical plasma membrane
155	P27659	RL3_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl3	Evidence at protein level	403	46110	cellular response to interf	5S rRNA binding [GO:000	cytoplasm [GO:0005737]
156	Q8VED5	K2C79_MOUSE	Keratin, type II cyto	Mus musculus (Mouse)	Krt79	Evidence at protein level	531	57552		enzyme binding [GO:001	extracellular exosome [G
157	P06728	APOA4_MOUSE	Apolipoprotein A-I	Mus musculus (Mouse)	Apoa4	Evidence at protein level	395	45029	cholesterol biosynthetic p	antioxidant activity [GO:(	blood microparticle [GO:(
158	P47963	RL13_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl13	Evidence at protein level	211	24305	translation [GO:0006412]	RNA binding [GO:000372	cytosolic large ribosomal
159	Q9R0P5	DEST_MOUSE	Destrin (Actin-depo	Mus musculus (Mouse)	Dstn	Evidence at protein level	165	18522	actin filament depolymer	actin filament binding [GC	cortical actin cytoskeleto
160	P80316	TCPE_MOUSE	T-complex protein	Mus musculus (Mouse)	Cct5	Evidence at protein level	541	59624	'de novo' protein folding	ATP binding [GO:000552	cell body [GO:0044297];
161	Q7TPV4	MBB1A_MOUSE	Myb-binding protei	Mus musculus (Mouse)	Mybbp1a	Evidence at protein level	1344	152037	cellular response to gluco	core promoter binding [G	cytoplasm [GO:0005737]
162	Q8VDM4	PSMD2_MOUSE	26S proteasome nc	Mus musculus (Mouse)	Psmd2	Evidence at protein level	908	100203	regulation of protein cata	enzyme regulator activity	extracellular exosome [G
163	Q80X90	FLNB_MOUSE	Filamin-B (FLN-B) (	Mus musculus (Mouse)	Flnb	Evidence at protein level	2602	277825	actin cytoskeleton organi	cadherin binding involved	brush border [GO:00059
164	P28653	PGS1_MOUSE	Biglycan (Bone/car	Mus musculus (Mouse)	Bgn	Evidence at protein level	369	41639	blood vessel remodeling [	extracellular matrix bindi	cell surface [GO:0009986
165	Q61765	K1H1_MOUSE	Keratin, type I cuti	Mus musculus (Mouse)	Krt31	Evidence at protein level	416	47117		structural molecule activi	extracellular exosome [G
166	Q99K48	NONO_MOUSE	Non-POU domain-c	Mus musculus (Mouse)	Nono	Evidence at protein level	473	54541	circadian rhythm [GO:00	chromatin binding [GO:0(	membrane [GO:0016020
167	Q91X72	HEMO_MOUSE	Hemopexin	Mus musculus (Mouse)	Hpx	Evidence at protein level	460	51318	cellular iron ion homeost	heme binding [GO:00200	blood microparticle [GO:(
168	P13020	GELS_MOUSE	Gelsolin (Actin-dep	Mus musculus (Mouse)	Gsn	Evidence at protein level	780	85942	actin filament capping [G	actin binding [GO:000377	actin cap [GO:0030478];
169	P11087	CO1A1_MOUSE	Collagen alpha-1(I)	Mus musculus (Mouse)	Col1a1	Evidence at protein level	1453	138032	blood vessel developmen	extracellular matrix struc	collagen trimer [GO:0005
170	Q9JHR7	IDE_MOUSE	Insulin-degrading e	Mus musculus (Mouse)	Ide	Evidence at protein level	1019	117772	beta-amyloid metabolic p	ATP binding [GO:000552	cell surface [GO:0009986
171	Q9JKF1	IQGA1_MOUSE	Ras GTPase-activat	Mus musculus (Mouse)	Iqgap1	Evidence at protein level	1657	188742	cellular response to calci	cadherin binding involved	actin cytoskeleton [GO:0
172	P35492	HUTH_MOUSE	Histidine ammonia	Mus musculus (Mouse)	Hal	Evidence at protein level	657	72258	histidine catabolic proces	histidine ammonia-lyase	cytoplasm [GO:0005737]
173	Q99M74	KRT82_MOUSE	Keratin, type II cuti	Mus musculus (Mouse)	Krt82	Evidence at protein level	516	57140		structural molecule activi	keratin filament [GO:004
174	Q9R1P4	PSA1_MOUSE	Proteasome subuni	Mus musculus (Mouse)	Psma1	Evidence at protein level	263	29547	immune system process [	lipopolysaccharide bindin	centrosome [GO:000581
175	Q61696	HS71A_MOUSE	Heat shock 70 kDa	Mus musculus (Mouse)	Hspa1a	Evidence at protein level	641	70079	DNA repair [GO:0006281	ATPase activity [GO:0016	blood microparticle [GO:(
176	Q8VHD8	HORN_MOUSE	Hornerin	Mus musculus (Mouse)	Hrnr	Evidence at protein level	2496	247587	hematopoietic progenitor	calcium ion binding [GO:(	cornified envelope [GO:0
177	P14148	RL7_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl7	Evidence at protein level	270	31420	cytoplasmic translation [(	DNA binding [GO:000367	cytoplasm [GO:0005737]
178	Q61598	GDIB_MOUSE	Rab GDP dissociati	Mus musculus (Mouse)	Gdi2	Evidence at protein level	445	50537	protein transport [GO:00	GTPase activator activity	extracellular exosome [G
179	Q99K85	SERC_MOUSE	Phosphoserine ami	Mus musculus (Mouse)	Psat1	Evidence at protein level	370	40473	L-serine biosynthetic proc	O-phospho-L-serine:2-ox	cytoplasm [GO:0005737]
180	P21812	MCPT4_MOUSE	Mast cell protease	Mus musculus (Mouse)	Mcpt4	Evidence at protein level	246	27204	protein processing [GO:0	peptidase activity [GO:00	intracellular [GO:00056
181	Q9D0E1	HNRPM_MOUSE	Heterogeneous nu	Mus musculus (Mouse)	Hnrnpm	Evidence at protein level	729	77649	alternative mRNA splicing	nucleotide binding [GO:0	catalytic step 2 spliceoso
182	O89086	RBM3_MOUSE	RNA-binding protei	Mus musculus (Mouse)	Rbm3	Evidence at protein level	153	16605	positive regulation of tran	nucleotide binding [GO:0	cytoplasm [GO:0005737]
183	Q9CX86	ROA0_MOUSE	Heterogeneous nu	Mus musculus (Mouse)	Hnrnpa0	Evidence at protein level	305	30530	3'-UTR-mediated mRNA s	AU-rich element binding [	intracellular ribonucleopr
184	Q9Z184	PADI3_MOUSE	Protein-arginine de	Mus musculus (Mouse)	Padi3	Evidence at protein level	664	75073	histone citrullination [GO	calcium ion binding [GO:(	cytoplasm [GO:0005737]
185	Q9CQV8	1433B_MOUSE	14-3-3 protein beta	Mus musculus (Mouse)	Ywhab	Evidence at protein level	246	28086	cytoplasmic sequestering	cadherin binding involved	cell-cell adherens junctio
186	Q9CZ13	UCR1_MOUSE	Cytochrome b-c1 c	Mus musculus (Mouse)	Uqcrc1	Evidence at protein level	480	52852	aerobic respiration [GO:0	metalloendopeptidase ac	cytosol [GO:0005829]; m
187	Q9WTP6	KAD2_MOUSE	Adenylate kinase 2	Mus musculus (Mouse)	Ak2	Evidence at protein level	239	26469	ADP biosynthetic process	adenylate kinase activity	extracellular exosome [G
188	P47738	ALDH2_MOUSE	Aldehyde dehydrog	Mus musculus (Mouse)	Aldh2	Evidence at protein level	519	56538	ethanol catabolic process	aldehyde dehydrogenase	extracellular exosome [G
189	Q99PL5	RRBP1_MOUSE	Ribosome-binding p	Mus musculus (Mouse)	Rrbp1	Evidence at protein level	1605	172879	protein transport [GO:00	receptor activity [GO:000	integral component of en
190	Q9CZU6	CISY_MOUSE	Citrate synthase, m	Mus musculus (Mouse)	Cs	Evidence at protein level	464	51737	carbohydrate metabolic p	citrate (Si)-synthase activ	extracellular exosome [G
191	Q8BGD9	IF4B_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif4b	Evidence at protein level	611	68840	cytoplasmic translation [(	nucleotide binding [GO:0	dendrite [GO:0030425]; e
192	Q99PT1	GDIR1_MOUSE	Rho GDP-dissociati	Mus musculus (Mouse)	Arhgdia	Evidence at protein level	204	23407	cellular response to mech	fatty acid binding [GO:00	cytosol [GO:0005829]; ex
193	P11983	TCPA_MOUSE	T-complex protein	Mus musculus (Mouse)	Tcp1	Evidence at protein level	556	60449	'de novo' protein folding	ATP binding [GO:000552	acrosomal vesicle [GO:00
194	Q9Z0N1	IF2G_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif2s3x	Evidence at protein level	472	51065	translational initiation [G	cadherin binding involved	cell-cell adherens junctio
195	Q61316	HSP74_MOUSE	Heat shock 70 kDa	Mus musculus (Mouse)	Hspa4	Evidence at protein level	841	94133	chaperone-mediated prot	ATP binding [GO:000552	cytosol [GO:0005829]; ex
196	O08529	CAN2_MOUSE	Calpain-2 catalytic	Mus musculus (Mouse)	Capn2	Evidence at protein level	700	79872	blastocyst development [	calcium-dependent syste	chromatin [GO:0000785]
197	P07901	HS90A_MOUSE	Heat shock protein	Mus musculus (Mouse)	Hsp90aa1	Evidence at protein level	733	84788	chaperone-mediated prot	ATPase activity [GO:0016	cytoplasm [GO:0005737]
198	P46935	NEDD4_MOUSE	E3 ubiquitin-protei	Mus musculus (Mouse)	Nedd4	Evidence at protein level	887	102706	adaptive immune respon	ionotropic glutamate rece	cell cortex [GO:0005938]
199	B1AQ75	KRT36_MOUSE	Keratin, type I cuti	Mus musculus (Mouse)	Krt36	Evidence at protein level	473	52790	regulation of keratinocyte	structural constituent of	extracellular exosome [G
200	Q9Z2K1	K1C16_MOUSE	Keratin, type I cyto	Mus musculus (Mouse)	Krt16	Evidence at protein level	469	51606	aging [GO:0007568]; esta	structural constituent of	cytoskeleton [GO:000585
201	Q91YQ5	RPN1_MOUSE	Dolichyl-diphospho	Mus musculus (Mouse)	Rpn1	Evidence at protein level	608	68528	protein N-linked glycosyla	dolichyl-diphosphooligosa	cytosol [GO:0005829]; er
202	Q9CQI6	COTL1_MOUSE	Coactosin-like prot	Mus musculus (Mouse)	Cotl1	Evidence at protein level	142	15944	defense response to fung	actin binding [GO:000377	cytoplasm [GO:0005737]
203	P80318	TCPG_MOUSE	T-complex protein	Mus musculus (Mouse)	Cct3	Evidence at protein level	545	60630	'de novo' protein folding	ATP binding [GO:000552	cell body [GO:0044297];
204	P42932	TCPQ_MOUSE	T-complex protein	Mus musculus (Mouse)	Cct8	Evidence at protein level	548	59555	'de novo' protein folding	ATP binding [GO:000552	cell body [GO:0044297];
205	P62281	RS11_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps11	Evidence at protein level	158	18431	osteoblast differentiation	RNA binding [GO:000372	cytoplasm [GO:0005737]
206	O54974	LEG7_MOUSE	Galectin-7 (Gal-7)	Mus musculus (Mouse)	Lgals7	Evidence at transcript level	136	15173	apoptotic process [GO:00	carbohydrate binding [GC	cytoplasm [GO:0005737]
207	P10518	HEM2_MOUSE	Delta-aminolevulin	Mus musculus (Mouse)	Alad	Evidence at protein level	330	36024	cellular response to interf	identical protein binding [	cytosol [GO:0005829]; ex
208	P19324	SERPH_MOUSE	Serpin H1 (47 kDa I	Mus musculus (Mouse)	Serpinh1	Evidence at protein level	417	46534	chondrocyte developmen	collagen binding [GO:000	cytoplasm [GO:0005737]
209	Q8BK67	RCC2_MOUSE	Protein RCC2	Mus musculus (Mouse)	Rcc2	Evidence at protein level	520	55983	activation of GTPase acti	microtubule binding [GO:	chromosome, centromeri
210	P68040	RACK1_MOUSE	Receptor of activat	Mus musculus (Mouse)	Rack1	Evidence at protein level	317	35077	activation of cysteine-typ	cadherin binding involved	cell body [GO:0044297];
211	Q8BMK4	CKAP4_MOUSE	Cytoskeleton-asso	Mus musculus (Mouse)	Ckap4	Evidence at protein level	575	63692		RNA binding [GO:000372	cell surface [GO:0009986
212	Q9CQ60	6PGL_MOUSE	6-phosphogluconol	Mus musculus (Mouse)	Pgls	Evidence at protein level	257	27254	carbohydrate metabolic p	6-phosphoglucono-lacton	cytoplasm [GO:0005737]
213	Q8CIT9	SBSN_MOUSE	Suprabasin	Mus musculus (Mouse)	Sbsn	Evidence at transcript level	700	72334			cytoplasm [GO:0005737]
214	P62806	H4_MOUSE	Histone H4	Mus musculus (Mouse)	Hist1h4a; Hist1	Evidence at protein level	103	11367	chromatin silencing at rD	DNA binding [GO:000367	extracellular exosome [G
215	Q9WVH9	FBLN5_MOUSE	Fibulin-5 (FIBL-5) (	Mus musculus (Mouse)	Fbln5	Evidence at protein level	448	50193	cell adhesion [GO:00071	calcium ion binding [GO:(	extracellular exosome [G
216	A2A5X5	KR161_MOUSE	Keratin-associated	Mus musculus (Mouse)	Krtap16-1	Inferred from homology	502	52020			keratin filament [GO:004
217	P62702	RS4X_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps4x	Evidence at protein level	263	29598	multicellular organism de	rRNA binding [GO:00198	cytoplasmic ribonucleopr
218	P62983	RS27A_MOUSE	Ubiquitin-40S ribos	Mus musculus (Mouse)	Rps27a	Evidence at protein level	156	17951	circadian rhythm [GO:00	metal ion binding [GO:00	cytoplasm [GO:0005737]
219	P62259	1433E_MOUSE	14-3-3 protein epsi	Mus musculus (Mouse)	Ywhae	Evidence at protein level	255	29174	cellular response to heat	cadherin binding involved	axon [GO:0030424]; cell-
220	Q8VDJ3	VIGLN_MOUSE	Vigilin (High densit	Mus musculus (Mouse)	Hdlbp	Evidence at protein level	1268	141743	cholesterol metabolic prc	cadherin binding involved	cell-cell adherens junctio
221	O08807	PRDX4_MOUSE	Peroxiredoxin-4 (EC	Mus musculus (Mouse)	Prdx4	Evidence at protein level	274	31053	4-hydroxyproline metabo	peroxidase activity [GO:0	cytoplasm [GO:0005737]
222	Q6P3A4	VSIG8_MOUSE	V-set and immuno	Mus musculus (Mouse)	Vsig8	Evidence at transcript level	417	44187		RNA binding [GO:000372	integral component of me
223	P54071	IDHP_MOUSE	Isocitrate dehydrog	Mus musculus (Mouse)	Idh2	Evidence at protein level	452	50906	2-oxoglutarate metabolic	isocitrate dehydrogenase	cytosol [GO:0005829]; ex
224	P60335	PCBP1_MOUSE	Poly(rC)-binding pr	Mus musculus (Mouse)	Pcbp1	Evidence at protein level	356	37498	mRNA processing [GO:00	cadherin binding involved	cell-cell adherens junctio
225	P35700	PRDX1_MOUSE	Peroxiredoxin-1 (EC	Mus musculus (Mouse)	Prdx1	Evidence at protein level	199	22176	cell proliferation [GO:000	cadherin binding involved	cell-cell adherens junctio
226	Q6NZJ6	IF4G1_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif4g1	Evidence at protein level	1600	176077	behavioral fear response	ATP binding [GO:000552	cell-cell adherens junctio
227	Q78PY7	SND1_MOUSE	Staphylococcal nuc	Mus musculus (Mouse)	Snd1	Evidence at protein level	910	102088	gene silencing by RNA [G	cadherin binding involved	cell-cell adherens junctio
228	P35175	CYT1_MOUSE	Stefin-1	Mus musculus (Mouse)	Stfa1	Inferred from homology	97	11007	negative regulation of en	cysteine-type endopeptid	cytoplasm [GO:0005737]
229	Q8K310	MATR3_MOUSE	Matrin-3	Mus musculus (Mouse)	Matr3	Evidence at protein level	846	94630	heart valve development	nucleotide binding [GO:0	membrane [GO:0016020

230	P50446	K2C6A_MOUSE	Keratin, type II cytc	Mus musculus (Mouse)	Krt6a	Evidence at protein level	553	59335	intermediate filament org	structural molecule activi	extracellular exosome [G
231	P62754	RS6_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps6	Evidence at protein level	249	28681	activation-induced cell de	protein kinase binding [G	cell body [GO:0044297];
232	P63242	IF5A1_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif5a	Evidence at protein level	154	16832	aging [GO:0007568]; apo	protein N-terminus bindi	annulate lamellae [GO:00
233	Q8BH64	EHD2_MOUSE	EH domain-contain	Mus musculus (Mouse)	Ehd2	Evidence at protein level	543	61174	cortical actin cytoskeleto	ATP binding [GO:0005524	caveola [GO:0005901]; c
234	P42208	SEPT2_MOUSE	Septin-2 (Neural pr	Mus musculus (Mouse)	Sept2	Evidence at protein level	361	41526	cell differentiation [GO:0	cadherin binding involved	actin cytoskeleton [GO:0
235	O70400	PDLI1_MOUSE	PDZ and LIM doma	Mus musculus (Mouse)	Pdlim1	Evidence at protein level	327	35774	regulation of transcriptio	cadherin binding involved	cell-cell adherens junctio
236	P97855	G3BP1_MOUSE	Ras GTPase-activat	Mus musculus (Mouse)	G3bp1	Evidence at protein level	465	51829	negative regulation of car	ATP binding [GO:0005524	cytoplasmic stress granul
237	Q9R0Q7	TEBP_MOUSE	Prostaglandin E syr	Mus musculus (Mouse)	Ptges3	Evidence at protein level	160	18721	cell proliferation [GO:000	DNA polymerase binding	actin filament [GO:00058
238	P51410	RL9_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl9	Evidence at transcript level	192	21881	cytoplasmic translation [(	RNA binding [GO:000372	cytosolic large ribosomal
239	Q925H6	KR193_MOUSE	Keratin-associated	Mus musculus (Mouse)	Krtap19-3	Evidence at transcript level	87	8823			intermediate filament [G
240	P08121	CO3A1_MOUSE	Collagen alpha-1(III	Mus musculus (Mouse)	Col3a1	Evidence at protein level	1464	138943	aging [GO:0007568]; aort	extracellular matrix struc	collagen trimer [GO:0005
241	Q8C1A5	THOP1_MOUSE	Thimet oligopeptid	Mus musculus (Mouse)	Thop1	Evidence at protein level	687	78026	intracellular signal transd	metal ion binding [GO:00	mitochondrial intermemb
242	Q61553	FSCN1_MOUSE	Fascin (Singed-like	Mus musculus (Mouse)	Fscn1	Evidence at protein level	493	54508	actin cytoskeleton organi	actin binding [GO:000377	actin cytoskeleton [GO:0
243	Q8BJY1	PSMD5_MOUSE	26S proteasome nc	Mus musculus (Mouse)	Psmd5	Evidence at protein level	504	55972	proteasome regulatory particle assembly [GO:0070		proteasome accessory co
244	Q9JK23	PSMG1_MOUSE	Proteasome assem	Mus musculus (Mouse)	Psmg1	Evidence at protein level	289	33104	cerebellar granule cell pre	proteasome binding [GO:	cytoplasm [GO:0005737]
245	Q9R0N0	GALK1_MOUSE	Galactokinase (EC 2	Mus musculus (Mouse)	Galk1	Evidence at protein level	392	42295	galactitol metabolic proc	ATP binding [GO:0005524	cytoplasm [GO:0005737]
246	P26443	DHE3_MOUSE	Glutamate dehydr	Mus musculus (Mouse)	Glud1	Evidence at protein level	558	61337	cerebellum development	ADP binding [GO:004353	cytoplasm [GO:0005737]
247	P70349	HINT1_MOUSE	Histidine triad nucl	Mus musculus (Mouse)	Hint1	Evidence at protein level	126	13777	intrinsic apoptotic signali	hydrolase activity [GO:00	cytosol [GO:0005829]; ex
248	Q8BKG3	PTK7_MOUSE	Inactive tyrosine-pr	Mus musculus (Mouse)	Ptk7	Evidence at protein level	1062	117532	actin cytoskeleton reorga	coreceptor activity involv	cell-cell junction [GO:000
249	Q99KJ8	DCTN2_MOUSE	Dynactin subunit 2	Mus musculus (Mouse)	Dctn2	Evidence at protein level	402	44117	cell proliferation [GO:000	identical protein binding	centrosome [GO:000581
250	Q9DAR7	DCPS_MOUSE	m7GpppX diphosph	Mus musculus (Mouse)	Dcps	Evidence at protein level	338	38988	cellular response to mena	m7G(5')pppN diphosphat	cytoplasm [GO:0005737]
251	P26350	PTMA_MOUSE	Prothymosin alpha	Mus musculus (Mouse)	Ptma	Evidence at protein level	111	12254	histone exchange [GO:00	histone binding [GO:0042	nucleus [GO:0005634]
252	P97429	ANXA4_MOUSE	Annexin A4 (Annex	Mus musculus (Mouse)	Anxa4	Evidence at protein level	319	35916	epithelial cell differentiat	calcium-dependent phos	apical plasma membrane
253	Q9Z110	P5CS_MOUSE	Delta-1-pyrroline-5	Mus musculus (Mouse)	Aldh18a1	Evidence at protein level	795	87266	cellular amino acid biosyr	ATP binding [GO:0005524	cytosol [GO:0005829]; m
254	P59999	ARPC4_MOUSE	Actin-related prote	Mus musculus (Mouse)	Arpc4	Evidence at protein level	168	19667	actin filament polymeriza	enzyme binding [GO:001	Arp2/3 protein complex [
255	P62245	RS15A_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps15a	Evidence at protein level	130	14840	positive regulation of cell	RNA binding [GO:000372	cytoplasm [GO:0005737]
256	Q6IRU2	TPM4_MOUSE	Tropomyosin alpha	Mus musculus (Mouse)	Tpm4	Evidence at protein level	248	28468	actin filament organizatic	actin filament binding [G	cortical cytoskeleton [GO
257	P30275	KCRU_MOUSE	Creatine kinase U-t	Mus musculus (Mouse)	Ckmt1	Evidence at protein level	418	47004	negative regulation of ap	ATP binding [GO:0005524	extracellular exosome [G
258	Q8CAY6	THIC_MOUSE	Acetyl-CoA acetyltr	Mus musculus (Mouse)	Acat2	Evidence at protein level	397	41298	fatty acid beta-oxidation	acetyl-CoA C-acetyltransf	cytoplasm [GO:0005737]
259	Q91VD9	NDUS1_MOUSE	NADH-ubiquinone	Mus musculus (Mouse)	Ndufs1	Evidence at protein level	727	79777	apoptotic mitochondrial	2 iron, 2 sulfur cluster bin	mitochondrial intermemb
260	Q80YX1	TENA_MOUSE	Tenascin (TN) (Hex	Mus musculus (Mouse)	Tnc	Evidence at protein level	2110	231807	bud outgrowth involved i	fibronectin binding [GO:0	basement membrane [GO
261	Q61191	HCFC1_MOUSE	Host cell factor 1 (H	Mus musculus (Mouse)	Hcfc1	Evidence at protein level	2045	210437	cell cycle [GO:0007049];	cadherin binding involved	Ada2/Gcn5/Ada3 transcr
262	P62918	RL8_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl8	Evidence at protein level	257	28025	cytoplasmic translation [(	RNA binding [GO:000372	cytosolic large ribosomal
263	Q9D3I6	KRA71_MOUSE	Keratin-associated	Mus musculus (Mouse)	Krtap7-1	Inferred from homology	87	9516			intermediate filament [G
264	Q61576	FKB10_MOUSE	Peptidyl-prolyl cis-t	Mus musculus (Mouse)	Fkbp10	Evidence at protein level	581	64697	chaperone-mediated prot	calcium ion binding [GO:(	cytoplasm [GO:0005737]
265	P68368	TBA4A_MOUSE	Tubulin alpha-4A cl	Mus musculus (Mouse)	Tuba4a	Evidence at protein level	448	49924	microtubule-based proce	enzyme binding [GO:001	cytoplasm [GO:0005737]
266	P06745	G6PI_MOUSE	Glucose-6-phospha	Mus musculus (Mouse)	Gpi	Evidence at protein level	558	62767	aldehyde catabolic proce	glucose-6-phosphate isor	ciliary membrane [GO:00
267	Q01405	SC23A_MOUSE	Protein transport p	Mus musculus (Mouse)	Sec23a	Evidence at protein level	765	86162	ER to Golgi vesicle-media	zinc ion binding [GO:000	COPII vesicle coat [GO:00
268	Q920B9	SP16H_MOUSE	FACT complex subu	Mus musculus (Mouse)	Supt16h	Evidence at protein level	1047	119825	DNA repair [GO:0006281	histone binding [GO:0042	chromosome [GO:00056
269	Q61554	FBN1_MOUSE	Fibrillin-1 [Cleaved	Mus musculus (Mouse)	Fbn1	Evidence at protein level	2873	312298	activation of protein kina	calcium ion binding [GO:(	basement membrane [GO
270	Q07076	ANXA7_MOUSE	Annexin A7 (Annex	Mus musculus (Mouse)	Anxa7	Evidence at protein level	463	49925	autophagy [GO:0006914]	calcium-dependent phos	chromaffin granule meml
271	O35326	SRSF5_MOUSE	Serine/arginine-ricl	Mus musculus (Mouse)	Srsf5	Evidence at protein level	269	30891	cellular response to insuli	nucleotide binding [GO:0	cytosol [GO:0005829]; nu
272	Q6PDM2	SRSF1_MOUSE	Serine/arginine-ricl	Mus musculus (Mouse)	Srsf1	Evidence at protein level	248	27745	alternative mRNA splicing	mRNA binding [GO:0003	catalytic step 2 spliceoso
273	Q9WVA4	TAGL2_MOUSE	Transgelin-2 (SM22	Mus musculus (Mouse)	Tagln2	Evidence at protein level	199	22395	epithelial cell differentiat	cadherin binding involved	cell-cell adherens junctio
274	Q9ER72	SYCC_MOUSE	Cysteine--tRNA liga	Mus musculus (Mouse)	Cars	Evidence at protein level	831	94860	cysteinyl-tRNA aminoacy	ATP binding [GO:0005524	cytoplasm [GO:0005737]
275	P62196	PRS8_MOUSE	26S protease regul	Mus musculus (Mouse)	Psmc5	Evidence at protein level	406	45626	modulation of synaptic tr	ATP binding [GO:0005524	blood microparticle [GO:(
276	P15089	CBPA3_MOUSE	Mast cell carboxyp	Mus musculus (Mouse)	Cpa3	Evidence at transcript level	417	48790	regulation of angiotensin	metallocarboxypeptidase	extracellular space [GO:0
277	Q91W90	TXND5_MOUSE	Thioredoxin domai	Mus musculus (Mouse)	Txndc5	Evidence at protein level	417	46415	apoptotic cell clearance [	protein disulfide isomera	endoplasmic reticulum lu
278	Q9CZ44	NSF1C_MOUSE	NSFL1 cofactor p47	Mus musculus (Mouse)	Nsfl1c	Evidence at protein level	370	40710	Golgi organization [GO:0(	phospholipid binding [GO	chromosome [GO:00056
279	P14869	RLA0_MOUSE	60S acidic ribosom	Mus musculus (Mouse)	Rplp0	Evidence at protein level	317	34216	cellular response to cAMI	peptide binding [GO:0042	cytoplasm [GO:0005737]
280	P01027	CO3_MOUSE	Complement C3 (H	Mus musculus (Mouse)	C3	Evidence at protein level	1663	186484	complement activation [(	C5L2 anaphylatoxin chem	blood microparticle [GO:(
281	P16381	DDX3L_MOUSE	Putative ATP-depe	Mus musculus (Mouse)	D1Pas1	Evidence at protein level	660	73141	cell differentiation [GO:0(	ATP binding [GO:0005524	cytoplasmic ribonucleopr
282	Q8BH97	RCN3_MOUSE	Reticulocalbin-3	Mus musculus (Mouse)	Rcn3	Evidence at protein level	328	38002		calcium ion binding [GO:(	endoplasmic reticulum lu
283	Q60597	ODO1_MOUSE	2-oxoglutarate deh	Mus musculus (Mouse)	Ogdh	Evidence at protein level	1023	116449	2-oxoglutarate metabolic	metal ion binding [GO:00	mitochondrial matrix [GO
284	Q9CWJ9	PUR9_MOUSE	Bifunctional purine	Mus musculus (Mouse)	Atic	Evidence at protein level	592	64217	'de novo' IMP biosynthet	cadherin binding involved	cell-cell adherens junctio
285	Q6P1B1	XPP1_MOUSE	Xaa-Pro aminopept	Mus musculus (Mouse)	Xpnpep1	Evidence at protein level	623	69591	bradykinin catabolic proc	aminopeptidase activity [	cytoplasm [GO:0005737]
286	Q8JZK9	HMCS1_MOUSE	Hydroxymethylglut	Mus musculus (Mouse)	Hmgcs1	Evidence at protein level	520	57569	brain development [GO:0	drug binding [GO:000814	cytosol [GO:0005829]
287	Q8BP47	SYNC_MOUSE	Asparagine--tRNA l	Mus musculus (Mouse)	Nars	Evidence at protein level	559	64279	asparaginyl-tRNA aminoa	asparagine-tRNA ligase a	cytosol [GO:0005829]; ex
288	P02772	FETA_MOUSE	Alpha-fetoprotein (	Mus musculus (Mouse)	Afp	Evidence at transcript level	605	67337	ovulation from ovarian fo	metal ion binding [GO:00	cytoplasm [GO:0005737]
289	P26638	SYSC_MOUSE	Serine--tRNA ligase	Mus musculus (Mouse)	Sars	Evidence at protein level	512	58389	selenocysteinyl-tRNA(Sec	ATP binding [GO:0005524	cytosol [GO:0005829]; ex
290	Q9DOI9	SYRC_MOUSE	Arginine--tRNA liga	Mus musculus (Mouse)	Rars	Evidence at protein level	660	75674	arginyl-tRNA aminoacylat	arginine binding [GO:000	aminoacyl-tRNA syntheta
291	Q6ZWN5	RS9_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps9	Evidence at protein level	194	22591	positive regulation of cell	5.8S rRNA binding [GO:15	cytoplasm [GO:0005737]
292	P35980	RL18_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl18	Evidence at protein level	188	21645	translation [GO:0006412]	structural constituent of	cytosol [GO:0005829]; cy
293	Q922R8	PDIA6_MOUSE	Protein disulfide-is	Mus musculus (Mouse)	Pdia6	Evidence at protein level	440	48100	apoptotic cell clearance [	protein disulfide isomera	cytosol [GO:0005829]; er
294	P30999	CTND1_MOUSE	Catenin delta-1 (Ca	Mus musculus (Mouse)	Ctnnd1	Evidence at protein level	938	104925	cell adhesion [GO:00071	cadherin binding [GO:004	bicellular tight junction [G
295	Q61171	PRDX2_MOUSE	Peroxiredoxin-2 (EC	Mus musculus (Mouse)	Prdx2	Evidence at protein level	198	21779	activation of MAPK activi	antioxidant activity [GO:(	cytosol [GO:0005829]; ex
296	O08632	KR195_MOUSE	Keratin-associated	Mus musculus (Mouse)	Krtap19-5	Evidence at transcript level	62	6688			intermediate filament [G
297	Q61398	PCOC1_MOUSE	Procollagen C-endc	Mus musculus (Mouse)	Pcolce	Evidence at protein level	468	50168	proteolysis [GO:0006508]	collagen binding [GO:000	extracellular exosome [G
298	P62814	VATB2_MOUSE	V-type proton ATP	Mus musculus (Mouse)	Atp6v1b2	Evidence at protein level	511	56551	ATP hydrolysis coupled p	ATP binding [GO:0005524	cytoplasm [GO:0005737]
299	Q8CIE6	COPA_MOUSE	Coatomer subunit a	Mus musculus (Mouse)	Copa	Evidence at protein level	1224	138432	ER to Golgi vesicle-media	structural molecule activi	COPI vesicle coat [GO:00
300	Q921H8	THIKA_MOUSE	3-ketoacyl-CoA thi	Mus musculus (Mouse)	Acaa1a	Evidence at protein level	424	43953	bile acid metabolic proce	acetate CoA-transferase a	intracellular membrane-b
301	Q9DBC7	KAP0_MOUSE	cAMP-dependent p	Mus musculus (Mouse)	Prkar1a	Evidence at protein level	381	43185	animal organ morphogen	cAMP binding [GO:00305	cAMP-dependent protein
302	O89023	TPP1_MOUSE	Tripeptidyl-peptida	Mus musculus (Mouse)	Tpp1	Evidence at protein level	562	61342	bone resorption [GO:004	endopeptidase activity [G	extracellular exosome [G
303	P97311	MCM6_MOUSE	DNA replication lic	Mus musculus (Mouse)	Mcm6	Evidence at protein level	821	92867	cell cycle [GO:0007049];	ATP binding [GO:0005524	MCM complex [GO:0042
304	Q76MZ3	2AAA_MOUSE	Serine/threonine-p	Mus musculus (Mouse)	Ppp2r1a	Evidence at protein level	589	65323	beta-catenin destruction	antigen binding [GO:0003	chromosome, centromeri
305	Q922D8	C1TC_MOUSE	C-1-tetrahydrofola	Mus musculus (Mouse)	Mthfd1	Evidence at protein level	935	101200	10-formyltetrahydrofolat	ATP binding [GO:0005524	cytosol [GO:0005829]; ex
306	Q61029	LAP2B_MOUSE	Lamina-associated	Mus musculus (Mouse)	Tmpo	Evidence at protein level	452	50373	regulation of transcriptio	cadherin binding involved	cell-cell adherens junctio
307	P08226	APOE_MOUSE	Apolipoprotein E (A	Mus musculus (Mouse)	Apoe	Evidence at protein level	311	35867	AMPA glutamate recepto	antioxidant activity [GO:(	blood microparticle [GO:(
308	P02468	LAMC1_MOUSE	Laminin subunit ga	Mus musculus (Mouse)	Lamc1	Evidence at protein level	1607	177298	axon guidance [GO:0007	extracellular matrix struc	basal lamina [GO:000560
309	Q9JLJ2	AL9A1_MOUSE	4-trimethylaminob	Mus musculus (Mouse)	Aldh9a1	Evidence at protein level	494	53515	carnitine biosynthetic pro	4-trimethylammoniobuty	cytosol [GO:0005829]; ex
310	P97461	RS5_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps5	Evidence at protein level	204	22889	regulation of translationa	mRNA binding [GO:0003	cytosolic small ribosomal
311	Q8C1I6	KR163_MOUSE	Keratin-associated	Mus musculus (Mouse)	Krtap16-3	Evidence at transcript level	86	8433			intermediate filament [G
312	Q2VIS4	FILA2_MOUSE	Filaggrin-2 (FLG-2)	Mus musculus (Mouse)	Flg2	Evidence at protein level	2362	251372		calcium ion binding [GO:(	cytoplasm [GO:0005737]
313	Q8K2B3	SDHA_MOUSE	Succinate dehydro	Mus musculus (Mouse)	Sdha	Evidence at protein level	664	72585	anaerobic respiration [GC	electron carrier activity [(	mitochondrial inner mem
314	O08709	PRDX6_MOUSE	Peroxiredoxin-6 (EC	Mus musculus (Mouse)	Prdx6	Evidence at protein level	224	24871	bleb assembly [GO:0032(	cadherin binding involved	cell-cell adherens junctio
315	Q9CXW4	RL11_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl11	Evidence at protein level	178	20252	protein localization to nu	RNA binding [GO:000372	cytoplasm [GO:0005737]
316	Q61035	SYHC_MOUSE	Histidine--tRNA liga	Mus musculus (Mouse)	Hars	Evidence at protein level	509	57432	histidyl-tRNA aminoacyla	ATP binding [GO:0005524	cytoplasm [GO:0005737]
317	Q922F4	TBB6_MOUSE	Tubulin beta-6 chai	Mus musculus (Mouse)	Tubb6	Evidence at protein level	447	50090	microtubule-based proce	GTPase activity [GO:0003	cytoplasm [GO:0005737]
318	P17751	TPIS_MOUSE	Triosephosphate is	Mus musculus (Mouse)	Tpi1	Evidence at protein level	299	32192	gluconeogenesis [GO:000	isomerase activity [GO:0(	cytosol [GO:0005829]; ex
319	Q9CZY3	UB2V1_MOUSE	Ubiquitin-conjugati	Mus musculus (Mouse)	Ube2v1	Evidence at protein level	147	16355	error-free postreplication	ubiquitin conjugating enz	cytoplasm [GO:0005737]
320	Q9JIK5	DDX21_MOUSE	Nucleolar RNA heli	Mus musculus (Mouse)	Ddx21	Evidence at protein level	851	93551	osteoblast differentiation	7SK snRNA binding [GO:0	membrane [GO:0016020
321	P80317	TCPZ_MOUSE	T-complex protein	Mus musculus (Mouse)	Cct6a	Evidence at protein level	531	58004	'de novo' protein folding	ATP binding [GO:0005524	acrosomal vesicle [GO:00
322	P54775	PRS6B_MOUSE	26S protease regul	Mus musculus (Mouse)	Psmc4	Evidence at protein level	418	47408	blastocyst development [	ATP binding [GO:0005524	cytosol [GO:0005829]; cy
323	Q8BJS4	SUN2_MOUSE	SUN domain-conta	Mus musculus (Mouse)	Sun2	Evidence at protein level	731	81605	centrosome localization [	identical protein binding	condensed nuclear chrom
324	Q8BFR5	EFTU_MOUSE	Elongation factor T	Mus musculus (Mouse)	Tufm	Evidence at protein level	452	49508	response to ethanol [GO:	GTPase activity [GO:0003	extracellular exosome [G
325	Q9D0R2	SYTC_MOUSE	Threonine--tRNA lig	Mus musculus (Mouse)	Tars	Evidence at protein level	722	83356	threonyl-tRNA aminoacyl	ATP binding [GO:0005524	actin cytoskeleton [GO:0
326	Q922Y1	UBXN1_MOUSE	UBX domain-contai	Mus musculus (Mouse)	Ubxn1	Evidence at protein level	297	33573	negative regulation of ER	ATPase binding [GO:0051	cytoplasm [GO:0005737]
327	P50580	PA2G4_MOUSE	Proliferation-assoc	Mus musculus (Mouse)	Pa2g4	Evidence at protein level	394	43699	negative regulation of ap	DNA binding [GO:000367	cytoplasm [GO:0005737]
328	Q8BL97	SRSF7_MOUSE	Serine/arginine-ricl	Mus musculus (Mouse)	Srsf7	Evidence at protein level	267	30818	mRNA processing [GO:00	nucleotide binding [GO:0	cytoplasm [GO:0005737]
329	P07214	SPRC_MOUSE	SPARC (Basement-r	Mus musculus (Mouse)	Sparc	Evidence at protein level	302	34450	bone development [GO:0	calcium ion binding [GO:(	basement membrane [GO
330	Q61753	SERA_MOUSE	D-3-phosphoglycer	Mus musculus (Mouse)	Phgdh	Evidence at protein level	533	56586	G1 to G0 transition [GO:0	NAD binding [GO:005128	extracellular exosome [G
331	Q99L47	F10A1_MOUSE	Hsc70-interacting p	Mus musculus (Mouse)	St13	Evidence at protein level	371	41656	chaperone cofactor-depe	dATP binding [GO:00325(	cytosol [GO:0005829]; ex
332	O55234	PSB5_MOUSE	Proteasome subuni	Mus musculus (Mouse)	Psmb5	Evidence at protein level	264	28532	proteasome-mediated ub	peptidase activity [GO:00	centrosome [GO:000581
333	P80315	TCPD_MOUSE	T-complex protein	Mus musculus (Mouse)	Cct4	Evidence at protein level	539	58066	'de novo' protein folding	ATP binding [GO:0005524	cell body [GO:0044297];
334	Q9R0P3	ESTD_MOUSE	S-formylglutathion	Mus musculus (Mouse)	Esd	Evidence at protein level	282	31320	formaldehyde catabolic p	carboxylic ester hydrolas	cytoplasmic vesicle [GO:(
335	Q9D1A2	CNDP2_MOUSE	Cytosolic non-speci	Mus musculus (Mouse)	Cndp2	Evidence at protein level	475	52767	proteolysis [GO:0006508]	alanylglutamate dipeptid	cytosol [GO:0005829]; ex
336	Q9JLI62	GLTP_MOUSE	Glycolipid transfer	Mus musculus (Mouse)	Gltp	Evidence at protein level	209	23690	glycolipid transport [GO:(	glycolipid binding [GO:00	cytosol [GO:0005829]; ex
337	P68372	TBB4B_MOUSE	Tubulin beta-4B ch	Mus musculus (Mouse)	Tubb4b	Evidence at protein level	445	49831	microtubule-based proce	double-stranded RNA bin	cytoplasm [GO:0005737]
338	Q9JK81	MYG1_MOUSE	UPF0160 protein M	Mus musculus (Mouse)	Myg1	Evidence at protein level	380	42723	locomotory exploration behavior [GO:0035641]		extracellular exosome [G
339	Q99J99	THTM_MOUSE	3-mercaptopyruvat	Mus musculus (Mouse)	Mpst	Evidence at protein level	297	33023	hydrogen sulfide biosynt	3-mercaptopyruvate sulfi	cell junction [GO:003005
340	Q9D2U9	H2B3A_MOUSE	Histone H2B type 3	Mus musculus (Mouse)	Hist3h2ba	Evidence at protein level	126	13994	nucleosome assembly [G	DNA binding [GO:000367	cytosol [GO:0005829]; ex
341	O54983	CRYM_MOUSE	Ketimine reductase	Mus musculus (Mouse)	Crym	Evidence at protein level	313	33523	negative regulation of tra	hormone binding [GO:00	cytoplasm [GO:0005737]
342	Q9WTI7	MYO1C_MOUSE	Unconventional my	Mus musculus (Mouse)	Myo1c	Evidence at protein level	1063	121944	membrane organization [	actin binding [GO:000377	basal plasma membrane
343	Q9Z204	HNRPC_MOUSE	Heterogeneous nu	Mus musculus (Mouse)	Hnrnpc	Evidence at protein level	313	34385	3'-UTR-mediated mRNA s	identical protein binding	catalytic step 2 spliceoso
344	Q9CRB3	HIUH_MOUSE	5-hydroxyisourate	Mus musculus (Mouse)	Urah	Evidence at protein level	118	13559	purine nucleobase metab	hydrolase activity [GO:00	mitochondrion [GO:0005
345	Q9CWK8	SNX2_MOUSE	Sorting nexin-2	Mus musculus (Mouse)	Snx2	Evidence at protein level	519	58471	early endosome to Golgi t	cadherin binding involved	cell-cell adherens junctio
346	P47911	RL6_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl6	Evidence at protein level	296	33510	cytoplasmic translation [(	cadherin binding involved	cell-cell adherens junctio

347	Q8CG70	P3H3_MOUSE	Prolyl 3-hydroxylas	Mus musculus (Mouse)	P3h3	Evidence at protein level	732	81701	collagen metabolic proce	iron ion binding [GO:005	endoplasmic reticulum [G
348	Q80X72	LRC15_MOUSE	Leucine-rich repeat	Mus musculus (Mouse)	Lrrc15	Evidence at transcript level	579	64177	cytokine-mediated signal	collagen binding [GO:000	cytoplasm [GO:0005737]
349	Q6WVG3	KCD12_MOUSE	BTB/POZ domain-c	Mus musculus (Mouse)	Kctd12	Evidence at protein level	327	35892	protein homooligomeriza	RNA binding [GO:000372	cell junction [GO:003005
350	Q11011	PSA_MOUSE	Puromycin-sensitiv	Mus musculus (Mouse)	Npepps	Evidence at protein level	920	103325	cellular response to hypo	aminopeptidase activity [	cytoplasm [GO:0005737]
351	P24270	CATA_MOUSE	Catalase (EC 1.11.1	Mus musculus (Mouse)	Cat	Evidence at protein level	527	59795	aerobic respiration [GO:0	aminoacylase activity [G	cytosol [GO:0005829]; er
352	P27573	MYP0_MOUSE	Myelin protein P0 (	Mus musculus (Mouse)	Mpz	Evidence at protein level	248	27622	cell aggregation [GO:0098743];	cell-cell adhesion vi	integral component of pla
353	P27546	MAP4_MOUSE	Microtubule-associ	Mus musculus (Mouse)	Map4	Evidence at protein level	1125	117429	cell division [GO:0051301	microtubule binding [GO:	axoneme [GO:0005930];
354	P23492	PNPH_MOUSE	Purine nucleoside p	Mus musculus (Mouse)	Pnp	Evidence at protein level	289	32277	apoptotic mitochondrial c	drug binding [GO:000814	cytoplasm [GO:0005737]
355	P08030	APT_MOUSE	Adenine phosphori	Mus musculus (Mouse)	Aprt	Evidence at protein level	180	19724	adenine metabolic proce	adenine binding [GO:000	cytosol [GO:0005829]; ex
356	P47757	CAPZB_MOUSE	F-actin-capping pro	Mus musculus (Mouse)	Capzb	Evidence at protein level	277	31345	actin cytoskeleton organi	beta-tubulin binding [GO:	actin filament [GO:00058
357	Q6URW6	MYH14_MOUSE	Myosin-14 (Myosir	Mus musculus (Mouse)	Myh14	Evidence at protein level	2000	228586	actin filament-based mov	actin-dependent ATPase	actomyosin [GO:0042641
358	O08547	SC22B_MOUSE	Vesicle-trafficking	Mus musculus (Mouse)	Sec22b	Evidence at protein level	215	24741	ER to Golgi vesicle-media	SNAP receptor activity [G	endoplasmic reticulum-G
359	P29758	OAT_MOUSE	Ornithine aminotra	Mus musculus (Mouse)	Oat	Evidence at protein level	439	48355	L-proline biosynthetic pro	identical protein binding |	mitochondrial matrix [GO
360	P26039	TLN1_MOUSE	Talin-1	Mus musculus (Mouse)	Tln1	Evidence at protein level	2541	269821	cell-substrate junction as	cadherin binding involved	cell-cell adherens junctio
361	P09803	CADH1_MOUSE	Cadherin-1 (ARC-1)	Mus musculus (Mouse)	Cdh1	Evidence at protein level	884	98256	adherens junction organi	alpha-catenin binding [G	actin cytoskeleton [GO:0
362	Q8K010	OPLA_MOUSE	5-oxoprolinase (EC	Mus musculus (Mouse)	Oplah	Evidence at protein level	1288	137611	glutathione metabolic pro	5-oxoprolinase (ATP-hydrolyzing) activity [GO:0017	
363	Q9Z1Q5	CLIC1_MOUSE	Chloride intracellul	Mus musculus (Mouse)	Clic1	Evidence at protein level	241	27013	chloride transport [GO:0	cadherin binding involved	blood microparticle [GO:0
364	Q148V8	FA83H_MOUSE	Protein FAM83H	Mus musculus (Mouse)	Fam83h	Evidence at protein level	1209	131115	biomineral tissue develop	keratin filament binding [	cytoplasm [GO:0005737]
365	P16460	ASSY_MOUSE	Argininosuccinate s	Mus musculus (Mouse)	Ass1	Evidence at protein level	412	46584	arginine biosynthetic pro	amino acid binding [GO:0	extracellular exosome [G
366	Q09PK2	APRV1_MOUSE	Retroviral-like aspa	Mus musculus (Mouse)	Asprv1	Evidence at protein level	339	37174	protein processing [GO:0	aspartic-type endopeptid	integral component of me
367	Q9DB20	ATPO_MOUSE	ATP synthase subu	Mus musculus (Mouse)	Atp5o	Evidence at protein level	213	23364	mitochondrial ATP synthe	drug binding [GO:000814	extracellular exosome [G
368	Q8R2Q0	TRI29_MOUSE	Tripartite motif-co	Mus musculus (Mouse)	Trim29	Evidence at protein level	587	65820	negative regulation of pro	cadherin binding involved	cell-cell adherens junctio
369	P50247	SAHH_MOUSE	Adenosylhomocyst	Mus musculus (Mouse)	Ahcy	Evidence at protein level	432	47688	one-carbon metabolic pro	adenosylhomocysteinase	cytosol [GO:0005829]; ex
370	P14131	RS16_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps16	Evidence at protein level	146	16445	maturation of SSU-rRNA	RNA binding [GO:000372	cytosolic small ribosomal
371	Q8BMJ2	SYLC_MOUSE	Leucine--tRNA liga	Mus musculus (Mouse)	Lars	Evidence at protein level	1178	134192	leucyl-tRNA aminoacylati	aminoacyl-tRNA editing a	cytosol [GO:0005829]; nu
372	Q8BMS1	ECHA_MOUSE	Trifunctional enzyn	Mus musculus (Mouse)	Hadha	Evidence at protein level	763	82670	fatty acid beta-oxidation	acetyl-CoA C-acyltransfer	extracellular matrix [GO:0
373	Q9R1P3	PSB2_MOUSE	Proteasome subuni	Mus musculus (Mouse)	Psmb2	Evidence at protein level	201	22906	proteolysis involved in ce	threonine-type endopept	cytosol [GO:0005829]; ex
374	Q8R081	HNRPL_MOUSE	Heterogeneous nu	Mus musculus (Mouse)	Hnrnpl	Evidence at protein level	586	63964	cellular response to amin	mRNA 3'-UTR binding [G	cytosol [GO:0005829]; ex
375	P55850	DSC3_MOUSE	Desmocollin-3	Mus musculus (Mouse)	Dsc3	Evidence at protein level	896	100203	homophilic cell adhesion	calcium ion binding [GO:0	cell junction [GO:003005
376	P01942	HBA_MOUSE	Hemoglobin subuni	Mus musculus (Mouse)	Hba	Evidence at protein level	142	15085	cellular oxidant detoxifica	heme binding [GO:00200	blood microparticle [GO:0
377	P80313	TCPH_MOUSE	T-complex protein	Mus musculus (Mouse)	Cct7	Evidence at protein level	544	59652	'de novo' protein folding	ATP binding [GO:0005524	cell body [GO:0044297];
378	Q8CI94	PYGB_MOUSE	Glycogen phospho	Mus musculus (Mouse)	Pygb	Evidence at protein level	843	96730	glycogen catabolic proce	glycogen phosphorylase a	axon [GO:0030424]; cyto
379	Q8VH51	RBM39_MOUSE	RNA-binding protei	Mus musculus (Mouse)	Rbm39	Evidence at protein level	530	59407	mRNA processing [GO:00	nucleotide binding [GO:0	microtubule cytoskeleton
380	P70698	PYRG1_MOUSE	CTP synthase 1 (EC	Mus musculus (Mouse)	Ctps1	Evidence at protein level	591	66682	'de novo' CTP biosyntheti	ATP binding [GO:0005524	membrane [GO:0016020
381	Q8CGN5	PLIN1_MOUSE	Perilipin-1 (Lipid dr	Mus musculus (Mouse)	Plin1	Evidence at protein level	517	55596	lipid catabolic process [GO:0016042]; triglyceride c		cytosol [GO:0005829]; er
382	P16110	LEG3_MOUSE	Galectin-3 (Gal-3) (	Mus musculus (Mouse)	Lgals3	Evidence at protein level	264	27515	cell differentiation [GO:0	carbohydrate binding [GO	cell surface [GO:0009986
383	Q7TPC1	CDSN_MOUSE	Corneodesmosin	Mus musculus (Mouse)	Cdsn	Evidence at transcript level	561	54313	single organismal cell-cell	protein homodimerizatio	desmosome [GO:003005
384	Q9CQQ7	AT5F1_MOUSE	ATP synthase F(0)	Mus musculus (Mouse)	Atp5f1	Evidence at protein level	256	28949	ATP hydrolysis coupled ca	ATPase activity [GO:0016	extracellular exosome [G
385	P62192	PRS4_MOUSE	26S protease regul	Mus musculus (Mouse)	Psmc1	Evidence at protein level	440	49185	negative regulation of ne	ATP binding [GO:0005524	cytosol [GO:0005829]; cy
386	Q922B2	SYDC_MOUSE	Aspartate--tRNA lig	Mus musculus (Mouse)	Dars	Evidence at protein level	501	57147	aspartyl-tRNA aminoacyl	aspartate-tRNA ligase act	cytosol [GO:0005829]; ex
387	Q3U0V1	FUBP2_MOUSE	Far upstream elem	Mus musculus (Mouse)	Khsrp	Evidence at protein level	748	76775	3'-UTR-mediated mRNA	DNA binding [GO:000367	cytoplasmic stress granul
388	Q61543	GSLG1_MOUSE	Golgi apparatus pro	Mus musculus (Mouse)	Glg1	Evidence at protein level	1175	133734	bone morphogenesis [GO	fibroblast growth factor b	extracellular exosome [G
389	Q8CDN6	TXNL1_MOUSE	Thioredoxin-like pro	Mus musculus (Mouse)	Txnl1	Evidence at protein level	289	32237	cell redox homeostasis [G	disulfide oxidoreductase	cytoplasm [GO:0005737]
390	Q99KP6	PRP19_MOUSE	Pre-mRNA-process	Mus musculus (Mouse)	Prpf19	Evidence at protein level	504	55239	cellular protein localizatio	identical protein binding |	catalytic step 2 spliceoso
391	Q8BTI8	SRRM2_MOUSE	Serine/arginine rep	Mus musculus (Mouse)	Srrm2	Evidence at protein level	2703	294840	mRNA processing [GO:00	RNA binding [GO:000372	Cajal body [GO:0015030]
392	Q62318	TIF1B_MOUSE	Transcription intern	Mus musculus (Mouse)	Trim28	Evidence at protein level	834	88847	convergent extension inv	chromatin binding [GO:0	chromatin [GO:0000785]
393	P35922	FMR1_MOUSE	Synaptic functional	Mus musculus (Mouse)	Fmr1	Evidence at protein level	614	68989	anterograde axonal trans	chromatin binding [GO:0	axon [GO:0030424]; axon
394	P63101	1433Z_MOUSE	14-3-3 protein zeta	Mus musculus (Mouse)	Ywhaz	Evidence at protein level	245	27771	establishment of Golgi lo	cadherin binding involved	blood microparticle [GO:0
395	Q9QUR6	PPCE_MOUSE	Prolyl endopeptida	Mus musculus (Mouse)	Prep	Evidence at protein level	710	80752	protein metabolic proces	serine-type endopeptidas	cytoplasm [GO:0005737]
396	O08553	DPYL2_MOUSE	Dihydropyrimidinas	Mus musculus (Mouse)	Dpysl2	Evidence at protein level	572	62278	axon guidance [GO:0007	hydrolase activity, acting	axon [GO:0030424]; cyto
397	P50608	FMOD_MOUSE	Fibromodulin (FM)	Mus musculus (Mouse)	Fmod	Evidence at transcript level	376	43055	collagen fibril organization [GO:0030199]		extracellular space [GO:0
398	P97821	CATC_MOUSE	Dipeptidyl peptidas	Mus musculus (Mouse)	Ctsc	Evidence at protein level	462	52376	aging [GO:0007568]; posi	chloride ion binding [GO:0	centrosome [GO:000581
399	Q9EQU5	SET_MOUSE	Protein SET (Phosp	Mus musculus (Mouse)	Set	Evidence at protein level	289	33378	negative regulation of ne	DNA binding [GO:000367	cytoplasm [GO:0005737]
400	P14211	CALR_MOUSE	Calreticulin (CRP55	Mus musculus (Mouse)	Calr	Evidence at protein level	416	47995	cardiac muscle cell differ	androgen receptor bindin	acrosomal vesicle [GO:00
401	P29699	FETUA_MOUSE	Alpha-2-HS-glycopr	Mus musculus (Mouse)	Ahsg	Evidence at protein level	345	37326	acute-phase response [G	cysteine-type endopeptid	blood microparticle [GO:0
402	P02088	HBB1_MOUSE	Hemoglobin subuni	Mus musculus (Mouse)	Hbb-b1	Evidence at protein level	147	15840	erythrocyte development	heme binding [GO:00200	hemoglobin complex [GO
403	Q8CCS6	PABP2_MOUSE	Polyadenylate-bind	Mus musculus (Mouse)	Pabpn1	Evidence at protein level	302	32297	cellular response to lipop	nucleotide binding [GO:0	cytoplasm [GO:0005737]
404	P63085	MK01_MOUSE	Mitogen-activated	Mus musculus (Mouse)	Mapk1	Evidence at protein level	358	41276	animal organ morphogen	ATP binding [GO:0005524	axon [GO:0030424]; cave
405	Q8R050	ERF3A_MOUSE	Eukaryotic peptide	Mus musculus (Mouse)	Gspt1	Evidence at protein level	636	68625	cytoplasmic translational	GTPase activity [GO:0003	cytosol [GO:0005829]; tra
406	Q9CQM9	GLRX3_MOUSE	Glutaredoxin-3 (PK	Mus musculus (Mouse)	Glrx3	Evidence at protein level	337	37778	[2Fe-2S] cluster assembly	electron carrier activity [(	cell cortex [GO:0009938]
407	Q91ZX7	LRP1_MOUSE	Prolow-density lipo	Mus musculus (Mouse)	Lrp1	Evidence at protein level	4545	504742	aorta morphogenesis [GO	apolipoprotein binding [G	clathrin-coated pit [GO:0
408	Q99JY0	ECHB_MOUSE	Trifunctional enzyn	Mus musculus (Mouse)	Hadhb	Evidence at protein level	475	51386	fatty acid beta-oxidation	acetyl-CoA C-acyltransfer	endoplasmic reticulum [G
409	P62322	LSM5_MOUSE	U6 snRNA-associat	Mus musculus (Mouse)	Lsm5	Inferred from homology	91	9937	mRNA catabolic process [	protein heterodimerizatio	cytoplasm [GO:0005737]
410	Q9D819	IPYR_MOUSE	Inorganic pyrophos	Mus musculus (Mouse)	Ppa1	Evidence at protein level	289	32667	phosphate-containing co	inorganic diphosphatase	cytoplasm [GO:0005737]
411	P63038	CH60_MOUSE	60 kDa heat shock	Mus musculus (Mouse)	Hspd1	Evidence at protein level	573	60955	'de novo' protein folding	ATP binding [GO:0005524	cell surface [GO:0009986
412	P70168	IMB1_MOUSE	Importin subunit be	Mus musculus (Mouse)	Kpnb1	Evidence at protein level	876	97184	astral microtubule organi	enzyme binding [GO:001	cytoplasm [GO:0005737]
413	Q3TXS7	PSMD1_MOUSE	26S proteasome no	Mus musculus (Mouse)	Psmd1	Evidence at protein level	953	105730	regulation of protein cata	enzyme regulator activity	extracellular exosome [G
414	Q9D8U8	SNX5_MOUSE	Sorting nexin-5	Mus musculus (Mouse)	Snx5	Evidence at protein level	404	46797	endocytosis [GO:0006897	cadherin binding involved	cell-cell adherens junctio
415	P70697	DCUP_MOUSE	Uroporphyrinogen	Mus musculus (Mouse)	Urod	Evidence at protein level	367	40692	heme biosynthetic proce	uroporphyrinogen decarb	cytosol [GO:0005829]; nu
416	P47754	CAZA2_MOUSE	F-actin-capping pro	Mus musculus (Mouse)	Capza2	Evidence at protein level	286	32967	barbed-end actin filament	capping [GO:0051016]	brush border [GO:00059
417	P54822	PUR8_MOUSE	Adenylosuccinate l	Mus musculus (Mouse)	Adsl	Evidence at protein level	484	54866	'de novo' AMP biosynthe	(S)-2-(5-amino-1-(5-phos	cytosol [GO:0005829]; m
418	Q32Q92	ACOT6_MOUSE	Acyl-coenzyme A th	Mus musculus (Mouse)	Acot6	Evidence at protein level	419	46769	acyl-CoA metabolic proce	acyl-CoA hydrolase activi	peroxisome [GO:0005777
419	Q9CYZ2	TPD54_MOUSE	Tumor protein D54	Mus musculus (Mouse)	Tpd52l2	Evidence at protein level	220	24043		protein heterodimerizatio	cytoplasm [GO:0005737]
420	Q9JIX8	ACINU_MOUSE	Apoptotic chromat	Mus musculus (Mouse)	Acin1	Evidence at protein level	1338	150719	apoptotic chromosome c	nucleotide binding [GO:0	ASAP complex [GO:0061
421	Q99JY9	ARP3_MOUSE	Actin-related prote	Mus musculus (Mouse)	Actr3	Evidence at protein level	418	47357	Arp2/3 complex-mediate	ATP binding [GO:0005524	Arp2/3 protein complex [
422	P60867	RS20_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps20	Evidence at protein level	119	13373	translation [GO:0006412]	RNA binding [GO:000372	cytosolic small ribosomal
423	Q9CYR6	AGM1_MOUSE	Phosphoacetylgluc	Mus musculus (Mouse)	Pgm3	Evidence at protein level	542	59453	carbohydrate metabolic p	magnesium ion binding [(	cytosol [GO:0005829]
424	Q02248	CTNB1_MOUSE	Catenin beta-1 (Be	Mus musculus (Mouse)	Ctnnb1	Evidence at protein level	781	85471	adherens junction assem	alpha-catenin binding [G	adherens junction [GO:00
425	Q91V92	ACLY_MOUSE	ATP-citrate syntha	Mus musculus (Mouse)	Acly	Evidence at protein level	1091	119728	acetyl-CoA biosynthetic p	ATP binding [GO:0005524	citrate lyase complex [GO
426	Q6ZWX6	IF2A_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif2s1	Evidence at protein level	315	36108	aging [GO:0007568]; cell	ribosome binding [GO:00	cytoplasm [GO:0005737]
427	Q8CGK3	LONM_MOUSE	Lon protease homo	Mus musculus (Mouse)	Lonp1	Evidence at protein level	949	105843	aging [GO:0007568]; cell	ADP binding [GO:004353	cytosol [GO:0005829]; m
428	P35486	ODPA_MOUSE	Pyruvate dehydrog	Mus musculus (Mouse)	Pdha1	Evidence at protein level	390	43232	acetyl-CoA biosynthetic p	pyruvate dehydrogenase	mitochondrial matrix [GO
429	Q8BP67	RL24_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl24	Evidence at protein level	157	17779	assembly of large subunit	cadherin binding involved	cell-cell adherens junctio
430	Q8R1B4	EIF3C_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif3c	Evidence at protein level	911	105531	positive regulation of mR	ribosome binding [GO:00	eukaryotic translation ini
431	Q8QZR5	ALAT1_MOUSE	Alanine aminotran	Mus musculus (Mouse)	Gpt	Evidence at protein level	496	55143	biosynthetic process [GO	L-alanine:2-oxoglutarate	cytoplasm [GO:0005737]
432	Q64010	CRK_MOUSE	Adapter molecule c	Mus musculus (Mouse)	Crk	Evidence at protein level	304	33815	cellular response to endo	ephrin receptor binding [(	actin cytoskeleton [GO:00
433	Q91WT9	CBS_MOUSE	Cystathionine beta	Mus musculus (Mouse)	Cbs	Evidence at protein level	561	61544	blood vessel remodeling [	carbon monoxide binding	cytoplasm [GO:0005737]
434	Q61205	PA1B3_MOUSE	Platelet-activating	Mus musculus (Mouse)	Pafah1b3	Evidence at protein level	232	25853	brain development [GO:0	1-alkyl-2-acetylglycerop	cytoplasm [GO:0005737]
435	Q8R317	UBQL1_MOUSE	Ubiquilin-1 (Proteir	Mus musculus (Mouse)	Ubqln1	Evidence at protein level	582	61976	aggrephagy [GO:0035973	identical protein binding |	aggresome [GO:0016235
436	Q9QXT0	CNPY2_MOUSE	Protein canopy hor	Mus musculus (Mouse)	Cnpy2	Evidence at protein level	182	20767	enzyme linked receptor	protein signaling pathway [	endoplasmic reticulum [G
437	Q9QXD6	F16P1_MOUSE	Fructose-1,6-bisph	Mus musculus (Mouse)	Fbp1	Evidence at protein level	338	36912	cellular response to drug	AMP binding [GO:001620	cytoplasm [GO:0005737]
438	P37804	TAGL_MOUSE	Transgelin (Actin-a	Mus musculus (Mouse)	Tagln	Evidence at protein level	201	22576	epithelial cell differentiation [GO:0030855]		cytoplasm [GO:0005737]
439	Q91YI0	ARLY_MOUSE	Argininosuccinate l	Mus musculus (Mouse)	Asl	Evidence at protein level	464	51739	ammonia assimilation cyc	argininosuccinate lyase a	cytoplasm [GO:0005737]
440	O35639	ANXA3_MOUSE	Annexin A3 (35-alp	Mus musculus (Mouse)	Anxa3	Evidence at protein level	323	36384	animal organ regeneratio	calcium-dependent phos	axon [GO:0030424]; cyto
441	P35505	FAAA_MOUSE	Fumarylacetoaceta	Mus musculus (Mouse)	Fah	Evidence at protein level	419	46176	arginine catabolic proces	fumarylacetoacetase acti	extracellular exosome [G
442	P31230	AIMP1_MOUSE	Aminoacyl tRNA sy	Mus musculus (Mouse)	Aimp1	Evidence at protein level	310	33997	angiogenesis [GO:000152	cytokine activity [GO:000	aminoacyl-tRNA syntheta
443	Q9WTM5	RUVB2_MOUSE	RuvB-like 2 (EC 3.6	Mus musculus (Mouse)	Ruvbl2	Evidence at protein level	463	51113	cellular response to estra	ADP binding [GO:004353	centrosome [GO:000581
444	P12382	PFKAL_MOUSE	ATP-dependent 6-p	Mus musculus (Mouse)	Pfkl	Evidence at protein level	780	85360	fructose 1,6-bisphosphat	6-phosphofructokinase a	6-phosphofructokinase c
445	Q8C1B7	SEP11_MOUSE	Septin-11	Mus musculus (Mouse)	Sept11	Evidence at protein level	431	49695	cell cycle [GO:0007049];	GTP binding [GO:0005525	axon [GO:0030424]; cell j
446	P54728	RD23B_MOUSE	UV excision repair	Mus musculus (Mouse)	Rad23b	Evidence at protein level	416	43513	cellular response to DNA	damaged DNA binding [G	cytosol [GO:0005829]; nu
447	Q8VDN2	AT1A1_MOUSE	Sodium/potassium	Mus musculus (Mouse)	Atp1a1	Evidence at protein level	1023	112982	cellular potassium ion ho	ADP binding [GO:004353	apical plasma membrane
448	Q60932	VDAC1_MOUSE	Voltage-dependent	Mus musculus (Mouse)	Vdac1	Evidence at protein level	296	32351	anion transport [GO:000	ion channel binding [GO:0	extracellular exosome [G
449	Q8R5J9	PRAF3_MOUSE	PRA1 family protei	Mus musculus (Mouse)	Arl6ip5	Evidence at protein level	188	21558	intrinsic apoptotic signaling pathway in response to		cytoskeleton [GO:000585
450	P35550	FBRL_MOUSE	rRNA 2'-O-methylt	Mus musculus (Mouse)	Fbl	Evidence at protein level	327	34307	box C/D snoRNA 3'-end p	ATPase binding [GO:0051	box C/D snoRNP complex
451	P15105	GLNA_MOUSE	Glutamine synthet	Mus musculus (Mouse)	Glul	Evidence at protein level	373	42120	ammonia assimilation cyc	ATP binding [GO:0005524	astrocyte projection [GO:
452	Q9WV32	ARC1B_MOUSE	Actin-related prote	Mus musculus (Mouse)	Arpc1b	Evidence at protein level	372	41064	Arp2/3 complex-mediate	actin filament binding [G	Arp2/3 protein complex [
453	Q8JZN5	ACAD9_MOUSE	Acyl-CoA dehydrog	Mus musculus (Mouse)	Acad9	Evidence at protein level	625	68722	mitochondrial respiratory	acyl-CoA dehydrogenase	dendrite [GO:0030425]; r
454	Q4KML4	ABRAL_MOUSE	Costars family prot	Mus musculus (Mouse)	Abracl	Evidence at protein level	81	9030			
455	O09061	PSB1_MOUSE	Proteasome subuni	Mus musculus (Mouse)	Psmb1	Evidence at protein level	240	26372	proteolysis involved in ce	threonine-type endopept	cytosol [GO:0005829]; ex
456	Q8VCW2	K1C25_MOUSE	Keratin, type I cyto	Mus musculus (Mouse)	Krt25	Evidence at protein level	446	48921	aging [GO:0007568]; cytc	protein heterodimerizatio	cytoplasm [GO:0005737]
457	Q62093	SRSF2_MOUSE	Serine/arginine-ric	Mus musculus (Mouse)	Srsf2	Evidence at protein level	221	25476	mitotic nuclear division [(	nucleotide binding [GO:0	cytosol [GO:0005829]; ex
458	Q8BGC4	PTGR3_MOUSE	Prostaglandin redu	Mus musculus (Mouse)	Zadh2	Evidence at protein level	377	40529	negative regulation of fat	13-prostaglandin reducta	mitochondrion [GO:0005
459	P51150	RAB7A_MOUSE	Ras-related protein	Mus musculus (Mouse)	Rab7a	Evidence at protein level	207	23490	early endosome to late en	GDP binding [GO:001900	autophagosome membra
460	P19783	COX41_MOUSE	Cytochrome c oxid	Mus musculus (Mouse)	Cox4i1	Evidence at protein level	169	19530	mitochondrial electron tr	cytochrome-c oxidase act	extracellular exosome [G
461	P62264	RS14_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps14	Evidence at protein level	151	16273	erythrocyte differentiatio	mRNA 5'-UTR binding [GC	cytosolic small ribosomal
462	Q3UDE2	TTL12_MOUSE	Tubulin--tyrosine li	Mus musculus (Mouse)	Ttll12	Evidence at protein level	639	74043	cellular protein modificat	ATP binding [GO:0005524]	
463	O35350	CAN1_MOUSE	Calpain-1 catalytic	Mus musculus (Mouse)	Capn1	Evidence at protein level	713	82106	mammary gland involutic	calcium-dependent cyste	cytosol [GO:0005829]; ex

464	P04117	FABP4_MOUSE	Fatty acid-binding p	Mus musculus (Mouse)	Fabp4	Evidence at protein level	132	14650	brown fat cell differentiat	fatty acid binding [GO:00	cytoplasm [GO:0005737]
465	P47962	RL5_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl5	Evidence at protein level	297	34401	ribosomal large subunit a	5S rRNA binding [GO:000	cytoplasm [GO:0005737]
466	P32261	ANT3_MOUSE	Antithrombin-III (A	Mus musculus (Mouse)	Serpinc1	Evidence at protein level	465	52004	acute inflammatory respo	heparin binding [GO:0008	blood microparticle [GO:0
467	Q00PI9	HNRL2_MOUSE	Heterogeneous nuc	Mus musculus (Mouse)	Hnrnpul2	Evidence at protein level	745	84940		RNA binding [GO:000372	membrane [GO:0016020
468	P62717	RL18A_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl18a	Evidence at protein level	176	20732	response to antineoplasti	RNA binding [GO:000372	cytosolic large ribosomal
469	P62962	PROF1_MOUSE	Profilin-1 (Profilin I	Mus musculus (Mouse)	Pfn1	Evidence at protein level	140	14957	actin cytoskeleton organi	actin binding [GO:000377	blood microparticle [GO:0
470	O54734	OST48_MOUSE	Dolichyl-diphospho	Mus musculus (Mouse)	Ddost	Evidence at protein level	441	49028	protein glycosylation [GO	dolichyl-diphosphooligosa	endoplasmic reticulum [G
471	Q9D1M0	SEC13_MOUSE	Protein SEC13 hom	Mus musculus (Mouse)	Sec13	Evidence at protein level	322	35566	ER to Golgi vesicle-media	identical protein binding |	cytosol [GO:0005829]; er
472	Q60716	P4HA2_MOUSE	Prolyl 4-hydroxylas	Mus musculus (Mouse)	P4ha2	Evidence at protein level	537	61002	peptidyl-proline hydroxyl	iron ion binding [GO:0005	cytosol [GO:0005829]; er
473	O88844	IDHC_MOUSE	Isocitrate dehydrog	Mus musculus (Mouse)	Idh1	Evidence at protein level	414	46674	2-oxoglutarate metabolic	(R)-2-hydroxyglutarate de	cell-cell adherens junctio
474	O08749	DLDH_MOUSE	Dihydrolipoyl dehy	Mus musculus (Mouse)	Dld	Evidence at protein level	509	54272	2-oxoglutarate metabolic	dihydrolipoyl dehydrogen	acrosomal matrix [GO:00
475	Q3THE2	ML12B_MOUSE	Myosin regulatory	Mus musculus (Mouse)	Myl12b	Evidence at protein level	172	19779	platelet aggregation [GO:	calcium ion binding [GO:0	apical part of cell [GO:00
476	Q9D2G2	ODO2_MOUSE	Dihydrolipoyllysine	Mus musculus (Mouse)	Dlst	Evidence at protein level	454	48995	L-lysine catabolic process	dihydrolipoyllysine-resid	extracellular exosome [G
477	P62960	YBOX1_MOUSE	Nuclease-sensitive	Mus musculus (Mouse)	Ybx1	Evidence at protein level	322	35730	CRD-mediated mRNA sta	chromatin binding [GO:0	CRD-mediated mRNA sta
478	Q8K411	PREP_MOUSE	Presequence prote	Mus musculus (Mouse)	Pitrm1	Evidence at protein level	1036	117372	proteolysis [GO:0006508	metal ion binding [GO:00	mitochondrial matrix [GO
479	Q9DCW4	ETFB_MOUSE	Electron transfer fl	Mus musculus (Mouse)	Etfb	Evidence at protein level	255	27623	fatty acid beta-oxidation	electron carrier activity [	cytosol [GO:0005829]; ex
480	Q61206	PA1B2_MOUSE	Platelet-activating	Mus musculus (Mouse)	Pafah1b2	Evidence at protein level	229	25581	brain development [GO:0	1-alkyl-2-acetylglycerop	cytoplasm [GO:0005737]
481	P28654	PGS2_MOUSE	Decorin (Bone prot	Mus musculus (Mouse)	Dcn	Evidence at protein level	354	39809	aging [GO:0007568]; cyto	extracellular matrix bindi	collagen type VI trimer [G
482	P61161	ARP2_MOUSE	Actin-related prote	Mus musculus (Mouse)	Actr2	Evidence at protein level	394	44761	actin cytoskeleton organi	ATP binding [GO:0005524	actin cap [GO:0030478];
483	Q505F5	LRC47_MOUSE	Leucine-rich repeat	Mus musculus (Mouse)	Lrrc47	Evidence at protein level	581	63590		phenylalanine-tRNA ligase activity [GO:0004826]; R	
484	Q3THG9	AASD1_MOUSE	Alanyl-tRNA editing	Mus musculus (Mouse)	Aarsd1	Evidence at protein level	412	44971	alanyl-tRNA aminoacylati	alanine-tRNA ligase activi	cytoplasm [GO:0005737]
485	P21845	TRYB2_MOUSE	Tryptase beta-2 (Tr	Mus musculus (Mouse)	Tpsb2	Evidence at protein level	276	30927	inflammatory response [G	heparin binding [GO:0008	extracellular region [GO:0
486	P67778	PHB_MOUSE	Prohibitin (B-cell re	Mus musculus (Mouse)	Phb	Evidence at protein level	272	29820	animal organ regeneratio	complement component	cell surface [GO:0009986
487	Q62186	SSRD_MOUSE	Translocon-associa	Mus musculus (Mouse)	Ssr4	Evidence at protein level	172	18937			endoplasmic reticulum m
488	Q3V1T4	P3H1_MOUSE	Prolyl 3-hydroxylas	Mus musculus (Mouse)	P3h1	Evidence at protein level	739	83651	bone development [GO:0	iron ion binding [GO:0005	basement membrane [GO
489	Q8CG76	ARK72_MOUSE	Aflatoxin B1 aldehy	Mus musculus (Mouse)	Akr7a2	Evidence at protein level	367	40612	daunorubicin metabolic p	oxidoreductase activity [	cytosol [GO:0005829]; ex
490	Q921F2	TADBP_MOUSE	TAR DNA-binding p	Mus musculus (Mouse)	Tardbp	Evidence at protein level	414	44548	3'-UTR-mediated mRNA s	double-stranded DNA bin	cytoplasm [GO:0005737]
491	P48758	CBR1_MOUSE	Carbonyl reductase	Mus musculus (Mouse)	Cbr1	Evidence at protein level	277	30641	drug metabolic process [G	15-hydroxyprostaglandin	cytoplasm [GO:0005737]
492	P61804	DAD1_MOUSE	Dolichyl-diphospho	Mus musculus (Mouse)	Dad1	Evidence at protein level	113	12497	apoptotic process [GO:00	dolichyl-diphosphooligosa	extracellular exosome [G
493	P16675	PPGB_MOUSE	Lysosomal protecti	Mus musculus (Mouse)	Ctsa	Evidence at protein level	474	53844	negative regulation of ch	serine-type carboxypeptid	extracellular exosome [G
494	P97496	SMRC1_MOUSE	SWI/SNF complex s	Mus musculus (Mouse)	Smarcc1	Evidence at protein level	1104	122890	animal organ morphogen	chromatin binding [GO:0	BAF-type complex [GO:00
495	P39061	COIA1_MOUSE	Collagen alpha-1(X	Mus musculus (Mouse)	Col18a1	Evidence at protein level	1774	182172	angiogenesis [GO:000152	metal ion binding [GO:00	basement membrane [GO
496	Q9EST1	GSDMA_MOUSE	Gasdermin-A (Gasc	Mus musculus (Mouse)	Gsdma	Evidence at transcript level	446	49593	apoptotic process [GO:0006915]		cytoplasm [GO:0005737]
497	O54724	PTRF_MOUSE	Polymerase I and tr	Mus musculus (Mouse)	Ptrf	Evidence at protein level	392	43954	regulation of transcriptio	RNA binding [GO:000372	caveola [GO:0005901]; cy
498	Q9CZX8	RS19_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps19	Evidence at protein level	145	16085	erythrocyte differentiatio	fibroblast growth factor b	cytoplasm [GO:0005737]
499	P16015	CAH3_MOUSE	Carbonic anhydrase	Mus musculus (Mouse)	Ca3	Evidence at protein level	260	29366	one-carbon metabolic pr	carbonate dehydratase a	cytosol [GO:0005829]
500	P41216	ACSL1_MOUSE	Long-chain-fatty-ac	Mus musculus (Mouse)	Acsl1	Evidence at protein level	699	77951	adiponectin-activated sig	ATP binding [GO:0005524	endoplasmic reticulum m
501	O08640	KRA14_MOUSE	Keratin-associated	Mus musculus (Mouse)	Krtap14	Evidence at transcript level	167	17919			intermediate filament [G
502	Q8BWT1	THIM_MOUSE	3-ketoacyl-CoA thi	Mus musculus (Mouse)	Acaa2	Evidence at protein level	397	41830	cellular response to hypo	acetyl-CoA C-acyltransfer	extracellular exosome [G
503	P26883	FKB1A_MOUSE	Peptidyl-prolyl cis-t	Mus musculus (Mouse)	Fkbp1a	Evidence at protein level	108	11923	amyloid fibril formation [	activin binding [GO:0048	axon terminus [GO:0043
504	Q62418	DBNL_MOUSE	Drebrin-like protein	Mus musculus (Mouse)	Dbnl	Evidence at protein level	436	48700	adaptive immune respon	actin binding [GO:000377	cell-cell adherens junctio
505	O70435	PSA3_MOUSE	Proteasome subuni	Mus musculus (Mouse)	Psma3	Evidence at protein level	255	28405	regulation of endopeptid	threonine-type endopept	cytosol [GO:0005829]; ex
506	Q9ERS2	NDUAD_MOUSE	NADH dehydrogena	Mus musculus (Mouse)	Ndufa13	Evidence at protein level	144	16860	apoptotic signaling pathw	ATP binding [GO:0005524	cytoplasm [GO:0005737]
507	O35902	DSG3_MOUSE	Desmoglein-3 (130	Mus musculus (Mouse)	Dsg3	Evidence at transcript level	993	107889	cell adhesion [GO:00071	calcium ion binding [GO:0	desmosome [GO:003005
508	Q9EST5	AN32B_MOUSE	Acidic leucine-rich n	Mus musculus (Mouse)	Anp32b	Evidence at protein level	272	31079	activation of cysteine-type endopeptidase activity i		cytoplasm [GO:0005737]
509	P05201	AATC_MOUSE	Aspartate aminotra	Mus musculus (Mouse)	Got1	Evidence at protein level	413	46248	2-oxoglutarate metabolic	carboxylic acid binding [G	axon terminus [GO:0043
510	Q68FL6	SYMC_MOUSE	Methionine--tRNA	Mus musculus (Mouse)	Mars	Evidence at protein level	902	101431	methionyl-tRNA aminoac	ATP binding [GO:0005524	cytoplasm [GO:0005737]
511	P70124	SPB5_MOUSE	Serpin B5 (Maspin)	Mus musculus (Mouse)	Serpinb5	Evidence at protein level	375	42111	extracellular matrix orgar	serine-type endopeptidas	cytoplasm [GO:0005737]
512	Q9DCT2	NDUS3_MOUSE	NADH dehydrogena	Mus musculus (Mouse)	Ndufs3	Evidence at protein level	263	30149	cellular respiration [GO:0	NADH dehydrogenase (ut	mitochondrial inner mem
513	Q9WUP7	UCHL5_MOUSE	Ubiquitin carboxyl-	Mus musculus (Mouse)	Uchl5	Evidence at protein level	329	37617	DNA recombination [GO:	endopeptidase inhibitor a	cytoplasm [GO:0005737]
514	Q64737	PUR2_MOUSE	Trifunctional purine	Mus musculus (Mouse)	Gart	Evidence at protein level	1010	107503	'de novo' IMP biosyntheti	ATP binding [GO:0005524	cytoplasm [GO:0005737]
515	P97807	FUMH_MOUSE	Fumarate hydratas	Mus musculus (Mouse)	Fh	Evidence at protein level	507	54357	fumarate metabolic proc	fumarate hydratase activ	extracellular exosome [G
516	Q5SUR0	PUR4_MOUSE	Phosphoribosylform	Mus musculus (Mouse)	Pfas	Evidence at protein level	1337	144629	'de novo' IMP biosyntheti	ATP binding [GO:0005524	cytoplasm [GO:0005737]
517	O70492	SNX3_MOUSE	Sorting nexin-3 (SD	Mus musculus (Mouse)	Snx3	Evidence at protein level	162	18757	endocytosis [GO:0006897	phosphatidylinositol-3,5-	clathrin-coated vesicle [G
518	P28656	NP1L1_MOUSE	Nucleosome assem	Mus musculus (Mouse)	Nap1l1	Evidence at protein level	391	45345	nucleosome assembly [G	RNA binding [GO:000372	melanosome [GO:004247
519	Q60692	PSB6_MOUSE	Proteasome subuni	Mus musculus (Mouse)	Psmb6	Evidence at protein level	238	25379	proteolysis involved in ce	cadherin binding involvec	cell-cell adherens junctio
520	A6BLY7	K1C28_MOUSE	Keratin, type I cyto	Mus musculus (Mouse)	Krt28	Evidence at protein level	462	50346		structural molecule activi	cytoplasm [GO:0005737]
521	Q64310	SURF4_MOUSE	Surfeit locus protei	Mus musculus (Mouse)	Surf4	Evidence at protein level	269	30381	Golgi organization [GO:0007030]; positive regulatio		endoplasmic reticulum-G
522	Q6IME9	K2C72_MOUSE	Keratin, type II cytc	Mus musculus (Mouse)	Krt72	Inferred from homology	520	56750		structural molecule activi	extracellular exosome [G
523	Q8VE37	RCC1_MOUSE	Regulator of chrom	Mus musculus (Mouse)	Rcc1	Evidence at protein level	421	44931	cell division [GO:0051301	chromatin binding [GO:0	condensed nuclear chrom
524	Q9DCN2	NB5R3_MOUSE	NADH-cytochrome	Mus musculus (Mouse)	Cyb5r3	Evidence at protein level	301	34128	cholesterol biosynthetic p	ADP binding [GO:004353	endoplasmic reticulum m
525	Q93092	TALDO_MOUSE	Transaldolase (EC 2	Mus musculus (Mouse)	Taldo1	Evidence at protein level	337	37387	carbohydrate metabolic p	monosaccharide binding	cytosol [GO:0005829]; ex
526	P12970	RL7A_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl7a	Evidence at protein level	266	29977	maturation of LSU-rRNA |	cadherin binding involvec	cell-cell adherens junctio
527	O88685	PRS6A_MOUSE	26S protease regul	Mus musculus (Mouse)	Psmc3	Evidence at protein level	442	49549	blastocyst development [	ATP binding [GO:0005524	cytosolic proteasome con
528	P02104	HBE_MOUSE	Hemoglobin subuni	Mus musculus (Mouse)	Hbb-y	Evidence at protein level	147	16137	negative regulation of tra	heme binding [GO:00200	blood microparticle [GO:0
529	Q7TMK9	HNRPQ_MOUSE	Heterogeneous nuc	Mus musculus (Mouse)	Syncrip	Evidence at protein level	623	69633	cellular response to interf	nucleotide binding [GO:0	catalytic step 2 spliceoso
530	P21844	CMA1_MOUSE	Chymase (EC 3.4.2	Mus musculus (Mouse)	Cma1	Evidence at protein level	247	27586	interleukin-1 beta biosyn	endopeptidase activity [G	extracellular region [GO:0
531	P22599	A1AT2_MOUSE	Alpha-1-antitrypsir	Mus musculus (Mouse)	Serpina1b	Evidence at protein level	413	45975	acute-phase response [G	glycoprotein binding [GO:	endoplasmic reticulum [G
532	Q8R5F8	ES8L1_MOUSE	Epidermal growth f	Mus musculus (Mouse)	Eps8l1	Evidence at protein level	716	80028	positive regulation of ruff	actin binding [GO:000377	cell-cell adherens junctio
533	P09405	NUCL_MOUSE	Nucleolin (Protein	Mus musculus (Mouse)	Ncl	Evidence at protein level	707	76723	angiogenesis [GO:000152	identical protein binding |	cell cortex [GO:0005938]
534	Q3UM45	PP1R7_MOUSE	Protein phosphatas	Mus musculus (Mouse)	Ppp1r7	Evidence at protein level	361	41292	chromosome segregation	[GO:0007059]; positive re	chromosome [GO:0005694
535	Q91Z53	GRHPR_MOUSE	Glyoxylate reducta	Mus musculus (Mouse)	Grhpr	Evidence at protein level	328	35329	dicarboxylic acid metabol	carboxylic acid binding [G	cytoplasm [GO:0005737]
536	P35173	CYT3_MOUSE	Stefin-3	Mus musculus (Mouse)	Stfa3	Inferred from homology	103	11640		cysteine-type endopeptid	cytoplasm [GO:0005737]
537	P56546	CTBP2_MOUSE	C-terminal-binding	Mus musculus (Mouse)	Ctbp2	Evidence at protein level	445	48957	negative regulation of tra	chromatin binding [GO:0	cell junction [GO:003005
538	P07607	TYSY_MOUSE	Thymidylate synth	Mus musculus (Mouse)	Tyms	Evidence at protein level	307	34958	aging [GO:0007568]; cart	cofactor binding [GO:004	cytoplasm [GO:0005737]
539	Q9R1Z8	VINEX_MOUSE	Vinexin (SH3 doma	Mus musculus (Mouse)	Sorbs3	Evidence at protein level	733	82349	actin filament organizatic	transcription factor bindi	cytoplasm [GO:0005737]
540	Q9QZD9	EIF3I_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif3i	Evidence at protein level	325	36461	translational initiation [G	translation initiation facto	eukaryotic translation ini
541	Q9DCJ9	NPL_MOUSE	N-acetylneuramina	Mus musculus (Mouse)	Npl	Evidence at protein level	320	35130	carbohydrate metabolic p	identical protein binding |	cytoplasm [GO:0005737]
542	Q91WQ3	SYYC_MOUSE	Tyrosine--tRNA liga	Mus musculus (Mouse)	Yars	Evidence at protein level	528	59105	tRNA aminoacylation for	ATP binding [GO:0005524	aminoacyl-tRNA synthetas
543	P62274	RS29_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps29	Inferred from homology	56	6677	translation [GO:0006412]	structural constituent of	cytosolic small ribosomal
544	P62137	PP1A_MOUSE	Serine/threonine-p	Mus musculus (Mouse)	Ppp1ca	Evidence at protein level	330	37540	branching morphogenesis	metal ion binding [GO:00	cell-cell adherens junctio
545	P49817	CAV1_MOUSE	Caveolin-1	Mus musculus (Mouse)	Cav1	Evidence at protein level	178	20539	angiogenesis [GO:000152	ATPase binding [GO:0051	acrosomal membrane [G
546	Q925I0	KR192_MOUSE	Keratin-associated	Mus musculus (Mouse)	Krtap19-2	Evidence at transcript level	141	13738			intermediate filament [G
547	P47811	MK14_MOUSE	Mitogen-activated	Mus musculus (Mouse)	Mapk14	Evidence at protein level	360	41287	angiogenesis [GO:000152	ATP binding [GO:0005524	cell [GO:0005623]; cytop
548	Q61033	LAP2A_MOUSE	Lamina-associated	Mus musculus (Mouse)	Tmpo	Evidence at protein level	693	75168	regulation of transcriptio	cadherin binding involvec	cell-cell adherens junctio
549	Q62432	SMAD2_MOUSE	Mothers against de	Mus musculus (Mouse)	Smad2	Evidence at protein level	467	52266	activin receptor signaling	activating transcription fa	activin responsive factor
550	P55849	DSC1_MOUSE	Desmocollin-1	Mus musculus (Mouse)	Dsc1	Evidence at protein level	886	98938	homophilic cell adhesion	calcium ion binding [GO:0	desmosome [GO:003005
551	P97454	SMAD5_MOUSE	Mothers against de	Mus musculus (Mouse)	Smad5	Evidence at protein level	465	52172	angiogenesis [GO:000152	metal ion binding [GO:00	cytoplasm [GO:0005737]
552	Q9WUU7	CATZ_MOUSE	Cathepsin Z (EC 3.4	Mus musculus (Mouse)	Ctsz	Evidence at protein level	306	33996	epithelial tube branching	cysteine-type endopeptid	endoplasmic reticulum [G
553	P60229	EIF3E_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif3e	Evidence at protein level	445	52221	nuclear-transcribed mRN	cadherin binding involvec	cell-cell adherens junctio
554	Q9DBG6	RPN2_MOUSE	Dolichyl-diphospho	Mus musculus (Mouse)	Rpn2	Evidence at protein level	631	69063	aging [GO:0007568]; prot	ribosome binding [GO:00	autophagosome membra
555	O55131	SEPT7_MOUSE	Septin-7 (CDC10 pr	Mus musculus (Mouse)	Sept7	Evidence at protein level	436	50550	cilium assembly [GO:006	cadherin binding involvec	actin cytoskeleton [GO:0
556	Q6ZQ58	LARP1_MOUSE	La-related protein	Mus musculus (Mouse)	Larp1	Evidence at protein level	1072	121125	cell proliferation [GO:000	cadherin binding involvec	cell-cell adherens junctio
557	P23927	CRYAB_MOUSE	Alpha-crystallin B c	Mus musculus (Mouse)	Cryab	Evidence at protein level	175	20069	apoptotic process involve	identical protein binding |	contractile fiber [GO:0004
558	Q9EPL8	IPO7_MOUSE	Importin-7 (Imp7) (	Mus musculus (Mouse)	Ipo7	Evidence at protein level	1038	119486	innate immune response	histone binding [GO:0042	cytosol [GO:0005829]; m
559	Q9DBP5	KCY_MOUSE	UMP-CMP kinase (	Mus musculus (Mouse)	Cmpk1	Evidence at protein level	196	22165	'de novo' pyrimidine nucl	ATP binding [GO:0005524	cytoplasm [GO:0005737]
560	O08579	EMD_MOUSE	Emerin	Mus musculus (Mouse)	Emd	Evidence at protein level	259	29436	cellular response to grow	actin binding [GO:000377	cell-cell adherens junctio
561	Q9R190	MTA2_MOUSE	Metastasis-associa	Mus musculus (Mouse)	Mta2	Evidence at protein level	668	75030	ATP-dependent chromati	histone deacetylase activ	histone deacetylase comp
562	Q99LC5	ETFA_MOUSE	Electron transfer fl	Mus musculus (Mouse)	Etfa	Evidence at protein level	333	35009	fatty acid beta-oxidation	electron carrier activity [	extracellular exosome [G
563	Q9D3B1	HACD2_MOUSE	Very-long-chain (3F	Mus musculus (Mouse)	Hacd2	Evidence at protein level	254	28402	fatty acid elongation [GO	3-hydroxyacyl-CoA dehyd	endoplasmic reticulum [G
564	Q8CH25	SLTM_MOUSE	SAFB-like transcrip	Mus musculus (Mouse)	Sltm	Evidence at protein level	1031	116919	apoptotic process [GO:00	double-stranded DNA bin	nuclear body [GO:0016607
565	Q9CPP0	NPM3_MOUSE	Nucleoplasmin-3	Mus musculus (Mouse)	Npm3	Evidence at protein level	175	19023	rRNA processing [GO:000	RNA binding [GO:000372	actin cytoskeleton [GO:0
566	Q9D8T7	SLIRP_MOUSE	SRA stem-loop-inte	Mus musculus (Mouse)	Slirp	Evidence at protein level	112	12605	flagellated sperm motility	nucleotide binding [GO:0	acrosomal vesicle [GO:00
567	Q61249	IGBP1_MOUSE	Immunoglobulin-bi	Mus musculus (Mouse)	Igbp1	Evidence at protein level	340	38971	B cell activation [GO:004	mitogen-activated protei	cytoplasm [GO:0005737]
568	Q8K354	CBR3_MOUSE	Carbonyl reductase	Mus musculus (Mouse)	Cbr3	Evidence at protein level	277	30953	cognition [GO:0050890];	3-keto sterol reductase a	cytosol [GO:0005829]; ex
569	Q62465	VAT1_MOUSE	Synaptic vesicle me	Mus musculus (Mouse)	Vat1	Evidence at protein level	406	43097	negative regulation of mi	oxidoreductase activity [	extracellular exosome [G
570	P62869	ELOB_MOUSE	Elongin-B (EloB) (El	Mus musculus (Mouse)	Elob	Evidence at protein level	118	13170	protein ubiquitination [GO:0016567]; regulation of		Cul2-RING ubiquitin ligas
571	P97351	RS3A_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps3a	Evidence at protein level	264	29885	cell differentiation [GO:0	RNA binding [GO:000372	cytosol [GO:0005829]; cy
572	P63087	PP1G_MOUSE	Serine/threonine-p	Mus musculus (Mouse)	Ppp1cc	Evidence at protein level	323	36984	cell cycle [GO:0007049];	metal ion binding [GO:00	cleavage furrow [GO:003
573	P10649	GSTM1_MOUSE	Glutathione S-tran	Mus musculus (Mouse)	Gstm1	Evidence at protein level	218	25970	cellular response to drug	glutathione transferase a	cytoplasm [GO:0005737]
574	Q60972	RBBP4_MOUSE	Histone-binding pr	Mus musculus (Mouse)	Rbbp4	Evidence at protein level	425	47656	ATP-dependent chromati	DNA-dependent ATPase a	CAF-1 complex [GO:0033
575	P40124	CAP1_MOUSE	Adenylyl cyclase-as	Mus musculus (Mouse)	Cap1	Evidence at protein level	474	51565	actin cytoskeleton organi	actin binding [GO:000377	cortical actin cytoskeleto
576	Q921F9	SAE2_MOUSE	SUMO-activating e	Mus musculus (Mouse)	Uba2	Evidence at protein level	638	70569	protein sumoylation [GO:	ATP binding [GO:0005524	cytoplasm [GO:0005737]
577	Q9CR00	PSMD9_MOUSE	26S proteasome no	Mus musculus (Mouse)	Psmd9	Evidence at protein level	222	24720	negative regulation of ins	bHLH transcription factor	cytoplasm [GO:0005737]
578	P26040	EZRI_MOUSE	Ezrin (Cytovillin) (V	Mus musculus (Mouse)	Ezr	Evidence at protein level	586	69407	actin cytoskeleton reorga	actin binding [GO:000377	actin cytoskeleton [GO:0
579	Q9QZM0	UBQL2_MOUSE	Ubiquilin-2 (Chap1	Mus musculus (Mouse)	Ubqln2	Evidence at protein level	638	67351	autophagy [GO:0006914];	negative regulation of cla	autophagosome [GO:000
580	O35344	IMA4_MOUSE	Importin subunit al	Mus musculus (Mouse)	Kpna3	Evidence at protein level	521	57773	NLS-bearing protein impo	nuclear localization sequ	cytosol [GO:0005829]; nu

581	Q99K51	PLST_MOUSE	Plastin-3 (T-plastin	Mus musculus (Mouse)	Pls3	Evidence at protein level	630	70742	actin crosslink formation	actin filament binding [G	actin filament [GO:00058
582	P84104	SRSF3_MOUSE	Serine/arginine-ric	Mus musculus (Mouse)	Srsf3	Evidence at protein level	164	19330	insulin receptor signaling	nucleotide binding [GO:0	cytoplasm [GO:0005737]
583	Q9QX47	SON_MOUSE	Protein SON (Nega	Mus musculus (Mouse)	Son	Evidence at protein level	2444	265651	microtubule cytoskeleton	DNA binding [GO:000367	nuclear speck [GO:00166
584	Q99LX0	PARK7_MOUSE	Protein DJ-1 (DJ-1)	Mus musculus (Mouse)	Park7	Evidence at protein level	189	20021	adult locomotory behavic	androgen receptor bindin	cell body [GO:0044297];
585	P10648	GSTA2_MOUSE	Glutathione S-tran	Mus musculus (Mouse)	Gsta2	Evidence at protein level	222	25542	glutathione metabolic pr	glutathione transferase a	cytosol [GO:0005829]; ex
586	Q9CWS0	DDAH1_MOUSE	N(G),N(G)-dimethy	Mus musculus (Mouse)	Ddah1	Evidence at protein level	285	31381	arginine catabolic proces	amino acid binding [GO:0	extracellular exosome [G
587	Q8BJU0	SGTA_MOUSE	Small glutamine-ric	Mus musculus (Mouse)	Sgta	Evidence at protein level	315	34322	negative regulation of ER	BAT3 complex binding [G	cytoplasm [GO:0005737]
588	P99026	PSB4_MOUSE	Proteasome subuni	Mus musculus (Mouse)	Psmb4	Evidence at protein level	264	29116	negative regulation of inf	lipopolysaccharide bindin	cytosol [GO:0005829]; ex
589	P49717	MCM4_MOUSE	DNA replication lic	Mus musculus (Mouse)	Mcm4	Evidence at protein level	862	96736	cell cycle [GO:0007049];	ATP binding [GO:000552	MCM complex [GO:0042
590	P51855	GSHB_MOUSE	Glutathione synthe	Mus musculus (Mouse)	Gss	Evidence at protein level	474	52247	aging [GO:0007568]; resp	ATP binding [GO:000552	cytosol [GO:0005829]; ex
591	Q64105	SPRE_MOUSE	Sepiapterin reducta	Mus musculus (Mouse)	Spr	Evidence at protein level	261	27883	cell morphogenesis invol	protein homodimerizatio	cytosol [GO:0005829]; ex
592	Q9D8S4	ORN_MOUSE	Oligoribonuclease,	Mus musculus (Mouse)	Rexo2	Evidence at protein level	237	26739	nucleobase-containing co	3'-5' exonuclease activity	focal adhesion [GO:0005
593	P60122	RUVB1_MOUSE	RuvB-like 1 (EC 3.6	Mus musculus (Mouse)	Ruvbl1	Evidence at protein level	456	50214	cell division [GO:0051301	ADP binding [GO:004353	cell-cell adherens junctio
594	Q9Z199	SPT4B_MOUSE	Transcription elong	Mus musculus (Mouse)	Supt4h1b	Evidence at transcript level	117	13194	chromatin organization [(	RNA polymerase II core b	DSIF complex [GO:00320
595	Q3U7R1	ESYT1_MOUSE	Extended synaptot	Mus musculus (Mouse)	Esyt1	Evidence at protein level	1092	121554	lipid transport [GO:0006	lipid binding [GO:0008285	endoplasmic reticulum [G
596	P61358	RL27_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl27	Evidence at protein level	136	15798	response to aldosterone [	RNA binding [GO:000372	cytosolic large ribosomal
597	P54923	ADPRH_MOUSE	[Protein ADP-ribos	Mus musculus (Mouse)	Adprh	Evidence at protein level	362	40068	cellular protein modificat	ADP-ribosylarginine hydr	intracellular [GO:000562
598	Q62422	OSTF1_MOUSE	Osteoclast-stimula	Mus musculus (Mouse)	Ostf1	Evidence at protein level	215	23783		SH3 domain binding [GO:	cytoplasm [GO:0005737]
599	Q60864	STIP1_MOUSE	Stress-induced-phc	Mus musculus (Mouse)	Stip1	Evidence at protein level	543	62582		RNA binding [GO:000372	cytosol [GO:0005829]; m
600	P97372	PSME2_MOUSE	Proteasome activat	Mus musculus (Mouse)	Psme2	Evidence at protein level	239	27057	antigen processing and pr	endopeptidase activator	cytoplasm [GO:0005737]
601	Q9D3D9	ATPD_MOUSE	ATP synthase subu	Mus musculus (Mouse)	Atp5d	Evidence at protein level	168	17600	ATP synthesis coupled pr	hydrogen ion transmemb	mitochondrial envelope [
602	Q6PD26	PIGS_MOUSE	GPI transamidase c	Mus musculus (Mouse)	Pigs	Evidence at protein level	555	61711	attachment of GPI anchor to protein [GO:0016255]		GPI-anchor transamidase
603	Q61823	PDCD4_MOUSE	Programmed cell d	Mus musculus (Mouse)	Pdcd4	Evidence at protein level	469	51702	apoptotic process [GO:00	RNA binding [GO:000372	cytoplasm [GO:0005737]
604	Q00896	A1AT3_MOUSE	Alpha-1-antitrypsir	Mus musculus (Mouse)	Serpina1c	Evidence at protein level	412	45823	response to cytokine [GO	glycoprotein binding [GO:	endoplasmic reticulum [G
605	Q9CQN1	TRAP1_MOUSE	Heat shock protein	Mus musculus (Mouse)	Trap1	Evidence at protein level	706	80209	negative regulation of cel	ATP binding [GO:000552	extracellular exosome [G
606	O88543	CSN3_MOUSE	COP9 signalosome	Mus musculus (Mouse)	Cops3	Evidence at protein level	423	47832	in utero embryonic development [GO:0001701]; pr		COP9 signalosome [GO:0
607	Q06890	CLUS_MOUSE	Clusterin (Apolipop	Mus musculus (Mouse)	Clu	Evidence at protein level	448	51656	cell morphogenesis [GO:(	misfolded protein binding	apical dendrite [GO:0097
608	O88342	WDR1_MOUSE	WD repeat-contain	Mus musculus (Mouse)	Wdr1	Evidence at protein level	606	66407	actin cytoskeleton organi	actin binding [GO:00037	actin cytoskeleton [GO:0
609	P09411	PGK1_MOUSE	Phosphoglycerate k	Mus musculus (Mouse)	Pgk1	Evidence at protein level	417	44550	epithelial cell differentiat	ATP binding [GO:000552	cytoplasm [GO:0005737]
610	Q9D8Y0	EFHD2_MOUSE	EF-hand domain-co	Mus musculus (Mouse)	Efhd2	Evidence at protein level	240	26791		cadherin binding involve	cell-cell adherens junctio
611	P70333	HNRH2_MOUSE	Heterogeneous nu	Mus musculus (Mouse)	Hnrnph2	Evidence at protein level	449	49280		nucleotide binding [GO:0	cytosol [GO:0005829]; in
612	Q64213	SF01_MOUSE	Splicing factor 1 (C	Mus musculus (Mouse)	Sf1	Evidence at protein level	653	70403	Leydig cell differentiation	pre-mRNA branch point b	cytoplasm [GO:0005737]
613	Q99M73	KRT84_MOUSE	Keratin, type II cuti	Mus musculus (Mouse)	Krt84	Evidence at transcript level	603	64983	regulation of keratinocyte	structural constituent of	extracellular exosome [G
614	Q62189	SNRPA_MOUSE	U1 small nuclear ri	Mus musculus (Mouse)	Snrpa	Evidence at protein level	287	31835	mRNA splicing, via splice	nucleotide binding [GO:0	spliceosomal complex [G
615	Q9JHW2	NIT2_MOUSE	Omega-amidase NI	Mus musculus (Mouse)	Nit2	Evidence at protein level	276	30502	asparagine metabolic pro	omega-amidase activity [	centrosome [GO:000581
616	Q4LDD4	ARAP1_MOUSE	Arf-GAP with Rho-(	Mus musculus (Mouse)	Arap1	Evidence at protein level	1452	162276	negative regulation of str	GTPase activator activity	cytoplasmic vesicle [GO:(
617	P62267	RS23_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps23	Evidence at protein level	143	15808	translation [GO:0006412]	RNA binding [GO:000372	cytosolic small ribosomal
618	Q9D2M8	UB2V2_MOUSE	Ubiquitin-conjugati	Mus musculus (Mouse)	Ube2v2	Evidence at protein level	145	16367	DNA double-strand break	ubiquitin protein ligase a	cytoplasm [GO:0005737]
619	P51660	DHB4_MOUSE	Peroxisomal multif	Mus musculus (Mouse)	Hsd17b4	Evidence at protein level	735	79482	androgen metabolic proc	17-beta-hydroxysteroid d	membrane [GO:0016020
620	Q91VH6	MEMO1_MOUSE	Protein MEMO1 (M	Mus musculus (Mouse)	Memo1	Evidence at protein level	297	33692	regulation of microtubule	peptide binding [GO:0042	cytosol [GO:0005829]; nu
621	A2A591	KRA31_MOUSE	Keratin-associated	Mus musculus (Mouse)	Krtap3-1	Inferred from homology	98	10271		structural molecule activi	keratin filament [GO:0004
622	Q9QXF8	GNMT_MOUSE	Glycine N-methyltr	Mus musculus (Mouse)	Gnmt	Evidence at protein level	293	32675	glycogen metabolic proce	folic acid binding [GO:00	cytosol [GO:0005829]
623	Q9CZ42	NNRD_MOUSE	ATP-dependent (S)	Mus musculus (Mouse)	Naxd	Evidence at protein level	343	36717		ADP-dependent NAD(P)H	cytosol [GO:0005829]; er
624	O55142	RL35A_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl35a	Evidence at protein level	110	12554	ribosomal large subunit b	RNA binding [GO:000372	cytosolic large ribosomal
625	P17426	AP2A1_MOUSE	AP-2 complex subu	Mus musculus (Mouse)	Ap2a1	Evidence at protein level	977	107664	endocytosis [GO:0006897	protein kinase binding [G	apical plasma membrane
626	P24527	LKHA4_MOUSE	Leukotriene A-4 hy	Mus musculus (Mouse)	Lta4h	Evidence at protein level	611	69051	leukotriene biosynthetic p	aminopeptidase activity [	cytoplasm [GO:0005737]
627	Q91YK8	LYPD3_MOUSE	Ly6/PLAUR domain	Mus musculus (Mouse)	Lypd3	Evidence at transcript level	363	37489	cell-matrix adhesion [GO:	laminin binding [GO:0043	anchored component of r
628	Q9D0F3	LMAN1_MOUSE	Protein ERGIC-53 (I	Mus musculus (Mouse)	Lman1	Evidence at protein level	517	57789	endoplasmic reticulum or	mannose binding [GO:00	endoplasmic reticulum-G
629	Q9DBG5	PLIN3_MOUSE	Perilipin-3 (Cargo s	Mus musculus (Mouse)	Plin3	Evidence at protein level	437	47262	transport [GO:0006810]	cadherin binding involve	cell-cell adherens junctio
630	Q8BT60	CPNE3_MOUSE	Copine-3 (Copine II	Mus musculus (Mouse)	Cpne3	Evidence at protein level	533	59585	cellular response to calci	calcium-dependent phos	cell junction [GO:003005
631	Q8C166	CPNE1_MOUSE	Copine-1 (Copine I)	Mus musculus (Mouse)	Cpne1	Evidence at protein level	536	58887	cellular response to calci	calcium ion binding [GO:(	cytoplasm [GO:0005737]
632	Q6A026	PDS5A_MOUSE	Sister chromatid co	Mus musculus (Mouse)	Pds5a	Evidence at protein level	1332	150327	cell division [GO:0051301]; DNA repair [GO:000628		chromatin [GO:0000785]
633	Q6ZQ38	CAND1_MOUSE	Cullin-associated N	Mus musculus (Mouse)	Cand1	Evidence at protein level	1230	136332	cell differentiation [GO:0030154]; negative regulati		cullin-RING ubiquitin ligas
634	Q9WUA2	SYFB_MOUSE	Phenylalanine--tRN	Mus musculus (Mouse)	Farsb	Evidence at protein level	589	65697	phenylalanyl-tRNA amino	ATP binding [GO:000552	membrane [GO:0016020
635	Q3UH93	PLXD1_MOUSE	Plexin-D1	Mus musculus (Mouse)	Plxnd1	Evidence at protein level	1925	211608	angiogenesis [GO:000152	protein domain specific b	integral component of pla
636	P06797	CATL1_MOUSE	Cathepsin L1 (EC 3.	Mus musculus (Mouse)	Ctsl	Evidence at protein level	334	37547	autophagic cell death [GO	aminopeptidase activity [	apical part of cell [GO:00
637	Q04207	TF65_MOUSE	Transcription facto	Mus musculus (Mouse)	Rela	Evidence at protein level	549	60212	acetaldehyde metabolic p	actinin binding [GO:0042	cytoplasm [GO:0005737]
638	Q61655	DD19A_MOUSE	ATP-dependent RN	Mus musculus (Mouse)	Ddx19a	Evidence at protein level	478	53933	mRNA transport [GO:005	ATP binding [GO:000552	catalytic step 2 spliceoso
639	Q64433	CH10_MOUSE	10 kDa heat shock	Mus musculus (Mouse)	Hspe1	Evidence at protein level	102	10963	chaperone mediated prot	ATP binding [GO:000552	extracellular exosome [G
640	Q9D6J6	NDUV2_MOUSE	NADH dehydrogen	Mus musculus (Mouse)	Ndufv2	Evidence at protein level	248	27285	cardiac muscle tissue dev	2 iron, 2 sulfur cluster bin	mitochondrial respirator
641	P53994	RAB2A_MOUSE	Ras-related protein	Mus musculus (Mouse)	Rab2a	Evidence at protein level	212	23548	Golgi organization [GO:0	GDP binding [GO:001900	endoplasmic reticulum-G
642	P53026	RL10A_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl10a	Evidence at protein level	217	24916	maturation of LSU-rRNA [	RNA binding [GO:000372	cytosolic large ribosomal
643	P63325	RS10_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps10	Evidence at protein level	165	18916	ribosomal small subunit a	RNA binding [GO:000372	cytosol [GO:0005829]; cy
644	Q9WV02	RBMX_MOUSE	RNA-binding motif	Mus musculus (Mouse)	Rbmx	Evidence at protein level	391	42301	cellular response to interf	chromatin binding [GO:0(	catalytic step 2 spliceoso
645	Q99L45	IF2B_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif2s2	Evidence at protein level	331	38092	in utero embryonic devel	metal ion binding [GO:00	cytoplasm [GO:0005737]
646	P19157	GSTP1_MOUSE	Glutathione S-tran	Mus musculus (Mouse)	Gstp1	Evidence at protein level	210	23609	animal organ regeneratio	dinitrosyl-iron complex bi	cytoplasm [GO:0005737]
647	Q9EPU0	RENT1_MOUSE	Regulator of nonse	Mus musculus (Mouse)	Upf1	Evidence at protein level	1124	123967	3'-UTR-mediated mRNA d	ATP binding [GO:000552	chromatin [GO:0000785]
648	P24547	IMDH2_MOUSE	Inosine-5'-monoph	Mus musculus (Mouse)	Impdh2	Evidence at protein level	514	55815	cellular response to interf	DNA binding [GO:000367	cytoplasm [GO:0005737]
649	Q99JI4	PSMD6_MOUSE	26S proteasome nc	Mus musculus (Mouse)	Psmd6	Evidence at protein level	389	45536	proteasome-mediated ubiquitin-dependent protein		extracellular exosome [G
650	O55143	AT2A2_MOUSE	Sarcoplasmic/endo	Mus musculus (Mouse)	Atp2a2	Evidence at protein level	1044	114858	calcium ion import into s	ATP binding [GO:000552	calcium ion-transporting
651	P30416	FKBP4_MOUSE	Peptidyl-prolyl cis-t	Mus musculus (Mouse)	Fkbp4	Evidence at protein level	458	51572	androgen receptor signali	ATP binding [GO:000552	axonal growth cone [GO:0
652	Q8CE93	FA26D_MOUSE	Protein FAM26D	Mus musculus (Mouse)	Fam26d	Evidence at transcript level	315	35429	ion transmembrane trans	cation channel activity [G	integral component of pla
653	Q3THK7	GUAA_MOUSE	GMP synthase [glu	Mus musculus (Mouse)	Gmps	Evidence at protein level	693	76723	glutamine metabolic proc	ATP binding [GO:000552	cytosol [GO:0005829]
654	Q91V98	CD248_MOUSE	Endosialin (Tumor	Mus musculus (Mouse)	Cd248	Evidence at protein level	765	81813	anatomical structure regr	calcium ion binding [GO:(	cytoplasm [GO:0005737]
655	Q9JK48	SHLB1_MOUSE	Endophilin-B1 (SH3	Mus musculus (Mouse)	Sh3glb1	Evidence at protein level	365	40855	'de novo' posttranslation	cadherin binding involve	autophagosome membra
656	Q80WJ7	LYRIC_MOUSE	Protein LYRIC (3D3	Mus musculus (Mouse)	Mtdh	Evidence at protein level	579	63846	bicellular tight junction a	double-stranded RNA bin	apical plasma membrane
657	P35979	RL12_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl12	Evidence at protein level	165	17805	ribosomal large subunit a	RNA binding [GO:000372	cytoplasm [GO:0005737]
658	P56395	CYB5_MOUSE	Cytochrome b5	Mus musculus (Mouse)	Cyb5a	Evidence at protein level	134	15241	fatty acid metabolic proc	enzyme binding [GO:001	cytosol [GO:0005829]; er
659	Q6PDQ2	CHD4_MOUSE	Chromodomain-he	Mus musculus (Mouse)	Chd4	Evidence at protein level	1915	217751	ATP-dependent chromati	ATP binding [GO:000552	centrosome [GO:000581
660	Q9DB77	QCR2_MOUSE	Cytochrome b-c1 c	Mus musculus (Mouse)	Uqcrc2	Evidence at protein level	453	48235	oxidation-reduction proc	metalloendopeptidase ac	extracellular exosome [G
661	Q05186	RCN1_MOUSE	Reticulocalbin-1	Mus musculus (Mouse)	Rcn1	Evidence at protein level	325	38113	camera-type eye develop	calcium ion binding [GO:(	endoplasmic reticulum [G
662	Q91VC3	IF4A3_MOUSE	Eukaryotic initiatio	Mus musculus (Mouse)	Eif4a3	Evidence at protein level	411	46840	associative learning [GO:	ATP binding [GO:000552	catalytic step 2 spliceoso
663	Q9Z2W0	DNPEP_MOUSE	Aspartyl aminopep	Mus musculus (Mouse)	Dnpep	Evidence at protein level	473	52207	peptide metabolic proces	identical protein binding	blood microparticle [GO:0
664	Q8BGE6	ATG4B_MOUSE	Cysteine protease a	Mus musculus (Mouse)	Atg4b	Evidence at protein level	393	44375	autophagosome assembl	cysteine-type endopeptid	cytoplasm [GO:0005737]
665	O09131	GSTO1_MOUSE	Glutathione S-tran	Mus musculus (Mouse)	Gsto1	Evidence at protein level	240	27498	cellular response to arser	glutathione dehydrogena	cytoplasm [GO:0005737]
666	P08003	PDIA4_MOUSE	Protein disulfide-is	Mus musculus (Mouse)	Pdia4	Evidence at protein level	638	71982	cell redox homeostasis [G	protein disulfide isomera	cell surface [GO:0009986
667	Q8BU30	SYIC_MOUSE	Isoleucine--tRNA lig	Mus musculus (Mouse)	Iars	Evidence at protein level	1262	144271	isoleucyl-tRNA aminoacyl	aminoacyl-tRNA editing a	cytoplasm [GO:0005737]
668	Q08857	CD36_MOUSE	Platelet glycoprote	Mus musculus (Mouse)	Cd36	Evidence at protein level	472	52698	amyloid fibril formation [	high-density lipoprotein p	apical part of cell [GO:00
669	Q9Z130	HNRDL_MOUSE	Heterogeneous nu	Mus musculus (Mouse)	Hnrnpdl	Evidence at protein level	301	33559	mRNA metabolic process	DNA binding [GO:000367	cytoplasm [GO:0005737]
670	Q61001	LAMA5_MOUSE	Laminin subunit alp	Mus musculus (Mouse)	Lama5	Evidence at protein level	3718	404054	animal organ morphogen	integrin binding [GO:000	basal lamina [GO:000560
671	P82198	BGH3_MOUSE	Transforming grow	Mus musculus (Mouse)	Tgfbi	Evidence at protein level	683	74597	angiogenesis [GO:000152	collagen binding [GO:000	basement membrane [GO
672	Q8VBV7	CSN8_MOUSE	COP9 signalosome	Mus musculus (Mouse)	Cops8	Evidence at protein level	209	23256	activation of NF-kappaB-inducing kinase activity [G		COP9 signalosome [GO:0
673	P14685	PSMD3_MOUSE	26S proteasome nc	Mus musculus (Mouse)	Psmd3	Evidence at protein level	530	60718	regulation of protein cata	enzyme regulator activity	extracellular exosome [G
674	Q9CQR2	RS21_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps21	Evidence at protein level	83	9141	endonucleolytic cleavage	protein N-terminus bindi	cytosolic small ribosomal
675	Q80X50	UBP2L_MOUSE	Ubiquitin-associate	Mus musculus (Mouse)	Ubap2l	Evidence at protein level	1107	116799	binding of sperm to zona	RNA binding [GO:000372	Ada2/Gcn5/Ada3 transcr
676	O08677	KNG1_MOUSE	Kininogen-1 [Cleav	Mus musculus (Mouse)	Kng1	Evidence at protein level	661	73102	blood coagulation [GO:0(	cysteine-type endopeptid	blood microparticle [GO:0
677	Q8R1F1	NIBL1_MOUSE	Niban-like protein	Mus musculus (Mouse)	Fam129b	Evidence at protein level	749	84819	gonadotropin secretion [(	cadherin binding involve	adherens junction [GO:00
678	Q8VCR7	ABHEB_MOUSE	Protein ABHD14B (	Mus musculus (Mouse)	Abhd14b	Evidence at protein level	210	22451	positive regulation of trar	hydrolase activity [GO:00	cytosol [GO:0005829]; ex
679	P51885	LUM_MOUSE	Lumican (Keratan s	Mus musculus (Mouse)	Lum	Evidence at protein level	338	38265	cartilage development [G	collagen binding [GO:000	extracellular exosome [G
680	P62301	RS13_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps13	Evidence at protein level	151	17222	negative regulation of RN	5.8S rRNA binding [GO:19	cytosolic small ribosomal
681	Q3UIU2	NDUB6_MOUSE	NADH dehydrogen	Mus musculus (Mouse)	Ndufb6	Evidence at protein level	128	15515	oxidation-reduction process [GO:0055114]		integral component of m
682	Q3TW96	UAP1L_MOUSE	UDP-N-acetylhexos	Mus musculus (Mouse)	Uap1l1	Evidence at protein level	507	56614	UDP-N-acetylglucosamin	UDP-N-acetylglucosamin	cytosol [GO:0005829]
683	Q9D2R0	AACS_MOUSE	Acetoacetyl-CoA sy	Mus musculus (Mouse)	Aacs	Evidence at protein level	672	75200	adipose tissue developme	acetoacetate-CoA ligase a	cytosol [GO:0005829]
684	P25444	RS2_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps2	Evidence at protein level	293	31231	cellular response to interf	cadherin binding involve	cell-cell adherens junctio
685	Q91V61	SFXN3_MOUSE	Sideroflexin-3	Mus musculus (Mouse)	Sfxn3	Evidence at protein level	321	35406	iron ion homeostasis [GO	ion transmembrane trans	integral component of m
686	P68510	1433F_MOUSE	14-3-3 protein eta	Mus musculus (Mouse)	Ywhah	Evidence at protein level	246	28212	cytoskeleton organizatior	actin binding [GO:00037	cytoplasm [GO:0005737]
687	P61087	UBE2K_MOUSE	Ubiquitin-conjugati	Mus musculus (Mouse)	Ube2k	Evidence at protein level	200	22407	cellular response to interf	ATP binding [GO:000552	cytoplasm [GO:0005737]
688	Q9CPU0	LGUL_MOUSE	Lactoylglutathione	Mus musculus (Mouse)	Glo1	Evidence at protein level	184	20810	carbohydrate metabolic p	lactoylglutathione lyase a	cytosol [GO:0005829]; ex
689	Q62348	TSN_MOUSE	Translin (EC 3.1.-.-)	Mus musculus (Mouse)	Tsn	Evidence at protein level	228	26201	RNA metabolic process [G	endonuclease activity [G	cytoplasm [GO:0005737]
690	O35295	PURB_MOUSE	Transcriptional acti	Mus musculus (Mouse)	Purb	Evidence at protein level	324	33901	apoptotic process [GO:00	double-stranded DNA bin	DNA replication factor A
691	Q60737	CSK21_MOUSE	Casein kinase II sub	Mus musculus (Mouse)	Csnk2a1	Evidence at protein level	391	45134	apoptotic process [GO:00	ATP binding [GO:000552	cytoplasm [GO:0005737]
692	P61082	UBC12_MOUSE	NEDD8-conjugating	Mus musculus (Mouse)	Ube2m	Evidence at protein level	183	20900	cellular protein modificat	ATP binding [GO:000552	cytoplasm [GO:0005737]
693	Q91VR5	DDX1_MOUSE	ATP-dependent RN	Mus musculus (Mouse)	Ddx1	Evidence at protein level	740	82500	DNA duplex unwinding [G	ATP binding [GO:000552	cleavage body [GO:0071
694	Q80UU9	PGRC2_MOUSE	Membrane-associa	Mus musculus (Mouse)	Pgrmc2	Evidence at protein level	217	23334		heme binding [GO:00200	endomembrane system [
695	Q8K3J1	NDUS8_MOUSE	NADH dehydrogen	Mus musculus (Mouse)	Ndufs8	Evidence at protein level	212	24038	mitochondrial respiratory	4 iron, 4 sulfur cluster bin	mitochondrial respirator
696	Q9D0M3	CY1_MOUSE	Cytochrome c1, he	Mus musculus (Mouse)	Cyc1	Evidence at protein level	325	35328	mitochondrial ATP synthe	electron transporter, trar	membrane [GO:0016020
697	O55222	ILK_MOUSE	Integrin-linked prot	Mus musculus (Mouse)	Ilk	Evidence at protein level	452	51373	branching involved in ure	ATP binding [GO:000552	cell-cell junction [GO:000

698	Q9Z1Q2	ABHGA_MOUSE	Protein ABHD16A (	Mus musculus (Mouse)	Abhd16a	Evidence at protein level	558	63086	monoacylglycerol catabol	acylglycerol lipase activit	integral component of me
699	O88207	CO5A1_MOUSE	Collagen alpha-1(V	Mus musculus (Mouse)	Col5a1	Evidence at protein level	1838	183677	blood vessel developmen	extracellular matrix struc	basement membrane [GO
700	P62827	RAN_MOUSE	GTP-binding nuclea	Mus musculus (Mouse)	Ran	Evidence at protein level	216	24423	actin cytoskeleton organi	cadherin binding involved	cell-cell adherens junctio
701	Q99P72	RTN4_MOUSE	Reticulon-4 (Neurit	Mus musculus (Mouse)	Rtn4	Evidence at protein level	1162	126613	axonal fasciculation [GO:	cadherin binding involved	cell-cell adherens junctio
702	P30412	PPIC_MOUSE	Peptidyl-prolyl cis-t	Mus musculus (Mouse)	Ppic	Evidence at protein level	212	22794	protein folding [GO:0006	cyclosporin A binding [GC	cytoplasm [GO:0005737]
703	Q9D967	MGDP1_MOUSE	Magnesium-depen	Mus musculus (Mouse)	Mdp1	Evidence at protein level	164	18582	fructosamine metabolic p	metal ion binding [GO:00	extracellular exosome [G
704	P47856	GFPT1_MOUSE	Glutamine--fructos	Mus musculus (Mouse)	Gfpt1	Evidence at protein level	697	78539	circadian regulation of ge	carbohydrate derivative b	extracellular exosome [G
705	Q9Z2U1	PSA5_MOUSE	Proteasome subuni	Mus musculus (Mouse)	Psma5	Evidence at protein level	241	26411	proteasome-mediated ub	threonine-type endopept	cytosol [GO:0005829]; ex
706	Q8BGC0	HTSF1_MOUSE	HIV Tat-specific fac	Mus musculus (Mouse)	Htatsf1	Evidence at protein level	757	86240	mRNA splicing, via splice	nucleotide binding [GO:0	nucleoplasm [GO:000565
707	P68134	ACTS_MOUSE	Actin, alpha skelet	Mus musculus (Mouse)	Acta1	Evidence at protein level	377	42051	cell growth [GO:0016049	ATP binding [GO:0005524	actin cytoskeleton [GO:00
708	Q9D6R2	IDH3A_MOUSE	Isocitrate dehydrog	Mus musculus (Mouse)	Idh3a	Evidence at protein level	366	39639	tricarboxylic acid cycle [G	isocitrate dehydrogenase	mitochondrion [GO:0005
709	Q04750	TOP1_MOUSE	DNA topoisomeras	Mus musculus (Mouse)	Top1	Evidence at protein level	767	90876	chromatin remodeling [G	chromatin binding [GO:0	cytoplasm [GO:0005737]
710	Q91WJ8	FUBP1_MOUSE	Far upstream elem	Mus musculus (Mouse)	Fubp1	Evidence at protein level	651	68540	cell growth [GO:0016049	DNA binding [GO:000367	nucleus [GO:0005634]
711	Q61881	MCM7_MOUSE	DNA replication lic	Mus musculus (Mouse)	Mcm7	Evidence at protein level	719	81211	cell cycle [GO:0007049];	ATP binding [GO:0005524	cytosol [GO:0005829]; M
712	P08752	GNAI2_MOUSE	Guanine nucleotide	Mus musculus (Mouse)	Gnai2	Evidence at protein level	355	40489	activation of MAPKK acti	G-protein beta/gamma-s	cell body [GO:0044297];
713	P00329	ADH1_MOUSE	Alcohol dehydroge	Mus musculus (Mouse)	Adh1	Evidence at protein level	375	39771	behavioral response to et	alcohol dehydrogenase (N	cytosol [GO:0005829]; in
714	P61089	UBE2N_MOUSE	Ubiquitin-conjugati	Mus musculus (Mouse)	Ube2n	Evidence at protein level	152	17138	DNA double-strand break	ATP binding [GO:0005524	cytoplasm [GO:0005737]
715	Q99JW2	ACY1_MOUSE	Aminoacylase-1 (A	Mus musculus (Mouse)	Acy1	Evidence at protein level	408	45781	cellular amino acid metab	aminoacylase activity [GC	cytoplasm [GO:0005737]
716	Q11136	PEPD_MOUSE	Xaa-Pro dipeptidas	Mus musculus (Mouse)	Pepd	Evidence at protein level	493	55029	collagen catabolic proces	aminopeptidase activity [	extracellular exosome [G
717	A2ADY9	DDI2_MOUSE	Protein DDI1 homo	Mus musculus (Mouse)	Ddi2	Evidence at protein level	399	44591	intestinal absorption [GO	aspartic-type endopeptid	brush border [GO:00059
718	P50544	ACADV_MOUSE	Very long-chain spe	Mus musculus (Mouse)	Acadvl	Evidence at protein level	656	70875	epithelial cell differentiat	acyl-CoA dehydrogenase	cytosol [GO:0005829]; m
719	P15626	GSTM2_MOUSE	Glutathione S-tran	Mus musculus (Mouse)	Gstm2	Evidence at protein level	218	25717	cellular detoxification of	enzyme binding [GO:001	cytoplasm [GO:0005737]
720	O70194	EIF3D_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif3d	Evidence at protein level	548	63989	cap-dependent translatio	mRNA cap binding [GO:0	eukaryotic translation ini
721	P51174	ACADL_MOUSE	Long-chain specific	Mus musculus (Mouse)	Acadl	Evidence at protein level	430	47908	carnitine catabolic proces	flavin adenine dinucleotic	mitochondrial matrix [GO
722	Q91YT0	NDUV1_MOUSE	NADH dehydrogen	Mus musculus (Mouse)	Ndufv1	Evidence at protein level	464	50834		4 iron, 4 sulfur cluster bin	cytosol [GO:0005829]; m
723	P10852	4F2_MOUSE	4F2 cell-surface an	Mus musculus (Mouse)	Slc3a2	Evidence at protein level	526	58337	carbohydrate metabolic p	cadherin binding involved	apical plasma membrane
724	P49722	PSA2_MOUSE	Proteasome subuni	Mus musculus (Mouse)	Psma2	Evidence at protein level	234	25927	ubiquitin-dependent prot	threonine-type endopept	cytosol [GO:0005829]; ex
725	Q9QYS9	QKI_MOUSE	Protein quaking (M	Mus musculus (Mouse)	Qki	Evidence at protein level	341	37671	3'-UTR-mediated mRNA	mRNA binding [GO:0003	cytoplasm [GO:0005737]
726	Q1HFZ0	NSUN2_MOUSE	tRNA (cytosine(34)	Mus musculus (Mouse)	Nsun2	Evidence at protein level	757	85452	cell division [GO:0051301	RNA binding [GO:000372	chromatoid body [GO:00
727	O35640	ANXA8_MOUSE	Annexin A8 (Annex	Mus musculus (Mouse)	Anxa8	Evidence at protein level	327	36724	blood coagulation [GO:00	actin filament binding [G	cytosol [GO:0005829]; ex
728	Q9D051	ODPB_MOUSE	Pyruvate dehydrog	Mus musculus (Mouse)	Pdhb	Evidence at protein level	359	38937	acetyl-CoA biosynthetic p	pyruvate dehydrogenase	extracellular exosome [G
729	P35235	PTN11_MOUSE	Tyrosine-protein ph	Mus musculus (Mouse)	Ptpn11	Evidence at protein level	597	68460	abortive mitotic cell cycle	cell adhesion molecule bi	cytoplasm [GO:0005737]
730	Q78ZA7	NP1L4_MOUSE	Nucleosome assem	Mus musculus (Mouse)	Nap1l4	Evidence at protein level	375	42679	nucleosome assembly [G	RNA binding [GO:000372	nucleus [GO:0005634]
731	Q7TMM9	TBB2A_MOUSE	Tubulin beta-2A ch	Mus musculus (Mouse)	Tubb2a	Evidence at protein level	445	49907	microtubule-based proce	GTPase activity [GO:0003	cytoplasm [GO:0005737]
732	Q05D44	IF2P_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif5b	Evidence at protein level	1216	137616	regulation of translationa	GTPase activity [GO:0003	cytoplasm [GO:0005737]
733	Q01279	EGFR_MOUSE	Epidermal growth f	Mus musculus (Mouse)	Egfr	Evidence at protein level	1210	134853	activation of MAPKK acti	actin filament binding [G	apical plasma membrane
734	Q7TQI3	OTUB1_MOUSE	Ubiquitin thioester	Mus musculus (Mouse)	Otub1	Evidence at protein level	271	31270	adaptive immune respon	NEDD8-specific protease	cytoplasm [GO:0005737]
735	Q7TMD7	DSG4_MOUSE	Desmoglein-4	Mus musculus (Mouse)	Dsg4	Evidence at protein level	1041	114449	BMP signaling pathway [(	calcium ion binding [GO:0	desmosome [GO:003005
736	Q3V188	ENDOU_MOUSE	Poly(U)-specific en	Mus musculus (Mouse)	Endou	Evidence at transcript level	412	47010	female pregnancy [GO:00	endoribonuclease activity	cytoplasm [GO:0005737]
737	Q60967	PAPS1_MOUSE	Bifunctional 3'-pho	Mus musculus (Mouse)	Papss1	Evidence at protein level	624	70794	3'-phosphoadenosine 5'-p	adenylylsulfate kinase ac	sulfate adenylyltransfera
738	P62880	GBB2_MOUSE	Guanine nucleotide	Mus musculus (Mouse)	Gnb2	Evidence at protein level	340	37331	G-protein coupled recept	calcium channel regulato	cell body [GO:0044297];
739	Q08AT1	RASLC_MOUSE	Ras-like protein fa	Mus musculus (Mouse)	Rasl12	Evidence at transcript level	266	29555	small GTPase mediated si	GTP binding [GO:0005525	intracellular [GO:000562
740	Q5BKS4	ERI2_MOUSE	ERI1 exoribonuclea	Mus musculus (Mouse)	Eri2	Evidence at transcript level	688	76524	exonucleolytic trimming t	exonuclease activity [GO:0004527]; nucleic acid bin	
741	Q9Z2L6	MINP1_MOUSE	Multiple inositol pc	Mus musculus (Mouse)	Minpp1	Evidence at protein level	481	54537		acid phosphatase activity	endoplasmic reticulum lu
742	Q9D8W5	PSD12_MOUSE	26S proteasome no	Mus musculus (Mouse)	Psmd12	Evidence at protein level	456	52895	proteasome-mediated ubiquitin-dependent protein catabolic process		cytoplasm [GO:0005737]
743	P11247	PERM_MOUSE	Myeloperoxidase (M	Mus musculus (Mouse)	Mpo	Evidence at protein level	718	81182	aging [GO:0007568]; defe	heme binding [GO:00200	azurophil granule [GO:00
744	Q7TSV4	PGM2_MOUSE	Phosphoglucomuta	Mus musculus (Mouse)	Pgm2	Evidence at protein level	620	68748	deoxyribose phosphate c	magnesium ion binding [(	cytosol [GO:0005829]; ex
745	Q9DB05	SNAA_MOUSE	Alpha-soluble NSF	Mus musculus (Mouse)	Napa	Evidence at protein level	295	33190	apical protein localizatior	protein complex binding [	extracellular exosome [G
746	O89094	CASPE_MOUSE	Caspase-14 (CASP-	Mus musculus (Mouse)	Casp14	Evidence at protein level	257	29458	cornification [GO:0007026	cysteine-type endopeptid	cytoplasm [GO:0005737]
747	P42227	STAT3_MOUSE	Signal transducer a	Mus musculus (Mouse)	Stat3	Evidence at protein level	770	88054	acute-phase response [G	chromatin DNA binding [(	cytoplasm [GO:0005737]
748	Q9QXZ0	MACF1_MOUSE	Microtubule-actin	Mus musculus (Mouse)	Macf1	Evidence at protein level	7354	831878	establishment or mainter	actin binding [GO:000377	actin cytoskeleton [GO:00
749	Q9CYD3	CRTAP_MOUSE	Cartilage-associate	Mus musculus (Mouse)	Crtap	Evidence at protein level	400	46169	chaperone-mediated prot	protein complex binding [	endoplasmic reticulum [G
750	Q9D7Q1	CHIT1_MOUSE	Chitotriosidase-1 (E	Mus musculus (Mouse)	Chit1	Evidence at protein level	464	51112	chitin catabolic process [(	chitin binding [GO:00080	extracellular space [GO:0
751	Q8K3F7	TDH_MOUSE	L-threonine 3-dehy	Mus musculus (Mouse)	Tdh	Evidence at protein level	373	41462	L-threonine catabolic pro	coenzyme binding [GO:0	mitochondrion [GO:0005
752	Q9DCH4	EIF3F_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif3f	Evidence at protein level	361	37984	IRES-dependent viral tran	thiol-dependent ubiquitin	eukaryotic translation ini
753	P27048	RSMB_MOUSE	Small nuclear ribon	Mus musculus (Mouse)	Snrpb	Evidence at protein level	231	23656	mRNA splicing, via splice	histone pre-mRNA DCP b	catalytic step 2 spliceoso
754	Q9Z1R2	BAG6_MOUSE	Large proline-rich p	Mus musculus (Mouse)	Bag6	Evidence at protein level	1154	121037	antigen processing and pr	Hsp70 protein binding [G	BAT3 complex [GO:0071
755	P06151	LDHA_MOUSE	L-lactate dehydrog	Mus musculus (Mouse)	Ldha	Evidence at protein level	332	36499	cellular response to extra	cadherin binding involved	cell-cell adherens junctio
756	Q61792	LASP1_MOUSE	LIM and SH3 doma	Mus musculus (Mouse)	Lasp1	Evidence at protein level	263	29994	ion transport [GO:0006811	actin filament binding [G	cell-cell adherens junctio
757	Q60865	CAPR1_MOUSE	Caprin-1 (Cytoplas	Mus musculus (Mouse)	Caprin1	Evidence at protein level	707	78169	negative regulation of tra	RNA binding [GO:000372	cytoplasmic stress granul
758	Q99KD5	UN45A_MOUSE	Protein unc-45 hon	Mus musculus (Mouse)	Unc45a	Evidence at protein level	944	103447	cell differentiation [GO:0	cadherin binding involved	cell-cell adherens junctio
759	Q61879	MYH10_MOUSE	Myosin-10 (Cellula	Mus musculus (Mouse)	Myh10	Evidence at protein level	1976	228996	actin cytoskeleton organi	actin-dependent ATPase	actomyosin [GO:0042641
760	P62874	GBB1_MOUSE	Guanine nucleotide	Mus musculus (Mouse)	Gnb1	Evidence at protein level	340	37377	cardiac muscle cell apopt	alkylglycerophosphoethe	cell body [GO:0044297];
761	Q61739	ITA6_MOUSE	Integrin alpha-6 (CI	Mus musculus (Mouse)	Itga6	Evidence at protein level	1091	122159	amelogenesis [GO:00971	cadherin binding involved	basal part of cell [GO:004
762	Q9JM14	NT5C_MOUSE	5'(3')-deoxyribonu	Mus musculus (Mouse)	Nt5c	Evidence at protein level	200	23076	deoxyribonucleotide cata	5'-nucleotidase activity [(	cytoplasm [GO:0005737]
763	P28658	ATX10_MOUSE	Ataxin-10 (Brain pr	Mus musculus (Mouse)	Atxn10	Evidence at protein level	475	53707	cilium assembly [GO:0060271]; nervous system dev		cytoplasm [GO:0005737]
764	Q9R1P1	PSB3_MOUSE	Proteasome subuni	Mus musculus (Mouse)	Psmb3	Evidence at protein level	205	22965	proteasome-mediated ub	endopeptidase activity [G	cytosol [GO:0005829]; ex
765	Q9JMA1	UBP14_MOUSE	Ubiquitin carboxyl-	Mus musculus (Mouse)	Usp14	Evidence at protein level	493	56002	chemical synaptic transm	endopeptidase inhibitor a	cell surface [GO:0009986
766	O55029	COPB2_MOUSE	Coatomer subunit I	Mus musculus (Mouse)	Copb2	Evidence at protein level	905	102449	ER to Golgi vesicle-media	structural molecule activi	COPI vesicle coat [GO:00
767	Q80U72	SCRIB_MOUSE	Protein scribble ho	Mus musculus (Mouse)	Scrib	Evidence at protein level	1612	174059	activation of GTPase acti	cadherin binding involved	basolateral plasma memb
768	Q923D2	BLVRB_MOUSE	Flavin reductase (N	Mus musculus (Mouse)	Blvrb	Evidence at protein level	206	22197	heme catabolic process [(	biliverdin reductase activ	cytosol [GO:0005829]; ex
769	P63330	PP2AA_MOUSE	Serine/threonine-p	Mus musculus (Mouse)	Ppp2ca	Evidence at protein level	309	35608	meiotic cell cycle [GO:00	GABA receptor binding [G	chromosome, centromeri
770	P35279	RAB6A_MOUSE	Ras-related protein	Mus musculus (Mouse)	Rab6a	Evidence at protein level	208	23590	antigen processing and pr	GTPase activity [GO:0003	cytoplasmic vesicle [GO:0
771	O08585	CLCA_MOUSE	Clathrin light chain	Mus musculus (Mouse)	Clta	Evidence at protein level	235	25604	cell division [GO:0051301	clathrin heavy chain bind	clathrin coat of coated pi
772	Q9D6Z1	NOP56_MOUSE	Nucleolar protein 5	Mus musculus (Mouse)	Nop56	Evidence at protein level	580	64464	rRNA modification [GO:0	cadherin binding involved	box C/D snoRNP complex
773	Q02819	NUCB1_MOUSE	Nucleobindin-1 (CA	Mus musculus (Mouse)	Nucb1	Evidence at protein level	459	53409	regulation of protein targ	calcium ion binding [GO:(	cis-Golgi network [GO:00
774	Q99PV0	PRP8_MOUSE	Pre-mRNA-process	Mus musculus (Mouse)	Prpf8	Evidence at protein level	2335	273616	cellular response to lipop	K63-linked polyubiquitin	catalytic step 2 spliceoso
775	P70441	NHRF1_MOUSE	Na(+)/H(+) exchang	Mus musculus (Mouse)	Slc9a3r1	Evidence at protein level	355	38600	actin cytoskeleton organi	beta-2 adrenergic recept	apical part of cell [GO:00
776	Q922Q8	LRC59_MOUSE	Leucine-rich repeat	Mus musculus (Mouse)	Lrrc59	Evidence at protein level	307	34877		cadherin binding involved	cell-cell adherens junctio
777	O08756	HCD2_MOUSE	3-hydroxyacyl-CoA	Mus musculus (Mouse)	Hsd17b10	Evidence at protein level	261	27419	tRNA processing [GO:000	3-hydroxy-2-methylbutyr	endoplasmic reticulum [G
778	Q6IFX4	K1C39_MOUSE	Keratin, type I cyto	Mus musculus (Mouse)	Krt39	Evidence at transcript level	482	54287		structural molecule activi	intermediate filament [G
779	Q640N1	AEBP1_MOUSE	Adipocyte enhance	Mus musculus (Mouse)	Aebp1	Evidence at protein level	1128	128365	negative regulation of tra	carboxypeptidase activity	cytoplasm [GO:0005737]
780	Q6P4T2	U520_MOUSE	U5 small nuclear ri	Mus musculus (Mouse)	Snrnp200	Evidence at protein level	2136	244547	mRNA splicing, via splice	ATP binding [GO:0005524	catalytic step 2 spliceoso
781	Q8BTZ7	GMPPB_MOUSE	Mannose-1-phosph	Mus musculus (Mouse)	Gmppb	Evidence at protein level	360	39917	GDP-mannose biosynthet	GTP binding [GO:0005525	cytoplasm [GO:0005737]
782	Q9Z2D0	MTMR9_MOUSE	Myotubularin-relat	Mus musculus (Mouse)	Mtmr9	Evidence at protein level	545	62908		enzyme regulator activity	cytoplasm [GO:0005737]
783	Q7TMF3	NDUAC_MOUSE	NADH dehydrogen	Mus musculus (Mouse)	Ndufa12	Evidence at protein level	145	17086	response to oxidative stre	electron carrier activity [(	cytosol [GO:0005829]; m
784	Q9DC50	OCTC_MOUSE	Peroxisomal carniti	Mus musculus (Mouse)	Crot	Evidence at protein level	612	70264	carnitine metabolic proce	carnitine O-octanoyltrans	intracellular membrane-b
785	Q9WVK4	EHD1_MOUSE	EH domain-contain	Mus musculus (Mouse)	Ehd1	Evidence at protein level	534	60603	cellular response to nerve	ATP binding [GO:0005524	cell-cell adherens junctio
786	P32067	LA_MOUSE	Lupus La protein ho	Mus musculus (Mouse)	Ssb	Evidence at protein level	415	47756	IRES-dependent viral tran	nucleotide binding [GO:0	intracellular ribonucleopr
787	P49586	PCY1A_MOUSE	Choline-phosphate	Mus musculus (Mouse)	Pcyt1a	Evidence at protein level	367	41667	CDP-choline pathway [GC	choline-phosphate cytidy	cytosol [GO:0005829]; er
788	P68254	1433T_MOUSE	14-3-3 protein thet	Mus musculus (Mouse)	Ywhaq	Evidence at protein level	245	27778	negative regulation of ion	protein domain specific b	cytoplasm [GO:0005737]
789	P39054	DYN2_MOUSE	Dynamin-2 (EC 3.6.	Mus musculus (Mouse)	Dnm2	Evidence at protein level	870	98145	aorta development [GO:0	GTPase activity [GO:0003	cell junction [GO:003005
790	P14115	RL27A_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl27a	Evidence at protein level	148	16605	translation [GO:0006412	RNA binding [GO:000372	cytosol [GO:0005829]; cy
791	Q9CQI3	GMFB_MOUSE	Glia maturation fac	Mus musculus (Mouse)	Gmfb	Evidence at protein level	142	16723	learning [GO:0007612]; locomotory behavior [GO:0		intracellular [GO:000562
792	Q61768	KINH_MOUSE	Kinesin-1 heavy ch	Mus musculus (Mouse)	Kif5b	Evidence at protein level	963	109551	axon guidance [GO:0007	ATP binding [GO:0005524	axonal growth cone [GO:0
793	Q64511	TOP2B_MOUSE	DNA topoisomeras	Mus musculus (Mouse)	Top2b	Evidence at protein level	1612	181909	axonogenesis [GO:0007	ATP binding [GO:0005524	cytosol [GO:0005829]; nu
794	P56567	CYTA_MOUSE	Cystatin-A (Cystatin	Mus musculus (Mouse)	Csta	Inferred from homology	97	10929		cysteine-type endopeptid	cornified envelope [GO:0
795	O55126	NIPS2_MOUSE	Protein NipSnap ho	Mus musculus (Mouse)	Gbas	Evidence at protein level	281	32933	ATP biosynthetic process [GO:0006754]; negative r		mitochondrion [GO:0005
796	Q9JHH9	COPZ2_MOUSE	Coatomer subunit z	Mus musculus (Mouse)	Copz2	Evidence at protein level	205	22934	protein transport [GO:0015031]; vesicle-mediated t		COPI-coated vesicle [GO:
797	P11352	GPX1_MOUSE	Glutathione peroxi	Mus musculus (Mouse)	Gpx1	Evidence at protein level	201	22329	angiogenesis involved in v	glutathione peroxidase ac	cytoplasm [GO:0005737]
798	P00493	HPRT_MOUSE	Hypoxanthine-guar	Mus musculus (Mouse)	Hprt1	Evidence at protein level	218	24570	adenine metabolic proce	guanine phosphoribosyltr	cytoplasm [GO:0005737]
799	P26231	CTNA1_MOUSE	Catenin alpha-1 (1(	Mus musculus (Mouse)	Ctnna1	Evidence at protein level	906	100106	actin filament organizatic	actin filament binding [G	acrosomal vesicle [GO:00
800	Q8BLX7	COGA1_MOUSE	Collagen alpha-1(X	Mus musculus (Mouse)	Col16a1	Evidence at protein level	1580	155805	cell adhesion [GO:00071	integrin binding [GO:000	collagen trimer [GO:0005
801	Q8QZT1	THIL_MOUSE	Acetyl-CoA acetyltr	Mus musculus (Mouse)	Acat1	Evidence at protein level	424	44816	acetyl-CoA biosynthetic p	acetyl-CoA C-acetyltransf	extracellular exosome [G
802	P01831	THY1_MOUSE	Thy-1 membrane g	Mus musculus (Mouse)	Thy1	Evidence at protein level	162	18080	angiogenesis [GO:000152	GPI anchor binding [GO:0	anchored component of e
803	Q8BP92	RCN2_MOUSE	Reticulocalbin-2 (Tr	Mus musculus (Mouse)	Rcn2	Evidence at protein level	320	37271		calcium ion binding [GO:(	endoplasmic reticulum [G
804	Q9CY58	PAIRB_MOUSE	Plasminogen activa	Mus musculus (Mouse)	Serbp1	Evidence at protein level	407	44714	regulation of apoptotic pr	cadherin binding involved	cell-cell adherens junctio
805	Q925H7	KR194_MOUSE	Keratin-associated	Mus musculus (Mouse)	Krtap19-4	Evidence at transcript level	84	8626			intermediate filament [G
806	Q8BU85	MSRB3_MOUSE	Methionine-R-sulfo	Mus musculus (Mouse)	Msrb3	Evidence at protein level	253	26832	protein repair [GO:00300	peptide-methionine (R)-S	endoplasmic reticulum [G
807	P41105	RL28_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl28	Evidence at protein level	137	15733	positive regulation of pro	RNA binding [GO:000372	cell body [GO:0044297];
808	P17710	HXK1_MOUSE	Hexokinase-1 (EC 2	Mus musculus (Mouse)	Hk1	Evidence at protein level	974	108303	canonical glycolysis [GO:(	ATP binding [GO:0005524	cilium [GO:0005929]; cyt
809	Q8BJW6	EIF2A_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif2a	Evidence at protein level	581	64403	positive regulation of sigr	cadherin binding involved	blood microparticle [GO:(
810	Q8CIV8	TBCE_MOUSE	Tubulin-specific ch	Mus musculus (Mouse)	Tbce	Evidence at protein level	524	59086	adult locomotory behavic	unfolded protein binding	cytoplasm [GO:0005737]
811	Q6P069	SORCN_MOUSE	Sorcin	Mus musculus (Mouse)	Sri	Evidence at protein level	198	21627	calcium ion transport [GC	calcium-dependent syste	axon [GO:0030424]; axor
812	O88898	P63_MOUSE	Tumor protein 63 (	Mus musculus (Mouse)	Tp63	Evidence at protein level	680	76789	anatomical structure forr	chromatin binding [GO:0	chromatin [GO:0000785]
813	Q9EPE9	AT131_MOUSE	Manganese-transp	Mus musculus (Mouse)	Atp13a1	Evidence at protein level	1200	132388	cellular calcium ion home	ATP binding [GO:0005524	endoplasmic reticulum m
814	Q6P9R2	OXSR1_MOUSE	Serine/threonine-p	Mus musculus (Mouse)	Oxsr1	Evidence at protein level	527	58214	cellular hypotonic respon	ATP binding [GO:0005524	cytoplasm [GO:0005737]

815	O35405	PLD3_MOUSE	Phospholipase D3 (	Mus musculus (Mouse)	Pld3	Evidence at protein level	488	54389	lipid catabolic process [G	N-acylphosphatidylethan	endoplasmic reticulum m
816	Q9CPQ1	COX6C_MOUSE	Cytochrome c oxid	Mus musculus (Mouse)	Cox6c	Evidence at protein level	76	8469		cytochrome-c oxidase act	integral component of m
817	Q99K30	ES8L2_MOUSE	Epidermal growth f	Mus musculus (Mouse)	Eps8l2	Evidence at protein level	729	82229	positive regulation of ruff	actin binding [GO:000377	cell-cell adherens junctio
818	O08586	PTEN_MOUSE	Phosphatidylinosit	Mus musculus (Mouse)	Pten	Evidence at protein level	403	47152	adult behavior [GO:0030	anaphase-promoting com	apical plasma membrane
819	P62254	UB2G1_MOUSE	Ubiquitin-conjugati	Mus musculus (Mouse)	Ube2g1	Evidence at protein level	170	19509	cellular protein catabolic	ATP binding [GO:0005524	cytoplasm [GO:0005737]
820	O08738	CASP6_MOUSE	Caspase-6 (CASP-6	Mus musculus (Mouse)	Casp6	Evidence at protein level	276	31595	epithelial cell differentiat	cysteine-type endopeptid	cytoplasm [GO:0005737]
821	Q9Z247	FKBP9_MOUSE	Peptidyl-prolyl cis-t	Mus musculus (Mouse)	Fkbp9	Evidence at protein level	570	62995	chaperone-mediated prot	calcium ion binding [GO:(	endoplasmic reticulum [G
822	Q9QZE5	COPG1_MOUSE	Coatomer subunit	Mus musculus (Mouse)	Copg1	Evidence at protein level	874	97513	intracellular protein trans	structural molecule activi	COPI vesicle coat [GO:00
823	Q9EP69	SAC1_MOUSE	Phosphatidylinositi	Mus musculus (Mouse)	Sacm1l	Evidence at protein level	587	66944	phosphatidylinositol dep	phosphatase activity [GO	AMPA glutamate recepto
824	Q8K0E8	FIBB_MOUSE	Fibrinogen beta ch	Mus musculus (Mouse)	Fgb	Evidence at protein level	481	54753	adaptive immune respon	chaperone binding [GO:0	blood microparticle [GO:(
825	P62818	S10A3_MOUSE	Protein S100-A3 (P	Mus musculus (Mouse)	S100a3	Evidence at transcript level	101	11747		calcium ion binding [GO:(	cytosol [GO:0005829]; nu
826	Q9CQW9	IFM3_MOUSE	Interferon-induced	Mus musculus (Mouse)	Ifitm3	Evidence at protein level	137	14954	defense response to virus	[GO:0051607]; negative r	apical part of cell [GO:00
827	Q8BKC5	IPO5_MOUSE	Importin-5 (Imp5) (	Mus musculus (Mouse)	Ipo5	Evidence at protein level	1097	123591	cellular response to amin	nuclear localization sequ	cytoplasm [GO:0005737]
828	Q8BMF4	ODP2_MOUSE	Dihydrolipoyllysine	Mus musculus (Mouse)	Dlat	Evidence at protein level	642	67942	glucose metabolic proces	dihydrolipoyllysine-resid	mitochondrial pyruvate d
829	P62320	SMD3_MOUSE	Small nuclear ribon	Mus musculus (Mouse)	Snrpd3	Evidence at protein level	126	13916	protein methylation [GO:	enzyme binding [GO:001	catalytic step 2 spliceoso
830	P63276	RS17_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps17	Evidence at protein level	135	15524	erythrocyte homeostasis	RNA binding [GO:000372	cytosolic small ribosomal
831	Q8BK64	AHSA1_MOUSE	Activator of 90 kDa	Mus musculus (Mouse)	Ahsa1	Evidence at protein level	338	38117	protein folding [GO:0006	ATPase activator activity	cell-cell adherens junctio
832	Q9R0P6	SC11A_MOUSE	Signal peptidase co	Mus musculus (Mouse)	Sec11a	Evidence at protein level	179	20626	signal peptide processing	peptidase activity [GO:00	extracellular exosome [G
833	Q7TSF1	DSG1B_MOUSE	Desmoglein-1-beta	Mus musculus (Mouse)	Dsg1b	Evidence at protein level	1060	114454	homophilic cell adhesion	calcium ion binding [GO:(	cytoplasmic side of plasm
834	P28271	ACOC_MOUSE	Cytoplasmic aconit	Mus musculus (Mouse)	Aco1	Evidence at protein level	889	98126	cellular iron ion homeost	4 iron, 4 sulfur cluster bin	cytoplasm [GO:0005737]
835	P52196	THTR_MOUSE	Thiosulfate sulfurtr	Mus musculus (Mouse)	Tst	Evidence at protein level	297	33466	epithelial cell differentiat	5S rRNA binding [GO:000	extracellular exosome [G
836	P10493	NID1_MOUSE	Nidogen-1 (NID-1)	Mus musculus (Mouse)	Nid1	Evidence at protein level	1245	136538	cell-matrix adhesion [GO:	calcium ion binding [GO:(	basal lamina [GO:000560
837	Q8VHN8	SDOS_MOUSE	Protein syndesmos	Mus musculus (Mouse)	Nudt16l1	Evidence at protein level	211	23414		hydrolase activity [GO:00	cytoplasm [GO:0005737]
838	Q91X96	MSS4_MOUSE	Guanine nucleotide	Mus musculus (Mouse)	Rabif	Evidence at protein level	123	13915	post-Golgi vesicle-mediat	guanyl-nucleotide exchan	cytosol [GO:0005829]; m
839	Q62376	RU17_MOUSE	U1 small nuclear ri	Mus musculus (Mouse)	Snrnp70	Evidence at protein level	448	51992	cellular response to retin	mRNA binding [GO:0003	commitment complex [G
840	Q8R323	RFC3_MOUSE	Replication factor (	Mus musculus (Mouse)	Rfc3	Evidence at protein level	356	40526	DNA-dependent DNA rep	DNA clamp loader activit	Ctf18 RFC-like complex [G
841	Q8CIG8	ANM5_MOUSE	Protein arginine N-	Mus musculus (Mouse)	Prmt5	Evidence at protein level	637	72680	circadian regulation of ge	chromatin binding [GO:0	cytoplasm [GO:0005737]
842	A2BDX3	MOCS3_MOUSE	Adenylyltransferas	Mus musculus (Mouse)	Mocs3	Evidence at protein level	460	49375	enzyme active site forma	ATP binding [GO:0005524	cytosol [GO:0005829]
843	Q3UFY7	5NT3B_MOUSE	7-methylguanosine	Mus musculus (Mouse)	Nt5c3b	Evidence at protein level	300	34425	nucleotide metabolic pro	5'-nucleotidase activity [(	cytoplasm [GO:0005737]
844	P08551	NFL_MOUSE	Neurofilament ligh	Mus musculus (Mouse)	Nefl	Evidence at protein level	543	61508	anterograde axonal trans	identical protein binding [	axon [GO:0030424]; axon
845	Q925H4	KR211_MOUSE	Keratin-associated	Mus musculus (Mouse)	Krtap21-1	Evidence at transcript level	128	12539	cell proliferation [GO:0008283];	developmental gro	intermediate filament [G
846	Q8QZY1	EIF3L_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif3l	Evidence at protein level	564	66613	translational initiation [G	RNA binding [GO:000372	eukaryotic translation ini
847	Q99KC8	VMA5A_MOUSE	von Willebrand fac	Mus musculus (Mouse)	Vwa5a	Evidence at protein level	793	87143			
848	Q9DBZ5	EIF3K_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif3k	Evidence at protein level	218	25087	regulation of translationa	ribosome binding [GO:00	cytosol [GO:0005829]; eu
849	Q9DB60	PGFS_MOUSE	Prostamide/prosta	Mus musculus (Mouse)	Fam213b	Evidence at protein level	201	21670	cyclooxygenase pathway	antioxidant activity [GO:(	cytoplasm [GO:0005737]
850	A2AGH6	MED12_MOUSE	Mediator of RNA p	Mus musculus (Mouse)	Med12	Evidence at protein level	2190	244561	androgen receptor signali	chromatin binding [GO:0(	mediator complex [GO:00
851	Q8BK06	FBX9_MOUSE	F-box only protein	Mus musculus (Mouse)	Fbxo9	Evidence at protein level	437	50760	fat cell differentiation [G	ubiquitin-protein transfer	cytoplasm [GO:0005737]
852	Q6PEB6	PHOCN_MOUSE	MOB-like protein p	Mus musculus (Mouse)	Mob4	Evidence at protein level	225	26032	transport [GO:0006810]	kinase binding [GO:0019	cytoplasm [GO:0005737]
853	P97310	MCM2_MOUSE	DNA replication lic	Mus musculus (Mouse)	Mcm2	Evidence at protein level	904	102078	apoptotic process [GO:00	ATP binding [GO:0005524	chromatin [GO:0000785]
854	Q08943	SSRP1_MOUSE	FACT complex subu	Mus musculus (Mouse)	Ssrp1	Evidence at protein level	708	80860	DNA repair [GO:0006281	chromatin binding [GO:0(	chromosome [GO:0005
855	P48025	KSYK_MOUSE	Tyrosine-protein ki	Mus musculus (Mouse)	Syk	Evidence at protein level	629	71376	activation of JUN kinase a	ATP binding [GO:0005524	B cell receptor complex [(
856	Q9QY76	VAPB_MOUSE	Vesicle-associated	Mus musculus (Mouse)	Vapb	Evidence at protein level	243	26946	activation of signaling pro	beta-tubulin binding [GO:	cell-cell adherens junctio
857	Q9QYJ0	DNJA2_MOUSE	DnaJ homolog subf	Mus musculus (Mouse)	Dnaja2	Evidence at protein level	412	45746	protein refolding [GO:004	ATPase activator activity	cytosol [GO:0005829]; ex
858	Q8CGY8	OGT1_MOUSE	UDP-N-acetylgluco	Mus musculus (Mouse)	Ogt	Evidence at protein level	1046	116952	apoptotic process [GO:00	catalytic activity [GO:000	cytoplasm [GO:0005737]
859	Q61166	MARE1_MOUSE	Microtubule-associ	Mus musculus (Mouse)	Mapre1	Evidence at protein level	268	30016	cell division [GO:0051301	cadherin binding involved	cell-cell adherens junctio
860	Q9D554	SF3A3_MOUSE	Splicing factor 3A s	Mus musculus (Mouse)	Sf3a3	Evidence at protein level	501	58842	mRNA processing [GO:00	RNA binding [GO:000372	catalytic step 2 spliceoso
861	Q920A5	RISC_MOUSE	Retinoid-inducible	Mus musculus (Mouse)	Scpep1	Evidence at protein level	452	50965	negative regulation of blo	serine-type carboxypepti	cytosol [GO:0005829]; ex
862	Q9CQR6	PPP6_MOUSE	Serine/threonine-p	Mus musculus (Mouse)	Ppp6c	Evidence at protein level	305	35159	cell cycle [GO:0007049];	metal ion binding [GO:00	cytosol [GO:0005829]
863	P02463	CO4A1_MOUSE	Collagen alpha-1(I	Mus musculus (Mouse)	Col4a1	Evidence at protein level	1669	160679	basement membrane org	extracellular matrix struc	basement membrane [GO
864	Q80TP3	UBR5_MOUSE	E3 ubiquitin-protei	Mus musculus (Mouse)	Ubr5	Evidence at protein level	2792	308352	cellular response to DNA	RNA binding [GO:000372	cytosol [GO:0005829]; m
865	Q6A0A9	F120A_MOUSE	Constitutive coacti	Mus musculus (Mouse)	FAM120A	Evidence at protein level	1112	121646		RNA binding [GO:000372	cytosol [GO:0005829]; m
866	Q99LJ6	GPX7_MOUSE	Glutathione peroxi	Mus musculus (Mouse)	Gpx7	Evidence at protein level	186	21061	response to oxidative stre	catalase activity [GO:000	endoplasmic reticulum [G
867	Q9CQU3	RER1_MOUSE	Protein RER1	Mus musculus (Mouse)	Rer1	Evidence at protein level	196	22988	neuromuscular junction c	acetylcholine receptor bi	cell surface [GO:0009986
868	Q9D1D4	TMEDA_MOUSE	Transmembrane er	Mus musculus (Mouse)	Tmed10	Evidence at protein level	219	24911	COPI-coated vesicle budd	syntaxin binding [GO:001	cis-Golgi network [GO:00
869	Q8BWF0	SSDH_MOUSE	Succinate-semialde	Mus musculus (Mouse)	Aldh5a1	Evidence at protein level	523	55968	acetate metabolic proces	succinate-semialdehyde	mitochondrion [GO:0005
870	Q9R0Q6	ARC1A_MOUSE	Actin-related prote	Mus musculus (Mouse)	Arpc1a	Evidence at protein level	370	41626	Arp2/3 complex-mediate	actin filament binding [G	Arp2/3 protein complex [
871	Q8CI51	PDLI5_MOUSE	PDZ and LIM doma	Mus musculus (Mouse)	Pdlim5	Evidence at protein level	591	63299	regulation of dendritic sp	cadherin binding involve	actin cytoskeleton [GO:0
872	P63024	VAMP3_MOUSE	Vesicle-associated	Mus musculus (Mouse)	Vamp3	Evidence at protein level	103	11480	calcium ion regulated exc	SNAP receptor activity [G	apical plasma membrane
873	Q62188	DPYL3_MOUSE	Dihydropyrimidina	Mus musculus (Mouse)	Dpysl3	Evidence at protein level	570	61936	actin crosslink formation	chondroitin sulfate bindir	cell body [GO:0044297];
874	Q8VHC3	SELM_MOUSE	Selenoprotein M (S	Mus musculus (Mouse)	Selenom	Evidence at protein level	145	16378	adipose tissue development	[GO:0060612]; cortico	endoplasmic reticulum [G
875	Q91WG4	ELP2_MOUSE	Elongator complex	Mus musculus (Mouse)	Elp2	Evidence at protein level	831	93093	proteasome assembly [G	endopeptidase activator	cytosol [GO:0005829]; El
876	Q8BMA6	SRP68_MOUSE	Signal recognition	Mus musculus (Mouse)	Srp68	Evidence at protein level	625	70574	protein targeting to ER [G	7S RNA binding [GO:0008	cytosol [GO:0005829]; er
877	Q9CXE7	TMED5_MOUSE	Transmembrane er	Mus musculus (Mouse)	Tmed5	Evidence at protein level	229	26172	Golgi ribbon formation [G	O:0090161]; protein tran	cis-Golgi network [GO:00
878	P97494	GSH1_MOUSE	Glutamate--cystein	Mus musculus (Mouse)	Gclc	Evidence at protein level	637	72571	aging [GO:0007568]; apo	ADP binding [GO:004353	cytosol [GO:0005829]; gl
879	P02089	HBB2_MOUSE	Hemoglobin subuni	Mus musculus (Mouse)	Hbb-b2	Evidence at protein level	147	15878	erythrocyte development	heme binding [GO:00200	hemoglobin complex [GO
880	Q9WTR5	CAD13_MOUSE	Cadherin-13 (Heart	Mus musculus (Mouse)	Cdh13	Evidence at protein level	714	78186	calcium-dependent cell-c	adiponectin binding [GO:	anchored component of r
881	P63268	ACTH_MOUSE	Actin, gamma-ente	Mus musculus (Mouse)	Actg2	Evidence at protein level	376	41877	mesenchyme migration [	ATP binding [GO:0005524	blood microparticle [GO:(
882	Q9CQJ0	ACO15_MOUSE	Acyl-coenzyme A th	Mus musculus (Mouse)	Them5	Evidence at transcript level	248	27865	cardiolipin acyl-chain rem	myristoyl-CoA hydrolase	mitochondrial matrix [GO
883	Q3V009	TMED1_MOUSE	Transmembrane er	Mus musculus (Mouse)	Tmed1	Evidence at protein level	227	25263	protein transport [GO:0015031]		endoplasmic reticulum [G
884	Q9CYR0	SSBP_MOUSE	Single-stranded DN	Mus musculus (Mouse)	Ssbp1	Evidence at protein level	152	17319	DNA replication [GO:000	chromatin binding [GO:0(	extracellular exosome [G
885	Q9CR68	UCRI_MOUSE	Cytochrome b-c1 c	Mus musculus (Mouse)	Uqcrfs1	Evidence at protein level	274	29368	response to antibiotic [G	2 iron, 2 sulfur cluster bin	mitochondrial inner mem
886	O35206	COFA1_MOUSE	Collagen alpha-1(X	Mus musculus (Mouse)	Col15a1	Evidence at protein level	1367	140472	cell adhesion [GO:00071	structural molecule activi	basement membrane [GO
887	Q9R257	HEBP1_MOUSE	Heme-binding prot	Mus musculus (Mouse)	Hebp1	Evidence at protein level	190	21067	heme metabolic process	heme binding [GO:00200	cytoplasm [GO:0005737]
888	P56380	AP4A_MOUSE	Bis(5'-nucleosyl)-te	Mus musculus (Mouse)	Nudt2	Evidence at protein level	147	16989	apoptotic process [GO:00	bis(5'-nucleosyl)-tetraph	mitochondrion [GO:0005
889	P68037	UB2L3_MOUSE	Ubiquitin-conjugati	Mus musculus (Mouse)	Ube2l3	Evidence at protein level	154	17862	cell cycle phase transition	ATP binding [GO:0005524	cytoplasm [GO:0005737]
890	P59017	B2L13_MOUSE	Bcl-2-like protein 1	Mus musculus (Mouse)	Bcl2l13	Evidence at protein level	434	46719	apoptotic process [GO:0006915];	regulation of apo	integral component of m
891	Q8VE97	SRSF4_MOUSE	Serine/arginine-ric	Mus musculus (Mouse)	Srsf4	Evidence at transcript level	489	55979	hematopoietic progenitor	nucleotide binding [GO:0	nuclear speck [GO:00166
892	Q8VDM6	HNRL1_MOUSE	Heterogeneous nu	Mus musculus (Mouse)	Hnrnpul1	Evidence at protein level	859	96002	regulation of transcriptio	enzyme binding [GO:001	intracellular ribonucleopr
893	Q9DC70	NDUS7_MOUSE	NADH dehydrogen	Mus musculus (Mouse)	Ndufs7	Evidence at protein level	224	24683	mitochondrial respiratory	4 iron, 4 sulfur cluster bin	mitochondrial inner mem
894	O08796	EF2K_MOUSE	Eukaryotic elongati	Mus musculus (Mouse)	Eef2k	Evidence at protein level	724	81739	cellular response to anox	ATP binding [GO:0005524	cytoplasm [GO:0005737]
895	Q9CZ30	OLA1_MOUSE	Obg-like ATPase 1 (	Mus musculus (Mouse)	Ola1	Evidence at protein level	396	44730	ATP metabolic process [G	ATPase activity [GO:0016	cell-cell adherens junctio
896	O08788	DCTN1_MOUSE	Dynactin subunit 1	Mus musculus (Mouse)	Dctn1	Evidence at protein level	1281	141676	centriole-centriole cohesi	microtubule binding [GO:	actin cytoskeleton [GO:0
897	O89112	LANC1_MOUSE	LanC-like protein 1	Mus musculus (Mouse)	Lancl1	Evidence at protein level	399	45341	signal transduction [GO:0	catalytic activity [GO:000	cytoplasm [GO:0005737]
898	P56959	FUS_MOUSE	RNA-binding protei	Mus musculus (Mouse)	Fus	Evidence at protein level	518	52673	cellular response to calci	DNA binding [GO:000367	cytoplasm [GO:0005737]
899	Q61545	EWS_MOUSE	RNA-binding protei	Mus musculus (Mouse)	Ewsr1	Evidence at protein level	655	68462	regulation of transcriptio	nucleotide binding [GO:0	cytoplasm [GO:0005737]
900	Q0GA42	CNNM1_MOUSE	Metal transporter (	Mus musculus (Mouse)	Cnnm1	Evidence at protein level	951	103980	ion transport [GO:0006811]		integral component of m
901	P52825	CPT2_MOUSE	Carnitine O-palmit	Mus musculus (Mouse)	Cpt2	Evidence at protein level	658	73981	fatty acid metabolic proc	carnitine O-palmitoyltran	mitochondrial inner mem
902	Q3U487	HECD3_MOUSE	E3 ubiquitin-protei	Mus musculus (Mouse)	Hectd3	Evidence at protein level	861	97347	proteasome-mediated ub	syntaxin binding [GO:001	perinuclear region of cytc
903	Q9ZDX1	AIFM1_MOUSE	Apoptosis-inducing	Mus musculus (Mouse)	Aifm1	Evidence at protein level	612	66765	activation of cysteine-typ	DNA binding [GO:000367	cytoplasm [GO:0005737]
904	P06801	MAOX_MOUSE	NADP-dependent n	Mus musculus (Mouse)	Me1	Evidence at protein level	572	63954	malate metabolic process	malate dehydrogenase (d	cytosol [GO:0005829]; m
905	Q9JI10	STK3_MOUSE	Serine/threonine-p	Mus musculus (Mouse)	Stk3	Evidence at protein level	497	56855	cell differentiation involv	ATP binding [GO:0005524	cytoplasm [GO:0005737]
906	Q3TLP5	ECHD2_MOUSE	Enoyl-CoA hydrata	Mus musculus (Mouse)	Echdc2	Evidence at protein level	296	31852	fatty acid beta-oxidation	enoyl-CoA hydratase acti	mitochondrion [GO:0005
907	Q9R0M3	SRPX_MOUSE	Sushi-repeat-conta	Mus musculus (Mouse)	Srpx	Evidence at transcript level	464	51574	autophagy [GO:0006914];	negative regulation of ce	autophagosome [GO:000
908	Q9DBL9	ABHD5_MOUSE	1-acylglycerol-3-ph	Mus musculus (Mouse)	Abhd5	Evidence at protein level	351	39155	cell differentiation [GO:0(	1-acylglycerol-3-phospha	cytosol [GO:0005829]; lip
909	Q60817	NACA_MOUSE	Nascent polypeptic	Mus musculus (Mouse)	Naca	Evidence at protein level	215	23384	cardiac ventricle develop	DNA binding [GO:000367	cytoplasm [GO:0005737]
910	Q9CR67	TMM33_MOUSE	Transmembrane pr	Mus musculus (Mouse)	Tmem33	Evidence at protein level	247	28031	cellular protein localizatic	structural constituent of	endoplasmic reticulum [G
911	Q8K2T1	NMRL1_MOUSE	NmrA-like family d	Mus musculus (Mouse)	Nmral1	Evidence at protein level	309	34376			nucleus [GO:0005634]; p
912	Q9CPV4	GLOD4_MOUSE	Glyoxalase domain	Mus musculus (Mouse)	Glod4	Evidence at protein level	298	33317		cadherin binding involve	cell-cell adherens junctio
913	P29416	HEXA_MOUSE	Beta-hexosaminida	Mus musculus (Mouse)	Hexa	Evidence at protein level	528	60613	adult walking behavior [G	acetylglucosaminyltransf	azurophil granule [GO:00
914	Q5FWK3	RHG01_MOUSE	Rho GTPase-activa	Mus musculus (Mouse)	Arhgap1	Evidence at protein level	439	50411	regulation of GTPase acti	cadherin binding involve	cell-cell adherens junctio
915	Q9CR57	RL14_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl14	Evidence at protein level	217	23564	ribosomal large subunit b	cadherin binding involve	cell-cell adherens junctio
916	Q9JIW9	RALB_MOUSE	Ras-related protein	Mus musculus (Mouse)	Ralb	Evidence at protein level	206	23349	apoptotic process [GO:00	ATPase binding [GO:0051	autophagosome [GO:000
917	Q8C2Q3	RBM14_MOUSE	RNA-binding protei	Mus musculus (Mouse)	Rbm14	Evidence at protein level	669	69449	centriole assembly [GO:0	ligand-dependent nuclear	cytoplasm [GO:0005737]
918	Q8VCN5	CGL_MOUSE	Cystathionine gam	Mus musculus (Mouse)	Cth	Evidence at protein level	398	43567	'de novo' L-methionine bi	cystathionine gamma-lya	cytoplasm [GO:0005737]
919	P50136	ODBA_MOUSE	2-oxoisovalerate de	Mus musculus (Mouse)	Bckdha	Evidence at protein level	442	50371	branched-chain amino ac	3-methyl-2-oxobutanoat	mitochondrial alpha-keto
920	Q8K1M6	DNM1L_MOUSE	Dynamin-1-like pro	Mus musculus (Mouse)	Dnm1l	Evidence at protein level	742	82658	cellular response to oxyge	GTPase activity [GO:0003	brush border [GO:00059
921	Q9JLJ5	ELOV1_MOUSE	Elongation of very l	Mus musculus (Mouse)	Elovl1	Evidence at protein level	279	32678	fatty acid elongation, mo	3-oxo-arachidoyl-CoA syn	endoplasmic reticulum [G
922	O35855	BCAT2_MOUSE	Branched-chain-am	Mus musculus (Mouse)	Bcat2	Evidence at protein level	393	44127	branched-chain amino ac	branched-chain-amino-ac	mitochondrion [GO:0005
923	P23953	EST1C_MOUSE	Carboxylesterase 1	Mus musculus (Mouse)	Ces1c	Evidence at protein level	554	61056		carboxylic ester hydrolas	endoplasmic reticulum lu
924	Q9JKR6	HYOU1_MOUSE	Hypoxia up-regulat	Mus musculus (Mouse)	Hyou1	Evidence at protein level	999	111181	cellular response to hypo	ATP binding [GO:0005524	endoplasmic reticulum ch
925	Q6NSR8	PEPL1_MOUSE	Probable aminopep	Mus musculus (Mouse)	Npepl1	Evidence at protein level	524	55940		aminopeptidase activity [	cytoplasm [GO:0005737]
926	Q921T2	TOIP1_MOUSE	Torsin-1A-interacti	Mus musculus (Mouse)	Tor1aip1	Evidence at protein level	595	66781	nuclear membrane organ	ATPase activator activity	integral component of m
927	Q9QYB1	CLIC4_MOUSE	Chloride intracellul	Mus musculus (Mouse)	Clic4	Evidence at protein level	253	28729	angiogenesis [GO:000152	chloride channel activity	apical part of cell [GO:00
928	Q8VCA8	SCRN2_MOUSE	Secernin-2	Mus musculus (Mouse)	Scrn2	Evidence at protein level	425	46601	exocytosis [GO:0006887]	dipeptidase activity [GO:(	extracellular exosome [G
929	Q62219	TGFI1_MOUSE	Transforming grow	Mus musculus (Mouse)	Tgfb1i1	Evidence at protein level	461	50101	cell fate commitment [GO	androgen receptor bindin	cytoplasm [GO:0005737]
930	P56135	ATPK_MOUSE	ATP synthase subu	Mus musculus (Mouse)	Atp5j2	Evidence at protein level	88	10344	ATP biosynthetic process	ATPase activity [GO:0016	extracellular exosome [G
931	P57759	ERP29_MOUSE	Endoplasmic reticu	Mus musculus (Mouse)	Erp29	Evidence at protein level	262	28823	activation of MAPK activity	[GO:0000187]; ER to Gc	cell surface [GO:0009986

932	Q9JIF0	ANM1_MOUSE	Protein arginine N-	Mus musculus (Mouse)	Prmt1	Evidence at protein level	371	42436	histone H4-R3 methylatic	[cytochrome c]-arginine !	cytosol [GO:0005829]; m
933	P63028	TCTP_MOUSE	Translationally-con	Mus musculus (Mouse)	Tpt1	Evidence at protein level	172	19462	cell differentiation [GO:0	calcium ion binding [GO:(	cytoplasm [GO:0005737]
934	Q9WUA3	PFKAP_MOUSE	ATP-dependent 6-p	Mus musculus (Mouse)	Pfkp	Evidence at protein level	784	85455	fructose 6-phosphate me	6-phosphofructokinase a	6-phosphofructokinase c
935	Q8BHL8	PSMF1_MOUSE	Proteasome inhibit	Mus musculus (Mouse)	Psmf1	Evidence at protein level	271	29664	negative regulation of pr	proteasome binding [GO:	cytosol [GO:0005829]; er
936	P36993	PPM1B_MOUSE	Protein phosphata	Mus musculus (Mouse)	Ppm1b	Evidence at protein level	390	42795	negative regulation of de	magnesium ion binding [(	cytosol [GO:0005829]; m
937	Q9DCD0	6PGD_MOUSE	6-phosphogluconat	Mus musculus (Mouse)	Pgd	Evidence at protein level	483	53247	D-gluconate metabolic pr	phosphogluconate dehyd	cytoplasm [GO:0005737]
938	P97298	PEDF_MOUSE	Pigment epithelium	Mus musculus (Mouse)	Serpinf1	Evidence at protein level	417	46234	aging [GO:0007568]; cell	serine-type endopeptidas	axon hillock [GO:004320
939	Q3TAS6	EMC10_MOUSE	ER membrane prot	Mus musculus (Mouse)	Emc10	Evidence at transcript level	258	27053			ER membrane protein co
940	Q9DD59	HINT2_MOUSE	Histidine triad nucl	Mus musculus (Mouse)	Hint2	Evidence at protein level	163	17320	apoptotic process [GO:00	hydrolase activity [GO:00	mitochondrion [GO:0005
941	Q501J6	DDX17_MOUSE	Probable ATP-depe	Mus musculus (Mouse)	Ddx17	Evidence at protein level	650	72399	alternative mRNA splicing	ATP binding [GO:0005524	membrane [GO:0016020
942	P39447	ZO1_MOUSE	Tight junction prote	Mus musculus (Mouse)	Tjp1	Evidence at protein level	1745	194742	blastocyst formation [GO	cadherin binding involved	adherens junction [GO:0
943	P58660	CAR10_MOUSE	Caspase recruitmer	Mus musculus (Mouse)	Card10	Evidence at protein level	1021	114414	activation of NF-kappaB-inducing kinase activity [G		intracellular [GO:000562
944	Q9CQ65	MTAP_MOUSE	S-methyl-5'-thioad	Mus musculus (Mouse)	Mtap	Evidence at protein level	283	31062	L-methionine salvage fro	S-methyl-5-thioadenosin	cytosol [GO:0005829]; ex
945	Q6EDY6	CARL1_MOUSE	F-actin-uncapping p	Mus musculus (Mouse)	Carmil1	Evidence at protein level	1374	151860	actin filament network fo	protein complex binding [	cell leading edge [GO:003
946	Q9CSU0	RPR1B_MOUSE	Regulation of nucle	Mus musculus (Mouse)	Rprd1b	Evidence at protein level	326	36884	dephosphorylation of RN	RNA polymerase II core b	centrosome [GO:000581
947	Q99MN9	PCCB_MOUSE	Propionyl-CoA carb	Mus musculus (Mouse)	Pccb	Evidence at protein level	541	58409		ATP binding [GO:0005524	mitochondrial matrix [GO
948	P62858	RS28_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps28	Evidence at protein level	69	7841	maturation of SSU-rRNA	RNA binding [GO:000372	cytosolic small ribosomal
949	P16388	KCNA1_MOUSE	Potassium voltage-	Mus musculus (Mouse)	Kcna1	Evidence at protein level	495	56409	brain development [GO:0	delayed rectifier potassiu	apical plasma membrane
950	Q9D7X3	DUS3_MOUSE	Dual specificity pro	Mus musculus (Mouse)	Dusp3	Evidence at protein level	185	20472	dephosphorylation [GO:0	MAP kinase phosphatase	cytosol [GO:0005829]; ex
951	Q99JY8	PLPP3_MOUSE	Phospholipid phosp	Mus musculus (Mouse)	Plpp3	Evidence at protein level	312	35216	Bergmann glial cell differ	integrin binding [GO:000	endoplasmic reticulum m
952	Q7TSG2	CTDP1_MOUSE	RNA polymerase II	Mus musculus (Mouse)	Ctdp1	Evidence at protein level	960	104554	cell division [GO:0051301	CTD phosphatase activity	actin cytoskeleton [GO:0
953	Q9ZI8	SUCB2_MOUSE	Succinate--CoA liga	Mus musculus (Mouse)	Suclg2	Evidence at protein level	433	46840	succinate metabolic proc	ATP binding [GO:0005524	mitochondrion [GO:0005
954	O35381	AN32A_MOUSE	Acidic leucine-rich	Mus musculus (Mouse)	Anp32a	Evidence at protein level	247	28538	regulation of transcription,	DNA-templated [GO:000	cytoplasm [GO:0005737]
955	P62315	SMD1_MOUSE	Small nuclear ribon	Mus musculus (Mouse)	Snrpd1	Evidence at protein level	119	13282	spliceosomal complex ass	RNA binding [GO:000372	catalytic step 2 spliceoso
956	Q70FJ1	AKAP9_MOUSE	A-kinase anchor pr	Mus musculus (Mouse)	Akap9	Evidence at protein level	3797	436214	microtubule nucleation [GO:0007020]; Sertoli cell d		centrosome [GO:000581
957	O35887	CALU_MOUSE	Calumenin (Crocalt	Mus musculus (Mouse)	Calu	Evidence at protein level	315	37064	platelet degranulation [G	calcium ion binding [GO:(	endoplasmic reticulum [G
958	Q571B6	WHAMM_MOUSE	WASP homolog-ass	Mus musculus (Mouse)	Whamm	Evidence at protein level	793	88997	actin filament organizatic	Arp2/3 complex binding [	cytoplasmic vesicle mem
959	P08730	K1C13_MOUSE	Keratin, type I cyto	Mus musculus (Mouse)	Krt13	Evidence at protein level	437	47754	cellular response to retin	structural molecule activi	extracellular exosome [G
960	Q9Z1T6	FYV1_MOUSE	1-phosphatidylinos	Mus musculus (Mouse)	Pikfyve	Evidence at protein level	2097	236877	intracellular signal transd	1-phosphatidylinositol-3-	cell-cell junction [GO:000
961	Q9WVL2	STAT2_MOUSE	Signal transducer a	Mus musculus (Mouse)	Stat2	Evidence at protein level	923	105417	defense response to virus	DNA binding [GO:000367	cytoplasm [GO:0005737]
962	Q9Z1D1	EIF3G_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif3g	Evidence at protein level	320	35638	translational initiation [G	nucleotide binding [GO:0	cytoplasm [GO:0005737]
963	Q99LR1	ABD12_MOUSE	Monoacylglycerol l	Mus musculus (Mouse)	Abhd12	Evidence at protein level	398	45270	acylglycerol catabolic pro	acylglycerol lipase activit	AMPA glutamate recepto
964	P47964	RL36_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl36	Inferred from homology	105	12216	cytoplasmic translation [(	structural constituent of	cytosolic large ribosomal
965	P54285	CACB3_MOUSE	Voltage-dependent	Mus musculus (Mouse)	Cacnb3	Evidence at protein level	484	54572	calcium ion transmembra	high voltage-gated calciu	apical plasma membrane
966	Q9QUI0	RHOA_MOUSE	Transforming prote	Mus musculus (Mouse)	Rhoa	Evidence at protein level	193	21782	actin cytoskeleton organi	GDP binding [GO:001900	apical junction complex [(
967	Q6ZWY6	U2D2B_MOUSE	Ubiquitin-conjugati	Mus musculus (Mouse)	Ube2d2b	Evidence at protein level	147	16659	protein K11-linked ubiqui	ATP binding [GO:0005524];	ubiquitin-protein transf
968	Q99020	ROAA_MOUSE	Heterogeneous nuc	Mus musculus (Mouse)	Hnrnpab	Evidence at protein level	285	30831	epithelial to mesenchyma	DNA binding [GO:000367	cytoplasm [GO:0005737]
969	Q8BK48	EST2E_MOUSE	Pyrethroid hydrola	Mus musculus (Mouse)	Ces2e	Evidence at protein level	559	62318		carboxylic ester hydrolas	endoplasmic reticulum [G
970	Q99K01	PDXD1_MOUSE	Pyridoxal-depende	Mus musculus (Mouse)	Pdxdc1	Evidence at protein level	787	87335	carboxylic acid metabolic	cadherin binding involved	cell-cell adherens junctio
971	Q6ZWQ0	SYNE2_MOUSE	Nesprin-2 (KASH d	Mus musculus (Mouse)	Syne2	Evidence at protein level	6874	782725	centrosome localization [	actin binding [GO:000377	aggresome [GO:0016235
972	Q9QYG0	NDRG2_MOUSE	Protein NDRG2 (N-	Mus musculus (Mouse)	Ndrg2	Evidence at protein level	371	40789	cell differentiation [GO:0030154]; negative regulati		cytoplasm [GO:0005737]
973	Q8BRF7	SCFD1_MOUSE	Sec1 family domair	Mus musculus (Mouse)	Scfd1	Evidence at protein level	639	72323	cell morphogenesis [GO:0000902]; negative regulat		cis-Golgi network [GO:00
974	P27931	IL1R2_MOUSE	Interleukin-1 recep	Mus musculus (Mouse)	Il1r2	Evidence at protein level	410	45645	negative regulation of cyt	interleukin-1, Type II, blo	cytoplasm [GO:0005737]
975	P68181	KAPCB_MOUSE	cAMP-dependent p	Mus musculus (Mouse)	Prkacb	Evidence at protein level	351	40708	adenylate cyclase-modul	ATP binding [GO:0005524	cAMP-dependent protein
976	Q922P9	GLYR1_MOUSE	Putative oxidoredu	Mus musculus (Mouse)	Glyr1	Evidence at protein level	546	59716		DNA binding [GO:000367	cytosol [GO:0005829]; Go
977	Q9D154	ILEUA_MOUSE	Leukocyte elastase	Mus musculus (Mouse)	Serpinb1a	Evidence at protein level	379	42575	regulation of protein cata	serine-type endopeptidas	cytoplasm [GO:0005737]
978	P68433	H31_MOUSE	Histone H3.1	Mus musculus (Mouse)	Hist1h3a; Hist1	Evidence at protein level	136	15404	chromatin silencing at rD	cadherin binding involved	cell-cell adherens junctio
979	O35286	DHX15_MOUSE	Pre-mRNA-splicing	Mus musculus (Mouse)	Dhx15	Evidence at protein level	795	91007	mRNA splicing, via splice	ATP binding [GO:0005524	cytoplasm [GO:0005737]
980	Q99M31	HSP7E_MOUSE	Heat shock 70 kDa	Mus musculus (Mouse)	Hspa14	Evidence at protein level	509	54650		ATP binding [GO:0005524	cytosol [GO:0005829]; m
981	Q8R4A3	DACT1_MOUSE	Dapper homolog 1	Mus musculus (Mouse)	Dact1	Evidence at protein level	778	84306	dendrite morphogenesis [	beta-catenin binding [GO	cell junction [GO:003005
982	Q9QZZ6	DERM_MOUSE	Dermatopontin (Ea	Mus musculus (Mouse)	Dpt	Evidence at protein level	201	23995	cell adhesion [GO:0007155]; collagen fibril organiza		extracellular exosome [G
983	P47945	MT4_MOUSE	Metallothionein-4	Mus musculus (Mouse)	Mt4	Evidence at transcript level	62	6277	cellular metal ion homeo	metal ion binding [GO:00	cytosol [GO:0005829]
984	P62311	LSM3_MOUSE	U6 snRNA-associat	Mus musculus (Mouse)	Lsm3	Evidence at protein level	102	11845	cytoplasmic mRNA proce	RNA binding [GO:000372	catalytic step 2 spliceoso
985	Q8VED9	LEGL_MOUSE	Galectin-related pr	Mus musculus (Mouse)	Lgalsl	Evidence at protein level	172	18956		carbohydrate binding [GC	intracellular [GO:000562
986	P09055	ITB1_MOUSE	Integrin beta-1 (Fib	Mus musculus (Mouse)	Itgb1	Evidence at protein level	798	88231	axon extension [GO:0048	actin binding [GO:000377	cell-cell adherens junctio
987	Q9D8C2	TSN13_MOUSE	Tetraspanin-13 (Ts	Mus musculus (Mouse)	Tspan13	Evidence at protein level	204	22219	cell surface receptor sign	calcium channel regulato	integral component of pla
988	Q9D6J5	NDUB8_MOUSE	NADH dehydrogen	Mus musculus (Mouse)	Ndufb8	Evidence at protein level	186	21876	mitochondrial electron tr	NADH dehydrogenase (ut	endoplasmic reticulum [G
989	Q99LF4	RTCB_MOUSE	tRNA-splicing ligas	Mus musculus (Mouse)	Rtcb	Evidence at protein level	505	55249	in utero embryonic devel	ATP binding [GO:0005524	cytoplasm [GO:0005737]
990	Q8VCW8	ACSF2_MOUSE	Acyl-CoA synthetas	Mus musculus (Mouse)	Acsf2	Evidence at protein level	615	67951	fatty acid metabolic proc	ATP binding [GO:0005524	mitochondrion [GO:0005
991	Q80SW1	SAHH2_MOUSE	Putative adenosylh	Mus musculus (Mouse)	Ahcyl1	Evidence at protein level	530	58951	angiotensin-activated sig	hydrolase activity [GO:00	apical plasma membrane
992	P08122	CO4A2_MOUSE	Collagen alpha-2(IV	Mus musculus (Mouse)	Col4a2	Evidence at protein level	1707	167325	angiogenesis [GO:000152	extracellular matrix struc	basement membrane [GO
993	Q6DIC0	SMCA2_MOUSE	Probable global tra	Mus musculus (Mouse)	Smarca2	Evidence at protein level	1577	180253	aortic smooth muscle cel	ATPase activity [GO:0016	BAF-type complex [GO:00
994	Q791V5	MTCH2_MOUSE	Mitochondrial carri	Mus musculus (Mouse)	Mtch2	Evidence at protein level	303	33499	cellular response to radiation [GO:0071478]; establ		extracellular exosome [G
995	Q99LN9	DOHH_MOUSE	Deoxyhypusine hyc	Mus musculus (Mouse)	Dohh	Evidence at protein level	302	32905	peptidyl-lysine modificati	deoxyhypusine monooxygenase activity [GO:00191	
996	Q9QXK7	CPSF3_MOUSE	Cleavage and polya	Mus musculus (Mouse)	Cpsf3	Evidence at protein level	684	77505	mRNA 3'-end processing	5'-3' exonuclease activity	intracellular ribonucleopr
997	Q8C570	RAE1L_MOUSE	mRNA export facto	Mus musculus (Mouse)	Rae1	Evidence at protein level	368	40965	cellular response to orgar	RNA binding [GO:000372	cytoplasm [GO:0005737]
998	Q9ERD7	TBB3_MOUSE	Tubulin beta-3 chai	Mus musculus (Mouse)	Tubb3	Evidence at protein level	450	50419	axon guidance [GO:0007	GTPase activity [GO:0003	axon [GO:0030424]; cell p
999	Q05144	RAC2_MOUSE	Ras-related C3 bot	Mus musculus (Mouse)	Rac2	Evidence at protein level	192	21441	actin cytoskeleton organi	GTPase activity [GO:0003	actin filament [GO:00058
1000	P31428	DPEP1_MOUSE	Dipeptidase 1 (EC 3	Mus musculus (Mouse)	Dpep1	Evidence at protein level	410	45722	antibiotic metabolic proc	cysteine-type endopeptid	anchored component of r
1001	Q9DBX3	SUSD2_MOUSE	Sushi domain-cont	Mus musculus (Mouse)	Susd2	Evidence at protein level	820	90641	immune response [GO:0	polysaccharide binding [G	extracellular exosome [G
1002	Q3U541	ESRP1_MOUSE	Epithelial splicing r	Mus musculus (Mouse)	Esrp1	Evidence at protein level	680	75549	alternative mRNA splicing	mRNA binding [GO:0003	nuclear body [GO:00166
1003	Q8R0G9	NU133_MOUSE	Nuclear pore comp	Mus musculus (Mouse)	Nup133	Evidence at protein level	1155	128620	chromatin organization [(	nucleocytoplasmic transp	condensed chromosome
1004	P62309	RUXG_MOUSE	Small nuclear ribon	Mus musculus (Mouse)	Snrpg	Evidence at protein level	76	8496	mRNA splicing, via splice	RNA binding [GO:000372	catalytic step 2 spliceoso
1005	Q0PHV7	DACT3_MOUSE	Dapper homolog 3	Mus musculus (Mouse)	Dact3	Evidence at protein level	610	63287	negative regulation of car	beta-catenin binding [GO	cytoplasm [GO:0005737]
1006	P42669	PURA_MOUSE	Transcriptional acti	Mus musculus (Mouse)	Pura	Evidence at protein level	321	34884	apoptotic process [GO:00	DNA binding [GO:000367	cytoplasm [GO:0005737]
1007	Q6A0A2	LAR4B_MOUSE	La-related protein 4	Mus musculus (Mouse)	Larp4b	Evidence at protein level	741	81627	positive regulation of trar	nucleotide binding [GO:0	cytoplasmic stress granul
1008	Q9QZ06	TOLIP_MOUSE	Toll-interacting pro	Mus musculus (Mouse)	Tollip	Evidence at protein level	274	30345	autophagy [GO:0006914]	kinase binding [GO:0019	cytoplasm [GO:0005737]
1009	Q9D892	ITPA_MOUSE	Inosine triphosphat	Mus musculus (Mouse)	Itpa	Evidence at protein level	198	21897	chromosome organizatio	dITP diphosphatase activi	cytoplasm [GO:0005737]
1010	Q9Z2M7	PMM2_MOUSE	Phosphomannomu	Mus musculus (Mouse)	Pmm2	Evidence at protein level	242	27657	GDP-mannose biosynthet	phosphomannomutase a	cytoplasm [GO:0005737]
1011	Q04447	KCRB_MOUSE	Creatine kinase B-t	Mus musculus (Mouse)	Ckb	Evidence at protein level	381	42713	cellular chloride ion home	ATP binding [GO:0005524	cytosol [GO:0005829]; de
1012	P97384	ANX11_MOUSE	Annexin A11 (Anne	Mus musculus (Mouse)	Anxa11	Evidence at protein level	503	54079	cell cycle [GO:0007049]; (	calcium-dependent phos	azurophil granule [GO:00
1013	P35278	RAB5C_MOUSE	Ras-related protein	Mus musculus (Mouse)	Rab5c	Evidence at protein level	216	23413	endosome organization [(	GDP binding [GO:001900	early endosome [GO:000
1014	Q8R4R6	NUP53_MOUSE	Nucleoporin NUP5	Mus musculus (Mouse)	Nup35	Evidence at protein level	325	34786	mRNA transport [GO:005	nucleocytoplasmic transp	nuclear membrane [GO:0
1015	Q91VA6	PDIP2_MOUSE	Polymerase delta-i	Mus musculus (Mouse)	Poldip2	Evidence at protein level	368	41870	mitochondrion morphoge	DNA binding [GO:000367	mitochondrial nucleoid [G
1016	Q3V1I0	LYG2_MOUSE	Lysozyme g-like pro	Mus musculus (Mouse)	Lyg2	Evidence at transcript level	213	23762	cell wall macromolecule (	lysozyme activity [GO:00	extracellular region [GO:0
1017	Q8BH59	CMC1_MOUSE	Calcium-binding mi	Mus musculus (Mouse)	Slc25a12	Evidence at protein level	677	74570	aspartate transport [GO:(	calcium ion binding [GO:(	integral component of me
1018	Q9QXX4	CMC2_MOUSE	Calcium-binding mi	Mus musculus (Mouse)	Slc25a13	Evidence at protein level	676	74467	aspartate transport [GO:(	calcium ion binding [GO:(	integral component of me
1019	Q99JF8	PSIP1_MOUSE	PC4 and SFRS1-inte	Mus musculus (Mouse)	Psip1	Evidence at protein level	528	59697	mRNA 5'-splice site recog	activating transcription fa	nuclear heterochromatin
1020	Q8K3I9	GLCI1_MOUSE	Glucocorticoid-ind	Mus musculus (Mouse)	Glcci1	Evidence at protein level	537	57479			cytoplasm [GO:0005737]
1021	P59235	NUP43_MOUSE	Nucleoporin Nup4	Mus musculus (Mouse)	Nup43	Evidence at protein level	380	41990	cell division [GO:0051301]; chromosome segregatic		condensed chromosome
1022	P36552	HEM6_MOUSE	Oxygen-dependent	Mus musculus (Mouse)	Cpox	Evidence at protein level	443	49715	heme biosynthetic proce	coproporphyrinogen oxid	cytosol [GO:0005829]; m
1023	Q91YP3	DEOC_MOUSE	Deoxyribose-phosp	Mus musculus (Mouse)	Dera	Evidence at protein level	318	34975	carbohydrate catabolic pr	deoxyribose-phosphate a	cytoplasm [GO:0005737]
1024	Q3U1J4	DDB1_MOUSE	DNA damage-bindi	Mus musculus (Mouse)	Ddb1	Evidence at protein level	1140	126853	histone H2A monoubiquit	damaged DNA binding [G	Cul4A-RING E3 ubiquitin l
1025	Q8QZZ7	TPRKB_MOUSE	EKC/KEOPS comple	Mus musculus (Mouse)	Tprkb	Evidence at protein level	175	19556	tRNA processing [GO:000	protein kinase binding [G	cytosol [GO:0005829]; nu
1026	P46978	STT3A_MOUSE	Dolichyl-diphospho	Mus musculus (Mouse)	Stt3a	Evidence at protein level	705	80598	co-translational protein n	dolichyl-diphosphooligos	integral component of me
1027	P47746	CNR1_MOUSE	Cannabinoid recep	Mus musculus (Mouse)	Cnr1	Evidence at protein level	473	52831	adenylate cyclase-modul	cannabinoid receptor act	actin cytoskeleton [GO:0
1028	Q80UF7	TCAM1_MOUSE	TIR domain-contair	Mus musculus (Mouse)	Ticam1	Evidence at protein level	732	79230	apoptotic signaling pathw	protein kinase binding [G	autophagosome [GO:000
1029	Q91VE0	S27A4_MOUSE	Long-chain fatty ac	Mus musculus (Mouse)	Slc27a4	Evidence at protein level	643	72319	fatty acid metabolic proc	long-chain fatty acid-CoA	brush border membrane
1030	Q9EQH3	VPS35_MOUSE	Vacuolar protein sc	Mus musculus (Mouse)	Vps35	Evidence at protein level	796	91713	lysosome organization [G	D1 dopamine receptor bi	cytoplasm [GO:0005737]
1031	Q64481	CP3AG_MOUSE	Cytochrome P450 3	Mus musculus (Mouse)	Cyp3a16	Evidence at transcript level	504	57870		aromatase activity [GO:0	endoplasmic reticulum m
1032	P23591	FCL_MOUSE	GDP-L-fucose synt	Mus musculus (Mouse)	Tsta3	Evidence at protein level	321	35878	'de novo' GDP-L-fucose b	coenzyme binding [GO:0(	extracellular exosome [G
1033	Q9DCG9	TR112_MOUSE	Multifunctional me	Mus musculus (Mouse)	Trmt112	Evidence at protein level	125	14141	peptidyl-glutamine meth	protein methyltransferas	extracellular exosome [G
1034	Q8CHY6	P66A_MOUSE	Transcriptional rep	Mus musculus (Mouse)	Gatad2a	Evidence at protein level	629	67334	anterior neuropore closur	metal ion binding [GO:00	nuclear speck [GO:00166
1035	P48962	ADT1_MOUSE	ADP/ATP transloca	Mus musculus (Mouse)	Slc25a4	Evidence at protein level	298	32904	apoptotic mitochondrial (	ATP:ADP antiporter activi	integral component of me
1036	Q62452	UD19_MOUSE	UDP-glucuronosylt	Mus musculus (Mouse)	Ugt1a9	Evidence at protein level	528	60008	xenobiotic glucuronidatio	drug binding [GO:000814	endoplasmic reticulum [G
1037	Q921G7	ETFD_MOUSE	Electron transfer fl	Mus musculus (Mouse)	Etfdh	Evidence at protein level	616	68091	electron transport chain [	4 iron, 4 sulfur cluster bir	integral component of mi
1038	P36916	GNL1_MOUSE	Guanine nucleotide	Mus musculus (Mouse)	Gnl1	Evidence at protein level	607	68771	cellular response to DNA	GTP binding [GO:0005525	nucleus [GO:0005634]
1039	P02469	LAMB1_MOUSE	Laminin subunit be	Mus musculus (Mouse)	Lamb1	Evidence at protein level	1786	197090	axon guidance [GO:0007	enzyme binding [GO:001	basal lamina [GO:000560
1040	Q8VEM8	MPCP_MOUSE	Phosphate carrier p	Mus musculus (Mouse)	Slc25a3	Evidence at protein level	357	39632	mitochondrial transport [	phosphate ion transmem	extracellular exosome [G
1041	Q91VW3	SH3L3_MOUSE	SH3 domain-bindin	Mus musculus (Mouse)	Sh3bgrl3	Evidence at protein level	93	10477	cell redox homeostasis [G	electron carrier activity [(	cytoplasm [GO:0005737]
1042	Q9CZA6	NDE1_MOUSE	Nuclear distributio	Mus musculus (Mouse)	Nde1	Evidence at protein level	344	38523	cell division [GO:0051301	identical protein binding [	centrosome [GO:000581
1043	Q925I1	ATAD3_MOUSE	ATPase family AAA	Mus musculus (Mouse)	Atad3	Evidence at protein level	591	66742	cell growth [GO:0016049	ATP binding [GO:0005524	integral component of me
1044	Q8R1F5	HYI_MOUSE	Putative hydroxypy	Mus musculus (Mouse)	Hyi	Evidence at protein level	277	30449		hydroxypyruvate isomerase activity [GO:0008903]	
1045	Q8BY87	UBP47_MOUSE	Ubiquitin carboxyl-	Mus musculus (Mouse)	Usp47	Evidence at protein level	1376	157455	base-excision repair [GO:	thiol-dependent ubiquitin	cytoplasm [GO:0005737]
1046	P15864	H12_MOUSE	Histone H1.2 (H1 V	Mus musculus (Mouse)	Hist1h1c	Evidence at protein level	212	21267	histone H3-K27 trimethyl	chromatin DNA binding [(	nuclear euchromatin [GO
1047	Q8VHE6	DYH5_MOUSE	Dynein heavy chair	Mus musculus (Mouse)	Dnah5	Evidence at protein level	4621	527558	cilium assembly [GO:006	ATPase activity [GO:0016	axonemal dynein comple
1048	Q7TPR4	ACTN1_MOUSE	Alpha-actinin-1 (Al	Mus musculus (Mouse)	Actn1	Evidence at protein level	892	103068	actin crosslink formation	actin filament binding [G	actin filament [GO:00058

1049	O55022	PGRC1_MOUSE	Membrane-associa	Mus musculus (Mouse)	Pgrmc1	Evidence at protein level	195	21694		heme binding [GO:00200	endomembrane system [
1050	P14152	MDHC_MOUSE	Malate dehydroger	Mus musculus (Mouse)	Mdh1	Evidence at protein level	334	36511	carbohydrate metabolic p	L-malate dehydrogenase	cytosol [GO:0005829]; ex
1051	P58771	TPM1_MOUSE	Tropomyosin alpha	Mus musculus (Mouse)	Tpm1	Evidence at protein level	284	32681	actin filament organizatio	actin filament binding [G	bleb [GO:0032059]; cytop
1052	Q6PGN1	ERFE_MOUSE	Erythroferrone (Co	Mus musculus (Mouse)	Erfe	Evidence at protein level	340	36265	cellular iron ion homeosta	hormone activity [GO:00	cell [GO:0005623]; extrac
1053	A6H6E2	MMRN2_MOUSE	Multimerin-2	Mus musculus (Mouse)	Mmrn2	Evidence at protein level	943	105206	angiogenesis [GO:0001525];	negative regulation of	basement membrane [GO
1054	Q9CQA3	SDHB_MOUSE	Succinate dehydro	Mus musculus (Mouse)	Sdhb	Evidence at protein level	282	31814	aerobic respiration [GO:0	2 iron, 2 sulfur cluster bin	extracellular exosome [G
1055	Q62425	NDUA4_MOUSE	Cytochrome c oxid	Mus musculus (Mouse)	Ndufa4	Evidence at protein level	82	9327		cytochrome-c oxidase act	extracellular exosome [G
1056	Q99LS3	SERB_MOUSE	Phosphoserine pho	Mus musculus (Mouse)	Psph	Evidence at protein level	225	25096	L-serine biosynthetic proc	calcium ion binding [GO:0	neuron projection [GO:00
1057	P62751	RL23A_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl23a	Evidence at protein level	156	17695	ribosomal large subunit a	nucleotide binding [GO:0	cytosolic large ribosomal
1058	Q00898	A1AT5_MOUSE	Alpha-1-antitrypsir	Mus musculus (Mouse)	Serpina1e	Evidence at protein level	413	45891	response to cytokine [GO	glycoprotein binding [GO:	endoplasmic reticulum [G
1059	Q8CAQ8	MIC60_MOUSE	MICOS complex sul	Mus musculus (Mouse)	Immt	Evidence at protein level	757	83900	cristae formation [GO:00	RNA binding [GO:000372	membrane [GO:0016020
1060	Q9D281	NXP20_MOUSE	Protein Noxp20 (Ne	Mus musculus (Mouse)	Fam114a1	Evidence at protein level	569	61013			cytosol [GO:0005829]; Go
1061	Q61024	ASNS_MOUSE	Asparagine synthet	Mus musculus (Mouse)	Asns	Evidence at protein level	561	64283	asparagine biosynthetic p	asparagine synthase (glut	cytosol [GO:0005829]
1062	O35215	DOPD_MOUSE	D-dopachrome dec	Mus musculus (Mouse)	Ddt	Evidence at protein level	118	13077	melanin biosynthetic proc	D-dopachrome decarboxy	cytoplasm [GO:0005737]
1063	Q61140	BCAR1_MOUSE	Breast cancer anti-	Mus musculus (Mouse)	Bcar1	Evidence at protein level	874	94285	actin filament organizatic	protein kinase binding [G	actin cytoskeleton [GO:0
1064	Q0VGB7	PP4R2_MOUSE	Serine/threonine-p	Mus musculus (Mouse)	Ppp4r2	Evidence at protein level	417	46479	hematopoietic progenitor	protein binding, bridging	cytoplasm [GO:0005737]
1065	P35802	GPM6A_MOUSE	Neuronal membrar	Mus musculus (Mouse)	Gpm6a	Evidence at protein level	278	31149	neural retina developmer	calcium channel activity [	axonal growth cone [GO:0
1066	P50518	VATE1_MOUSE	V-type proton ATP	Mus musculus (Mouse)	Atp6v1e1	Evidence at protein level	226	26157	ATP hydrolysis coupled pr	ATPase binding [GO:0051	apical plasma membrane
1067	P83882	RL36A_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl36a	Evidence at protein level	106	12441	translation [GO:0006412]	structural constituent of	cytosolic large ribosomal
1068	P46061	RAGP1_MOUSE	Ran GTPase-activat	Mus musculus (Mouse)	Rangap1	Evidence at protein level	589	63531	cellular response to vasop	cadherin binding involved	aggresome [GO:0016235
1069	Q3UHD3	MTUS2_MOUSE	Microtubule-associ	Mus musculus (Mouse)	Mtus2	Evidence at protein level	1353	147356		microtubule binding [GO:	cytoplasm [GO:0005737]
1070	Q9R0Y5	KAD1_MOUSE	Adenylate kinase is	Mus musculus (Mouse)	Ak1	Evidence at protein level	194	21540	ATP metabolic process [G	adenylate kinase activity	cytoplasm [GO:0005737]
1071	Q9QZS0	CO4A3_MOUSE	Collagen alpha-3(I	Mus musculus (Mouse)	Col4a3	Evidence at protein level	1669	161726	activation of cysteine-typ	extracellular matrix struc	basement membrane [GO
1072	Q9EQP2	EHD4_MOUSE	EH domain-contain	Mus musculus (Mouse)	Ehd4	Evidence at protein level	541	61481	cellular response to grow	ATP binding [GO:0005524	cell-cell adherens junctio
1073	P40336	VP26A_MOUSE	Vacuolar protein so	Mus musculus (Mouse)	Vps26a	Evidence at protein level	327	38114	intracellular protein trans	protein transporter activi	cytosol [GO:0005829]; ea
1074	Q07105	GDF9_MOUSE	Growth/differentia	Mus musculus (Mouse)	Gdf9	Evidence at transcript level	441	49649	BMP signaling pathway [(	cytokine activity [GO:000	cytoplasm [GO:0005737]
1075	P58871	TB182_MOUSE	182 kDa tankyrase-	Mus musculus (Mouse)	Tnks1bp1	Evidence at protein level	1720	181825	cellular response to ionizi	ankyrin repeat binding [G	CCR4-NOT complex [GO:0
1076	Q9R1A9	TREX2_MOUSE	Three prime repair	Mus musculus (Mouse)	Trex2	Evidence at transcript level	236	25955	DNA metabolic process [(	3'-5'-exodeoxyribonuclea	nucleus [GO:0005634]
1077	A2CG49	KALRN_MOUSE	Kalirin (EC 2.7.11.1	Mus musculus (Mouse)	Kalrn	Evidence at protein level	2964	337000	adult locomotory behavic	ATP binding [GO:0005524	cytoskeleton [GO:000585
1078	Q9WVJ3	CBPQ_MOUSE	Carboxypeptidase (	Mus musculus (Mouse)	Cpq	Evidence at protein level	470	51813	peptide catabolic process	carboxypeptidase activity	cytoplasm [GO:0005737]
1079	Q8BMZ5	SEN34_MOUSE	tRNA-splicing endo	Mus musculus (Mouse)	Tsen34	Evidence at transcript level	316	34196	mRNA processing [GO:00	lyase activity [GO:00168	nucleolus [GO:0005730];
1080	Q80UM7	MOGS_MOUSE	Mannosyl-oligosac	Mus musculus (Mouse)	Mogs	Evidence at protein level	834	91831	oligosaccharide metaboli	mannosyl-oligosaccharid	endoplasmic reticulum [G
1081	P50431	GLYC_MOUSE	Serine hydroxymet	Mus musculus (Mouse)	Shmt1	Evidence at protein level	478	52601	cellular response to tetra	glycine hydroxymethyltra	cytosol [GO:0005829]; ex
1082	P68369	TBA1A_MOUSE	Tubulin alpha-1A ch	Mus musculus (Mouse)	Tuba1a	Evidence at protein level	451	50136	microtubule-based proce	GTPase activity [GO:0003	cytoplasmic microtubule
1083	Q7TNG5	EMAL2_MOUSE	Echinoderm microt	Mus musculus (Mouse)	Eml2	Evidence at protein level	649	70734	negative regulation of mi	microtubule binding [GO:	cytoplasm [GO:0005737]
1084	O54941	SMCE1_MOUSE	SWI/SNF-related m	Mus musculus (Mouse)	Smarce1	Evidence at protein level	411	46638	ATP-dependent chromati	ligand-dependent nuclear	BAF-type complex [GO:0
1085	Q9QUH0	GLRX1_MOUSE	Glutaredoxin-1 (Th	Mus musculus (Mouse)	Glrx	Evidence at protein level	107	11871	cell redox homeostasis [(	electron carrier activity [(	cytoplasm [GO:0005737]
1086	Q9CPW5	SSRB_MOUSE	Translocon-associa	Mus musculus (Mouse)	Ssr2	Evidence at protein level	183	20019	cotranslational protein targeting to membrane [GO		endoplasmic reticulum [G
1087	Q924C1	XPO5_MOUSE	Exportin-5 (Exp5) (I	Mus musculus (Mouse)	Xpo5	Evidence at protein level	1204	136973	positive regulation of RN	mRNA binding [GO:0003	cytoplasm [GO:0005737]
1088	P29391	FRIL1_MOUSE	Ferritin light chain	Mus musculus (Mouse)	Ftl1	Evidence at protein level	183	20802	intracellular sequestering	ferric iron binding [GO:00	autolysosome [GO:00447
1089	Q91VK1	BZW2_MOUSE	Basic leucine zippe	Mus musculus (Mouse)	Bzw2	Evidence at protein level	419	48063	cell differentiation [GO:0	cadherin binding involved	cell-cell adherens junctio
1090	P20782	ACHE_MOUSE	Acetylcholine rece	Mus musculus (Mouse)	Chrne	Evidence at transcript level	493	54914	neuromuscular synaptic t	acetylcholine-gated catio	acetylcholine-gated chan
1091	Q9QZQ1	AFAD_MOUSE	Afadin (Afadin adh	Mus musculus (Mouse)	Afdn	Evidence at protein level	1820	206499	adherens junction mainte	cadherin binding involved	adherens junction [GO:00
1092	Q9QZ25	VNN3_MOUSE	Vascular non-inflar	Mus musculus (Mouse)	Vnn3	Evidence at protein level	500	56305	pantothenate metabolic p	pantetheine hydrolase ac	anchored component of r
1093	O54984	ASNA_MOUSE	ATPase Asna1 (EC 3	Mus musculus (Mouse)	Asna1	Evidence at protein level	348	38823	transport [GO:0006810]	ATPase activity [GO:0016	endoplasmic reticulum [G
1094	Q9ERK4	XPO2_MOUSE	Exportin-2 (Exp2) (I	Mus musculus (Mouse)	Cse1l	Evidence at protein level	971	110455	intracellular protein transport [GO:0006886]		cytosol [GO:0005829]; ex
1095	Q8K3W2	LRC10_MOUSE	Leucine-rich repeat	Mus musculus (Mouse)	Lrrc10	Evidence at protein level	274	31263	cardiac muscle cell devel	actin binding [GO:000377	cytoskeleton [GO:000585
1096	Q61425	HCDH_MOUSE	Hydroxyacyl-coenz	Mus musculus (Mouse)	Hadh	Evidence at protein level	314	34464	fatty acid beta-oxidation	3-hydroxyacyl-CoA dehyd	cytoplasm [GO:0005737]
1097	Q571I9	A16A1_MOUSE	Aldehyde dehydrog	Mus musculus (Mouse)	Aldh16a1	Evidence at protein level	802	84756		aldehyde dehydrogenase	extracellular exosome [G
1098	Q91VZ6	SMAP1_MOUSE	Stromal membrane	Mus musculus (Mouse)	Smap1	Evidence at protein level	440	47660	positive regulation of eryt	clathrin binding [GO:003	cytoplasm [GO:0005737]
1099	P41241	CSK_MOUSE	Tyrosine-protein ki	Mus musculus (Mouse)	Csk	Evidence at protein level	450	50716	adaptive immune respon	ATP binding [GO:0005524	cell-cell junction [GO:000
1100	Q91WT4	DJC17_MOUSE	DnaJ homolog subf	Mus musculus (Mouse)	Dnajc17	Evidence at protein level	303	34465	negative regulation of tra	nucleotide binding [GO:0	cytoplasm [GO:0005737]
1101	Q9D0L8	MCES_MOUSE	mRNA cap guanine	Mus musculus (Mouse)	Rnmt	Evidence at protein level	465	53291	7-methylguanosine mRN	mRNA (guanine-N7-)-met	fibrillar center [GO:0001
1102	Q80U93	NU214_MOUSE	Nuclear pore comp	Mus musculus (Mouse)	Nup214	Evidence at protein level	2085	212979	mitotic nuclear division [(	nuclear export signal rece	cytoplasmic side of nucle
1103	P07742	RIR1_MOUSE	Ribonucleoside-dip	Mus musculus (Mouse)	Rrm1	Evidence at protein level	792	90210	cell proliferation in forebr	ATP binding [GO:0005524	cell projection [GO:0042
1104	P62830	RL23_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl23	Evidence at protein level	140	14865	translation [GO:0006412]	large ribosomal subunit r	cytosolic large ribosomal
1105	Q9CQT5	POMP_MOUSE	Proteasome matur	Mus musculus (Mouse)	Pomp	Evidence at protein level	141	15766	proteasome assembly [GO:0043248]		cytoplasm [GO:0005737]
1106	Q9WVB6	LENEP_MOUSE	Lens epithelial cell	Mus musculus (Mouse)	Lenep	Predicted	61	6923	multicellular organism development [GO:0007275]		cytoplasm [GO:0005737]
1107	Q9D824	FIP1_MOUSE	Pre-mRNA 3'-end-p	Mus musculus (Mouse)	Fip1l1	Evidence at protein level	581	64959	mRNA polyadenylation [(	RNA binding [GO:000372	mRNA cleavage and poly
1108	Q61074	PPM1G_MOUSE	Protein phosphatas	Mus musculus (Mouse)	Ppm1g	Evidence at protein level	542	58728	cell cycle arrest [GO:0007	metal ion binding [GO:00	membrane [GO:0016020
1109	Q91VX2	UBAP2_MOUSE	Ubiquitin-associate	Mus musculus (Mouse)	Ubap2	Evidence at protein level	1132	117966	positive regulation of gen	cadherin binding involved	cell-cell adherens junctio
1110	Q501J7	PHAR4_MOUSE	Phosphatase and a	Mus musculus (Mouse)	Phactr4	Evidence at protein level	694	76632	actin cytoskeleton organi	actin binding [GO:000377	cytoplasm [GO:0005737]
1111	P49919	CDN1C_MOUSE	Cyclin-dependent k	Mus musculus (Mouse)	Cdkn1c	Evidence at protein level	348	37372	adrenal gland developme	cyclin-dependent protein	cytoplasm [GO:0005737]
1112	Q8C7B8	ZSWM4_MOUSE	Zinc finger SWIM d	Mus musculus (Mouse)	Zswim4	Evidence at transcript level	1101	122445		zinc ion binding [GO:0008270]	
1113	Q3UPH7	ARH40_MOUSE	Rho guanine nucle	Mus musculus (Mouse)	Arhgef40	Evidence at protein level	1517	165132	regulation of Rho protein	Rho guanyl-nucleotide ex	cytoplasm [GO:0005737]
1114	Q80W04	TMCC2_MOUSE	Transmembrane ar	Mus musculus (Mouse)	Tmcc2	Evidence at protein level	706	77054			integral component of me
1115	P12815	PDCD6_MOUSE	Programmed cell d	Mus musculus (Mouse)	Pdcd6	Evidence at protein level	191	21867	activation of cysteine-typ	binding, bridging [GO:006	cytoplasm [GO:0005737]
1116	Q9D1E6	TBCB_MOUSE	Tubulin-folding cof	Mus musculus (Mouse)	Tbcb	Evidence at protein level	244	27386	cell differentiation [GO:0030154]; nervous system (		cytoplasm [GO:0005737]
1117	Q9CRB9	MIC19_MOUSE	MICOS complex sul	Mus musculus (Mouse)	Chchd3	Evidence at protein level	227	26335	cristae formation [GO:00	phosphatase binding [GO	cytoplasm [GO:0005737]
1118	Q6GQT6	SCAP_MOUSE	Sterol regulatory el	Mus musculus (Mouse)	Scap	Evidence at protein level	1276	139611	aging [GO:0007568]; chol	cholesterol binding [GO:0	endoplasmic reticulum m
1119	Q8BWY3	ERF1_MOUSE	Eukaryotic peptide	Mus musculus (Mouse)	Etf1	Evidence at protein level	437	49031	nuclear-transcribed mRN	RNA binding [GO:000372	cytoplasm [GO:0005737]
1120	Q8BL66	EEA1_MOUSE	Early endosome an	Mus musculus (Mouse)	Eea1	Evidence at protein level	1411	160915	endocytosis [GO:0006897	1-phosphatidylinositol bi	axonal spine [GO:004430
1121	Q6ZWY3	RS27L_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps27l	Evidence at protein level	84	9477	cellular response to DNA	cysteine-type endopeptid	cytosolic small ribosomal
1122	Q80TH2	ERBIN_MOUSE	Erbin (Densin-180-i	Mus musculus (Mouse)	Erbin	Evidence at protein level	1402	157248	cellular response to tumc	integrin binding [GO:000	basolateral plasma memb
1123	O35678	MGLL_MOUSE	Monoglyceride lipa	Mus musculus (Mouse)	Mgll	Evidence at protein level	303	33388	acylglycerol catabolic pro	acylglycerol lipase activit	axon [GO:0030424]; cyto
1124	P11859	ANGT_MOUSE	Angiotensinogen (S	Mus musculus (Mouse)	Agt	Evidence at protein level	477	51990	activation of NF-kappaB-i	serine-type endopeptidas	blood microparticle [GO:0
1125	Q9Z2U0	PSA7_MOUSE	Proteasome subuni	Mus musculus (Mouse)	Psma7	Evidence at protein level	248	27855	ubiquitin-dependent prot	identical protein binding	cytosol [GO:0005829]; ex
1126	Q9D0F9	PGM1_MOUSE	Phosphoglucomuta	Mus musculus (Mouse)	Pgm1	Evidence at protein level	562	61418	galactose catabolic proce	magnesium ion binding [(	actin cytoskeleton [GO:0
1127	P81117	NUCB2_MOUSE	Nucleobindin-2 (DN	Mus musculus (Mouse)	Nucb2	Evidence at protein level	420	50304	cellular calcium ion home	calcium ion binding [GO:(	cytoplasm [GO:0005737]
1128	Q9CPQ3	TOM22_MOUSE	Mitochondrial impo	Mus musculus (Mouse)	Tomm22	Evidence at protein level	142	15537	protein import into mitoc	protein transmembrane t	integral component of me
1129	Q8R1I1	QCR9_MOUSE	Cytochrome b-c1 c	Mus musculus (Mouse)	Uqcr10	Evidence at protein level	64	7446	aerobic respiration [GO:0009060]; hydrogen ion tra		extracellular exosome [G
1130	Q61937	NPM_MOUSE	Nucleophosmin (NI	Mus musculus (Mouse)	Npm1	Evidence at protein level	292	32560	cardiac muscle hypertrop	ATP binding [GO:0005524	centrosome [GO:000581
1131	Q3TDN2	FAF2_MOUSE	FAS-associated fact	Mus musculus (Mouse)	Faf2	Evidence at protein level	445	52471	lipid particle organization	lipase binding [GO:00354	endoplasmic reticulum [G
1132	Q7TNV0	DEK_MOUSE	Protein DEK	Mus musculus (Mouse)	Dek	Evidence at protein level	380	43159	chromatin remodeling [G	chromatin binding [GO:0(	contractile fiber [GO:0043
1133	Q9Z1Z0	USO1_MOUSE	General vesicular t	Mus musculus (Mouse)	Uso1	Evidence at protein level	959	106983	ER to Golgi vesicle-media	cadherin binding involved	cell-cell adherens junctio
1134	Q9DC69	NDUA9_MOUSE	NADH dehydrogena	Mus musculus (Mouse)	Ndufa9	Evidence at protein level	377	42525	response to glucose [GO:	NADH dehydrogenase act	mitochondrial inner mem
1135	Q9JI99	SGPP1_MOUSE	Sphingosine-1-phos	Mus musculus (Mouse)	Sgpp1	Evidence at protein level	430	47744	extrinsic apoptotic signali	sphingosine-1-phosphate	endoplasmic reticulum [G
1136	P61027	RAB10_MOUSE	Ras-related protein	Mus musculus (Mouse)	Rab10	Evidence at protein level	200	22541	antigen processing and pr	cadherin binding involved	cell-cell adherens junctio
1137	P97363	SPTC2_MOUSE	Serine palmitoyltra	Mus musculus (Mouse)	Sptlc2	Evidence at protein level	560	62982	ceramide biosynthetic pr	pyridoxal phosphate bind	integral component of me
1138	P62855	RS26_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps26	Evidence at protein level	115	13015	negative regulation of RN	cadherin binding involved	cell-cell adherens junctio
1139	G3X9C2	FBX50_MOUSE	F-box only protein	Mus musculus (Mouse)	Nccrp1	Evidence at protein level	266	30408	positive regulation of cell	proliferation [GO:000828	cytoplasm [GO:0005737]
1140	P45376	ALDR_MOUSE	Aldose reductase (A	Mus musculus (Mouse)	Akr1b1	Evidence at protein level	316	35732	cellular response to hydr	alditol:NADP+ 1-oxidored	cell projection cytoplasm
1141	Q9Z0G0	GIPC1_MOUSE	PDZ domain-contai	Mus musculus (Mouse)	Gipc1	Evidence at protein level	333	36129	chemical synaptic transm	actin binding [GO:000377	brush border [GO:0005900
1142	Q61247	A2AP_MOUSE	Alpha-2-antiplasmi	Mus musculus (Mouse)	Serpinf2	Evidence at protein level	491	54972	acute-phase response [G	protease binding [GO:000	blood microparticle [GO:0
1143	Q3TIU4	PDE12_MOUSE	2',5'-phosphodiest	Mus musculus (Mouse)	Pde12	Evidence at protein level	608	67514	mRNA processing [GO:00	metal ion binding [GO:00	mitochondrial matrix [GO
1144	O55135	IF6_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif6	Evidence at protein level	245	26511	assembly of large subunit	ribosomal large subunit b	cytoplasm [GO:0005737]
1145	P97770	THUM3_MOUSE	THUMP domain-co	Mus musculus (Mouse)	Thumpd3	Evidence at protein level	505	56431		methyltransferase activit	cytosol [GO:0005829]; nu
1146	P34884	MIF_MOUSE	Macrophage migra	Mus musculus (Mouse)	Mif	Evidence at protein level	115	12504	carboxylic acid metabolic	chemoattractant activity	cell surface [GO:0009986
1147	Q9Z287	KR121_MOUSE	Keratin-associated	Mus musculus (Mouse)	Krtap12-1	Evidence at transcript level	130	13119			keratin filament [GO:004
1148	Q9JKB3	YBOX3_MOUSE	Y-box-binding prote	Mus musculus (Mouse)	Ybx3	Evidence at protein level	361	38814	cellular hyperosmotic res	DNA binding [GO:000367	cytoplasm [GO:0005737]
1149	P35174	CYT2_MOUSE	Stefin-2	Mus musculus (Mouse)	Stfa2	Inferred from homology	103	11842	negative regulation of en	cysteine-type endopeptid	cytoplasm [GO:0005737]
1150	Q91W50	CSDE1_MOUSE	Cold shock domain	Mus musculus (Mouse)	Csde1	Evidence at protein level	798	88791	nuclear-transcribed mRN	DNA binding [GO:000367	CRD-mediated mRNA sta
1151	P58021	TM9S2_MOUSE	Transmembrane 9	Mus musculus (Mouse)	Tm9sf2	Evidence at protein level	662	75330			endosome membrane [G
1152	P85094	ISC2A_MOUSE	Isochorismatase do	Mus musculus (Mouse)	Isoc2a	Evidence at protein level	206	22417	metabolic process [GO:0(	catalytic activity [GO:000	cytoplasm [GO:0005737]
1153	Q8CDW1	F228A_MOUSE	Protein FAM228A	Mus musculus (Mouse)	Fam228a	Evidence at transcript level	299	34457			
1154	O54891	LEG6_MOUSE	Galectin-6 (Gal-6)	Mus musculus (Mouse)	Lgals6	Evidence at transcript level	301	34112		carbohydrate binding [GO:0030246]	
1155	Q61233	PLSL_MOUSE	Plastin-2 (65 kDa m	Mus musculus (Mouse)	Lcp1	Evidence at protein level	627	70149	actin crosslink formation	actin filament binding [G	actin cytoskeleton [GO:0
1156	P28352	APEX1_MOUSE	DNA-(apurinic or ap	Mus musculus (Mouse)	Apex1	Evidence at protein level	317	35490	aging [GO:0007568]; base	3'-5' exonuclease activity	centrosome [GO:000581
1157	Q924K8	MTA3_MOUSE	Metastasis-associa	Mus musculus (Mouse)	Mta3	Evidence at protein level	591	67077	negative regulation of tra	chromatin binding [GO:0(	cohesin complex [GO:000
1158	Q9CY64	BIEA_MOUSE	Biliverdin reductase	Mus musculus (Mouse)	Blvra	Evidence at protein level	295	33525	heme catabolic process [(	biliverdin reductase activ	cytosol [GO:0005829]; ex
1159	Q9D7P7	CLIC3_MOUSE	Chloride intracellul	Mus musculus (Mouse)	Clic3	Evidence at protein level	237	26846	chloride transport [GO:0(	chloride channel activity	chloride channel complex
1160	P52912	TIA1_MOUSE	Nucleolysin TIA-1 (I	Mus musculus (Mouse)	Tia1	Evidence at protein level	386	42800	apoptotic process [GO:00	AU-rich element binding [	cytoplasm [GO:0005737]
1161	Q8R146	APEH_MOUSE	Acylamino-acid-rel	Mus musculus (Mouse)	Apeh	Evidence at protein level	732	81581	beta-amyloid metabolic p	identical protein binding	cytosol [GO:0005829]; ex
1162	Q9D1L0	CHCH2_MOUSE	Coiled-coil-helix-co	Mus musculus (Mouse)	Chchd2	Evidence at transcript level	153	15661	mitochondrion organizati	sequence-specific DNA bi	mitochondrial intermemb
1163	Q61555	FBN2_MOUSE	Fibrillin-2 [Cleaved	Mus musculus (Mouse)	Fbn2	Evidence at protein level	2907	313818	bone trabecula formatior	calcium ion binding [GO:(	extracellular matrix [GO:0
1164	Q7TSN7	IGSF5_MOUSE	Immunoglobulin su	Mus musculus (Mouse)	Igsf5	Evidence at protein level	370	40292	single organismal cell-cell	PDZ domain binding [GO:	apical plasma membrane
1165	Q62351	TFR1_MOUSE	Transferrin receptc	Mus musculus (Mouse)	Tfrc	Evidence at protein level	763	85731	cellular iron ion homeosta	double-stranded RNA bin	basolateral plasma memb

1166	P62900	RL31_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl31	Evidence at protein level	125	14463	translation [GO:0006412]	RNA binding [GO:000372	cytosolic large ribosomal
1167	Q9QZQ8	H2AY_MOUSE	Core histone macr	Mus musculus (Mouse)	H2afy	Evidence at protein level	372	39735	chromatin silencing [GO:0	chromatin binding [GO:0(	Barr body [GO:0001740];
1168	Q9WTQ5	AKA12_MOUSE	A-kinase anchor pr	Mus musculus (Mouse)	Akap12	Evidence at protein level	1684	180695	positive regulation of cAM	adenylate cyclase binding	cytoskeleton [GO:000585
1169	Q9JLF6	TGM1_MOUSE	Protein-glutamine	Mus musculus (Mouse)	Tgm1	Evidence at protein level	815	89826	animal organ morphogen	metal ion binding [GO:00	cell-cell adherens junctio
1170	P17918	PCNA_MOUSE	Proliferating cell nu	Mus musculus (Mouse)	Pcna	Evidence at protein level	261	28785	base-excision repair, gap-	chromatin binding [GO:0(	centrosome [GO:000581
1171	Q8BGW1	FTO_MOUSE	Alpha-ketoglutarat	Mus musculus (Mouse)	Fto	Evidence at protein level	502	58007	adipose tissue developme	DNA-N1-methyladenine	nuclear speck [GO:00166
1172	Q6P542	ABCF1_MOUSE	ATP-binding casset	Mus musculus (Mouse)	Abcf1	Evidence at protein level	837	94945	positive regulation of trar	ATPase activity [GO:0016	cytoplasm [GO:0005737]
1173	O08884	KRA62_MOUSE	Keratin-associated	Mus musculus (Mouse)	Krtap6-2	Evidence at transcript level	159	15262			intermediate filament [G
1174	P18572	BASI_MOUSE	Basigin (Basic immu	Mus musculus (Mouse)	Bsg	Evidence at protein level	389	42445	decidualization [GO:0046	cadherin binding involved	acrosomal membrane [G
1175	P70677	CASP3_MOUSE	Caspase-3 (CASP-3	Mus musculus (Mouse)	Casp3	Evidence at protein level	277	31475	apoptotic process [GO:00	aspartic-type endopeptid	cytoplasm [GO:0005737]
1176	P46735	MYO1B_MOUSE	Unconventional my	Mus musculus (Mouse)	Myo1b	Evidence at protein level	1107	128564	actin filament-based mov	actin filament binding [G	actin filament [GO:00058
1177	A2ASQ1	AGRIN_MOUSE	Agrin [Cleaved into	Mus musculus (Mouse)	Agrn	Evidence at protein level	1950	207539	cell differentiation [GO:0	acetylcholine receptor re	basal lamina [GO:00560
1178	P05213	TBA1B_MOUSE	Tubulin alpha-1B ch	Mus musculus (Mouse)	Tuba1b	Evidence at protein level	451	50152	cellular response to interl	double-stranded RNA bin	cytoplasmic microtubule
1179	Q9JJ59	ABCB9_MOUSE	ATP-binding casset	Mus musculus (Mouse)	Abcb9	Evidence at transcript level	762	83963	peptide transport [GO:00	ATP binding [GO:0005524	endoplasmic reticulum m
1180	Q9D358	PPAC_MOUSE	Low molecular weig	Mus musculus (Mouse)	Acp1	Evidence at protein level	158	18192		acid phosphatase activity	cytoplasm [GO:0005737]
1181	Q3UQ28	PXDN_MOUSE	Peroxidasin homolo	Mus musculus (Mouse)	Pxdn	Evidence at protein level	1475	165103	extracellular matrix orgar	extracellular matrix struc	endoplasmic reticulum [G
1182	Q9JI90	RNF14_MOUSE	E3 ubiquitin-protei	Mus musculus (Mouse)	Rnf14	Evidence at protein level	485	54926	positive regulation of pro	androgen receptor bindin	cytoplasm [GO:0005737]
1183	Q61699	HS105_MOUSE	Heat shock protein	Mus musculus (Mouse)	Hsph1	Evidence at protein level	858	96407	chaperone mediated prot	adenyl-nucleotide exchar	cytoplasm [GO:0005737]
1184	Q9CQJ4	RING2_MOUSE	E3 ubiquitin-protei	Mus musculus (Mouse)	Rnf2	Evidence at protein level	336	37623	anterior/posterior axis sp	chromatin binding [GO:0(	euchromatin [GO:00007
1185	Q0VBK2	K2C80_MOUSE	Keratin, type II cyto	Mus musculus (Mouse)	Krt80	Evidence at protein level	452	50660		structural molecule activi	cytoplasm [GO:0005737]
1186	P09470	ACE_MOUSE	Angiotensin-conver	Mus musculus (Mouse)	Ace	Evidence at protein level	1312	150918	arachidonic acid secretio	actin binding [GO:000377	cytoplasm [GO:0005737]
1187	P55264	ADK_MOUSE	Adenosine kinase (	Mus musculus (Mouse)	Adk	Evidence at protein level	361	40149	adenosine salvage [GO:0(	adenosine kinase activity	cytosol [GO:0005829]; nu
1188	Q07456	AMBP_MOUSE	Protein AMBP [Cle	Mus musculus (Mouse)	Ambp	Evidence at protein level	349	39029	protein catabolic process	heme binding [GO:00200	blood microparticle [GO:(
1189	Q8VCM7	FIBG_MOUSE	Fibrinogen gamma	Mus musculus (Mouse)	Fgg	Evidence at protein level	436	49391	adaptive immune respon	cell adhesion molecule bi	blood microparticle [GO:(
1190	Q8R5C5	ACTY_MOUSE	Beta-centractin (Ac	Mus musculus (Mouse)	Actr1b	Evidence at protein level	376	42281		ATP binding [GO:0005524	centrosome [GO:000581
1191	Q64449	MRC2_MOUSE	C-type mannose re	Mus musculus (Mouse)	Mrc2	Evidence at protein level	1479	167074	collagen catabolic proces	carbohydrate binding [GO	cell surface [GO:0009986
1192	P62082	RS7_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps7	Evidence at transcript level	194	22127	cell differentiation [GO:0(	poly(U) RNA binding [GO:	cytosolic small ribosomal
1193	O09167	RL21_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl21	Evidence at protein level	160	18562	translation [GO:0006412]	RNA binding [GO:000372	cytosolic large ribosomal
1194	Q80WS3	FBLL1_MOUSE	rRNA/tRNA 2'-O-m	Mus musculus (Mouse)	Fbll1	Evidence at protein level	314	33339	box C/D snoRNA 3'-end p	histone-glutamine methy	box C/D snoRNP complex
1195	Q9D880	TIM50_MOUSE	Mitochondrial impo	Mus musculus (Mouse)	Timm50	Evidence at protein level	353	39776	mitochondrial membrane	interleukin-2 receptor bin	integral component of me
1196	P05063	ALDOC_MOUSE	Fructose-bisphosp	Mus musculus (Mouse)	Aldoc	Evidence at protein level	363	39395	epithelial cell differentiat	cytoskeletal protein bindi	extracellular exosome [G
1197	Q9R1P0	PSA4_MOUSE	Proteasome subuni	Mus musculus (Mouse)	Psma4	Evidence at protein level	261	29471	ubiquitin-dependent prot	threonine-type endopept	cytosol [GO:0005829]; ex
1198	Q9CZU3	SK2L2_MOUSE	Superkiller viralicid	Mus musculus (Mouse)	Skiv2l2	Evidence at protein level	1040	117636	maturation of 5.8S rRNA	ATP binding [GO:0005524	catalytic step 2 spliceoso
1199	Q8C6K9	CO6A6_MOUSE	Collagen alpha-6(V	Mus musculus (Mouse)	Col6a6	Evidence at protein level	2265	246323	cell adhesion [GO:0007155]		collagen trimer [GO:0005
1200	Q99MR6	SRRT_MOUSE	Serrate RNA effecto	Mus musculus (Mouse)	Srrt	Evidence at protein level	875	100452	cell proliferation [GO:000	DNA binding [GO:000367	cytoplasm [GO:0005737]
1201	Q9D1Q6	ERP44_MOUSE	Endoplasmic reticu	Mus musculus (Mouse)	Erp44	Evidence at protein level	406	46853	cell redox homeostasis [G	protein disulfide isomera:	cell surface [GO:0009986
1202	A2AN08	UBR4_MOUSE	E3 ubiquitin-protei	Mus musculus (Mouse)	Ubr4	Evidence at protein level	5180	572290	protein ubiquitination inv	ubiquitin-protein transfer	centrosome [GO:000581
1203	P62889	RL30_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl30	Evidence at protein level	115	12784	liver regeneration [GO:00	RNA binding [GO:000372	cytosolic large ribosomal
1204	P97379	G3BP2_MOUSE	Ras GTPase-activat	Mus musculus (Mouse)	G3bp2	Evidence at protein level	482	54088	mRNA transport [GO:005	mRNA binding [GO:0003	cytosol [GO:0005829]; in
1205	Q91UZ5	IMPA2_MOUSE	Inositol monophosp	Mus musculus (Mouse)	Impa2	Evidence at protein level	290	31716	inositol biosynthetic proc	inositol monophosphate	cytoplasm [GO:0005737]
1206	Q9JKF6	NECT1_MOUSE	Nectin-1 (Herpes vi	Mus musculus (Mouse)	Nectin1	Evidence at protein level	515	57035	axon guidance [GO:0007	carbohydrate binding [GO	apical junction complex [
1207	O08582	GTPB1_MOUSE	GTP-binding protei	Mus musculus (Mouse)	Gtpbp1	Evidence at protein level	668	72301	positive regulation of mR	GTPase activity [GO:0003	cytoplasmic exosome (RN
1208	Q60668	HNRPD_MOUSE	Heterogeneous nuc	Mus musculus (Mouse)	Hnrnpd	Evidence at protein level	355	38354	3'-UTR-mediated mRNA	AT DNA binding [GO:000	cytosol [GO:0005829]; ex
1209	P46664	PURA2_MOUSE	Adenylosuccinate s	Mus musculus (Mouse)	Adss	Evidence at protein level	456	50021	'de novo' AMP biosynthet	adenylosuccinate synthas	cytoplasm [GO:0005737]
1210	Q91YJ2	SNX4_MOUSE	Sorting nexin-4	Mus musculus (Mouse)	Snx4	Evidence at protein level	450	51778	endocytic recycling [GO:0	epidermal growth factor	cytoplasm [GO:0005737]
1211	Q91ZW3	SMCA5_MOUSE	SWI/SNF-related m	Mus musculus (Mouse)	Smarca5	Evidence at protein level	1051	121627	ATP-dependent chromati	ATPase activity [GO:0016	chromatin silencing comp
1212	A3KMP2	TTC38_MOUSE	Tetratricopeptide r	Mus musculus (Mouse)	Ttc38	Evidence at protein level	465	52224			extracellular exosome [G
1213	P55096	ABCD3_MOUSE	ATP-binding casset	Mus musculus (Mouse)	Abcd3	Evidence at protein level	659	75475	fatty acid beta-oxidation	ATPase activity [GO:0016	integral component of me
1214	Q99LB6	MAT2B_MOUSE	Methionine adenos	Mus musculus (Mouse)	Mat2b	Evidence at protein level	334	37393	one-carbon metabolic pr	enzyme binding [GO:001	extracellular exosome [G
1215	Q61599	GDIR2_MOUSE	Rho GDP-dissociati	Mus musculus (Mouse)	Arhgdib	Evidence at protein level	200	22851	cellular response to redo	GTPase activator activity	cytosol [GO:0005829]; ex
1216	Q9JIF7	COPB_MOUSE	Coatomer subunit I	Mus musculus (Mouse)	Copb1	Evidence at protein level	953	107066	ER to Golgi vesicle-media	structural molecule activi	COPI-coated vesicle [GO:
1217	Q99K41	EMIL1_MOUSE	EMILIN-1 (Elastin n	Mus musculus (Mouse)	Emilin1	Evidence at protein level	1017	107585	cell adhesion [GO:000715	extracellular matrix const	collagen trimer [GO:0005
1218	Q9JMH9	MY18A_MOUSE	Unconventional my	Mus musculus (Mouse)	Myo18a	Evidence at protein level	2050	232755	actomyosin structure org	actin filament binding [G	actomyosin [GO:0042641
1219	Q9CR60	GOT1B_MOUSE	Vesicle transport p	Mus musculus (Mouse)	Golt1b	Evidence at protein level	138	15422	positive regulation of I-ka	signal transducer activity	endoplasmic reticulum [G
1220	Q9D7Z7	LYPD5_MOUSE	Ly6/PLAUR domain	Mus musculus (Mouse)	Lypd5	Evidence at transcript level	256	27450	cell-matrix adhesion [GO:	laminin binding [GO:0043	anchored component of r
1221	O88986	KBL_MOUSE	2-amino-3-ketobut	Mus musculus (Mouse)	Gcat	Evidence at protein level	416	44931	biosynthetic process [GO	glycine C-acetyltransfera	mitochondrial inner mem
1222	Q9D952	EVPL_MOUSE	Envoplakin (210 kD	Mus musculus (Mouse)	Evpl	Evidence at protein level	2035	232012	keratinization [GO:00314	cadherin binding involved	cell-cell adherens junctio
1223	Q8VBZ3	CLPT1_MOUSE	Cleft lip and palate	Mus musculus (Mouse)	Clptm1	Evidence at protein level	664	75291	cell differentiation [GO:0030154];	multicellular orga	external side of plasma m
1224	Q9D7H3	RTCA_MOUSE	RNA 3'-terminal ph	Mus musculus (Mouse)	RtcA	Evidence at protein level	366	39254	RNA processing [GO:000	ATP binding [GO:0005524	nucleoplasm [GO:0005
1225	Q9D7G0	PRPS1_MOUSE	Ribose-phosphate	Mus musculus (Mouse)	Prps1	Evidence at protein level	318	34834	5-phosphoribose 1-dipho	ADP binding [GO:004353	protein complex [GO:004
1226	Q91Z31	PTBP2_MOUSE	Polypyrimidine trac	Mus musculus (Mouse)	Ptbp2	Evidence at protein level	531	57489	cerebellum development	mRNA binding [GO:0003	growth cone [GO:003042
1227	P67984	RL22_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl22	Evidence at protein level	128	14759	alpha-beta T cell differen	heparin binding [GO:000	cytoplasm [GO:0005737]
1228	P00405	COX2_MOUSE	Cytochrome c oxid	Mus musculus (Mouse)	Mtco2	Evidence at protein level	227	25976	ATP synthesis coupled ele	copper ion binding [GO:0	extracellular exosome [G
1229	Q9DBE8	ALG2_MOUSE	Alpha-1,3/1,6-man	Mus musculus (Mouse)	Alg2	Evidence at protein level	415	47405	dolichol-linked oligosacch	alpha-1,3-mannosyltrans	cytoplasm [GO:0005737]
1230	P15379	CD44_MOUSE	CD44 antigen (Extr	Mus musculus (Mouse)	Cd44	Evidence at protein level	778	85617	branching involved in pro	hyaluronic acid binding [C	basolateral plasma memb
1231	Q8BSY0	ASPH_MOUSE	Aspartyl/asparagin	Mus musculus (Mouse)	Asph	Evidence at protein level	741	83042	activation of cysteine-typ	calcium ion binding [GO:(	cortical endoplasmic retic
1232	Q60598	SRC8_MOUSE	Src substrate corta	Mus musculus (Mouse)	Cttn	Evidence at protein level	546	61250	actin cytoskeleton reorga	cadherin binding involved	actin filament [GO:00058
1233	Q3UKJ7	SMU1_MOUSE	WD40 repeat-cont	Mus musculus (Mouse)	Smu1	Evidence at transcript level	513	57544			cytoplasm [GO:0005737]
1234	P61982	1433G_MOUSE	14-3-3 protein gam	Mus musculus (Mouse)	Ywhag	Evidence at protein level	247	28303	cellular response to insuli	actin binding [GO:000377	cytoplasmic vesicle memb
1235	Q99MN1	SYK_MOUSE	Lysine--tRNA ligase	Mus musculus (Mouse)	Kars	Evidence at protein level	595	67840	lysyl-tRNA aminoacylatio	ATP binding [GO:0005524	cytosol [GO:0005829]; m
1236	Q9R0U0	SRS10_MOUSE	Serine/arginine-rich	Mus musculus (Mouse)	Srsf10	Evidence at protein level	262	31301	cytosolic transport [GO:0	nucleotide binding [GO:0(	cytosol [GO:0005829]; nu
1237	P97449	AMPN_MOUSE	Aminopeptidase N	Mus musculus (Mouse)	Anpep	Evidence at protein level	966	109651	angiogenesis [GO:000152	metalloaminopeptidase a	cytoplasm [GO:0005737]
1238	Q8C0I1	ADAS_MOUSE	Alkyldihydroxyacet	Mus musculus (Mouse)	Agps	Evidence at protein level	645	71684	ether lipid biosynthetic pr	alkylglycerone-phosphate	membrane [GO:0016020
1239	Q63844	MK03_MOUSE	Mitogen-activated	Mus musculus (Mouse)	Mapk3	Evidence at protein level	380	43066	animal organ morphogen	ATP binding [GO:0005524	caveola [GO:0005901]; cy
1240	Q8CH72	TRI32_MOUSE	E3 ubiquitin-protei	Mus musculus (Mouse)	Trim32	Evidence at protein level	655	72057	actin ubiquitination [GO:0	identical protein binding [	cytoplasm [GO:0005737]
1241	Q9CX34	SGT1_MOUSE	Protein SGT1 homo	Mus musculus (Mouse)	Sugt1	Evidence at protein level	336	38159	positive regulation by host of	symbiont catalytic act	cytoplasm [GO:0005737]
1242	Q9D1H7	GET4_MOUSE	Golgi to ER traffic p	Mus musculus (Mouse)	Get4	Evidence at protein level	327	36525	cytoplasmic sequestering	chaperone binding [GO:0	BAT3 complex [GO:0071
1243	Q9Z2D6	MECP2_MOUSE	Methyl-CpG-bindin	Mus musculus (Mouse)	Mecp2	Evidence at protein level	484	52307	adult locomotory behavic	chromatin binding [GO:0(	cytoplasm [GO:0005737]
1244	Q9WVG6	CARM1_MOUSE	Histone-arginine m	Mus musculus (Mouse)	Carm1	Evidence at protein level	608	65854	aging [GO:0007568]; end	histone-arginine N-meth	cytoplasm [GO:0005737]
1245	Q9Z148	EHMT2_MOUSE	Histone-lysine N-m	Mus musculus (Mouse)	Ehmt2	Evidence at protein level	1263	138039	behavioral response to co	C2H2 zinc finger domain	nuclear chromatin [GO:0(
1246	P46718	PDCD2_MOUSE	Programmed cell d	Mus musculus (Mouse)	Pdcd2	Evidence at transcript level	343	38342	activation of cysteine-typ	DNA binding [GO:000367	cytoplasm [GO:0005737]
1247	P42567	EPS15_MOUSE	Epidermal growth f	Mus musculus (Mouse)	Eps15	Evidence at protein level	897	98471	clathrin coat assembly [G	cadherin binding involved	aggresome [GO:0016235
1248	Q8C754	VPS52_MOUSE	Vacuolar protein so	Mus musculus (Mouse)	Vps52	Evidence at protein level	723	82044	ectodermal cell differenti	Rab GTPase binding [GO:(	cytosol [GO:0005829]; EA
1249	B1AZI6	THOC2_MOUSE	THO complex subu	Mus musculus (Mouse)	Thoc2	Evidence at protein level	1594	182773	blastocyst development [	mRNA binding [GO:0003	nuclear speck [GO:00166
1250	Q8R2T8	TF3C5_MOUSE	General transcripti	Mus musculus (Mouse)	Gtf3c5	Evidence at transcript level	520	60502	RNA polymerase III type	DNA binding [GO:000367	nucleoplasm [GO:0005
1251	P35282	RAB21_MOUSE	Ras-related protein	Mus musculus (Mouse)	Rab21	Evidence at protein level	222	24106	anterograde axonal trans	GDP binding [GO:001900	axon cytoplasm [GO:190
1252	P62878	RBX1_MOUSE	E3 ubiquitin-protei	Mus musculus (Mouse)	Rbx1	Evidence at protein level	108	12274	DNA repair [GO:0006281	cullin family protein bindi	anaphase-promoting com
1253	P52432	RPAC1_MOUSE	DNA-directed RNA	Mus musculus (Mouse)	Polr1c	Evidence at protein level	346	39107	chromatin silencing at rD	DNA binding [GO:000367	DNA-directed RNA polym
1254	Q9Z160	COG1_MOUSE	Conserved oligome	Mus musculus (Mouse)	Cog1	Evidence at protein level	980	109050	intra-Golgi vesicle-mediated transport [GO:000689		Golgi apparatus [GO:000
1255	Q80TM9	NISCH_MOUSE	Nischarin (Imidazol	Mus musculus (Mouse)	Nisch	Evidence at protein level	1593	175012	actin cytoskeleton organi	integrin binding [GO:000	cytosol [GO:0005829]; ea
1256	P0CB42	ALKB1_MOUSE	Nucleic acid dioxyg	Mus musculus (Mouse)	Alkbh1	Evidence at protein level	389	43746	cell differentiation [GO:0(	1-ethyladenine demethyl	mitochondrion [GO:0005
1257	E9Q1P8	IZBP2_MOUSE	Interferon regulato	Mus musculus (Mouse)	Irf2bp2	Evidence at protein level	570	59292	negative regulation of tra	metal ion binding [GO:00	cytoplasm [GO:0005737]
1258	Q8BR90	CE051_MOUSE	UPF0600 protein C	Mus musculus (Mouse)		Evidence at protein level	294	33471			cytosol [GO:0005829]; nu
1259	P43883	PLIN2_MOUSE	Perilipin-2 (Adipopl	Mus musculus (Mouse)	Plin2	Evidence at protein level	425	46646	lipid storage [GO:0019915];	long-chain fatty acid tr	cytoplasm [GO:0005737]
1260	Q8VEJ4	NLE1_MOUSE	Notchless protein h	Mus musculus (Mouse)	Nle1	Evidence at protein level	485	53134	hematopoietic stem cell homeostasis [GO:0061484		nucleolus [GO:0005730];
1261	O35382	EXOC4_MOUSE	Exocyst complex co	Mus musculus (Mouse)	Exoc4	Evidence at protein level	975	110545	chemical synaptic transm	PDZ domain binding [GO:	cytoplasm [GO:0005737]
1262	Q8CB77	ELOA1_MOUSE	Elongin-A (EloA) (El	Mus musculus (Mouse)	Eloa	Evidence at protein level	773	87161	regulation of transcription,	DNA-templated [GO:000	elongin complex [GO:007
1263	Q6Y7W8	GGYF2_MOUSE	GRB10-interacting	Mus musculus (Mouse)	Gigyf2	Evidence at protein level	1291	149193	adult locomotory behavic	cadherin binding involved	cell-cell adherens junctio
1264	Q9D753	EXOS8_MOUSE	Exosome complex	Mus musculus (Mouse)	Exosc8	Evidence at protein level	276	29949	RNA catabolic process [G	AU-rich element binding	cytoplasm [GO:0005737]
1265	O89050	MKLN1_MOUSE	Muskelin	Mus musculus (Mouse)	Mkln1	Evidence at protein level	735	84878	actin cytoskeleton reorganization [GO:0031532];	ce	cell cortex [GO:0005938]
1266	Q8QZY9	SF3B4_MOUSE	Splicing factor 3B s	Mus musculus (Mouse)	Sf3b4	Evidence at protein level	424	44356	mRNA processing [GO:00	nucleotide binding [GO:0(	spliceosomal complex [G
1267	O88630	GOSR1_MOUSE	Golgi SNAP receptc	Mus musculus (Mouse)	Gosr1	Evidence at protein level	250	28489	ER to Golgi vesicle-media	SNAP receptor activity [G	cis-Golgi network [GO:00
1268	Q9D2N9	VP33A_MOUSE	Vacuolar protein so	Mus musculus (Mouse)	Vps33a	Evidence at protein level	598	67555	autophagosome maturation [GO:0097352];	endoso	autophagosome [GO:000
1269	P24472	GSTA4_MOUSE	Glutathione S-tran	Mus musculus (Mouse)	Gsta4	Evidence at protein level	222	25564	cellular response to lithiu	drug binding [GO:000814	mitochondrion [GO:0005
1270	O54785	LIMK2_MOUSE	LIM domain kinase	Mus musculus (Mouse)	Limk2	Evidence at protein level	638	72202	intracellular signal transd	ATP binding [GO:0005524	cis-Golgi network [GO:00
1271	Q91VY9	ZN622_MOUSE	Zinc finger protein	Mus musculus (Mouse)	Znf622	Evidence at protein level	476	53451	intrinsic apoptotic signali	RNA binding [GO:000372	cytosol [GO:0005829]; cy
1272	Q9ZDY1	DCTN3_MOUSE	Dynactin subunit 3	Mus musculus (Mouse)	Dctn3	Evidence at protein level	186	20978	cytokinesis [GO:0000910];	microtubule-based proc	centrosome [GO:000581
1273	Q5NCQ5	DPH1_MOUSE	2-(3-amino-3-carb	Mus musculus (Mouse)	Dph1	Evidence at protein level	438	48004	cell proliferation [GO:000	transferase activity [GO:(	cell junction [GO:003005
1274	Q9QZ08	NAGK_MOUSE	N-acetyl-D-glucosa	Mus musculus (Mouse)	Nagk	Evidence at protein level	343	37268	N-acetylglucosamine met	ATP binding [GO:0005524	extracellular exosome [G
1275	Q9D6K8	FUND2_MOUSE	FUN14 domain-con	Mus musculus (Mouse)	Fundc2	Evidence at protein level	151	16564	mitophagy [GO:0000422]		integral component of mi
1276	P53564	CUX1_MOUSE	Homeobox protein	Mus musculus (Mouse)	Cux1	Evidence at protein level	1515	165596	auditory receptor cell diff	chromatin binding [GO:0(	cytoplasm [GO:0005737]
1277	Q9D6Y9	GLGB_MOUSE	1,4-alpha-glucan-b	Mus musculus (Mouse)	Gbe1	Evidence at protein level	702	80364	glycogen biosynthetic prc	1,4-alpha-glucan branchi	extracellular exosome [G
1278	Q8VE80	THOC3_MOUSE	THO complex subu	Mus musculus (Mouse)	Thoc3	Evidence at transcript level	351	38738	mRNA export from nucle	RNA binding [GO:000372	nuclear chromosome, tel
1279	Q8VBT9	ASPC1_MOUSE	Tether containing U	Mus musculus (Mouse)	Aspscr1	Evidence at protein level	550	59796	glucose homeostasis [GO:0042593];	intracellular pr	cytoplasmic side of plasm
1280	Q64442	DHSO_MOUSE	Sorbitol dehydroge	Mus musculus (Mouse)	Sord	Evidence at protein level	357	38249	flagellated sperm motility	D-xylulose reductase acti	extracellular exosome [G
1281	Q9JHL1	NHRF2_MOUSE	Na(+)/H(+) exchang	Mus musculus (Mouse)	Slc9a3r2	Evidence at protein level	337	37403	negative regulation of ph	beta-catenin binding [GO	apical plasma membrane
1282	Q6QD59	SEC20_MOUSE	Vesicle transport p	Mus musculus (Mouse)	Bnip1	Evidence at protein level	228	26175	apoptotic process [GO:00	SNAP receptor activity [G	cytoplasm [GO:0005737]

1283	Q8BLY2	SYTC2_MOUSE	Probable threonine	Mus musculus (Mouse)	Tarsl2	Evidence at protein level	790	91318	threonyl-tRNA aminoacyl	ATP binding [GO:000552	cytoplasm [GO:0005737]
1284	Q80XP8	FA76B_MOUSE	Protein FAM76B	Mus musculus (Mouse)	Fam76b	Evidence at protein level	339	38556			nuclear speck [GO:00166
1285	Q99104	MYO5A_MOUSE	Unconventional my	Mus musculus (Mouse)	Myo5a	Evidence at protein level	1853	215538	actin filament-based mov	actin binding [GO:000377	actin filament [GO:00058
1286	Q99K28	ARFG2_MOUSE	ADP-ribosylation fa	Mus musculus (Mouse)	Arfgap2	Evidence at protein level	520	56598	protein transport [GO:00	GTPase activator activity	cytosol [GO:0005829]; Go
1287	Q8CHW4	EI2BE_MOUSE	Translation initiatio	Mus musculus (Mouse)	Eif2b5	Evidence at protein level	717	80086	aging [GO:0007568]; astr	guanyl-nucleotide exchan	cytoplasm [GO:0005737]
1288	Q9DCC4	P5CR3_MOUSE	Pyrroline-5-carboxy	Mus musculus (Mouse)	Pycrl	Evidence at protein level	274	28721	cytidine deamination [GC	cytidine deaminase activi	cytosol [GO:0005829]
1289	Q61749	EI2BD_MOUSE	Translation initiatio	Mus musculus (Mouse)	Eif2b4	Evidence at protein level	524	57624	cellular response to stim	translation initiation fact	cytoplasm [GO:0005737]
1290	Q9JMA2	TGT_MOUSE	Queuine tRNA-ribo	Mus musculus (Mouse)	Qtrt1	Evidence at protein level	403	44093	queuosine biosynthetic p	metal ion binding [GO:00	cytoplasm [GO:0005737]
1291	Q3UFF7	LYPL1_MOUSE	Lysophospholipase	Mus musculus (Mouse)	Lypla1	Evidence at protein level	239	26354	negative regulation of Go	carboxylic ester hydrolas	cytosol [GO:0005829]; ex
1292	Q9D110	MTHFS_MOUSE	5-formyltetrahydro	Mus musculus (Mouse)	Mthfs	Evidence at transcript level	203	23202	folic acid-containing com	5-formyltetrahydrofolate	cytoplasm [GO:0005737]
1293	Q9DBR3	ARMC8_MOUSE	Armadillo repeat-c	Mus musculus (Mouse)	Armc8	Evidence at protein level	673	75364			
1294	Q6ZPY7	KDM3B_MOUSE	Lysine-specific dem	Mus musculus (Mouse)	Kdm3b	Evidence at protein level	1562	170875	histone H3-K9 demethyla	chromatin DNA binding [(	chromatin [GO:0000785]
1295	Q8CCJ3	UFL1_MOUSE	E3 UFM1-protein li	Mus musculus (Mouse)	Ufl1	Evidence at protein level	793	89520	negative regulation of ap	ligase activity [GO:00168	cytoplasm [GO:0005737]
1296	Q3UHD6	SNX27_MOUSE	Sorting nexin-27	Mus musculus (Mouse)	Snx27	Evidence at protein level	539	60989	endosomal transport [GO	phosphatidylinositol-3-ph	cytosol [GO:0005829]; ea
1297	Q9QUR7	PIN1_MOUSE	Peptidyl-prolyl cis-t	Mus musculus (Mouse)	Pin1	Evidence at protein level	165	18370	cell cycle [GO:0007049];	beta-catenin binding [GO	cytosol [GO:0005829]; m
1298	P56812	PDCD5_MOUSE	Programmed cell d	Mus musculus (Mouse)	Pdcd5	Evidence at protein level	126	14275	apoptotic process [GO:00	acetyltransferase activat	cytoplasm [GO:0005737]
1299	Q99JX7	NXF1_MOUSE	Nuclear RNA expor	Mus musculus (Mouse)	Nxf1	Evidence at protein level	618	70300	mRNA export from nucle	mRNA binding [GO:0003	cytoplasm [GO:0005737]
1300	Q9WUK2	IF4H_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif4h	Evidence at protein level	248	27341	cytoplasmic translation [(	cadherin binding involved	cell-cell adherens junctio
1301	P62141	PP1B_MOUSE	Serine/threonine-p	Mus musculus (Mouse)	Ppp1cb	Evidence at protein level	327	37187	cell cycle [GO:0007049];	metal ion binding [GO:00	cytoplasm [GO:0005737]
1302	Q9JK92	HSPB8_MOUSE	Heat shock protein	Mus musculus (Mouse)	Hspb8	Evidence at protein level	196	21533		identical protein binding	cytoplasm [GO:0005737]
1303	Q9JJW6	ALRF2_MOUSE	Aly/REF export fact	Mus musculus (Mouse)	Alyref2	Evidence at protein level	218	23730	mRNA processing [GO:00	nucleotide binding [GO:0	cytoplasm [GO:0005737]
1304	Q8BG81	PDIP3_MOUSE	Polymerase delta-i	Mus musculus (Mouse)	Poldip3	Evidence at protein level	420	46132	poly(A)+ mRNA export fro	nucleotide binding [GO:0	nuclear speck [GO:00166
1305	O35343	IMA3_MOUSE	Importin subunit al	Mus musculus (Mouse)	Kpna4	Evidence at protein level	521	57923	NLS-bearing protein impo	nuclear localization sequ	cytosol [GO:0005829]; ex
1306	Q8C0C7	SYFA_MOUSE	Phenylalanine--tRN	Mus musculus (Mouse)	Farsa	Evidence at protein level	508	57599	phenylalanyl-tRNA amino	ATP binding [GO:000552	cytoplasm [GO:0005737]
1307	Q9D0D5	T2EA_MOUSE	General transcripti	Mus musculus (Mouse)	Gtf2e1	Evidence at protein level	440	49593	regulation of transcriptio	metal ion binding [GO:00	cytosol [GO:0005829]; nu
1308	Q99JV5	STAR4_MOUSE	StAR-related lipid t	Mus musculus (Mouse)	Stard4	Evidence at protein level	224	25579	cholesterol esterification	cholesterol binding [GO:0	cytoplasmic vesicle [GO:0
1309	Q62084	PP14B_MOUSE	Protein phosphatas	Mus musculus (Mouse)	Ppp1r14b	Evidence at protein level	147	15957	innate immune response	protein phosphatase inhi	cytoplasm [GO:0005737]
1310	Q61070	EI24_MOUSE	Etoposide-induced	Mus musculus (Mouse)	Ei24	Evidence at protein level	340	38933	autophagy [GO:0006914];	cellular response to UV-C	cytosol [GO:0005829]; er
1311	Q8JZM7	CDC73_MOUSE	Parafibromin (Cell	Mus musculus (Mouse)	Cdc73	Evidence at protein level	531	60577	cell cycle [GO:0007049];	RNA polymerase II core b	Cdc73/Paf1 complex [GO
1312	Q8CHP8	PGP_MOUSE	Glycerol-3-phosph	Mus musculus (Mouse)	Pgp	Evidence at protein level	321	34541	dephosphorylation [GO:0	glycerol-1-phosphatase a	cytosol [GO:0005829]
1313	Q60930	VDAC2_MOUSE	Voltage-dependent	Mus musculus (Mouse)	Vdac2	Evidence at protein level	295	31733	anion transport [GO:000	nucleotide binding [GO:0	extracellular exosome [G
1314	P63323	RS12_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps12	Evidence at protein level	132	14525	translation [GO:0006412	RNA binding [GO:000372	cytosol [GO:0005829]; cy
1315	P21981	TGM2_MOUSE	Protein-glutamine	Mus musculus (Mouse)	Tgm2	Evidence at protein level	686	77061	apoptotic cell clearance [	calcium ion binding [GO:(	cytoplasm [GO:0005737]
1316	Q80Y55	BSDC1_MOUSE	BSD domain-contai	Mus musculus (Mouse)	Bsdc1	Evidence at protein level	427	46953			
1317	Q8R5H1	UBP15_MOUSE	Ubiquitin carboxyl-	Mus musculus (Mouse)	Usp15	Evidence at protein level	981	112325	BMP signaling pathway [(	cysteine-type endopeptid	cytoplasm [GO:0005737]
1318	Q8CA72	GAN_MOUSE	Gigaxonin	Mus musculus (Mouse)	Gan	Evidence at protein level	597	67671	cytoskeleton organization	[GO:0007010]; protein ul	Cul3-RING ubiquitin ligas
1319	Q9JHQ5	LZTL1_MOUSE	Leucine zipper tran	Mus musculus (Mouse)	Lztfl1	Evidence at protein level	299	34773	negative regulation of pro	identical protein binding	cytosol [GO:0005829]
1320	Q8CBW3	ABI1_MOUSE	Abl interactor 1 (Ab	Mus musculus (Mouse)	Abi1	Evidence at protein level	481	52288	actin polymerization or d	cadherin binding involved	cell-cell adherens junctio
1321	Q8R4U7	LUZP1_MOUSE	Leucine zipper prot	Mus musculus (Mouse)	Luzp1	Evidence at protein level	1068	119311	artery development [GO:0060840]; neural fold ben		extracellular exosome [G
1322	P45481	CBP_MOUSE	CREB-binding prote	Mus musculus (Mouse)	Crebbp	Evidence at protein level	2441	265494	cellular response to hepa	acetyltransferase activity	condensed chromosome
1323	Q99NB8	UBQL4_MOUSE	Ubiquilin-4 (Ataxin-	Mus musculus (Mouse)	Ubqln4	Evidence at protein level	596	63506	autophagy [GO:0006914]	identical protein binding	autophagosome [GO:000
1324	Q60772	CDN2C_MOUSE	Cyclin-dependent k	Mus musculus (Mouse)	Cdkn2c	Evidence at protein level	168	18066	cell cycle arrest [GO:0007	cyclin-dependent protein	cytoplasm [GO:0005737]
1325	Q9JKP7	DPOE3_MOUSE	DNA polymerase e	Mus musculus (Mouse)	Pole3	Evidence at protein level	145	16629	histone H3 acetylation [G	DNA binding [GO:000367	Ada2/Gcn5/Ada3 transcr
1326	Q3TZX8	NOL9_MOUSE	Polynucleotide 5'-h	Mus musculus (Mouse)	Nol9	Evidence at protein level	714	80840	cleavage in ITS2 between	ATP binding [GO:000552	intermediate filament cyt
1327	P60670	NPL4_MOUSE	Nuclear protein loc	Mus musculus (Mouse)	Nploc4	Evidence at protein level	608	68017	Golgi organization [GO:0	ubiquitin binding [GO:00	cytosol [GO:0005829]; er
1328	A6H630	ARMT1_MOUSE	Protein-glutamate	Mus musculus (Mouse)	Armt1	Evidence at protein level	439	50549	cellular response to DNA	enzyme binding [GO:0019899]; protein carboxyl O-r	
1329	P62627	DLRB1_MOUSE	Dynein light chain r	Mus musculus (Mouse)	Dynlrb1	Evidence at protein level	96	10990	microtubule-based move	dynein intermediate chai	centrosome [GO:000581
1330	Q9CR98	F136A_MOUSE	Protein FAM136A	Mus musculus (Mouse)	Fam136a	Evidence at protein level	138	15674			cytoplasm [GO:0005737]
1331	Q9Z120	TRMB_MOUSE	tRNA (guanine-N(7	Mus musculus (Mouse)	Mettl1	Evidence at protein level	268	30603	RNA (guanine-N7)-methy	tRNA (guanine-N7-)-met	cytosol [GO:0005829]; nu
1332	Q9D2U5	LSMD1_MOUSE	N-alpha-acetyltran	Mus musculus (Mouse)	Naa38	Evidence at protein level	125	13430	negative regulation of apoptotic process	[GO:0043	cytoplasm [GO:0005737]
1333	Q9Z0N2	IF2H_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif2s3y	Evidence at protein level	472	51131		GTPase activity [GO:0003	eukaryotic translation ini
1334	O88939	ZBT7A_MOUSE	Zinc finger and BTB	Mus musculus (Mouse)	Zbtb7a	Evidence at protein level	569	60281	cartilage development [G	DNA binding [GO:000367	nucleus [GO:0005634]
1335	Q921I9	EXOS4_MOUSE	Exosome complex	Mus musculus (Mouse)	Exosc4	Evidence at protein level	245	26250	defense response to virus	AU-rich element binding	cytoplasm [GO:0005737]
1336	Q8BIQ5	CSTF2_MOUSE	Cleavage stimulatio	Mus musculus (Mouse)	Cstf2	Evidence at protein level	580	61341	cellular response to nerve	mRNA binding [GO:0003	cleavage body [GO:0071
1337	Q6DVA0	LEMD2_MOUSE	LEM domain-conta	Mus musculus (Mouse)	Lemd2	Evidence at protein level	511	57507	heart formation [GO:006	chromatin DNA binding [(	integral component of nu
1338	Q9WU56	TRUA_MOUSE	tRNA pseudouridin	Mus musculus (Mouse)	Pus1	Evidence at protein level	423	47502	mRNA pseudouridine syn	ligand-dependent nuclea	mitochondrion [GO:0005
1339	Q9QXS6	DREB_MOUSE	Drebrin (Developm	Mus musculus (Mouse)	Dbn1	Evidence at protein level	706	77287	actin filament organizatio	cadherin binding involved	actin cytoskeleton [GO:0
1340	P42230	STA5A_MOUSE	Signal transducer a	Mus musculus (Mouse)	Stat5a	Evidence at protein level	793	90831	2-oxoglutarate metabolic	DNA binding [GO:000367	cytoplasm [GO:0005737]
1341	Q9DBW3	NATD1_MOUSE	Protein NATD1 (Ge	Mus musculus (Mouse)	Natd1	Evidence at protein level	110	12731			
1342	Q91YU6	LZTS2_MOUSE	Leucine zipper puta	Mus musculus (Mouse)	Lzts2	Evidence at protein level	671	72578	cell division [GO:0051301];	kidney development [GO	cytoplasm [GO:0005737]
1343	Q9D9V3	ECHD1_MOUSE	Ethylmalonyl-CoA	Mus musculus (Mouse)	Echdc1	Evidence at protein level	322	35467	fatty acid beta-oxidation	carboxy-lyase activity [GO	cytosol [GO:0005829]; ex
1344	Q9ET01	PYGL_MOUSE	Glycogen phosphor	Mus musculus (Mouse)	Pygl	Evidence at protein level	850	97463	5-phosphoribose 1-dipho	AMP binding [GO:001620	cytoplasm [GO:0005737]
1345	Q8VI93	OAS3_MOUSE	2'-5'-oligoadenylat	Mus musculus (Mouse)	Oas3	Evidence at protein level	1138	126333	defense response to virus	2'-5'-oligoadenylate synt	cytoplasm [GO:0005737]
1346	Q8C181	MBNL2_MOUSE	Muscleblind-like pr	Mus musculus (Mouse)	Mbnl2	Evidence at transcript level	373	40156	mRNA processing [GO:00	metal ion binding [GO:00	cytoplasm [GO:0005737]
1347	Q3TUH1	TAM41_MOUSE	Phosphatidate cyti	Mus musculus (Mouse)	Tamm41	Evidence at protein level	337	37828	cardiolipin biosynthetic p	phosphatidate cytidylyltr	extrinsic component of m
1348	P21550	ENOB_MOUSE	Beta-enolase (EC 4	Mus musculus (Mouse)	Eno3	Evidence at protein level	434	47025	aging [GO:0007568]; glyc	magnesium ion binding [(	cytosol [GO:0005829]; ex
1349	P31725	S10A9_MOUSE	Protein S100-A9 (C	Mus musculus (Mouse)	S100a9	Evidence at protein level	113	13049	actin cytoskeleton reorga	antioxidant activity [GO:(	cell junction [GO:003005
1350	Q6NS46	RRP5_MOUSE	Protein RRP5 homc	Mus musculus (Mouse)	Pdcd11	Evidence at protein level	1862	207779	mRNA processing [GO:00	RNA binding [GO:000372	cytosol [GO:0005829]; nu
1351	Q99PM3	TF2AA_MOUSE	Transcription initia	Mus musculus (Mouse)	Gtf2a1	Evidence at transcript level	378	41614	regulation of transcriptio	DNA binding [GO:000367	cytoplasm [GO:0005737]
1352	Q8BZ20	PAR12_MOUSE	Poly [ADP-ribose] p	Mus musculus (Mouse)	Parp12	Evidence at protein level	711	79917		metal ion binding [GO:00	nucleus [GO:0005634]
1353	Q9CQ56	USE1_MOUSE	Vesicle transport p	Mus musculus (Mouse)	Use1	Evidence at protein level	270	30594	endoplasmic reticulum organization	[GO:0007029];	endoplasmic reticulum [G
1354	Q8VD04	GRAP1_MOUSE	GRIP1-associated p	Mus musculus (Mouse)	Gripap1	Evidence at protein level	806	92715			blood microparticle [GO:(
1355	Q8CAK3	RYDEN_MOUSE	Repressor of yield	Mus musculus (Mouse)	Ryden	Evidence at transcript level	290	33015	defense response to virus	RNA binding [GO:000372	cytoplasm [GO:0005737]
1356	Q60604	ADSV_MOUSE	Adseverin (Gelsolin	Mus musculus (Mouse)	Scin	Evidence at protein level	715	80254	actin filament capping [G	calcium ion binding [GO:(	brush border [GO:00059
1357	Q8JZL3	THTPA_MOUSE	Thiamine-triphosp	Mus musculus (Mouse)	Thtpa	Evidence at protein level	224	24264	dephosphorylation [GO:0	magnesium ion binding [(	cytoplasm [GO:0005737]
1358	Q9QYH6	MAGD1_MOUSE	Melanoma-associa	Mus musculus (Mouse)	Maged1	Evidence at protein level	775	85670	circadian regulation of ge	identical protein binding	chromatin [GO:0000785]
1359	Q8VBW6	ULA1_MOUSE	NEDD8-activating	Mus musculus (Mouse)	Nae1	Evidence at protein level	534	60274	mitotic DNA replication c	NEDD8 activating enzym	plasma membrane [GO:0
1360	Q9JMB0	GKAP1_MOUSE	G kinase-anchoring	Mus musculus (Mouse)	Gkap1	Evidence at protein level	366	41763	G-protein coupled receptor	signaling pathway coup	Golgi apparatus [GO:000
1361	Q3UJB9	EDC4_MOUSE	Enhancer of mRNA	Mus musculus (Mouse)	Edc4	Evidence at protein level	1406	152484	deadenylation-independent	decapping of nuclear-tr	membrane [GO:0016020
1362	Q8C650	SEP10_MOUSE	Septin-10	Mus musculus (Mouse)	Sept10	Evidence at protein level	452	52422	cell cycle [GO:0007049];	GTP binding [GO:000552	cytoplasm [GO:0005737]
1363	Q03963	E2AK2_MOUSE	Interferon-induced	Mus musculus (Mouse)	Eif2ak2	Evidence at protein level	515	58280	activation of MAPKK activ	ATP binding [GO:000552	cytoplasm [GO:0005737]
1364	Q99JF5	MVD1_MOUSE	Diphosphomevalor	Mus musculus (Mouse)	Mvd	Evidence at protein level	401	44072	cholesterol biosynthetic p	ATP binding [GO:000552	cytosol [GO:0005829]
1365	Q6WKZ8	UBR2_MOUSE	E3 ubiquitin-protei	Mus musculus (Mouse)	Ubr2	Evidence at protein level	1755	199155	cellular response to leuci	leucine binding [GO:0070	cytoplasm [GO:0005737]
1366	Q9D6K7	TTC33_MOUSE	Tetratricopeptide r	Mus musculus (Mouse)	Ttc33	Evidence at protein level	262	29371			
1367	O54692	ZW10_MOUSE	Centromere/kinetc	Mus musculus (Mouse)	Zw10	Evidence at protein level	779	88063	cell division [GO:0051301];	ER to Golgi vesicle-medi	condensed chromosome
1368	Q8VEE0	RPE_MOUSE	Ribulose-phosphat	Mus musculus (Mouse)	Rpe	Evidence at protein level	228	24945	carbohydrate metabolic p	identical protein binding	cytosol [GO:0005829]; ex
1369	Q9D1F4	AKTS1_MOUSE	Proline-rich AKT1 s	Mus musculus (Mouse)	Akt1s1	Evidence at protein level	257	27483	negative regulation of cell	size [GO:0045792]; nega	cytosol [GO:0005829]; TO
1370	P45591	COF2_MOUSE	Cofilin-2 (Cofilin, m	Mus musculus (Mouse)	Cfl2	Evidence at protein level	166	18710	actin filament depolymer	actin filament binding [G	actin cytoskeleton [GO:0
1371	Q60973	RBBP7_MOUSE	Histone-binding pro	Mus musculus (Mouse)	Rbbp7	Evidence at protein level	425	47790	cellular heat acclimation	RNA binding [GO:000372	cytosol [GO:0005829]; ES
1372	Q9WUR9	KAD4_MOUSE	Adenylate kinase 4	Mus musculus (Mouse)	Ak4	Evidence at protein level	223	25062	AMP metabolic process [(	adenylate kinase activity	extracellular exosome [G
1373	Q8CBY8	DCTN4_MOUSE	Dynactin subunit 4	Mus musculus (Mouse)	Dctn4	Evidence at protein level	467	53057	nuclear migration [GO:00	protein N-terminus bindi	centrosome [GO:000581
1374	P21619	LMNB2_MOUSE	Lamin-B2	Mus musculus (Mouse)	Lmnb2	Evidence at protein level	596	67318		structural molecule activi	lamin filament [GO:0005
1375	Q99KP3	CRYL1_MOUSE	Lambda-crystallin h	Mus musculus (Mouse)	Cryl1	Evidence at protein level	319	35209	fatty acid metabolic proc	3-hydroxyacyl-CoA dehyd	cytosol [GO:0005829]; ex
1376	P54227	STMN1_MOUSE	Stathmin (Leukemi	Mus musculus (Mouse)	Stmn1	Evidence at protein level	149	17274	axonogenesis [GO:00074	tubulin binding [GO:0015	cytoplasm [GO:0005737]
1377	P15307	REL_MOUSE	Proto-oncogene c-r	Mus musculus (Mouse)	Rel	Evidence at protein level	587	64960	cytokine production [GO:	chromatin binding [GO:0	cytoplasm [GO:0005737]
1378	Q8K2I1	FNTB_MOUSE	Protein farnesyltra	Mus musculus (Mouse)	Fntb	Evidence at protein level	437	48820	negative regulation of cel	drug binding [GO:000814	microtubule associated c
1379	Q8VDC1	FYCO1_MOUSE	FYVE and coiled-co	Mus musculus (Mouse)	Fyco1	Evidence at protein level	1437	162336	'de novo' protein folding	metal ion binding [GO:00	autophagosome [GO:000
1380	Q91V01	MBOA5_MOUSE	Lysophospholipid a	Mus musculus (Mouse)	Lpcat3	Evidence at protein level	487	56147	phospholipid biosynthetic	1-acylglycerophosphocho	endoplasmic reticulum m
1381	Q9CQV7	TIM14_MOUSE	Mitochondrial impo	Mus musculus (Mouse)	Dnajc19	Evidence at protein level	116	12437	genitalia development [G	0048806]; protein trans	integral component of m
1382	Q9D0M0	EXOS7_MOUSE	Exosome complex	Mus musculus (Mouse)	Exosc7	Evidence at protein level	291	31825	rRNA processing [GO:000	RNA binding [GO:000372	cytosol [GO:0005737]
1383	Q9QZV9	NXT1_MOUSE	NTF2-related expor	Mus musculus (Mouse)	Nxt1	Evidence at protein level	140	15847	mRNA transport [GO:005	Ran GTPase binding [GO:	cytosol [GO:0005829]; nu
1384	O35465	FKBP8_MOUSE	Peptidyl-prolyl cis-t	Mus musculus (Mouse)	Fkbp8	Evidence at protein level	402	43529	apoptotic process [GO:00	FK506 binding [GO:00055	cytosol [GO:0005829]; er
1385	Q9CY62	RN181_MOUSE	E3 ubiquitin-protei	Mus musculus (Mouse)	Rnf181	Evidence at protein level	165	19101	proteasome-mediated ub	ubiquitin protein ligase activity	[GO:0061630]; ubiq
1386	Q9QYI5	DNJB2_MOUSE	DnaJ homolog subf	Mus musculus (Mouse)	Dnajb2	Evidence at protein level	324	35593	chaperone-mediated prot	ATPase activator activity	cytoplasm [GO:0005737]
1387	Q64514	TPP2_MOUSE	Tripeptidyl-peptida	Mus musculus (Mouse)	Tpp2	Evidence at protein level	1262	139879		aminopeptidase activity [	cytosol [GO:0005829]; nu
1388	Q5U458	DJC11_MOUSE	DnaJ homolog subf	Mus musculus (Mouse)	Dnajc11	Evidence at protein level	559	63233			extracellular exosome [G
1389	P61965	WDR5_MOUSE	WD repeat-contain	Mus musculus (Mouse)	Wdr5	Evidence at protein level	334	36588	cilium assembly [GO:006	histone acetyltransferase	Ada2/Gcn5/Ada3 transcr
1390	Q8BUV3	GEPH_MOUSE	Gephyrin [Includes	Mus musculus (Mouse)	Gphn	Evidence at protein level	769	83282	establishment of synaptic	ATP binding [GO:000552	cell junction [GO:003005
1391	Q9D428	GOG7B_MOUSE	Golgin subfamily A	Mus musculus (Mouse)	GOLGA7B	Evidence at protein level	167	18335	peptidyl-L-cysteine S-palmitoylation	[GO:0018230];	Golgi membrane [GO:000
1392	P47199	QOR_MOUSE	Quinone oxidoredu	Mus musculus (Mouse)	Cryz	Evidence at protein level	331	35269	protein homotetrameriza	mRNA 3'-UTR binding [GO	cytosol [GO:0005829]; ex
1393	Q3TRM8	HXK3_MOUSE	Hexokinase-3 (EC 2	Mus musculus (Mouse)	Hk3	Evidence at protein level	922	100101	cellular glucose homeost	ATP binding [GO:000552	cytosol [GO:0005829]; m
1394	Q9CQX2	CYB5B_MOUSE	Cytochrome b5 typ	Mus musculus (Mouse)	Cyb5b	Evidence at protein level	146	16318	oxidation-reduction proce	enzyme activator activity	integral component of m
1395	Q8BGA5	KRR1_MOUSE	KRR1 small subunit	Mus musculus (Mouse)	Krr1	Evidence at transcript level	380	43538	maturation of SSU-rRNA	RNA binding [GO:000372	cytoplasm [GO:0005737]
1396	Q8BHS3	RBM22_MOUSE	Pre-mRNA-splicing	Mus musculus (Mouse)	Rbm22	Evidence at protein level	420	46896	cellular response to drug	calcium-dependent prote	catalytic step 2 spliceoso
1397	Q99JI6	THUM1_MOUSE	THUMP domain-co	Mus musculus (Mouse)	Thumpd1	Evidence at protein level	350	38885	tRNA modification [GO:0	RNA binding [GO:0003723]	
1398	Q9D662	SC23B_MOUSE	Protein transport p	Mus musculus (Mouse)	Sec23b	Evidence at protein level	767	86437	ER to Golgi vesicle-media	zinc ion binding [GO:000	COPII vesicle coat [GO:00
1399	Q8CG72	ARHL2_MOUSE	Poly(ADP-ribose) gl	Mus musculus (Mouse)	Adprhl2	Evidence at protein level	370	39414	cellular response to super	metal ion binding [GO:00	cytoplasm [GO:0005737]

1400	Q99L88	SNTB1_MOUSE	Beta-1-syntrophin	Mus musculus (Mouse)	Sntb1	Evidence at protein level	537	58081		structural molecule activi	cytoplasm [GO:0005737]
1401	Q8BZM1	GLMN_MOUSE	Glomulin (FK506-bi	Mus musculus (Mouse)	Glmn	Evidence at protein level	596	67756	cell surface receptor sign	hepatocyte growth factor	Cul2-RING ubiquitin ligas
1402	Q8BWQ6	CP062_MOUSE	UPF0505 protein C	Mus musculus (Mouse)		Evidence at protein level	963	109077	Golgi to plasma membrane transport [GO:0006893		early endosome [GO:000
1403	P23506	PIMT_MOUSE	Protein-L-isoaspart	Mus musculus (Mouse)	Pcmt1	Evidence at protein level	227	24634	protein methylation [GO:	protein-L-isoaspartate (D	cytoplasm [GO:0005737]
1404	Q60605	MYL6_MOUSE	Myosin light polype	Mus musculus (Mouse)	Myl6	Evidence at protein level	151	16930	muscle contraction [GO:0	actin-dependent ATPase	brush border [GO:00059
1405	Q3U308	CTU2_MOUSE	Cytoplasmic tRNA	Mus musculus (Mouse)	Ctu2	Evidence at protein level	514	56105	tRNA thio-modification [G	sulfurtransferase activity	cytosol [GO:0005829]; pr
1406	P58742	AAAS_MOUSE	Aladin (Adracalin)	Mus musculus (Mouse)	Aaas	Evidence at protein level	546	59431	fertilization [GO:0009566];	learning [GO:0007612];	centrosome [GO:000581
1407	Q6PFY1	FCSD1_MOUSE	F-BAR and double S	Mus musculus (Mouse)	Fchsd1	Evidence at transcript level	688	76256	neuromuscular synaptic transmission [GO:0007274		neuromuscular junction [
1408	P62737	ACTA_MOUSE	Actin, aortic smoot	Mus musculus (Mouse)	Acta2	Evidence at protein level	377	42009	glomerular mesangial cell	ATP binding [GO:0005524	actin cytoskeleton [GO:0
1409	Q8BZ21	KAT6A_MOUSE	Histone acetyltrans	Mus musculus (Mouse)	Kat6a	Evidence at protein level	2003	224919	aorta morphogenesis [GC	acetyltransferase activity	cytosol [GO:0005829]; M
1410	A0JNT9	BICL1_MOUSE	BICD family-like ca	Mus musculus (Mouse)	Bicdl1	Evidence at protein level	577	65287	Golgi to secretory granul	dynactin binding [GO:003	centrosome [GO:000581
1411	Q9WVF7	DPOE1_MOUSE	DNA polymerase e	Mus musculus (Mouse)	Pole	Evidence at protein level	2283	262100	base-excision repair, gap-	4 iron, 4 sulfur cluster bin	epsilon DNA polymerase
1412	Q9D8S3	ARFG3_MOUSE	ADP-ribosylation fa	Mus musculus (Mouse)	Arfgap3	Evidence at protein level	523	57456	protein secretion [GO:000	GTPase activator activity	cytosol [GO:0005829]; Go
1413	F8VPU2	FARP1_MOUSE	FERM, RhoGEF and	Mus musculus (Mouse)	Farp1	Evidence at protein level	1048	118875	dendrite morphogenesis	Rac guanyl-nucleotide exc	cell junction [GO:003005
1414	Q9CQC8	SPG21_MOUSE	Maspardin (Acid cl	Mus musculus (Mouse)	Spg21	Evidence at protein level	308	34952		CD4 receptor binding [GC	cytosol [GO:0005829]; in
1415	Q61210	ARHG1_MOUSE	Rho guanine nuclec	Mus musculus (Mouse)	Arhgef1	Evidence at protein level	920	102805	regulation of Rho protein	GTPase activator activity	cytosol [GO:0005829]; pl
1416	Q9D114	MESH1_MOUSE	Guanosine-3',5'-bis	Mus musculus (Mouse)	Hddc3	Evidence at protein level	179	20262		guanosine-3',5'-bis(diphosphate)	3'-diphosphatase
1417	Q9D2V8	MFS10_MOUSE	Major facilitator su	Mus musculus (Mouse)	Mfsd10	Evidence at protein level	456	49369	apoptotic process [GO:00	organic anion transmemb	brush border membrane
1418	Q99PF4	CAD23_MOUSE	Cadherin-23 (Otoca	Mus musculus (Mouse)	Cdh23	Evidence at protein level	3354	369623	auditory receptor cell diff	calcium ion binding [GO:0	centrosome [GO:000581
1419	Q99PG6	TS1R1_MOUSE	Taste receptor type	Mus musculus (Mouse)	Tas1r1	Evidence at transcript level	842	93426	sensory perception of um	G-protein coupled recept	integral component of me
1420	P19137	LAMA1_MOUSE	Laminin subunit alp	Mus musculus (Mouse)	Lama1	Evidence at protein level	3084	338172	axon guidance [GO:00074	extracellular matrix struc	basal lamina [GO:000560
1421	Q8K4R4	PITC1_MOUSE	Cytoplasmic phosp	Mus musculus (Mouse)	Pitpnc1	Evidence at protein level	332	38384	phosphatidylinositol met	phosphatidic acid binding	cytoplasm [GO:0005737]
1422	Q8K284	TF3C1_MOUSE	General transcripti	Mus musculus (Mouse)	Gtf3c1	Evidence at protein level	2101	237476	5S class rRNA transcriptic	RNA polymerase III type	intracellular ribonucleopr
1423	Q8C167	PPCEL_MOUSE	Prolyl endopeptida	Mus musculus (Mouse)	Prepl	Evidence at protein level	725	83194		serine-type endopeptidas	cytoskeleton [GO:000585
1424	Q99ME2	WDR6_MOUSE	WD repeat-contain	Mus musculus (Mouse)	Wdr6	Evidence at protein level	1125	121898	cell cycle arrest [GO:0007	RNA binding [GO:000372	cytoplasm [GO:0005737]
1425	Q8C142	ARH_MOUSE	Low density lipopro	Mus musculus (Mouse)	Ldlrap1	Evidence at protein level	308	33975	amyloid precursor protei	AP-2 adaptor complex bir	AP-1 adaptor complex [G
1426	Q3UA06	PCH2_MOUSE	Pachytene checkpo	Mus musculus (Mouse)	Trip13	Evidence at protein level	432	48377	double-strand break repa	ATP binding [GO:0005524	male germ cell nucleus [G
1427	Q9QYF9	NDRG3_MOUSE	Protein NDRG3 (N-	Mus musculus (Mouse)	Ndrg3	Evidence at protein level	375	41555			cytoplasm [GO:0005737]
1428	O88291	ZN326_MOUSE	DBIRD complex sub	Mus musculus (Mouse)	Znf326	Evidence at protein level	580	65225	mRNA processing [GO:00	DNA binding [GO:000367	DBIRD complex [GO:0044
1429	O88746	TOM1_MOUSE	Target of Myb prot	Mus musculus (Mouse)	Tom1	Evidence at protein level	492	54325	intracellular protein trans	clathrin binding [GO:003	cytoplasm [GO:0005737]
1430	P83940	ELOC_MOUSE	Elongin-C (EloC) (El	Mus musculus (Mouse)	Eloc	Evidence at protein level	112	12473	positive regulation of transcription elongation from		elongin complex [GO:007
1431	Q8BM39	PRP18_MOUSE	Pre-mRNA-splicing	Mus musculus (Mouse)	Prpf18	Evidence at protein level	342	39890	generation of catalytic spliceosome for second tran		nuclear speck [GO:00166
1432	Q9CWY8	RNH2A_MOUSE	Ribonuclease H2 su	Mus musculus (Mouse)	Rnaseh2a	Evidence at protein level	301	33513	mismatch repair [GO:000	metal ion binding [GO:00	cytosol [GO:0005829]; nu
1433	Q8CI32	BAG5_MOUSE	BAG family molecu	Mus musculus (Mouse)	Bag5	Evidence at protein level	447	50943	Golgi organization [GO:0	chaperone binding [GO:0	cytosol [GO:0005829]; in
1434	O09044	SNP23_MOUSE	Synaptosomal-assc	Mus musculus (Mouse)	Snap23	Evidence at protein level	210	23261	exocytosis [GO:0006887]	SNAP receptor activity [G	azurophil granule [GO:00
1435	Q9EPQ7	STAR5_MOUSE	StAR-related lipid t	Mus musculus (Mouse)	Stard5	Evidence at protein level	213	23922	cholesterol import [GO:0	bile acid binding [GO:003	mitochondrion [GO:0005
1436	P60060	SC61G_MOUSE	Protein transport p	Mus musculus (Mouse)	Sec61g	Inferred from homology	68	7741	protein targeting [GO:000	P-P-bond-hydrolysis-drive	endoplasmic reticulum m
1437	Q5I1X5	IASPP_MOUSE	RelA-associated inh	Mus musculus (Mouse)	Ppp1r13l	Evidence at protein level	824	88976	apoptotic process [GO:00	cadherin binding involved	cell-cell adherens junctio
1438	P58466	CTDS1_MOUSE	Carboxy-terminal d	Mus musculus (Mouse)	Ctdsp1	Evidence at protein level	261	29266	negative regulation of G1	CTD phosphatase activity	extracellular exosome [G
1439	Q9CWL8	CTBL1_MOUSE	Beta-catenin-like p	Mus musculus (Mouse)	Ctnnbl1	Evidence at protein level	563	64980	apoptotic process [GO:00	enzyme binding [GO:001	membrane [GO:0016020
1440	Q9D8Z1	ASCC1_MOUSE	Activating signal co	Mus musculus (Mouse)	Ascc1	Evidence at protein level	356	41280	regulation of transcriptio	RNA binding [GO:000372	neuromuscular junction [
1441	Q9CXA2	T3HPD_MOUSE	Trans-L-3-hydroxy	Mus musculus (Mouse)	L3hypdh	Evidence at protein level	354	37804	metabolic process [GO:0	hydro-lyase activity [GO:0016836];	trans-L-3-hydro
1442	Q6PIP5	NUDC1_MOUSE	NudC domain-cont	Mus musculus (Mouse)	Nudcd1	Evidence at protein level	582	66705			cytosol [GO:0005829]; nu
1443	Q8BPM2	M4K5_MOUSE	Mitogen-activated	Mus musculus (Mouse)	Map4k5	Evidence at protein level	847	95045	intracellular signal transd	ATP binding [GO:0005524	cytoplasm [GO:0005737]
1444	Q9JJ28	FLII_MOUSE	Protein flightless-1	Mus musculus (Mouse)	Flii	Evidence at protein level	1271	144803	actin cytoskeleton organi	actin binding [GO:000377	brush border [GO:00059
1445	O55137	ACOT1_MOUSE	Acyl-coenzyme A t	Mus musculus (Mouse)	Acot1	Evidence at protein level	419	46136	acyl-CoA metabolic proce	acyl-CoA hydrolase activi	cytoplasm [GO:0005737]
1446	Q9CQ71	RFA3_MOUSE	Replication protein	Mus musculus (Mouse)	Rpa3	Evidence at protein level	121	13584	base-excision repair [GO:	damaged DNA binding [G	DNA replication factor A
1447	Q9D0R4	DDX56_MOUSE	Probable ATP-depe	Mus musculus (Mouse)	Ddx56	Evidence at transcript level	546	61212	positive regulation of neu	ATP binding [GO:0005524	membrane [GO:0016020
1448	Q9JHU2	PALMD_MOUSE	Palmdelphin	Mus musculus (Mouse)	Palmd	Evidence at protein level	551	62700	regulation of cell shape [GO:0008360]		cytoplasm [GO:0005737]
1449	Q9R060	NUBP1_MOUSE	Cytosolic Fe-S clust	Mus musculus (Mouse)	Nubp1	Evidence at protein level	320	34085	cell growth [GO:0016049	4 iron, 4 sulfur cluster bin	centriole [GO:0005814];
1450	O70404	VAMP8_MOUSE	Vesicle-associated	Mus musculus (Mouse)	Vamp8	Evidence at protein level	101	11451	autophagosome docking	chloride channel inhibitor	azurophil granule membr
1451	Q9DCL2	FA96A_MOUSE	MIP18 family prote	Mus musculus (Mouse)	Fam96a	Evidence at protein level	160	18418	chromosome segregation	metal ion binding [GO:00	cytosol [GO:0005829]; nu
1452	P70202	LXN_MOUSE	Latexin (Endogenou	Mus musculus (Mouse)	Lxn	Evidence at protein level	222	25492	detection of temperature	heparin binding [GO:000	cytoplasm [GO:0005737]
1453	Q64261	CDK6_MOUSE	Cyclin-dependent k	Mus musculus (Mouse)	Cdk6	Evidence at protein level	326	37028	cell dedifferentiation [GO	ATP binding [GO:0005524	centrosome [GO:000581
1454	Q9JMD3	PCTL_MOUSE	PCTP-like protein (I	Mus musculus (Mouse)	Stard10	Evidence at protein level	291	32951	bile acid secretion [GO:0	lipid binding [GO:0008289	cytosol [GO:0005829]; in
1455	Q9CX80	CYGB_MOUSE	Cytoglobin (Histogl	Mus musculus (Mouse)	Cygb	Evidence at protein level	190	21466	fatty acid oxidation [GO:0	catalase activity [GO:000	cytoplasm [GO:0005737]
1456	Q9QZB9	DCTN5_MOUSE	Dynactin subunit 5	Mus musculus (Mouse)	Dctn5	Evidence at protein level	182	20141	aorta development [GO:0035904];	coronary vascula	centrosome [GO:000581
1457	Q8BGS2	BOLA2_MOUSE	BolA-like protein 2	Mus musculus (Mouse)	Bola2	Evidence at protein level	86	10215	[2Fe-2S] cluster assembly [GO:0044571];	protein m	cytoplasm [GO:0005737]
1458	Q9Z2L7	CRLF3_MOUSE	Cytokine receptor-l	Mus musculus (Mouse)	Crlf3	Evidence at protein level	442	49559	G1/S transition of mitotic	identical protein binding	cytoplasm [GO:0005737]
1459	Q62448	IF4G2_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif4g2	Evidence at protein level	906	102106	cellular macromolecule b	cadherin binding involved	cell-cell adherens junctio
1460	O55239	NNMT_MOUSE	Nicotinamide N-me	Mus musculus (Mouse)	Nnmt	Evidence at protein level	264	29598	animal organ regeneratio	nicotinamide N-methyltra	cytosol [GO:0005829]
1461	Q8K274	KT3K_MOUSE	Ketosamine-3-kina	Mus musculus (Mouse)	Fn3krp	Evidence at protein level	309	34468		kinase activity [GO:0016301]	
1462	Q9CPS7	PNO1_MOUSE	RNA-binding protei	Mus musculus (Mouse)	Pno1	Evidence at protein level	248	27454		RNA binding [GO:000372	nucleolus [GO:0005730];
1463	Q9D7J7	CPNS2_MOUSE	Calpain small subu	Mus musculus (Mouse)	Capns2	Evidence at transcript level	247	27190		calcium-dependent syste	cytoplasm [GO:0005737]
1464	Q8BUK6	HOOK3_MOUSE	Protein Hook homc	Mus musculus (Mouse)	Hook3	Evidence at protein level	718	83218	cytoplasmic microtubule	dynein light intermediate	centriolar satellite [GO:0
1465	Q9Z1E3	IKBA_MOUSE	NF-kappa-B inhibit	Mus musculus (Mouse)	Nfkbia	Evidence at protein level	314	35071	cellular response to cytok	enzyme binding [GO:001	cytoplasm [GO:0005737]
1466	O35654	DPOD2_MOUSE	DNA polymerase d	Mus musculus (Mouse)	Pold2	Evidence at protein level	469	51355	cellular response to DNA	DNA binding [GO:000367	delta DNA polymerase co
1467	P70362	UFD1_MOUSE	Ubiquitin fusion de	Mus musculus (Mouse)	Ufd1l	Evidence at protein level	307	34481	ER-associated misfolded	K48-linked polyubiquitin	cytoplasm [GO:0005737]
1468	Q9CX30	YIF1B_MOUSE	Protein YIF1B (YIP1	Mus musculus (Mouse)	Yif1b	Evidence at protein level	311	33983	ER to Golgi vesicle-mediated transport [GO:000688		endoplasmic reticulum-G
1469	Q8BVL3	SNX17_MOUSE	Sorting nexin-17	Mus musculus (Mouse)	Snx17	Evidence at protein level	470	52797	aorta development [GO:0	low-density lipoprotein p	cytoplasm [GO:0005737]
1470	Q9JKY0	RCD1_MOUSE	Cell differentiation	Mus musculus (Mouse)	Rqcd1	Evidence at protein level	299	33601	cytokine-mediated signal	protein domain specific b	CCR4-NOT complex [GO:0
1471	P49300	CLC10_MOUSE	C-type lectin doma	Mus musculus (Mouse)	Clec10a	Evidence at protein level	304	34596	connective tissue replace	carbohydrate binding [GC	integral component of me
1472	Q9CX00	IST1_MOUSE	IST1 homolog	Mus musculus (Mouse)	Ist1	Evidence at protein level	362	39468	abscission [GO:0009838]	cadherin binding involved	cell-cell adherens junctio
1473	Q921Z5	TFIP8_MOUSE	Tumor necrosis fac	Mus musculus (Mouse)	Tnfaip8	Evidence at protein level	198	22960	defense response to Gra	cysteine-type endopeptid	cytoplasm [GO:0005737]
1474	P62849	RS24_MOUSE	40S ribosomal prot	Mus musculus (Mouse)	Rps24	Evidence at protein level	133	15423	erythrocyte homeostasis	nucleotide binding [GO:0	cytosolic small ribosomal
1475	Q64008	RAB34_MOUSE	Ras-related protein	Mus musculus (Mouse)	Rab34	Evidence at protein level	259	29101	antigen processing and pr	GTPase activity [GO:0003	cytoplasmic vesicle [GO:0
1476	Q9JKY5	HIP1R_MOUSE	Huntingtin-interact	Mus musculus (Mouse)	Hip1r	Evidence at protein level	1068	119426	activation of cysteine-typ	actin binding [GO:000377	apical plasma membrane
1477	Q3UJ81	NEPR1_MOUSE	Nuclear envelope p	Mus musculus (Mouse)	Cnep1r1	Evidence at protein level	125	14267	lipid metabolic process [GO:0006629];	positive regu	cytoplasm [GO:0005737]
1478	Q9CPZ6	ORML3_MOUSE	ORM1-like protein	Mus musculus (Mouse)	Ormdl3	Evidence at transcript level	153	17477	cellular sphingolipid homeostasis [GO:0090156];	ce	endoplasmic reticulum [G
1479	Q9CQZ0	ORML2_MOUSE	ORM1-like protein	Mus musculus (Mouse)	Ormdl2	Evidence at protein level	153	17390	cellular sphingolipid homeostasis [GO:0090156];	ce	endoplasmic reticulum [G
1480	Q91YN5	UAP1_MOUSE	UDP-N-acetylhexos	Mus musculus (Mouse)	Uap1	Evidence at protein level	522	58609	UDP-N-acetylglucosamin	identical protein binding	cytosol [GO:0005829]; nu
1481	Q60710	SAMH1_MOUSE	Deoxynucleoside tr	Mus musculus (Mouse)	Samhd1	Evidence at protein level	627	72650	dATP catabolic process [G	dGTPase activity [GO:000	nucleoplasm [GO:0005654
1482	Q6NXJ0	WWC2_MOUSE	Protein WWC2 (WW	Mus musculus (Mouse)	Wwc2	Evidence at protein level	1187	132620	negative regulation of hip	kinase binding [GO:0019	cytosol [GO:0005829]
1483	Q3TC93	H1BP3_MOUSE	HCLS1-binding prot	Mus musculus (Mouse)	Hs1bp3	Evidence at protein level	395	43691	cell surface receptor sign	phosphatidylinositol bind	endoplasmic reticulum [G
1484	Q8K3W0	BRE_MOUSE	BRCA1-A complex s	Mus musculus (Mouse)	Bre	Evidence at protein level	383	43545	apoptotic process [GO:00	polyubiquitin binding [GC	BRCA1-A complex [GO:00
1485	Q9D211	C2AIL_MOUSE	CDKN2AIP N-termi	Mus musculus (Mouse)	Cdkn2aipnl	Inferred from homology	116	13209	signal transduction [GO:0007165]		nucleolus [GO:0005730];
1486	P62965	RABP1_MOUSE	Cellular retinoic aci	Mus musculus (Mouse)	Crabp1	Evidence at protein level	137	15592	retinoic acid catabolic pro	retinal binding [GO:0016	cytoplasm [GO:0005737]
1487	P22935	RABP2_MOUSE	Cellular retinoic aci	Mus musculus (Mouse)	Crabp2	Evidence at transcript level	138	15746	embryonic forelimb morp	cyclin binding [GO:00303	cytoplasm [GO:0005737]
1488	P43274	H14_MOUSE	Histone H1.4 (H1 V	Mus musculus (Mouse)	Hist1h1e	Evidence at protein level	219	21977	histone H3-K27 trimethyl	chromatin DNA binding [(	extracellular exosome [G
1489	Q9CSN1	SNW1_MOUSE	SNW domain-conta	Mus musculus (Mouse)	Snw1	Evidence at protein level	536	61475	cellular response to retin	Notch binding [GO:00051	catalytic step 2 spliceoso
1490	Q9DBG9	TX1B3_MOUSE	Tax1-binding prote	Mus musculus (Mouse)	Tax1bp3	Evidence at protein level	124	13723	activation of GTPase acti	beta-catenin binding [GO	actin cytoskeleton [GO:0
1491	P63044	VAMP2_MOUSE	Vesicle-associated	Mus musculus (Mouse)	Vamp2	Evidence at protein level	116	12691	calcium ion regulated exc	calcium-dependent prote	cell junction [GO:003005
1492	Q8BI08	MAL2_MOUSE	Protein MAL2	Mus musculus (Mouse)	Mal2	Evidence at protein level	175	19094	membrane raft polarizati	structural constituent of	apical plasma membrane
1493	Q9CXD9	LRC17_MOUSE	Leucine-rich repeat	Mus musculus (Mouse)	Lrrc17	Evidence at transcript level	443	51852	bone marrow development [GO:0048539];	negative	extracellular space [GO:0
1494	P53657	KPYR_MOUSE	Pyruvate kinase PK	Mus musculus (Mouse)	Pklr	Evidence at protein level	574	62309	cellular response to insuli	ATP binding [GO:0005524	cytoplasm [GO:0005737]
1495	Q921F4	HNRLL_MOUSE	Heterogeneous nuc	Mus musculus (Mouse)	Hnrnpll	Evidence at protein level	591	64125	mRNA processing [GO:00	mRNA binding [GO:00037	intracellular ribonucleopr
1496	Q8BPG6	SUMF2_MOUSE	Sulfatase-modifyin	Mus musculus (Mouse)	Sumf2	Evidence at protein level	308	34737		metal ion binding [GO:00	endoplasmic reticulum [G
1497	O08543	EFNA5_MOUSE	Ephrin-A5 (AL-1) (E	Mus musculus (Mouse)	Efna5	Evidence at protein level	228	26339	axon guidance [GO:0007	chemorepellent activity	adherens junction [GO:00
1498	Q62172	RBP1_MOUSE	RalA-binding protei	Mus musculus (Mouse)	Ralbp1	Evidence at protein level	648	75043	endocytosis [GO:0006897	ATPase activity [GO:0016	intracellular [GO:000562
1499	P06684	CO5_MOUSE	Complement C5 (H	Mus musculus (Mouse)	C5	Evidence at protein level	1680	188878	complement activation, a	endopeptidase inhibitor a	extracellular exosome [G
1500	P58802	TB10A_MOUSE	TBC1 domain famil	Mus musculus (Mouse)	Tbc1d10a	Evidence at protein level	500	56202	activation of cysteine-typ	cadherin binding involved	cell-cell adherens junctio
1501	Q61990	PCBP2_MOUSE	Poly(rC)-binding pr	Mus musculus (Mouse)	Pcbp2	Evidence at protein level	362	38222	defense response to virus	C-rich single-stranded DN	cytoplasm [GO:0005737]
1502	Q61955	KLK8_MOUSE	Kallikrein-8 (mK8) (	Mus musculus (Mouse)	Klk8	Evidence at protein level	260	28524	cell death [GO:0008219];	serine-type endopeptidas	cytoplasm [GO:0005737]
1503	O70589	CSKP_MOUSE	Peripheral plasma	Mus musculus (Mouse)	Cask	Evidence at protein level	926	105109	calcium ion import [GO:0	ATP binding [GO:0005524	basement membrane [GO
1504	Q61411	RASH_MOUSE	GTPase HRas (H-Ra	Mus musculus (Mouse)	Hras	Evidence at protein level	189	21298	cell aging [GO:0007569];	GTPase activity [GO:0003	Golgi apparatus [GO:000
1505	Q6ZPJ3	UBE2O_MOUSE	(E3-independent) E	Mus musculus (Mouse)	Ube2o	Evidence at protein level	1288	140834	positive regulation of BM	ATP binding [GO:0005524	cytoplasm [GO:0005737]
1506	Q61292	LAMB2_MOUSE	Laminin subunit be	Mus musculus (Mouse)	Lamb2	Evidence at protein level	1799	196579	astrocyte development [(	integrin binding [GO:000	basal lamina [GO:000560
1507	O88544	CSN4_MOUSE	COP9 signalosome	Mus musculus (Mouse)	Cops4	Evidence at protein level	406	46285	protein deneddylation [GO:0000338]		cell junction [GO:003005
1508	F6ZDS4	TPR_MOUSE	Nucleoprotein TPR	Mus musculus (Mouse)	Tpr	Evidence at protein level	2431	273990	cell division [GO:0051301	chromatin binding [GO:0	cytoplasm [GO:0005737]
1509	Q6PAV2	HERC4_MOUSE	Probable E3 ubiquit	Mus musculus (Mouse)	Herc4	Evidence at protein level	1057	118412	cell differentiation [GO:0	ubiquitin protein ligase a	cytosol [GO:0005829]; fit
1510	Q9EQG3	SCEL_MOUSE	Sciellin	Mus musculus (Mouse)	Scel	Evidence at protein level	652	72972	embryo development [GC	zinc ion binding [GO:000	cytoplasm [GO:0005737]
1511	Q8R5A6	TB22A_MOUSE	TBC1 domain famil	Mus musculus (Mouse)	Tbc1d22a	Evidence at protein level	516	59362	activation of GTPase acti	14-3-3 protein binding [G	endomembrane system [
1512	Q920E5	FPPS_MOUSE	Farnesyl pyrophosp	Mus musculus (Mouse)	Fdps	Evidence at protein level	353	40582	cholesterol biosynthetic p	dimethylallyltranstransfe	cytosol [GO:0005829]; m
1513	Q8VDP3	MICA1_MOUSE	[F-actin]-methionir	Mus musculus (Mouse)	Mical1	Evidence at protein level	1048	116785	actin filament depolymer	actin binding [GO:000377	cytoplasm [GO:0005737]
1514	Q64321	ZBT7B_MOUSE	Zinc finger and BTB	Mus musculus (Mouse)	Zbtb7b	Evidence at protein level	544	58918	cell differentiation [GO:0	DNA binding [GO:000367	nucleoplasm [GO:0005654
1515	O08638	MYH11_MOUSE	Myosin-11 (Myosin	Mus musculus (Mouse)	Myh11	Evidence at protein level	1972	227028	cardiac muscle fiber deve	ATP binding [GO:0005524	brush border [GO:00059
1516	Q8BTZ4	APC5_MOUSE	Anaphase-promoti	Mus musculus (Mouse)	Anapc5	Evidence at protein level	740	83098	cell division [GO:0051301	protein phosphatase bind	anaphase-promoting com

1517	Q99KF1	TMED9_MOUSE	Transmembrane er	Mus musculus (Mouse)	Tmed9	Evidence at protein level	235	27127	COPI coating of Golgi vesi	syntaxin binding [GO:001	endoplasmic reticulum [G
1518	P97371	PSME1_MOUSE	Proteasome activat	Mus musculus (Mouse)	Psme1	Evidence at protein level	249	28673	antigen processing and pr	endopeptidase activator	cytoplasm [GO:0005737]
1519	Q9ER88	RT29_MOUSE	28S ribosomal prot	Mus musculus (Mouse)	Dap3	Evidence at protein level	391	44699	apoptotic mitochondrial	RNA binding [GO:000372	mitochondrial matrix [GO
1520	Q8CFZ4	GPC3_MOUSE	Glypican-3 [Cleave	Mus musculus (Mouse)	Gpc3	Evidence at transcript level	579	65332	animal organ morphogen	peptidyl-dipeptidase inhi	anchored component of p
1521	Q3UL36	ARGL1_MOUSE	Arginine and glutar	Mus musculus (Mouse)	Arglu1	Evidence at protein level	271	32887		cadherin binding involve	cell-cell adherens junctio
1522	Q8BK62	OLFL3_MOUSE	Olfactomedin-like p	Mus musculus (Mouse)	Olfml3	Evidence at transcript level	406	45746	multicellular organism development [GO:0007275]		extracellular space [GO:0
1523	O35604	NPC1_MOUSE	Niemann-Pick C1 p	Mus musculus (Mouse)	Npc1	Evidence at protein level	1277	142885	adult walking behavior [G	cholesterol binding [GO:0	endoplasmic reticulum [G
1524	Q8BP27	SFR1_MOUSE	Swi5-dependent re	Mus musculus (Mouse)	Sfr1	Evidence at protein level	319	35183	cellular response to estro	ligand-dependent nuclea	nucleus [GO:0005634]; S
1525	Q9DBR7	MYPT1_MOUSE	Protein phosphatas	Mus musculus (Mouse)	Ppp1r12a	Evidence at protein level	1029	114996	cellular response to drug	14-3-3 protein binding [G	A band [GO:0031672]; ac
1526	O55242	SGMR1_MOUSE	Sigma non-opioid i	Mus musculus (Mouse)	Sigmar1	Evidence at protein level	223	25250	lipid transport [GO:00068	opioid receptor activity [	cell junction [GO:003005
1527	Q63836	SBP2_MOUSE	Selenium-binding p	Mus musculus (Mouse)	Selenbp2	Evidence at protein level	472	52610	protein transport [GO:00	selenium binding [GO:00	cytosol [GO:0005829]; ex
1528	Q8K2B0	SC65_MOUSE	Synaptonemal com	Mus musculus (Mouse)	P3h4	Evidence at transcript level	443	51132			nucleolus [GO:0005730]
1529	Q9CYZ6	CS060_MOUSE	Uncharacterized pr	Mus musculus (Mouse)		Evidence at protein level	169	18706			
1530	Q99KX1	MLF2_MOUSE	Myeloid leukemia f	Mus musculus (Mouse)	Mlf2	Evidence at protein level	247	28055	defense response [GO:0006952]		cytoplasm [GO:0005737]
1531	E9PZQ0	RYR1_MOUSE	Ryanodine recepto	Mus musculus (Mouse)	Ryr1	Evidence at protein level	5035	565039	calcium ion transport [GO	calcium channel activity [	cell cortex [GO:0005938]
1532	O35130	NEP1_MOUSE	Ribosomal RNA sm	Mus musculus (Mouse)	Emg1	Evidence at protein level	244	26974	blastocyst development [	RNA binding [GO:000372	nucleolus [GO:0005730];
1533	P61294	RAB6B_MOUSE	Ras-related protein	Mus musculus (Mouse)	Rab6b	Evidence at protein level	208	23462	intra-Golgi vesicle-mediat	GTP binding [GO:0005525	cytoplasmic vesicle [GO:0
1534	Q5SUE8	ANR40_MOUSE	Ankyrin repeat don	Mus musculus (Mouse)	Ankrd40	Evidence at protein level	363	40560			
1535	Q8BFS6	CPPED_MOUSE	Serine/threonine-p	Mus musculus (Mouse)	Cpped1	Evidence at protein level	312	35248		metal ion binding [GO:00	cytosol [GO:0005829]; ex
1536	P58137	ACOT8_MOUSE	Acyl-coenzyme A th	Mus musculus (Mouse)	Acot8	Evidence at protein level	320	35827	acyl-CoA metabolic proce	acyl-CoA hydrolase activi	mitochondrion [GO:0005
1537	P97823	LYPA1_MOUSE	Acyl-protein thioes	Mus musculus (Mouse)	Lypla1	Evidence at protein level	230	24688	fatty acid metabolic proc	carboxylic ester hydrolase	cytosol [GO:0005829]; ex
1538	Q62384	ZPR1_MOUSE	Zinc finger protein	Mus musculus (Mouse)	Zpr1	Evidence at protein level	459	50715	apoptotic process involve	receptor tyrosine kinase l	axon [GO:0030424]; Caja
1539	P59326	YTHD1_MOUSE	YTH domain-contai	Mus musculus (Mouse)	Ythdf1	Evidence at protein level	559	60879	positive regulation of tran	N6-methyladenosine-con	cytoplasm [GO:0005737]
1540	P26369	U2AF2_MOUSE	Splicing factor U2A	Mus musculus (Mouse)	U2af2	Evidence at protein level	475	53517	mRNA splicing, via splice	C2H2 zinc finger domain	commitment complex [G
1541	Q8K021	SCAM1_MOUSE	Secretory carrier-a	Mus musculus (Mouse)	Scamp1	Evidence at protein level	338	38029	exocytosis [GO:0006887];	protein transport [GO:00	integral component of me
1542	Q9CQ26	STABP_MOUSE	STAM-binding prot	Mus musculus (Mouse)	Stambp	Evidence at protein level	424	48514	mitotic cytokinesis [GO:0	metal ion binding [GO:00	cleavage furrow [GO:0003
1543	O88485	DC1I1_MOUSE	Cytoplasmic dyneir	Mus musculus (Mouse)	Dync1i1	Evidence at protein level	628	70725	vesicle transport along m	dynein light chain binding	condensed chromosome
1544	Q8CIN4	PAK2_MOUSE	Serine/threonine-p	Mus musculus (Mouse)	Pak2	Evidence at protein level	524	57930	apoptotic process [GO:00	ATP binding [GO:000552	cell-cell adherens junctio
1545	Q9ERL7	GMFG_MOUSE	Glia maturation fac	Mus musculus (Mouse)	Gmfg	Evidence at protein level	142	16748	actin filament debranchir	Arp2/3 complex binding [	intracellular [GO:000562
1546	O70493	SNX12_MOUSE	Sorting nexin-12 (S	Mus musculus (Mouse)	Snx12	Evidence at protein level	165	19116	endocytosis [GO:0006897	enzyme binding [GO:001	early endosome [GO:000
1547	Q8BH61	F13A_MOUSE	Coagulation factor	Mus musculus (Mouse)	F13a1	Evidence at protein level	732	83207	blood coagulation [GO:00	metal ion binding [GO:00	blood microparticle [GO:0
1548	P04231	HB23_MOUSE	H-2 class II histoco	Mus musculus (Mouse)	H2-Eb1	Evidence at protein level	232	26647	antigen processing and presentation of exogenous		extracellular exosome [G
1549	Q9R059	FHL3_MOUSE	Four and a half LIM	Mus musculus (Mouse)	Fhl3	Evidence at protein level	289	31795	actin cytoskeleton organi	actin binding [GO:000377	focal adhesion [GO:0005
1550	P97447	FHL1_MOUSE	Four and a half LIM	Mus musculus (Mouse)	Fhl1	Evidence at protein level	280	31889	cell differentiation [GO:0	ion channel binding [GO:0	cytoplasm [GO:0005737]
1551	P70429	EVL_MOUSE	Ena/VASP-like prot	Mus musculus (Mouse)	Evl	Evidence at protein level	414	44337	actin filament-based mov	profilin binding [GO:0005	cytoplasm [GO:0005737]
1552	Q9DB90	SMG9_MOUSE	Protein SMG9	Mus musculus (Mouse)	Smg9	Evidence at protein level	520	57621	brain development [GO:0	identical protein binding	intracellular [GO:000562
1553	P70460	VASP_MOUSE	Vasodilator-stimula	Mus musculus (Mouse)	Vasp	Evidence at protein level	375	39667	actin cytoskeleton organi	cadherin binding involve	bicellular tight junction [G
1554	Q61189	ICLN_MOUSE	Methylosome subu	Mus musculus (Mouse)	Clns1a	Evidence at protein level	236	26021	cell volume homeostasis	protein heterodimerizatio	cytoskeleton [GO:000585
1555	Q3UUJ4	STRAA_MOUSE	STE20-related kina	Mus musculus (Mouse)	Strada	Evidence at protein level	431	48236	activation of protein kina	ATP binding [GO:000552	cytoplasm [GO:0005737]
1556	Q99JR1	SFXN1_MOUSE	Sideroflexin-1	Mus musculus (Mouse)	Sfxn1	Evidence at protein level	322	35649	erythrocyte differentiatio	ion transmembrane trans	integral component of me
1557	Q9QYY0	GAB1_MOUSE	GRB2-associated-b	Mus musculus (Mouse)	Gab1	Evidence at protein level	695	76812	activation of JUN kinase a	signal transducer activity	cytoplasm [GO:0005737]
1558	Q9CQ49	NCBP2_MOUSE	Nuclear cap-bindin	Mus musculus (Mouse)	Ncbp2	Evidence at protein level	156	18017	gene silencing by RNA [G	mRNA binding [GO:0003	cytoplasm [GO:0005737]
1559	Q3TTL0	CC038_MOUSE	Uncharacterized pr	Mus musculus (Mouse)		Evidence at transcript level	348	39532	apoptotic process [GO:0006915]		
1560	Q9DBS5	KLC4_MOUSE	Kinesin light chain	Mus musculus (Mouse)	Klc4	Evidence at protein level	619	68613		microtubule motor activi	cytoplasm [GO:0005737]
1561	Q91V12	BACH_MOUSE	Cytosolic acyl coen	Mus musculus (Mouse)	Acot7	Evidence at protein level	381	42537	coenzyme A biosynthetic	carboxylic ester hydrolase	cell body [GO:0044297];
1562	P32233	DRG1_MOUSE	Developmentally-r	Mus musculus (Mouse)	Drg1	Evidence at protein level	367	40512		GTP binding [GO:0005525	cytosol [GO:0005829]; m
1563	Q8BFW7	LPP_MOUSE	Lipoma-preferred p	Mus musculus (Mouse)	Lpp	Evidence at protein level	613	65891	cell adhesion [GO:0007155	zinc ion binding [GO:0008	cytosol [GO:0005829]; fo
1564	Q91YR1	TWF1_MOUSE	Twinfilin-1 (Protein	Mus musculus (Mouse)	Twf1	Evidence at protein level	350	40079	barbed-end actin filamen	actin monomer binding [	actin cytoskeleton [GO:0
1565	P84089	ERH_MOUSE	Enhancer of rudim	Mus musculus (Mouse)	Erh	Evidence at protein level	104	12259	cell cycle [GO:0007049];	methyl-CpG binding [GO:	membrane [GO:0016020
1566	P17183	ENOG_MOUSE	Gamma-enolase (E	Mus musculus (Mouse)	Eno2	Evidence at protein level	434	47297	glycolytic process [GO:00	magnesium ion binding [	cytoplasm [GO:0005737]
1567	O08789	MNT_MOUSE	Max-binding protei	Mus musculus (Mouse)	Mnt	Evidence at transcript level	591	63274	cell aging [GO:0007569];	chromatin binding [GO:0	nucleoplasm [GO:0005659
1568	P70122	SBDS_MOUSE	Ribosome maturati	Mus musculus (Mouse)	Sbds	Evidence at protein level	250	28781	bone marrow developme	microtubule binding [GO:	cytoplasm [GO:0005737]
1569	Q9DCV7	K2C7_MOUSE	Keratin, type II cytc	Mus musculus (Mouse)	Krt7	Evidence at protein level	457	50709		structural molecule activi	cytoplasm [GO:0005737]
1570	Q62388	ATM_MOUSE	Serine-protein kina	Mus musculus (Mouse)	Atm	Evidence at protein level	3066	349418	brain development [GO:0	1-phosphatidylinositol-3-	chromosome, telomeric r
1571	O70305	ATX2_MOUSE	Ataxin-2 (Spinocere	Mus musculus (Mouse)	Atxn2	Evidence at protein level	1285	136485	cerebellar Purkinje cell di	epidermal growth factor	cytoplasm [GO:0005737]
1572	Q9WV86	KTNA1_MOUSE	Katanin p60 ATPas	Mus musculus (Mouse)	Katna1	Evidence at protein level	491	55949	cell division [GO:0051301	ATPase activity [GO:0016	axon [GO:0030424]; cent
1573	P81069	GABP2_MOUSE	GA-binding protein	Mus musculus (Mouse)	Gabpb2	Evidence at protein level	414	45658	positive regulation of tran	protein heterodimerizatio	nucleus [GO:0005634]
1574	Q8CAV0	YBEY_MOUSE	Putative ribonuclea	Mus musculus (Mouse)	Ybey	Evidence at protein level	164	18989	rRNA processing [GO:000	metal ion binding [GO:00	mitochondrion [GO:0005
1575	Q8QZS1	HIBCH_MOUSE	3-hydroxyisobutyry	Mus musculus (Mouse)	Hibch	Evidence at protein level	385	43038	valine catabolic process [	3-hydroxyisobutyryl-CoA	extracellular exosome [G
1576	Q8BH47	SC22A_MOUSE	Vesicle-trafficking p	Mus musculus (Mouse)	Sec22a	Evidence at transcript level	307	35025	ER to Golgi vesicle-media	SNAP receptor activity [G	endoplasmic reticulum m
1577	P47739	AL3A1_MOUSE	Aldehyde dehydrog	Mus musculus (Mouse)	Aldh3a1	Evidence at protein level	453	50481	aging [GO:0007568]; cell	3-chloroallyl aldehyde de	cytoplasm [GO:0005737]
1578	G5E870	TRIPC_MOUSE	E3 ubiquitin-protei	Mus musculus (Mouse)	Trip12	Evidence at protein level	2025	224128	cellular response to DNA	thyroid hormone recepto	nuclear speck [GO:00166
1579	P31786	ACBP_MOUSE	Acyl-CoA-binding p	Mus musculus (Mouse)	Dbi	Evidence at protein level	87	10000	behavioral fear response	lipid binding [GO:0008289	extracellular exosome [G
1580	Q8K363	DDX18_MOUSE	ATP-dependent RN	Mus musculus (Mouse)	Ddx18	Evidence at protein level	660	74181	cellular response to estra	ATP binding [GO:000552	chromosome [GO:00056
1581	P51125	ICAL_MOUSE	Calpastatin (Calpai	Mus musculus (Mouse)	Cast	Evidence at protein level	788	84922	negative regulation of pe	cadherin binding involve	cell-cell adherens junctio
1582	Q99P30	NUDT7_MOUSE	Peroxisomal coenz	Mus musculus (Mouse)	Nudt7	Evidence at protein level	236	26857	acetyl-CoA catabolic proc	acetyl-CoA hydrolase acti	peroxisome [GO:0005777
1583	Q61151	2A5E_MOUSE	Serine/threonine-p	Mus musculus (Mouse)	Ppp2r5e	Evidence at protein level	467	54713	signal transduction [GO:0	protein phosphatase reg	cytoplasm [GO:0005737]
1584	Q9D4J1	EFHD1_MOUSE	EF-hand domain-co	Mus musculus (Mouse)	Efhd1	Evidence at protein level	240	27000	neuron projection develo	calcium ion binding [GO:	extracellular exosome [G
1585	Q9CR86	CHSP1_MOUSE	Calcium-regulated	Mus musculus (Mouse)	Carhsp1	Evidence at protein level	148	16062	regulation of mRNA stabi	DNA binding [GO:000367	cytosol [GO:0005829]; ex
1586	Q64374	RGN_MOUSE	Regucalcin (RC) (Gl	Mus musculus (Mouse)	Rgn	Evidence at protein level	299	33407	aging [GO:0007568]; cell	calcium ion binding [GO:	cytoplasm [GO:0005737]
1587	Q8BUN5	SMAD3_MOUSE	Mothers against de	Mus musculus (Mouse)	Smad3	Evidence at protein level	425	48081	activation of cysteine-typ	bHLH transcription factor	cytoplasm [GO:0005737]
1588	P48774	GSTM5_MOUSE	Glutathione S-tran	Mus musculus (Mouse)	Gstm5	Evidence at protein level	224	26635	cellular detoxification of	enzyme binding [GO:001	cytoplasm [GO:0005737]
1589	Q6NZM9	HDAC4_MOUSE	Histone deacetylas	Mus musculus (Mouse)	Hdac4	Evidence at protein level	1076	118562	cellular response to mech	activating transcription fa	A band [GO:0031672]; ac
1590	Q08093	CNN2_MOUSE	Calponin-2 (Calpon	Mus musculus (Mouse)	Cnn2	Evidence at protein level	305	33156	actomyosin structure org	cadherin binding involve	cell-cell adherens junctio
1591	Q9QZL0	RIPK3_MOUSE	Receptor-interactir	Mus musculus (Mouse)	Ripk3	Evidence at protein level	486	53322	activation of protein kina	ATP binding [GO:000552	cytosol [GO:0005829]; in
1592	Q9DBN5	LONP2_MOUSE	Lon protease homc	Mus musculus (Mouse)	Lonp2	Evidence at protein level	852	94526	misfolded or incompleteh	ATP binding [GO:000552	cytoplasm [GO:0005737]
1593	P49945	FRIL2_MOUSE	Ferritin light chain	Mus musculus (Mouse)	Ftl2	Inferred from homology	183	20843	intracellular sequestering	ferric iron binding [GO:00	cytoplasm [GO:0005737]
1594	Q9DBF1	AL7A1_MOUSE	Alpha-aminoadipic	Mus musculus (Mouse)	Aldh7a1	Evidence at protein level	539	58861	glycine betaine biosynthe	betaine-aldehyde dehydr	cytosol [GO:0005829]; ex
1595	P52293	IMA1_MOUSE	Importin subunit al	Mus musculus (Mouse)	Kpna2	Evidence at protein level	529	57928	NLS-bearing protein impo	histone deacetylase bindi	cytosol [GO:0005829]; m
1596	Q9JLR9	HIG1A_MOUSE	HIG1 domain famil	Mus musculus (Mouse)	Higd1a	Evidence at protein level	95	10425	cellular response to glucose starvation [GO:004214		integral component of me
1597	Q60960	IMA5_MOUSE	Importin subunit al	Mus musculus (Mouse)	Kpna1	Evidence at protein level	538	60183	NLS-bearing protein impo	nuclear localization sequ	cytosol [GO:0005829]; de
1598	Q3UB74	TBRG1_MOUSE	Transforming grow	Mus musculus (Mouse)	Tbrg1	Evidence at protein level	406	44881	cell cycle arrest [GO:0007050];	DNA replication [GO	nucleus [GO:0005634]
1599	Q99JX4	EIF3M_MOUSE	Eukaryotic translat	Mus musculus (Mouse)	Eif3m	Evidence at protein level	374	42517	cytoplasmic translational	translation initiation facto	eukaryotic translation ini
1600	Q91W40	KLC3_MOUSE	Kinesin light chain	Mus musculus (Mouse)	Klc3	Evidence at protein level	508	56006	axo-dendritic transport [G	kinesin binding [GO:0019	ciliary rootlet [GO:00352
1601	Q9D8C4	IN35_MOUSE	Interferon-induced	Mus musculus (Mouse)	Ifi35	Evidence at protein level	286	31876			nucleus [GO:0005634]
1602	Q8VHK9	DHX36_MOUSE	ATP-dependent RN	Mus musculus (Mouse)	Dhx36	Evidence at protein level	1001	113883	ossification [GO:0001503	ATP binding [GO:000552	chromosome, telomeric r
1603	P04184	KITH_MOUSE	Thymidine kinase,	Mus musculus (Mouse)	Tk1	Evidence at protein level	233	25776	DNA biosynthetic process	ATP binding [GO:000552	cytoplasm [GO:0005737]
1604	P08553	NFM_MOUSE	Neurofilament me	Mus musculus (Mouse)	Nefm	Evidence at protein level	848	95916	axo-dendritic transport [G	structural molecule activi	axon [GO:0030424]; mye
1605	O70439	STX7_MOUSE	Syntaxin-7	Mus musculus (Mouse)	Stx7	Evidence at protein level	261	29821	intracellular protein trans	chloride channel inhibitor	azurophil granule [GO:00
1606	Q9D0F6	RFC5_MOUSE	Replication factor C	Mus musculus (Mouse)	Rfc5	Evidence at protein level	339	38096	DNA-dependent DNA rep	ATP binding [GO:000552	Ctf18 RFC-like complex [G
1607	Q99JB3	ATG5_MOUSE	Autophagy protein	Mus musculus (Mouse)	Atg5	Evidence at protein level	275	32402	aggrephagy [GO:0035973];	antigen processing and	Atg12-Atg5-Atg16 compl
1608	Q9CQK7	RWDD1_MOUSE	RWD domain-cont	Mus musculus (Mouse)	Rwdd1	Evidence at protein level	243	27785	cytoplasmic translation [GO:0002181]		polysome [GO:0005844]
1609	P10922	H10_MOUSE	Histone H1.0 (Histo	Mus musculus (Mouse)	H1f0	Evidence at transcript level	194	20861	nucleosome assembly [G	chromatin DNA binding [	actin cytoskeleton [GO:0
1610	Q924Z6	XPO6_MOUSE	Exportin-6 (Exp6) (I	Mus musculus (Mouse)	Xpo6	Evidence at protein level	1125	128664	protein export from nucle	protein transporter activi	cytosol [GO:0005829]; nu
1611	P70271	PDLI4_MOUSE	PDZ and LIM doma	Mus musculus (Mouse)	Pdlim4	Evidence at protein level	330	35556		zinc ion binding [GO:0008270]	
1612	Q8K2Q7	BROX_MOUSE	BRO1 domain-cont	Mus musculus (Mouse)	Brox	Evidence at protein level	411	46202			extracellular exosome [G
1613	Q9QYK4	H6ST3_MOUSE	Heparan-sulfate 6-	Mus musculus (Mouse)	Hs6st3	Evidence at protein level	470	55037	heparan sulfate proteogl	heparan sulfate 6-O-sulfc	integral component of me
1614	Q7TT37	ELP1_MOUSE	Elongator complex	Mus musculus (Mouse)	Ikbkap	Evidence at protein level	1333	149584	positive regulation of cell	phosphorylase kinase reg	cytoplasm [GO:0005737]
1615	Q8BUL6	PKHA1_MOUSE	Pleckstrin homolog	Mus musculus (Mouse)	Plekha1	Evidence at protein level	383	43371	androgen metabolic proc	PDZ domain binding [GO:	cytoplasm [GO:0005737]
1616	Q6P5F9	XPO1_MOUSE	Exportin-1 (Exp1) (I	Mus musculus (Mouse)	Xpo1	Evidence at protein level	1071	123093	mRNA transport [GO:005	nuclear export signal rece	annulate lamellae [GO:00
1617	Q3TV70	NR2CA_MOUSE	Nuclear receptor 2	Mus musculus (Mouse)	Nr2c2ap	Evidence at protein level	140	15857			extracellular exosome [G
1618	Q6ZWM4	LSM8_MOUSE	U6 snRNA-associat	Mus musculus (Mouse)	Lsm8	Evidence at protein level	96	10403	mRNA splicing, via splice	RNA binding [GO:000372	spliceosomal complex [G
1619	Q8CF66	LTOR4_MOUSE	Ragulator complex	Mus musculus (Mouse)	Lamtor4	Evidence at protein level	99	10678	cellular response to amin	guanyl-nucleotide exchan	intracellular membrane-b
1620	P05784	K1C18_MOUSE	Keratin, type I cyto	Mus musculus (Mouse)	Krt18	Evidence at protein level	423	47538	extrinsic apoptotic signali	cadherin binding involve	cell-cell adherens junctio
1621	P70245	EBP_MOUSE	3-beta-hydroxyster	Mus musculus (Mouse)	Ebp	Evidence at protein level	230	26215	cholesterol biosynthetic p	C-8 sterol isomerase acti	cytoplasmic vesicle [GO:0
1622	Q9CZX9	EMC4_MOUSE	ER membrane prot	Mus musculus (Mouse)	Emc4	Evidence at protein level	183	20117	apoptotic process [GO:0006915];	protein folding in	ER membrane protein co
1623	Q9JKV1	ADRM1_MOUSE	Proteasomal ubiqu	Mus musculus (Mouse)	Adrm1	Evidence at protein level	407	42060	adipose tissue developme	endopeptidase activator	cytosol [GO:0005829]; nu
1624	P50207	HXC13_MOUSE	Homeobox protein	Mus musculus (Mouse)	Hoxc13	Evidence at transcript level	328	35193	anatomical structure mor	chromatin binding [GO:0	nucleus [GO:0005634]
1625	Q3TB82	PKHF1_MOUSE	Pleckstrin homolog	Mus musculus (Mouse)	Plekhf1	Evidence at transcript level	279	31158	apoptotic process [GO:00	metal ion binding [GO:00	endosome [GO:0005768]
1626	Q9CQE0	RN138_MOUSE	E3 ubiquitin-protei	Mus musculus (Mouse)	Rnf138	Evidence at transcript level	245	28299	DNA double-strand break	protein kinase binding [G	nucleus [GO:0005634]; si
1627	Q9DA73	CCD89_MOUSE	Coiled-coil domain-	Mus musculus (Mouse)	Ccdc89	Evidence at protein level	370	43241			cytoplasm [GO:0005737]
1628	Q9D6F9	TBB4A_MOUSE	Tubulin beta-4A ch	Mus musculus (Mouse)	Tubb4a	Evidence at protein level	444	49586	cell projection organizatic	GTPase activity [GO:0003	cell projection [GO:0042
1629	O89019	INVS_MOUSE	Inversin (Inversion	Mus musculus (Mouse)	Invs	Evidence at protein level	1062	117129	animal organ development [GO:0048513];	embryor	ciliary base [GO:0097546
1630	Q8BMA3	CNKR3_MOUSE	Connector enhance	Mus musculus (Mouse)	Cnksr3	Evidence at protein level	555	61870	negative regulation of ERK1 and ERK2 cascade [GO:		cytoplasm [GO:0005737]
1631	Q8BHD1	POC1B_MOUSE	POC1 centriolar pro	Mus musculus (Mouse)	Poc1b	Evidence at transcript level	476	53504	cell proliferation [GO:0008283];	cilium assembly [G	centriole [GO:0005814];
1632	Q8BXG3	IFT57_MOUSE	Intraflagellar transp	Mus musculus (Mouse)	Ift57	Evidence at protein level	429	48772	activation of cysteine-typ	DNA binding [GO:000367	axoneme [GO:0005930];
1633	Q9JKN5	OLIG1_MOUSE	Oligodendrocyte tr	Mus musculus (Mouse)	Olig1	Evidence at protein level	260	27141	neuron fate commitment	DNA binding [GO:000367	nucleus [GO:0005634]; tr

1634	O35646	CAN6_MOUSE	Calpain-6	Mus musculus (Mouse)	Capn6	Evidence at protein level	641	74543	microtubule bundle form	calcium-dependent cyste	cytoplasm [GO:0005737]
1635	Q9D2X8	CH076_MOUSE	Uncharacterized pr	Mus musculus (Mouse)		Evidence at protein level	372	41643			
1636	Q5SUA5	MYO1G_MOUSE	Unconventional my	Mus musculus (Mouse)	Myo1g	Evidence at protein level	1024	117227	cell gliding [GO:0071976]	ATP binding [GO:0005524	extracellular exosome [G
1637	Q64462	CP4B1_MOUSE	Cytochrome P450 4	Mus musculus (Mouse)	Cyp4b1	Evidence at protein level	511	58900	biphenyl metabolic proce	aromatase activity [GO:0	endoplasmic reticulum m
1638	Q63870	CO7A1_MOUSE	Collagen alpha-1(V	Mus musculus (Mouse)	Col7a1	Evidence at protein level	2944	295232	cell adhesion [GO:0007159	identical protein binding	basement membrane [GO
1639	Q5MPP0	FA2H_MOUSE	Fatty acid 2-hydrox	Mus musculus (Mouse)	Fa2h	Evidence at protein level	372	42981	central nervous system m	fatty acid alpha-hydroxyl	endoplasmic reticulum [G
1640	Q9DCF9	SSRG_MOUSE	Translocon-associa	Mus musculus (Mouse)	Ssr3	Evidence at protein level	185	21064	SRP-dependent cotranslational protein targeting to		endoplasmic reticulum m
1641	Q9JIA7	SPHK2_MOUSE	Sphingosine kinase	Mus musculus (Mouse)	Sphk2	Evidence at protein level	617	65618	blood vessel developmen	ATP binding [GO:0005524	cytosol [GO:0005829]; in
1642	P70699	LYAG_MOUSE	Lysosomal alpha-gl	Mus musculus (Mouse)	Gaa	Evidence at protein level	953	106248	cardiac muscle contractic	alpha-1,4-glucosidase act	extracellular exosome [G
1643	Q8BW10	NOB1_MOUSE	RNA-binding protei	Mus musculus (Mouse)	Nob1	Evidence at protein level	403	45464	cleavage involved in rRNA	endoribonuclease activity	cytoplasm [GO:0005737]
1644	Q8VHY0	CSPG4_MOUSE	Chondroitin sulfate	Mus musculus (Mouse)	Cspg4	Evidence at protein level	2327	252309	activation of MAPK activi	protein kinase binding [G	apical plasma membrane
1645	P19536	COX5B_MOUSE	Cytochrome c oxid	Mus musculus (Mouse)	Cox5b	Evidence at protein level	128	13813	mitochondrial ATP synthe	cytochrome-c oxidase act	mitochondrial inner mem
1646	B2RXR6	ANR44_MOUSE	Serine/threonine-p	Mus musculus (Mouse)	Ankrd44	Evidence at protein level	993	107385			
1647	O55111	DSG2_MOUSE	Desmoglein-2	Mus musculus (Mouse)	Dsg2	Evidence at protein level	1122	122385	bundle of His cell-Purkinje	calcium ion binding [GO:0	apical plasma membrane
1648	Q61475	DAF1_MOUSE	Complement decay	Mus musculus (Mouse)	Cd55	Evidence at protein level	390	42618	complement activation, c	lipid binding [GO:0008289	anchored component of r
1649	Q03350	TSP2_MOUSE	Thrombospondin-2	Mus musculus (Mouse)	Thbs2	Evidence at protein level	1172	129882	cell adhesion [GO:0007159	calcium ion binding [GO:0	basement membrane [GO
1650	Q9DBH5	LMAN2_MOUSE	Vesicular integral-m	Mus musculus (Mouse)	Lman2	Evidence at protein level	358	40430	positive regulation of pha	carbohydrate binding [GO	cell surface [GO:0009986
1651	P01668	KV3AG_MOUSE	Ig kappa chain V-III	Mus musculus (Mouse)		Evidence at protein level	110	11950		antigen binding [GO:0003823]	
1652	D3Z750	MRO2A_MOUSE	Maestro heat-like r	Mus musculus (Mouse)	Mroh2a	Evidence at protein level	1679	190012			
1653	Q0VF22	CC138_MOUSE	Coiled-coil domain-	Mus musculus (Mouse)	Ccdc138	Evidence at protein level	680	77947			
1654	Q2MV57	TECT2_MOUSE	Tectonic-2	Mus musculus (Mouse)	Tctn2	Evidence at protein level	700	77111	cilium assembly [GO:0060271]; protein localization		cytoplasm [GO:0005737]
1655	O70374	MTG8R_MOUSE	Protein CBFA2T2 (M	Mus musculus (Mouse)	Cbfa2t2	Evidence at protein level	594	65904	epithelial cell differentiat	metal ion binding [GO:00	nucleus [GO:0005634]
1656	Q9D1M7	FKB11_MOUSE	Peptidyl-prolyl cis-t	Mus musculus (Mouse)	Fkbp11	Evidence at protein level	201	22137	chaperone-mediated prot	FK506 binding [GO:0005	cytoplasm [GO:0005737]
1657	Q9Z239	PLM_MOUSE	Phospholemman (F	Mus musculus (Mouse)	Fxyd1	Evidence at protein level	92	10323	positive regulation of sod	chloride channel activity	chloride channel complex
1658	Q99KG7	HPS4_MOUSE	Hermansky-Pudlak	Mus musculus (Mouse)	Hps4	Evidence at protein level	671	72662	blood coagulation [GO:00	guanyl-nucleotide exchan	BLOC-3 complex [GO:003
1659	Q8BFY9	TNPO1_MOUSE	Transportin-1 (Imp	Mus musculus (Mouse)	Tnpo1	Evidence at protein level	898	102357	NLS-bearing protein impo	nuclear localization sequ	cytoplasm [GO:0005737]
1660	Q62507	COCH_MOUSE	Cochlin (COCH-5B2	Mus musculus (Mouse)	Coch	Evidence at protein level	552	59950	defense response to bact	collagen binding [GO:000	extracellular exosome [G
1661	Q8C0L0	TMX4_MOUSE	Thioredoxin-relate	Mus musculus (Mouse)	Tmx4	Evidence at protein level	335	37131	cell redox homeostasis [G	protein disulfide isomera	endoplasmic reticulum [G
1662	Q9D180	CFA57_MOUSE	Cilia- and flagella-a	Mus musculus (Mouse)	Cfap57	Evidence at protein level	1249	144934			
1663	Q60751	IGF1R_MOUSE	Insulin-like growth	Mus musculus (Mouse)	Igf1r	Evidence at protein level	1373	155788	adrenal gland developme	ATP binding [GO:0005524	alphav-beta3 integrin-IGF
1664	Q7TSF0	DSG1C_MOUSE	Desmoglein-1-gam	Mus musculus (Mouse)	Dsg1c	Evidence at protein level	911	100516	homophilic cell adhesion	calcium ion binding [GO:0	desmosome [GO:003005
1665	P10287	CADH3_MOUSE	Cadherin-3 (Placen	Mus musculus (Mouse)	Cdh3	Evidence at protein level	822	90612	canonical Wnt signaling p	calcium ion binding [GO:0	cell-cell adherens junctio
1666	Q9JHH6	CBPB2_MOUSE	Carboxypeptidase I	Mus musculus (Mouse)	Cpb2	Evidence at protein level	422	48871	blood coagulation [GO:00	carboxypeptidase activity	cell [GO:0005623]; extrac
1667	Q6PIC6	AT1A3_MOUSE	Sodium/potassium	Mus musculus (Mouse)	Atp1a3	Evidence at protein level	1013	111692	adult locomotory behavic	ATP binding [GO:0005524	axon [GO:0030424]; cyto
1668	P47809	MP2K4_MOUSE	Dual specificity mit	Mus musculus (Mouse)	Map2k4	Evidence at protein level	397	44114	activation of JUN kinase a	ATP binding [GO:0005524	axon [GO:0030424]; cyto
1669	Q8BXZ1	TMX3_MOUSE	Protein disulfide-is	Mus musculus (Mouse)	Tmx3	Evidence at protein level	456	51848	cell redox homeostasis [G	protein disulfide isomera	cell surface [GO:0009986
1670	Q8R007	NECT4_MOUSE	Nectin-4 (Ig superfa	Mus musculus (Mouse)	Nectin4	Evidence at transcript level	508	55657	cell recognition [GO:0008	cell adhesion molecule bi	adherens junction [GO:00
1671	Q9JJE7	FADS3_MOUSE	Fatty acid desatura	Mus musculus (Mouse)	Fads3	Evidence at transcript level	449	51469	fatty acid biosynthetic pr	oxidoreductase activity [(	endoplasmic reticulum m
1672	P39749	FEN1_MOUSE	Flap endonuclease	Mus musculus (Mouse)	Fen1	Evidence at protein level	378	42315	DNA repair [GO:0006281	5'-3' exonuclease activity	membrane [GO:0016020
1673	Q9QYJ3	DNJB1_MOUSE	DnaJ homolog subf	Mus musculus (Mouse)	Dnajb1	Evidence at protein level	340	38167	chaperone cofactor-depe	ATPase activator activity	cell-cell adherens junctio
1674	Q8CAK1	CAF17_MOUSE	Putative transferas	Mus musculus (Mouse)	Iba57	Evidence at protein level	358	38399	heme biosynthetic proce	RNA binding [GO:000372	mitochondrial matrix [GO
1675	Q7TQK5	CCD93_MOUSE	Coiled-coil domain-	Mus musculus (Mouse)	Ccdc93	Evidence at protein level	629	72603	Golgi to plasma membrane transport [GO:0006893		early endosome [GO:000
1676	Q8BLN6	UNC80_MOUSE	Protein unc-80 hon	Mus musculus (Mouse)	Unc80	Evidence at protein level	3261	363504			integral component of me
1677	P07309	TTHY_MOUSE	Transthyretin (Prea	Mus musculus (Mouse)	Ttr	Evidence at protein level	147	15776	retinol metabolic process	identical protein binding	extracellular exosome [G
1678	P49935	CATH_MOUSE	Pro-cathepsin H (Ca	Mus musculus (Mouse)	Ctsh	Evidence at protein level	333	37170	bradykinin catabolic proc	aminopeptidase activity [	alveolar lamellar body [G
1679	P53395	ODB2_MOUSE	Lipoamide acyltran	Mus musculus (Mouse)	Dbt	Evidence at protein level	482	53247	metabolic process [GO:0	dihydrolipoyllysine-resid	mitochondrial nucleoid [G
1680	Q99KV1	DJB11_MOUSE	DnaJ homolog subf	Mus musculus (Mouse)	Dnajb11	Evidence at protein level	358	40555	mRNA modification [GO:0	unfolded protein binding	cytoplasm [GO:0005737]
1681	Q99MR8	MCCA_MOUSE	Methylcrotonoyl-C	Mus musculus (Mouse)	Mccc1	Evidence at protein level	717	79344	leucine catabolic process	ATP binding [GO:0005524	3-methylcrotonyl-CoA ca
1682	Q9Z2I2	FKB1B_MOUSE	Peptidyl-prolyl cis-t	Mus musculus (Mouse)	Fkbp1b	Evidence at protein level	108	11798	chaperone-mediated prot	calcium channel inhibitor	calcium channel complex
1683	Q3V132	ADT4_MOUSE	ADP/ATP transloca	Mus musculus (Mouse)	Slc25a31	Evidence at protein level	320	35258	mitochondrial transport [	transmembrane transpor	integral component of me
1684	Q6NT99	DUS23_MOUSE	Dual specificity pro	Mus musculus (Mouse)	Dusp23	Evidence at protein level	150	16637	dephosphorylation [GO:0	phosphatase activity [GO	cytoplasm [GO:0005737]
1685	Q9JHI5	IVD_MOUSE	Isovaleryl-CoA deh	Mus musculus (Mouse)	Ivd	Evidence at protein level	424	46325	leucine catabolic process	flavin adenine dinucleotic	mitochondrial matrix [GO
1686	P03953	CFAD_MOUSE	Complement factor	Mus musculus (Mouse)	Cfd	Evidence at protein level	259	28057	complement activation, a	serine-type endopeptidas	extracellular exosome [G
1687	Q8BH04	PCKGM_MOUSE	Phosphoenolpyruv	Mus musculus (Mouse)	Pck2	Evidence at protein level	640	70528	gluconeogenesis [GO:000	GTP binding [GO:0005525	extracellular exosome [G
1688	P47753	CAZA1_MOUSE	F-actin-capping pro	Mus musculus (Mouse)	Capza1	Evidence at protein level	286	32940	barbed-end actin filamen	cadherin binding involved	brush border [GO:0005900
1689	Q8BVE8	NSD2_MOUSE	Histone-lysine N-m	Mus musculus (Mouse)	Nsd2	Evidence at protein level	1365	152253	atrial septum primum mo	chromatin binding [GO:0	chromosome [GO:0005694
1690	Q8CE08	PPAP_MOUSE	Prostatic acid phos	Mus musculus (Mouse)	Acpp	Evidence at transcript level	381	43717	adenosine metabolic proc	5'-nucleotidase activity [(	extracellular exosome [G
1691	Q920A7	AFG31_MOUSE	AFG3-like protein 1	Mus musculus (Mouse)	Afg3l1	Evidence at protein level	789	87047	cristae formation [GO:00	ATP binding [GO:0005524	m-AAA complex [GO:000
1692	Q8CCK0	H2AW_MOUSE	Core histone macro	Mus musculus (Mouse)	H2afy2	Evidence at protein level	372	40092	brain development [GO:0	chromatin DNA binding [(	Barr body [GO:0001740];
1693	P25976	UBF1_MOUSE	Nucleolar transcrip	Mus musculus (Mouse)	Ubtf	Evidence at protein level	765	89509	chromatin silencing at rD	chromatin binding [GO:0	fibrillar center [GO:00016
1694	O35943	FRDA_MOUSE	Frataxin, mitochon	Mus musculus (Mouse)	Fxn	Evidence at protein level	207	22924	adult walking behavior [G	2 iron, 2 sulfur cluster bin	cytosol [GO:0005829]; m
1695	Q07417	ACADS_MOUSE	Short-chain specific	Mus musculus (Mouse)	Acads	Evidence at protein level	412	44890	fatty acid metabolic proc	acyl-CoA dehydrogenase	mitochondrial matrix [GO
1696	Q99N93	RM16_MOUSE	39S ribosomal prot	Mus musculus (Mouse)	Mrpl16	Evidence at protein level	251	28804	mitochondrial translation	rRNA binding [GO:00198	mitochondrial large ribos
1697	Q8BK72	RT27_MOUSE	28S ribosomal prot	Mus musculus (Mouse)	Mrps27	Evidence at protein level	415	47779			mitochondrion [GO:0005
1698	P0CW03	LY6C2_MOUSE	Lymphocyte antige	Mus musculus (Mouse)	Ly6c2	Evidence at protein level	131	14090			anchored component of r
1699	Q9CXI5	MANF_MOUSE	Mesencephalic astr	Mus musculus (Mouse)	Manf	Evidence at protein level	179	20374	dopaminergic neuron diff	RNA binding [GO:000372	endoplasmic reticulum [G
1700	Q9ESB3	HRG_MOUSE	Histidine-rich glyco	Mus musculus (Mouse)	Hrg	Evidence at protein level	525	59163	angiogenesis [GO:000152	cysteine-type endopeptid	blood microparticle [GO:0
1701	A2ALW5	DJC25_MOUSE	DnaJ homolog subf	Mus musculus (Mouse)	Dnajc25	Evidence at protein level	357	41937			integral component of me
1702	Q921M3	SF3B3_MOUSE	Splicing factor 3B s	Mus musculus (Mouse)	Sf3b3	Evidence at protein level	1217	135550	mRNA splicing, via splice	RNA binding [GO:000372	catalytic step 2 spliceoso
1703	Q99KN2	CIAO1_MOUSE	Probable cytosolic	Mus musculus (Mouse)	Ciao1	Evidence at protein level	339	37633	chromosome segregation	transcription factor activi	CIA complex [GO:009736
1704	Q9WVJ2	PSD13_MOUSE	26S proteasome no	Mus musculus (Mouse)	Psmd13	Evidence at protein level	376	42809	meiosis I [GO:0007127]; p	endopeptidase activity [G	cytosol [GO:0005829]; ex
1705	P61255	RL26_MOUSE	60S ribosomal prot	Mus musculus (Mouse)	Rpl26	Evidence at protein level	145	17258	ribosomal large subunit b	RNA binding [GO:000372	cytosolic large ribosomal
1706	Q8BFQ4	WDR82_MOUSE	WD repeat-contain	Mus musculus (Mouse)	Wdr82	Evidence at protein level	313	35079	histone H3-K4 methylatic	chromatin binding [GO:0	chromatin [GO:0000785]
1707	Q9D3U0	PUS10_MOUSE	Putative tRNA pseu	Mus musculus (Mouse)	Pus10	Evidence at protein level	527	59710	tRNA pseudouridine synt	pseudouridine synthase activity	[GO:0009982]; RNA
1708	Q8VCH8	UBXN4_MOUSE	UBX domain-conta	Mus musculus (Mouse)	Ubxn4	Evidence at protein level	506	56472	response to unfolded protein	[GO:0006986]; ubiqui	cytosol [GO:0005829]; er
1709	Q99JI9	MEP50_MOUSE	Methylosome prot	Mus musculus (Mouse)	Wdr77	Evidence at protein level	342	36943	negative regulation of cel	ligand-dependent nuclear	cytoplasm [GO:0005737]
1710	Q9CW03	SMC3_MOUSE	Structural mainten	Mus musculus (Mouse)	Smc3	Evidence at protein level	1217	141556	cell division [GO:0051301	ATP binding [GO:0005524	chromatin [GO:0000785]
1711	Q9QYR9	ACOT2_MOUSE	Acyl-coenzyme A th	Mus musculus (Mouse)	Acot2	Evidence at protein level	453	49657	acyl-CoA metabolic proce	acyl-CoA hydrolase activi	extracellular exosome [G
1712	Q9Z2V4	PCKGC_MOUSE	Phosphoenolpyruv	Mus musculus (Mouse)	Pck1	Evidence at protein level	622	69355	aging [GO:0007568]; cell	carboxylic acid binding [G	cytosol [GO:0005829]; ex
1713	Q01320	TOP2A_MOUSE	DNA topoisomeras	Mus musculus (Mouse)	Top2a	Evidence at protein level	1528	172790	apoptotic chromosome c	ATP binding [GO:0005524	centriole [GO:0005814]; c
1714	Q61835	FXYD3_MOUSE	FXYD domain-conta	Mus musculus (Mouse)	Fxyd3	Evidence at transcript level	88	9526	regulation of catalytic act	ATPase binding [GO:0051	chloride channel complex
1715	Q3U492	KCP_MOUSE	Kielin/chordin-like	Mus musculus (Mouse)	Kcp	Evidence at protein level	1550	166628	hematopoietic progenitor	cell differentiation [GO:0	extracellular space [GO:0
1716	P49117	NR2C2_MOUSE	Nuclear receptor su	Mus musculus (Mouse)	Nr2c2	Evidence at protein level	596	65239	cell differentiation [GO:0	protein heterodimerizatic	nucleoplasm [GO:0005654
1717	Q8BI79	CCD40_MOUSE	Coiled-coil domain-	Mus musculus (Mouse)	Ccdc40	Evidence at protein level	1192	136772	axonemal dynein complex	assembly [GO:0070286];	axoneme [GO:0005930];
1718	E9QAU8	RN165_MOUSE	E3 ubiquitin-protei	Mus musculus (Mouse)	Rnf165	Evidence at protein level	347	39736	axonogenesis [GO:00074	ubiquitin protein ligase ac	cytoplasm [GO:0005737]
1719	Q8C522	ENDD1_MOUSE	Endonuclease dom	Mus musculus (Mouse)	Endod1	Evidence at protein level	501	55262		endonuclease activity [G	extracellular exosome [G
1720	Q9ESY9	GILT_MOUSE	Gamma-interferon	Mus musculus (Mouse)	Ifi30	Evidence at protein level	248	27784	antigen processing and pr	disulfide oxidoreductase a	cell junction [GO:003005
1721	P62342	SELT_MOUSE	Selenoprotein T (Se	Mus musculus (Mouse)	Selenot	Evidence at protein level	195	22292	cell redox homeostasis [G	thioredoxin-disulfide redu	endoplasmic reticulum [G
1722	Q62095	DDX3Y_MOUSE	ATP-dependent RN	Mus musculus (Mouse)	Ddx3y	Evidence at protein level	658	73428	regulation of gene expres	ATP binding [GO:0005524	cytoplasmic ribonucleopr
1723	P17156	HSP72_MOUSE	Heat shock-related	Mus musculus (Mouse)	Hspa2	Evidence at protein level	633	69642	male meiosis [GO:000714	ATP binding [GO:0005524	blood microparticle [GO:0
1724	Q9CR21	ACPM_MOUSE	Acyl carrier protein	Mus musculus (Mouse)	Ndufab1	Evidence at protein level	156	17370	lipid A biosynthetic proce	ACP phosphopantetheine	cytosol [GO:0005829]; m
1725	Q8R164	BPHL_MOUSE	Valacyclovir hydrol	Mus musculus (Mouse)	Bphl	Evidence at protein level	291	32851		hydrolase activity [GO:00	extracellular exosome [G
1726	P32921	SYWC_MOUSE	Tryptophan--tRNA	Mus musculus (Mouse)	Wars	Evidence at protein level	481	54358	angiogenesis [GO:000152	ATP binding [GO:0005524	cytoplasm [GO:0005737]
1727	Q9Z1T2	TSP4_MOUSE	Thrombospondin-4	Mus musculus (Mouse)	Thbs4	Evidence at protein level	963	106366	behavioral response to pa	calcium ion binding [GO:0	basement membrane [GO
1728	Q9EP72	EMC7_MOUSE	ER membrane prot	Mus musculus (Mouse)	Emc7	Evidence at protein level	241	26310		carbohydrate binding [GO	ER membrane protein co
1729	Q8VHI3	OFUT2_MOUSE	GDP-fucose protein	Mus musculus (Mouse)	Pofut2	Evidence at protein level	429	49429	fucose metabolic process	fucosyltransferase activit	endoplasmic reticulum [G
1730	O55125	NIPS1_MOUSE	Protein NipSnap ho	Mus musculus (Mouse)	Nipsnap1	Evidence at protein level	284	33363	sensory perception of pai	neurotransmitter binding	membrane [GO:0016020
1731	Q8BGV3	TACD2_MOUSE	Tumor-associated c	Mus musculus (Mouse)	Tacstd2	Evidence at protein level	317	35574	cell-cell adhesion [GO:0098609]; negative regulatio		basal plasma membrane
1732	O88456	CPNS1_MOUSE	Calpain small subu	Mus musculus (Mouse)	Capns1	Evidence at protein level	269	28463		calcium-dependent cyste	cytosol [GO:0005829]; ex
1733	Q9DCT5	SDF2_MOUSE	Stromal cell-derive	Mus musculus (Mouse)	Sdf2	Evidence at protein level	211	23159	ER-associated misfolded p	dolichyl-phosphate-mann	endoplasmic reticulum m
1734	Q9Z1Q3	LY66D_MOUSE	Lymphocyte antige	Mus musculus (Mouse)	Ly6g6d	Evidence at protein level	135	14092	acetylcholine receptor sig	acetylcholine receptor inh	anchored component of r
1735	Q80VP1	EPN1_MOUSE	Epsin-1 (EPS-15-int	Mus musculus (Mouse)	Epn1	Evidence at protein level	575	60212	embryonic organ develop	lipid binding [GO:0008289	clathrin-coated pit [GO:0
1736	Q8R3N6	THOC1_MOUSE	THO complex subu	Mus musculus (Mouse)	Thoc1	Evidence at protein level	657	75436	apoptotic process [GO:00	DNA binding [GO:000367	cytoplasm [GO:0005737]
1737	Q05895	TSP3_MOUSE	Thrombospondin-3	Mus musculus (Mouse)	Thbs3	Evidence at protein level	956	104119	bone trabecula formatior	calcium ion binding [GO:0	extracellular region [GO:0
1738	Q9DGG0	RT30_MOUSE	28S ribosomal prot	Mus musculus (Mouse)	Mrps30	Evidence at protein level	442	49939	translation [GO:0006412]	RNA binding [GO:000372	mitochondrion [GO:0005
1739	Q9DCM0	ETHE1_MOUSE	Persulfide dioxyger	Mus musculus (Mouse)	Ethe1	Evidence at protein level	254	27739	glutathione metabolic pr	iron ion binding [GO:000	cytoplasm [GO:0005737]
1740	O35114	SCRB2_MOUSE	Lysosome membra	Mus musculus (Mouse)	Scarb2	Evidence at protein level	478	54044	positive regulation of neu	enzyme binding [GO:001	extracellular exosome [G
1741	Q8BYJ6	TBCD4_MOUSE	TBC1 domain famil	Mus musculus (Mouse)	Tbc1d4	Evidence at protein level	1307	147451	activation of GTPase activ	GTPase activator activity	cytoplasmic vesicle memb
1742	Q05920	PYC_MOUSE	Pyruvate carboxyla	Mus musculus (Mouse)	Pc	Evidence at protein level	1178	129685	gluconeogenesis [GO:000	ATP binding [GO:0005524	cytoplasm [GO:0005737]
1743	Q9CXT8	MPPB_MOUSE	Mitochondrial-proc	Mus musculus (Mouse)	Pmpcb	Evidence at protein level	489	54614	aerobic respiration [GO:0	metalloendopeptidase ac	mitochondrial inner mem
1744	Q6PER3	MARE3_MOUSE	Microtubule-associ	Mus musculus (Mouse)	Mapre3	Evidence at protein level	281	31966	cell division [GO:0051301	identical protein binding	cytoplasm [GO:0005737]
1745	Q6J1H4	UTF1_MOUSE	Undifferentiated er	Mus musculus (Mouse)	Utf1	Evidence at protein level	339	36408	male gonad development	HMG box domain binding	nucleus [GO:0005634]
1746	Q8CIM3	D2HDH_MOUSE	D-2-hydroxyglutara	Mus musculus (Mouse)	D2hgdh	Evidence at protein level	535	58576	cellular protein metabolic	(R)-2-hydroxyglutarate de	mitochondrion [GO:0005
1747	O08810	U5S1_MOUSE	116 kDa U5 small n	Mus musculus (Mouse)	Eftud2	Evidence at protein level	971	109361	mRNA processing [GO:00	GTPase activity [GO:0003	Cajal body [GO:0015030]
1748	Q9DC23	DJC10_MOUSE	DnaJ homolog subf	Mus musculus (Mouse)	Dnajc10	Evidence at protein level	793	90583	cell redox homeostasis [G	ATPase activator activity	endoplasmic reticulum [G
1749	Q9R097	SPIT1_MOUSE	Kunitz-type protea	Mus musculus (Mouse)	Spint1	Evidence at protein level	507	56591	branching involved in lab	serine-type endopeptidas	extracellular exosome [G
1750	Q9DCS3	MECR_MOUSE	Enoyl-[acyl-carrier-	Mus musculus (Mouse)	Mecr	Evidence at protein level	373	40343	fatty acid biosynthetic pr	ligand-dependent nuclear	cytosol [GO:0005829]; m

1751	P97493	THIOM_MOUSE	Thioredoxin, mitoc	Mus musculus (Mouse)	Txn2	Evidence at protein level	166	18255	cell redox homeostasis [G	peptide-methionine (R)-S	dendrite [GO:0030425]; r
1752	P70195	PSB7_MOUSE	Proteasome subuni	Mus musculus (Mouse)	Psmb7	Evidence at protein level	277	29891	positive regulation of pro	threonine-type endopept	cytosol [GO:0005829]; ex
1753	P39098	MA1A2_MOUSE	Mannosyl-oligosac	Mus musculus (Mouse)	Man1a2	Evidence at protein level	641	72871	glycoprotein metabolic pr	calcium ion binding [GO:(	endoplasmic reticulum [G
1754	Q8BP48	MAP11_MOUSE	Methionine amino	Mus musculus (Mouse)	Metap1	Evidence at protein level	386	43221	platelet aggregation [GO:	aminopeptidase activity [	cytoplasm [GO:0005737]
1755	Q5NCF2	TPPC1_MOUSE	Trafficking protein	Mus musculus (Mouse)	Trappc1	Evidence at protein level	145	16882	ER to Golgi vesicle-media	Rab guanyl-nucleotide ex	endoplasmic reticulum [G
1756	Q99L04	DHRS1_MOUSE	Dehydrogenase/re	Mus musculus (Mouse)	Dhrs1	Evidence at protein level	313	34005		oxidoreductase activity [(	endoplasmic reticulum [G
1757	O54946	DNJB6_MOUSE	DnaJ homolog subf	Mus musculus (Mouse)	Dnajb6	Evidence at protein level	365	39807	actin cytoskeleton organi	ATPase activator activity	cytoplasm [GO:0005737]
1758	Q9R1T2	SAE1_MOUSE	SUMO-activating e	Mus musculus (Mouse)	Sae1	Evidence at protein level	350	38620	positive regulation of pro	ATP-dependent protein b	nucleus [GO:0005634]; SI
1759	Q9D187	MIP18_MOUSE	Mitotic spindle-ass	Mus musculus (Mouse)	Fam96b	Evidence at protein level	163	17667	chromosome segregation	[GO:0007059]; iron-sulfu	CIA complex [GO:009736
1760	Q8K2C7	OS9_MOUSE	Protein OS-9	Mus musculus (Mouse)	Os9	Evidence at protein level	672	76108	negative regulation of ret	carbohydrate binding [GC	endoplasmic reticulum lu
1761	Q8C7Q4	RBM4_MOUSE	RNA-binding protei	Mus musculus (Mouse)	Rbm4	Evidence at protein level	361	40046	cap-independent translat	miRNA binding [GO:0035	cytoplasm [GO:0005737]
1762	P57784	RU2A_MOUSE	U2 small nuclear ri	Mus musculus (Mouse)	Snrpa1	Evidence at protein level	255	28357	mRNA splicing, via splice	RNA binding [GO:000372	catalytic step 2 spliceoso
1763	O35226	PSMD4_MOUSE	26S proteasome nc	Mus musculus (Mouse)	Psmd4	Evidence at protein level	376	40704	proteasome assembly [GI	identical protein binding |	cytosol [GO:0005829]; nu
1764	Q8BX70	VP13C_MOUSE	Vacuolar protein sc	Mus musculus (Mouse)	Vps13c	Evidence at protein level	3748	420089	mitochondrion organization	[GO:0007005]; negativ	cytosol [GO:0005829]; ex
1765	P16254	SRP14_MOUSE	Signal recognition p	Mus musculus (Mouse)	Srp14	Evidence at protein level	110	12510	protein targeting to ER [G	7S RNA binding [GO:0008	extracellular exosome [GI
1766	P97825	HN1_MOUSE	Hematological and	Mus musculus (Mouse)	Hn1	Evidence at protein level	154	16081			nuclear membrane [GO:0
1767	Q8BYA0	TBCD_MOUSE	Tubulin-specific ch	Mus musculus (Mouse)	Tbcd	Evidence at protein level	1196	133321	adherens junction assem	beta-tubulin binding [GO:	adherens junction [GO:0(
1768	Q6PCM1	KDM3A_MOUSE	Lysine-specific dem	Mus musculus (Mouse)	Kdm3a	Evidence at protein level	1323	147847	androgen receptor signali	androgen receptor bindin	chromatin [GO:0000785]
1769	P56183	RRP1_MOUSE	Ribosomal RNA prc	Mus musculus (Mouse)	Rrp1	Evidence at protein level	494	54777	rRNA processing [GO:000	RNA binding [GO:000372	nucleolus [GO:0005730];
1770	Q99JT9	MTND_MOUSE	1,2-dihydroxy-3-ke	Mus musculus (Mouse)	Adi1	Evidence at protein level	179	21524	L-methionine salvage fro	acireductone dioxygenas	cytoplasm [GO:0005737]
1771	Q9EQQ9	OGA_MOUSE	Protein O-GlcNAca	Mus musculus (Mouse)	Mgea5	Evidence at protein level	916	103162	glycoprotein metabolic pr	beta-N-acetylglucosamin	cytosol [GO:0005829]; m
1772	P01867	IGG2B_MOUSE	Ig gamma-2B chain	Mus musculus (Mouse)	Igh-3	Evidence at protein level	404	44259	B cell receptor signaling p	antigen binding [GO:0003	blood microparticle [GO:(
1773	Q9D687	S6A19_MOUSE	Sodium-dependent	Mus musculus (Mouse)	Slc6a19	Evidence at protein level	634	71367	neutral amino acid transp	neurotransmitter:sodium	brush border membrane
1774	P00375	DYR_MOUSE	Dihydrofolate redu	Mus musculus (Mouse)	Dhfr	Evidence at protein level	187	21606	axon regeneration [GO:0(	dihydrofolate reductase a	cytoplasm [GO:0005737]
1775	Q9CPT4	MYDGF_MOUSE	Myeloid-derived gr	Mus musculus (Mouse)	Mydgf	Evidence at protein level	166	17982	angiogenesis [GO:0001525];	apoptotic process [GO	endoplasmic reticulum-G
1776	Q9JLJ1	SELK_MOUSE	Selenoprotein K (Se	Mus musculus (Mouse)	Selenok	Evidence at protein level	94	10642	calcium ion transport [GC	identical protein binding |	endoplasmic reticulum [G
1777	P54818	GALC_MOUSE	Galactocerebrosida	Mus musculus (Mouse)	Galc	Evidence at protein level	684	77256	carbohydrate metabolic p	galactosylceramidase act	extracellular exosome [GI

ST1B Supplementary Table 1B: Peptides identified by shotgun proteomics prior to TAILS (preTAILS) with an unlabeled N-terminus (i.e. free, acetylated, or after pyro-Glu formation).

Abbreviations: aa - amino acids; PEP - Posterior Error Probability; Score - Andromeda score for the best associated MS/MS spectrum; Ratio H/L - ratio between heavy and light label partners; NaN - non-quantifiable ratio.

Index	Sequence	Leading razor protein	Unique (Groups)	Unique (Proteins)	Start position	End position	Length (# aa)	Amino acid before	Amino acid after	Missed cleavages	Mass (Da)	Charges	PEP	Score	Ratio H/L	Ratio H/L normalized	Ratio H/L count
1	AAAAAAAAAAGAAGGR	sp|Q8CCS6-2|PABP2_MOUSE	yes	no	2	17	16	M	G	0	1197.621	2	2.87E-04	134.68	NaN	NaN	0
2	AAAAAAGPEMVR	sp|P63085|MK01_MOUSE	yes	yes	2	13	12	M	G	0	1113.560	2	1.23E-02	83.18	NaN	NaN	0
3	AAAAATAATKGNGGGSGR	sp|Q9D3B1|HACD2_MOUSE	yes	yes	2	19	18	M	V	0	1487.744	2	4.68E-02	37.77	1.58	1.03	2
4	AAAAGAVVASAASGPAEGKKITEL	sp|Q8CH25-2|SLTM_MOUSE	yes	no	2	26	25	M	V	0	2295.255	3	3.29E-02	39.19	1.23	0.78	6
5	AAAAVVEFQR	sp|Q8BG32|PSD11_MOUSE	yes	yes	2	11	10	M	A	0	1060.567	2	1.14E-02	117.70	NaN	NaN	0
6	AAAITSDLLESLGR	sp|Q62009-5|POSTN_MOUSE	yes	no	254	267	14	R	D	0	1415.762	2	3.07E-04	151.99	NaN	NaN	0
7	AAAQIGNSFR	sp|Q9CZD3|SYG_MOUSE	yes	yes	312	321	10	F	N	0	1033.531	2	3.26E-03	148.73	NaN	NaN	0
8	AACFGLQPGCLR	sp|Q8C1A5|THOP1_MOUSE	yes	yes	425	436	12	H	Q	0	1348.638	2	3.08E-04	119.53	1.39	1.15	1
9	AADISQWAGPLCLQEVDEPPQHA	sp|P70296|PEBP1_MOUSE	yes	yes	2	26	25	M	V	0	2800.360	2;3	1.33E-09	152.07	NaN	NaN	0
10	AADKDGNVTCER	sp|Q61553|FSCN1_MOUSE	yes	yes	71	82	12	L	E	0	1334.589	2	1.18E-02	65.04	1.32	1.05	1
11	AADVGKAGAER	sp|P51881|ADT2_MOUSE	yes	yes	142	152	11	L	E	0	1043.536	2	1.86E-04	132.79	1.67	1.02	4
12	AAEFVPSFLR	sp|Q8R050-2|ERF3A_MOUSE	yes	no	82	91	10	H	G	0	1135.603	2	1.31E-02	91.66	0.05	0.04	2
13	AAFGLSEAGFNTACLTKLFPTR	sp|Q8K2B3|DHSA_MOUSE	yes	yes	76	97	22	R	S	0	2371.200	3	1.40E-05	77.08	1.79	1.27	2
14	AAFQLGSPWR	sp|P47738|ALDH2_MOUSE	yes	yes	87	96	10	R	R	0	1131.583	2	3.98E-02	74.84	NaN	NaN	0
15	AAFVLPEFTR	sp|Q64674|SPEE_MOUSE	yes	yes	286	295	10	R	K	0	1149.618	2	1.32E-02	110.38	NaN	NaN	0
16	AAGAAAALAFLNQESR	sp|Q9CPP0|NPM3_MOUSE	yes	yes	2	17	16	M	A	0	1559.806	2	4.50E-04	121.99	NaN	NaN	0
17	AAGAAEAGEAAVAVVEVGSAQQ	sp|Q9CQM9|GLRX3_MOUSE	yes	yes	2	29	28	M	L	0	2742.382	2;3	6.35E-04	74.91	NaN	NaN	0
18	AAGKGLSGGFSSR	sp|Q6NXH9|K2C73_MOUSE	yes	no	33	45	13	R	S	0	1193.615	3	1.06E-02	61.41	1.45	0.85	1
19	AAGLLSTFR	sp|O35206|COFA1_MOUSE	yes	yes	1222	1230	9	R	A	0	934.524	2	2.21E-02	103.55	NaN	NaN	0
20	AAGPLESSGKEEITQLKER	sp|Q99PL5|RRBP1_MOUSE	yes	yes	1529	1547	19	R	L	0	2042.064	4	7.31E-02	44.39	1.45	0.89	5
21	AAGTLYTYPENWR	sp|Q9D8N0|EF1G_MOUSE	yes	yes	2	14	13	M	A	0	1540.731	2	9.67E-03	78.32	NaN	NaN	0
22	AAGVPSASITWR	sp|Q05793|PGBM_MOUSE	yes	yes	1978	1989	12	R	K	0	1214.641	2	2.38E-02	73.63	NaN	NaN	0
23	AAIDYQKVVR	sp|Q3THS6|METK2_MOUSE	yes	yes	75	84	10	R	E	0	1161.651	3	8.94E-03	75.39	1.40	1.10	3
24	AAKLAPEFAKR	sp|O08709|PRDX6_MOUSE	yes	yes	54	64	11	R	N	0	1200.698	3	2.64E-02	56.09	1.07	1.03	3
25	AAKVLEQLTGQTPVFSKAR	sp|Q9CXW4|RL11_MOUSE	yes	yes	36	54	19	R	Y	0	2043.148	3	1.86E-02	57.37	0.94	0.93	1
26	AALEELVR	sp|Q61035|SYHC_MOUSE	yes	yes	5	12	8	R	L	0	899.508	2	4.37E-02	102.95	NaN	NaN	0
27	AALPSHVVTMLDNFPTNLHPMSC	sp|Q9CZU6|CISY_MOUSE	yes	yes	145	183	39	R	A	0	4165.073	4	6.96E-04	56.31	NaN	NaN	0
28	AALSGANVLTLIEKDIR	sp|Q91ZX7|LRP1_MOUSE	yes	yes	2362	2378	17	R	T	0	1783.020	3	1.75E-05	100.43	1.73	1.16	1
29	AALSGLLHR	sp|Q99JY0|ECHB_MOUSE	yes	yes	83	91	9	R	T	0	936.551	2	1.97E-02	117.89	NaN	NaN	0
30	AALVDLEPGTMDSVR	sp|Q922F4|TBB6_MOUSE	yes	yes	63	77	15	R	S	0	1572.782	2	1.07E-03	101.20	NaN	NaN	0
31	AANATTNPSQLLPLELVDKCIGSR	sp|P62322|LSM5_MOUSE	yes	yes	2	25	24	M	I	0	2567.338	3	6.60E-03	61.96	1.36	0.99	3
32	AANVPAGTEVVCAPPTAYIDFAR	sp|P17751|TPIS_MOUSE	yes	yes	81	103	23	N	Q	0	2389.174	2	1.27E-05	111.99	NaN	NaN	0
33	AAPFTLEYR	sp|Q9D819|IPYR_MOUSE	yes	yes	10	18	9	R	V	0	1066.545	2	1.84E-03	118.50	0.08	0.07	2
34	AAPGVDLTQLLNNMR	sp|P02535-3|K1C10_MOUSE	no	no	297	311	15	N	N	0	1611.840	2	1.11E-04	153.81	NaN	NaN	0
35	AAPTVDLNR	sp|Q61897|KT33B_MOUSE	no	no	215	223	9	D	V	0	955.509	2	2.30E-02	102.07	NaN	NaN	0
36	AAQAVSLLR	sp|Q8BJY1|PSMD5_MOUSE	yes	yes	2	10	9	M	E	0	927.550	2	1.90E-02	121.64	NaN	NaN	0
37	AASAIKGLSALR	sp|Q9D8T7-2|SLIRP_MOUSE	yes	no	2	13	12	M	S	0	1156.693	2	2.14E-04	123.95	1.09	1.01	5
38	AASEDELLLPR	sp|Q61249|IGBP1_MOUSE	yes	yes	2	12	11	M	L	0	1212.635	2	3.91E-02	94.77	NaN	NaN	0
39	AASIFGGAKPVDTAAR	sp|Q8BGD9|IF4B_MOUSE	yes	yes	357	372	16	R	E	0	1530.815	3	1.63E-04	82.53	0.89	0.70	2
40	AATFFGEVVKAPCR	sp|Q9JK23|PSMG1_MOUSE	yes	yes	2	15	14	M	A	0	1551.787	2	1.15E-06	153.39	1.19	1.01	4
41	AATNRPNSIDPALR	sp|Q01853|TERA_MOUSE	yes	yes	345	358	14	M	R	1	1494.790	3	1.13E-03	107.11	NaN	NaN	0
42	AATSPALFNR	sp|Q9JHU4|DYHC1_MOUSE	yes	yes	3077	3086	10	R	C	0	1046.551	2	9.25E-03	126.07	NaN	NaN	0
43	AATTGSGVKVPR	sp|Q9CZY3|UB2V1_MOUSE	yes	no	2	13	12	M	N	0	1142.641	2	4.06E-17	213.63	1.19	0.93	8
44	AAVEEGIVLGGGCALLR	sp|P63038|CH60_MOUSE	yes	no	430	446	17	R	C	0	1683.898	2	1.59E-02	67.33	NaN	NaN	0
45	AAVENLPTFLVELSR	sp|P70168|IMB1_MOUSE	yes	yes	28	42	15	R	V	0	1657.904	2	6.39E-04	120.70	NaN	NaN	0
46	AAVESLGFILFR	sp|Q3TXS7|PSMD1_MOUSE	yes	yes	617	628	12	R	T	0	1321.739	2	4.35E-03	105.46	NaN	NaN	0
47	AAVIGDVIR	sp|Q9JIK5|DDX21_MOUSE	yes	yes	496	504	9	R	V	0	912.539	2	2.20E-02	104.20	NaN	NaN	0
48	AAVKTLNPKAEVAR	sp|P80317|TCPZ_MOUSE	yes	yes	2	15	14	M	A	0	1466.857	3	5.40E-03	68.04	1.17	0.96	6
49	AAVPELLEQQEEDR	sp|Q9D8U8|SNX5_MOUSE	yes	yes	2	15	14	M	S	0	1625.790	2	4.61E-02	57.41	NaN	NaN	0
50	AAVPSGASTGIYEALELR	sp|P17182|ENOA_MOUSE	yes	no	33	50	18	R	D	0	1803.937	2;3	4.02E-04	116.51	NaN	NaN	0
51	AAVQQLQAEGLSPR	sp|Q8K354|CBR3_MOUSE	yes	yes	45	58	14	R	F	0	1466.784	2	5.08E-04	145.00	NaN	NaN	0
52	AAWGEETDYTPVWCMR	sp|P70697|DCUP_MOUSE	yes	yes	22	37	16	R	Q	0	1970.829	2	2.12E-02	64.52	NaN	NaN	0
53	AAWRPPR	sp|Q9R0N0|GALK1_MOUSE	yes	yes	2	8	7	M	V	1	852.472	2	4.02E-02	107.49	NaN	NaN	0
54	AAYKLVLIR	sp|Q9DBJ1|PGAM1_MOUSE	yes	yes	2	10	9	M	H	0	1045.665	2	7.29E-06	168.27	1.25	0.98	9
55	ACEGGKFATVEVTDKPVDEALR	sp|Q9R257|HEBP1_MOUSE	yes	yes	35	56	22	R	E	0	2391.174	4	1.01E-05	83.42	0.99	0.80	1
56	ACGLIIFR	sp|P56380|AP4A_MOUSE	yes	yes	5	12	8	R	R	0	948.522	2	3.88E-02	120.65	NaN	NaN	0
57	ACGLNFADLMGR	sp|Q62465|VAT1_MOUSE	yes	yes	98	109	12	R	Q	0	1323.606	2	1.99E-03	134.13	NaN	NaN	0
58	ACGLVASNLNLKPGECLKVR	sp|P16045|LEG1_MOUSE	yes	yes	2	21	20	M	G	0	2198.166	2;3;4	1.30E-09	128.59	1.12	1.08	29
59	ACVTGKPISQGGIHGR	sp|P26443|DHE3_MOUSE	yes	yes	253	268	16	H	I	0	1636.847	4	7.50E-03	58.89	1.46	1.12	2
60	ACYGVLR	sp|P62908|RS3_MOUSE	yes	yes	118	124	7	R	F	0	837.417	2	8.83E-02	89.90	NaN	NaN	0
61	ADDTFEALR	sp|P62869|ELOB_MOUSE	yes	yes	81	89	9	R	I	0	1036.483	2	7.25E-03	149.72	NaN	NaN	0
62	ADEIAKAQVAQPGGDTIFGKIIR	sp|P70349|HINT1_MOUSE	yes	yes	2	24	23	M	K	0	2397.302	2;3;4	4.75E-07	112.85	0.87	0.85	3
63	ADGSSLPEWVTDNAGTLHFAR	sp|Q8BKG3|PTK7_MOUSE	yes	yes	531	551	21	R	V	0	2243.061	3	4.97E-05	124.20	NaN	NaN	0
64	ADGYEPPVQESV	sp|P97351|RS3A_MOUSE	yes	no	253	264	12	R	-	0	1289.578	2	2.16E-02	74.39	NaN	NaN	0
65	ADGYVLEGKELEFYLR	sp|P62242|RS8_MOUSE	yes	yes	185	200	16	R	K	0	1900.957	3	6.52E-03	71.98	1.08	1.02	5
66	ADHQPLTEASYVNLPTIALCNTDS	sp|P14206|RSSA_MOUSE	yes	yes	129	155	27	R	Y	0	2995.471	2;3	4.69E-17	170.27	NaN	NaN	0
67	ADIDKLNIDSIIQR	sp|P63087|PP1G_MOUSE	yes	no	2	15	14	M	L	0	1612.878	2	3.47E-05	125.50	1.58	0.97	1
68	ADIVENQVMDTR	sp|P10649|GSTM1_MOUSE	yes	yes	97	108	12	R	M	0	1389.656	2	9.84E-04	147.26	NaN	NaN	0
69	ADKEAAFDDAVEER	sp|Q60972|RBBP4_MOUSE	yes	yes	2	15	14	M	V	0	1564.701	2	1.19E-05	133.86	1.37	0.92	7
70	ADLAEEYSKDR	sp|P68037|UB2L3_MOUSE	yes	yes	123	133	11	R	K	0	1295.599	3	1.92E-03	94.77	1.21	1.05	4
71	ADLEEQLSDEEKVR	sp|P47754|CAZA2_MOUSE	yes	yes	2	15	14	M	I	0	1659.795	2	1.92E-06	152.00	1.29	0.97	8
72	ADLPTLGFTHFQPAQLTTVGKR	sp|P54822|PUR8_MOUSE	yes	yes	150	171	22	R	C	0	2397.281	4	1.02E-02	48.05	0.91	0.88	1
73	ADMQNLVER	sp|P40124|CAP1_MOUSE	yes	yes	2	10	9	M	L	0	1074.513	2	1.78E-02	128.81	NaN	NaN	0
74	ADPEAAWEPTEAEAR	sp|Q9Z1F9|SAE2_MOUSE	yes	yes	211	225	15	R	A	0	1641.727	2	3.53E-02	58.08	NaN	NaN	0
75	ADPKYADLPGIAR	sp|Q99KJ8|DCTN2_MOUSE	yes	yes	2	14	13	M	N	0	1385.730	2	3.70E-03	72.89	1.15	0.96	6
76	ADSHGELDLAR	sp|Q32Q92-2|ACOT6_MOUSE	yes	no	54	64	11	R	T	0	1182.563	3	4.26E-03	126.71	NaN	NaN	0
77	ADTAPQLKR	sp|Q9DAR7|DCPS_MOUSE	yes	yes	2	10	9	M	K	0	998.551	2	1.82E-02	138.98	0.95	0.90	3
78	ADTLDPALLRPGR	sp|P54775|PRS6B_MOUSE	yes	yes	314	326	13	R	L	1	1393.768	3	9.28E-03	79.49	NaN	NaN	0
79	ADVDLYQVR	sp|Q9CR00|PSMD9_MOUSE	yes	yes	65	73	9	R	T	0	1077.546	2	2.29E-02	80.69	NaN	NaN	0
80	ADVESQFPDWIR	sp|Q8BJS4-3|SUN2_MOUSE	yes	no	433	444	12	R	Q	0	1461.689	2	3.68E-04	156.36	NaN	NaN	0
81	ADVGKAGAER	sp|P51881|ADT2_MOUSE	yes	yes	143	152	10	A	E	0	972.499	2	4.00E-03	91.96	1.34	0.94	2
82	AEAESWYQTKYEELQVTAGR	sp|Q8BGZ7|K2C75_MOUSE	no	no	337	356	20	R	H	0	2358.113	3	4.45E-08	103.90	1.63	1.10	3
83	AEAGDNLGALVR	sp|Q8BFR5-2|EFTU_MOUSE	yes	no	316	327	12	R	G	0	1184.615	2	2.11E-03	132.56	NaN	NaN	0
84	AEDDEDDDVDTKKQKTEEDD	sp|P26350|PTMA_MOUSE	yes	no	92	111	20	V	-	0	2338.941	3	4.14E-03	54.23	0.80	0.81	4
85	AEDGSVIDYELIDQDAR	sp|P07356|ANXA2_MOUSE	yes	yes	180	196	17	R	E	0	1907.875	2	2.43E-08	194.58	NaN	NaN	0
86	AEENALQQKACGSETMQKKQR	sp|E9Q557|DESP_MOUSE	yes	yes	1282	1302	21	R	L	0	2434.169	5	7.38E-02	42.64	1.89	1.38	2
87	AEEYEFLTPMEEAPKGMLAR	sp|Q99PT1|GDIR1_MOUSE	yes	yes	153	172	20	R	G	0	2311.087	3	2.04E-08	117.65	1.07	0.99	7
88	AEGAAQLSEER	sp|P59017|B2L13_MOUSE	yes	yes	370	380	11	R	A	0	1159.547	2	1.83E-02	83.18	NaN	NaN	0
89	AEGESEAPNPEPR	sp|Q8VE97|SRSF4_MOUSE	yes	yes	424	436	13	R	A	0	1381.611	2	1.37E-03	129.54	NaN	NaN	0
90	AEGQVLVLDGR	sp|P19253|RL13A_MOUSE	yes	yes	2	12	11	M	G	0	1155.625	2	1.96E-02	80.32	NaN	NaN	0
91	AEGSDVANAVLDGADCIMLSGET	sp|P52480|KPYM_MOUSE	no	no	343	376	34	R	M	0	3493.634	3	3.76E-10	138.80	1.08	1.02	3
92	AEIDMLDIR	sp|P97429|ANXA4_MOUSE	yes	yes	276	284	9	R	A	0	1074.538	2	1.93E-02	119.68	NaN	NaN	0
93	AEIENAKCQR	sp|Q9Z2T6|KRT85_MOUSE	no	no	351	360	10	T	A	0	1217.582	2	2.93E-04	137.89	1.68	1.15	3
94	AEIINHLADLLTDQR	sp|Q9Z110-2|P5CS_MOUSE	yes	no	384	398	15	R	E	0	1720.911	3	5.72E-04	129.05	NaN	NaN	0
95	AEKELSEQIEKALQLEEER	sp|P26040|EZRI_MOUSE	yes	yes	361	379	19	R	R	0	2271.159	4	5.24E-03	68.64	1.08	1.04	1
96	AEKYEWDVAEAR	sp|P58252|EF2_MOUSE	yes	yes	636	647	12	L	K	0	1465.684	2	3.32E-03	75.59	1.21	0.99	4
97	AELAKVEEEIVTLR	sp|Q9CYZ2|TPD54_MOUSE	yes	yes	51	64	14	R	Q	0	1598.888	3	8.93E-02	46.32	0.84	0.78	1
98	AELECKIQER	sp|Q61897|KT33B_MOUSE	yes	no	82	91	10	N	N	0	1274.629	2	6.20E-05	151.98	1.46	1.01	3

99	AELEEVTLDGKPLQALR	sp|Q9JIX8-4|ACINU_MOUSE	yes	no	60	76	17	M	V	0	1881.021	2	3.47E-08	134.14	1.16	0.83	5
100	AELNPWPEYINTR	sp|Q9D0R2|SYTC_MOUSE	yes	yes	44	56	13	R	L	0	1601.784	2	6.44E-03	88.08	NaN	NaN	0
101	AELSEEALLSVLPTIR	sp|P56399|UBP5_MOUSE	yes	yes	2	17	16	M	V	0	1739.967	2	1.36E-03	99.34	NaN	NaN	0
102	AELTALESLIEMGFPR	sp|Q922Y1|UBXN1_MOUSE	yes	yes	2	17	16	M	G	0	1775.913	2	6.44E-04	107.50	NaN	NaN	0
103	AENFFILR	sp|P59999|ARPC4_MOUSE	yes	yes	98	105	8	R	R	0	1008.539	2	3.87E-02	121.09	NaN	NaN	0
104	AENGESSGPPRPSR	sp|Q9QZM0|UBQL2_MOUSE	yes	yes	2	15	14	M	G	1	1439.675	2	3.28E-02	64.10	NaN	NaN	0
105	AENPGLENHR	sp|O35344|IMA4_MOUSE	yes	yes	2	11	10	M	I	0	1135.537	2	5.46E-02	108.70	NaN	NaN	0
106	AENYDISPADR	sp|Q02053|UBA1_MOUSE	yes	yes	870	880	11	R	H	0	1249.558	2	6.92E-03	114.23	NaN	NaN	0
107	AEPEDHYFLLTEPPLNTPENR	sp|Q99JY9|ARP3_MOUSE	yes	yes	103	123	21	R	E	0	2481.181	3	1.02E-02	62.00	NaN	NaN	0
108	AEPYCSVLPGFTFIQHLPLSER	sp|Q8VDM6-2|HNRL1_MOUSE	yes	no	288	309	22	R	I	0	2560.278	3	8.96E-04	83.44	NaN	NaN	0
109	AEQVALSR	sp|Q00612|G6PD1_MOUSE	yes	yes	2	9	8	M	T	0	872.472	2	4.97E-02	97.97	NaN	NaN	0
110	AESMLQQADKLGCR	sp|Q99K51|PLST_MOUSE	yes	yes	337	350	14	R	Q	0	1605.760	3	7.27E-04	77.78	1.32	1.21	4
111	AETECQNAEYQQLLDIKTR	sp|P02535-3|K1C10_MOUSE	yes	no	412	430	19	R	L	0	2309.096	2;3	3.63E-37	252.77	2.23	1.26	13
112	AEVATGDDKKR	sp|O70456|1433S_MOUSE	yes	yes	132	142	11	L	I	0	1188.610	2	4.96E-24	237.53	1.19	1.05	6
113	AEVQKLQMEAPHIIVGTPGR	sp|P60843|IF4A1_MOUSE	yes	yes	142	161	20	R	V	0	2173.168	3;4	9.01E-17	179.58	1.50	1.23	8
114	AEYEALAEQNR	sp|Q9Z320|K1C27_MOUSE	no	no	252	262	11	R	R	0	1292.600	2	2.47E-04	162.38	NaN	NaN	0
115	AEYEALAEQNRR	sp|Q9Z320|K1C27_MOUSE	no	no	252	263	12	R	D	1	1448.701	2;3	6.22E-05	177.10	NaN	NaN	0
116	AEYVVTKLDDLINWAR	sp|Q9DC70|NDUS7_MOUSE	yes	yes	71	86	16	R	R	0	1905.000	3	1.63E-04	82.59	1.32	0.89	1
117	AFDTGLNLSPDR	sp|O08796|EF2K_MOUSE	yes	yes	618	629	12	R	C	0	1304.636	2	1.47E-02	77.19	NaN	NaN	0
118	AFEDDDITHVEGSVDPIR	sp|Q9CZ30-2|OLA1_MOUSE	yes	no	126	143	18	R	D	0	2013.928	3	5.70E-03	82.88	NaN	NaN	0
119	AFFSEVER	sp|P50580|PA2G4_MOUSE	yes	yes	264	271	8	R	R	0	983.471	2	4.00E-02	116.25	NaN	NaN	0
120	AFGYYGPLR	sp|P84104-2|SRSF3_MOUSE	yes	no	29	37	9	R	S	0	1042.524	2	1.76E-03	133.12	13.16	10.28	2
121	AFHNEAQVNPER	sp|P11983|TCPA_MOUSE	yes	no	469	480	12	R	K	0	1410.664	3	3.89E-03	110.98	NaN	NaN	0
122	AFKALIAAQYSGAQVR	sp|Q9D8N0|EF1G_MOUSE	yes	yes	15	30	16	R	V	0	1692.931	3	4.68E-03	65.04	1.12	0.99	3
123	AFKAWAVAR	sp|P07724|ALBU_MOUSE	yes	no	234	242	9	R	L	0	1018.571	2;3	1.02E-05	162.97	1.22	1.03	10
124	AFKDTGKTPVEPEVAIHR	sp|P60867|RS20_MOUSE	yes	yes	2	19	18	M	I	0	1994.059	3;4	3.61E-07	105.90	1.17	0.96	16
125	AFLEVLAKSFEISPNR	sp|Q60847|COCA1_MOUSE	yes	no	461	476	16	R	V	0	1819.983	3	3.08E-03	69.33	2.12	1.44	1
126	AFLQGGQEATDIALLLR	sp|O08788-2|DCTN1_MOUSE	yes	no	769	785	17	R	D	0	1814.989	2	3.46E-03	90.35	NaN	NaN	0
127	AFPNPYADYNKSLAENYFDSTGR	sp|O89112|LANC1_MOUSE	yes	yes	5	27	23	R	L	0	2639.193	3	3.16E-02	39.66	1.20	1.13	4
128	AFSCASACGPR	sp|P97861|KRT86_MOUSE	no	no	11	21	11	R	P	0	1182.491	2	1.44E-03	146.71	NaN	NaN	0
129	AFSCASACGPRPGR	sp|P97861|KRT86_MOUSE	no	no	11	24	14	R	C	1	1492.666	2;3	5.49E-07	194.98	NaN	NaN	0
130	AFSYYGPLR	sp|Q8BL97-3|SRSF7_MOUSE	yes	no	30	38	9	R	T	0	1072.534	2	5.78E-03	152.63	NaN	NaN	0
131	AFVNVLTR	sp|P19096|FAS_MOUSE	yes	yes	1524	1531	8	H	G	0	918.529	2	4.37E-02	102.95	NaN	NaN	0
132	AFVRPSGTEDIVR	sp|Q9CYR6|AGM1_MOUSE	yes	yes	493	505	13	R	V	1	1445.763	3	1.55E-03	106.32	NaN	NaN	0
133	AGDHPVELLAR	sp|P07214|SPRC_MOUSE	yes	yes	207	217	11	E	D	0	1176.625	2	1.78E-02	84.31	NaN	NaN	0
134	AGDKDDITEPAVCALR	sp|Q02257|PLAK_MOUSE	yes	yes	445	460	16	R	H	0	1729.831	2;3	4.91E-09	153.72	1.63	1.04	7
135	AGDREDITEPAICALR	sp|Q02248|CTNB1_MOUSE	yes	yes	454	469	16	R	H	1	1785.868	3	3.78E-03	86.50	0.16	0.10	1
136	AGDWKCPNPTCENMNFSWR	sp|P56959|FUS_MOUSE	yes	yes	416	434	19	R	N	0	2368.978	3	1.88E-08	120.40	1.32	1.09	5
137	AGDWQCPNPGCGNQNFAWR	sp|Q61545|EWS_MOUSE	yes	yes	518	536	19	R	T	0	2233.917	2	6.57E-04	103.13	NaN	NaN	0
138	AGELTEDEVER	sp|P62270|RS18_MOUSE	yes	yes	56	66	11	R	V	0	1246.568	2	3.30E-04	155.97	NaN	NaN	0
139	AGGADQFSKPEAR	sp|Q6P253-4|DMKN_MOUSE	yes	no	440	452	13	R	Q	0	1332.642	3	9.28E-06	146.36	1.18	0.94	6
140	AGGEGGVTLGQPHLSR	sp|Q9Z0N1|IF2G_MOUSE	yes	yes	2	17	16	M	Q	0	1534.785	2	5.67E-08	190.19	NaN	NaN	0
141	AGGGSFGGGSLYGGGGSR	sp|Q61414|K1C15_MOUSE	yes	no	24	41	18	R	S	0	1499.675	2	8.38E-09	192.85	NaN	NaN	0
142	AGGIETIANEYSDR	sp|Q61316|HSP74_MOUSE	yes	yes	20	33	14	R	C	0	1494.695	2	1.01E-03	124.07	NaN	NaN	0
143	AGGLDWPEATEGPPSR	sp|Q9QY23|PKP3_MOUSE	yes	no	226	241	16	R	T	0	1638.764	2	7.76E-03	75.02	NaN	NaN	0
144	AGGRVSLEGGTLR	sp|Q0GA42|CNNM1_MOUSE	yes	yes	51	63	13	T	A	1	1271.695	3	1.47E-02	54.65	1.76	1.08	2
145	AGIAIKLAKDR	sp|O08529|CAN2_MOUSE	yes	yes	2	12	11	M	E	0	1154.714	2;3	2.19E-03	91.55	1.56	1.47	11
146	AGIEGPLLASEVER	sp|Q9QX47-2|SON_MOUSE	yes	no	1775	1788	14	R	D	0	1439.762	2	6.55E-03	81.63	NaN	NaN	0
147	AGIKVTVAGLAGKDPVQCSR	sp|Q99LX0|PARK7_MOUSE	yes	yes	29	48	20	R	D	0	2026.099	4	3.23E-03	59.34	1.05	1.03	3
148	AGKDLVSSLTSGLLTIGDR	sp|Q91V92|ACLY_MOUSE	yes	yes	906	924	19	R	F	0	1902.042	3	1.09E-02	49.19	1.09	1.05	3
149	AGKIVVNLTGR	sp|P62245|RS15A_MOUSE	yes	yes	58	68	11	R	L	0	1126.682	3	7.39E-04	115.41	1.33	0.93	5
150	AGKPVICATQMLESMIKKPR	sp|P52480|KPYM_MOUSE	no	no	320	339	20	R	P	0	2257.211	5	4.03E-06	131.67	1.06	0.97	1
151	AGKPVLHYFNAR	sp|P10648|GSTA2_MOUSE	yes	no	2	13	12	M	G	0	1371.741	3	9.59E-04	97.73	1.16	0.93	4
152	AGLGHPSAFGR	sp|Q9CWS0|DDAH1_MOUSE	yes	yes	2	12	11	M	A	0	1068.547	2	3.46E-04	155.00	NaN	NaN	0
153	AGLLEPEVFHLNPAR	sp|P52825|CPT2_MOUSE	yes	yes	168	182	15	R	S	0	1661.889	3	1.05E-03	101.30	NaN	NaN	0
154	AGLNCSTETMPIKINLIAPPR	sp|Q6ZWX6|IF2A_MOUSE	yes	yes	214	234	21	R	Y	0	2295.208	3	2.23E-03	61.28	1.30	0.79	1
155	AGLNSLEAVKR	sp|Q6IRU2|TPM4_MOUSE	yes	yes	2	12	11	M	K	0	1156.656	2	1.38E-16	207.88	1.01	0.85	6
156	AGLPCQDLEFVQFHPTGIYGAGCL	sp|Q8K2B3|DHSA_MOUSE	yes	yes	283	312	30	R	G	0	3365.563	3	2.19E-08	107.17	NaN	NaN	0
157	AGLPLPAALAFVPR	sp|Q3U487|HECD3_MOUSE	yes	yes	32	45	14	R	E	0	1391.829	2	7.09E-03	79.49	NaN	NaN	0
158	AGLQFPVGR	sp|Q8CGP6|H2A1H_MOUSE	yes	no	22	30	9	R	V	0	943.524	2	5.78E-03	152.63	NaN	NaN	0
159	AGSSSGSGVQGASAGGLAADASR	sp|P11088|FILA_MOUSE	yes	yes	47	69	23	R	R	0	1919.893	2;3	7.31E-21	216.19	NaN	NaN	0
160	AGTEEEEEEEEQSR	sp|Q9JK23|PSMG1_MOUSE	yes	yes	16	29	14	R	R	0	1650.649	2	1.09E-03	112.42	NaN	NaN	0
161	AGTGVDNVDLEAATR	sp|Q61753|SERA_MOUSE	yes	yes	76	90	15	R	K	0	1487.722	2	1.22E-04	153.20	NaN	NaN	0
162	AGTLSITEFADMLSGNAGGFR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	4126	4146	21	R	S	0	2114.010	3	3.82E-03	74.79	NaN	NaN	0
163	AGTTTIEAVKR	sp|P21107-2|TPM3_MOUSE	yes	yes	2	12	11	M	K	0	1145.640	2	3.72E-24	243.13	0.98	0.73	9
164	AGTVVLDDVELR	sp|P25206|MCM3_MOUSE	yes	yes	2	13	12	M	E	0	1285.688	2	5.43E-02	63.09	NaN	NaN	0
165	AGVHIKLPLLSKDNR	sp|P30275|KCRU_MOUSE	yes	yes	327	341	15	R	F	0	1659.978	4	4.48E-03	82.65	1.12	1.12	1
166	AGVLAHLEEER	sp|Q8VDD5|MYH9_MOUSE	no	no	765	775	11	R	D	0	1222.631	2;3	5.47E-03	121.02	NaN	NaN	0
167	AGVTCIILPAENR	sp|Q8CGK3|LONM_MOUSE	yes	yes	894	906	13	R	K	0	1412.745	2	1.10E-03	94.12	20.04	16.15	1
168	AHVIVMAATNRPNSIDPALR	sp|Q01853|TERA_MOUSE	yes	yes	339	358	20	R	R	1	2145.148	3	2.59E-03	89.47	NaN	NaN	0
169	AIAELGIYPAVDPLDSTSR	sp|P56480|ATPB_MOUSE	yes	yes	388	406	19	R	I	0	1987.026	2;3	2.09E-04	120.90	NaN	NaN	0
170	AIASATEGGSVPQIR	sp|Q9Z0X1|AIFM1_MOUSE	yes	yes	112	126	15	R	A	0	1455.768	2	2.80E-03	91.81	NaN	NaN	0
171	AIEINPDSAQPYKWR	sp|Q99L47|F10A1_MOUSE	yes	yes	173	187	15	R	G	0	1786.900	3	9.21E-04	75.76	1.09	1.03	5
172	AIFASGSPFDPVTLPDGR	sp|P06801|MAOX_MOUSE	yes	yes	428	445	18	R	T	0	1845.926	2	3.84E-04	117.18	NaN	NaN	0
173	AIFMIPTNPPPTFR	sp|Q9JI10-2|STK3_MOUSE	yes	no	159	172	14	R	K	0	1600.844	2	5.91E-02	50.90	NaN	NaN	0
174	AIGIDPGYSKAYGR	sp|Q8BJU0-2|SGTA_MOUSE	yes	no	151	164	14	R	M	0	1466.752	3	1.38E-02	51.73	1.00	0.77	3
175	AIHSWLTR	sp|P99026|PSB4_MOUSE	yes	yes	132	139	8	R	A	0	982.535	3	2.79E-02	143.73	NaN	NaN	0
176	AIKPDGVQR	sp|Q01768|NDKB_MOUSE	yes	no	10	18	9	I	G	0	982.556	2	6.75E-03	93.10	1.00	0.84	5
177	AIKYLNQDYETLR	sp|O08529|CAN2_MOUSE	yes	yes	24	36	13	R	N	0	1625.841	3	1.03E-05	145.31	1.52	1.29	5
178	AILAELTGR	sp|P35486|ODPA_MOUSE	yes	yes	133	141	9	R	R	0	942.550	2	2.14E-02	107.69	NaN	NaN	0
179	AILKANLR	sp|Q01853|TERA_MOUSE	yes	yes	655	662	8	V	K	0	897.576	2	4.89E-04	162.50	1.41	1.12	5
180	AILVDLEPGTMDSVR	sp|P99024|TBB5_MOUSE	no	no	63	77	15	R	S	0	1614.829	2	2.16E-05	113.40	7.20	5.88	8
181	AISTLNGLR	sp|P70372|ELAV1_MOUSE	yes	yes	77	85	9	R	L	0	943.545	2	2.86E-02	96.67	NaN	NaN	0
182	AITAIKGVGR	sp|P62270|RS18_MOUSE	yes	yes	29	38	10	F	R	0	984.608	2	1.78E-06	172.56	1.15	1.05	4
183	AITGASLADIMAKR	sp|Q8BP67|RL24_MOUSE	yes	yes	81	94	14	R	N	0	1416.776	2;3	4.95E-04	88.08	1.01	0.88	11
184	AIVAIENPADVSVISSR	sp|P14206|RSSA_MOUSE	yes	yes	64	80	17	R	N	0	1739.942	2;3	1.65E-04	135.09	NaN	NaN	0
185	AIVAKQVLLGR	sp|P19253|RL13A_MOUSE	yes	yes	21	31	11	A	K	0	1166.750	2	3.16E-02	51.28	1.04	0.98	1
186	AIYQATYR	sp|O55234|PSB5_MOUSE	yes	yes	218	225	8	R	D	0	984.503	2	2.40E-02	150.40	NaN	NaN	0
187	AKELLGQGLLLR	sp|Q8R1B4|EIF3C_MOUSE	yes	yes	640	651	12	R	S	0	1309.808	3	1.85E-03	81.71	1.31	1.11	5
188	AKFEELNMDLFR	sp|P20029|GRP78_MOUSE	yes	yes	326	337	12	R	S	0	1511.744	2;3	9.06E-05	131.69	1.18	0.97	11
189	AKFYPEDVSEELIQDITQR	sp|P26041|MOES_MOUSE	yes	yes	82	100	19	R	L	0	2280.127	3	2.89E-08	115.57	1.16	0.93	4
190	AKIAQGAMYR	sp|P14824|ANXA6_MOUSE	yes	yes	2	11	10	M	G	0	1107.586	2	4.71E-06	157.66	1.08	0.98	9
191	AKLDELEGALHQAKEELAR	sp|Q9R0H5|K2C71_MOUSE	no	no	393	411	19	R	M	0	2120.123	3;4	2.68E-08	116.60	1.30	0.86	5
192	AKLEAAVAEAEQQGEAALADAR	sp|Q9Z2T6|KRT85_MOUSE	yes	yes	361	382	22	R	C	0	2211.113	2;3	2.40E-16	157.90	1.81	1.05	6
193	AKPDEFSALCDLLGTR	sp|Q3UPL0-2|SC31A_MOUSE	yes	no	620	635	16	Y	L	0	1791.883	3	8.80E-03	53.92	1.42	1.33	3
194	AKVAPEEVSEVIFGHVLTAGCGQN	sp|Q8CAY6|THIC_MOUSE	yes	yes	45	71	27	R	Q	0	2865.444	4	1.05E-15	173.05	1.03	0.97	1
195	AKYNQILR	sp|P17182|ENOA_MOUSE	yes	yes	405	412	8	L	I	0	1004.577	2	8.67E-03	103.74	1.12	0.97	4
196	ALADDDFLTVTGKTVR	sp|P49717|MCM4_MOUSE	yes	yes	845	860	16	R	L	0	1720.900	3	2.85E-02	45.62	1.44	1.12	4
197	ALAEGLGVIACIGEKLDER	sp|P17751|TPIS_MOUSE	yes	yes	167	185	19	H	E	0	2013.057	3	2.27E-05	95.21	1.10	0.94	4
198	ALAEGVLLR	sp|P51855|GSHB_MOUSE	yes	yes	26	34	9	R	S	0	940.571	2	1.93E-02	120.15	NaN	NaN	0
199	ALAEIAKAELDDTPMR	sp|Q8VIJ6|SFPQ_MOUSE	yes	yes	335	350	16	R	G	0	1742.887	3	1.94E-06	104.20	0.90	0.67	2
200	ALALAQEILPQAPIAVR	sp|Q3TLP5-3|ECHD2_MOUSE	yes	no	123	139	17	R	L	0	1773.051	2	6.22E-03	77.75	NaN	NaN	0
201	ALAPQLAR	sp|Q64105|SPRE_MOUSE	yes	yes	23	30	8	R	L	0	838.502	2	4.25E-02	107.32	NaN	NaN	0

202	ALDDISESIKELQFYR	sp|Q9D8S4|ORN_MOUSE	yes	yes	196	211	16	R	N	0	1925.974	3	1.47E-02	49.60	0.95	0.88	1
203	ALDEGDIALLKTYGQSTYSR	sp|P46471|PRS7_MOUSE	yes	yes	24	43	20	R	Q	0	2200.101	3	3.82E-05	84.25	1.08	0.98	5
204	ALDEYYDKHFTEFVPLR	sp|P50516-2|VATA_MOUSE	yes	no	460	476	17	R	T	0	2142.042	4	6.21E-02	34.40	0.98	0.92	2
205	ALDTMNFDVIKGKPVR	sp|P29341|PABP1_MOUSE	yes	yes	68	83	16	R	I	0	1802.971	4	6.65E-03	59.71	1.05	0.93	6
206	ALEEANTELEVKIR	sp|Q61781|K1C14_MOUSE	no	no	141	154	14	R	D	0	1613.863	2;3	4.81E-05	122.97	1.71	1.08	17
207	ALEEERPSLR	sp|Q91VI7|RINI_MOUSE	yes	yes	444	453	10	R	I	1	1198.631	3	2.05E-02	94.69	NaN	NaN	0
208	ALEHFTDLYDIKR	sp|Q68FD5|CLH1_MOUSE	yes	yes	626	638	13	R	A	0	1619.831	4	4.50E-03	71.56	1.21	0.94	5
209	ALEKIDLKFIDTTSKFGHGR	sp|P27659|RL3_MOUSE	yes	yes	359	378	20	R	F	0	2275.233	5	8.68E-03	69.36	0.81	0.74	1
210	ALELEQELR	sp|Q8QZR5|ALAT1_MOUSE	yes	yes	45	53	9	R	Q	0	1099.587	2	1.93E-02	119.75	NaN	NaN	0
211	ALELEQER	sp|P26041|MOES_MOUSE	yes	no	372	379	8	R	K	0	986.503	2	2.89E-02	141.93	NaN	NaN	0
212	ALEQANTELEVKIR	sp|Q61414|K1C15_MOUSE	yes	no	118	131	14	R	D	0	1612.878	3	9.11E-04	76.76	2.07	1.29	4
213	ALEQQVEEMKTQLEELEDELQAT	sp|Q8VDD5|MYH9_MOUSE	yes	yes	1529	1557	29	R	L	0	3415.667	4	5.83E-04	93.60	0.90	0.64	1
214	ALESSIAPIVIFASNR	sp|P60122|RUVB1_MOUSE	yes	yes	318	333	16	R	G	0	1686.931	2;3	1.28E-03	99.75	NaN	NaN	0
215	ALETVPKDLR	sp|Q9Z199|SPT4B_MOUSE	yes	no	2	11	10	M	H	0	1140.650	2	2.46E-03	100.88	0.98	0.78	3
216	ALFDFNGNDEEDLPFKKGDILR	sp|Q64010-2|CRK_MOUSE	yes	no	139	160	22	R	I	0	2552.255	4	2.21E-03	55.45	1.05	0.97	4
217	ALFNLIDTFPLR	sp|Q9R0M3-2|SRPX_MOUSE	yes	no	353	364	12	M	K	0	1418.792	2	1.09E-02	86.91	NaN	NaN	0
218	ALFPPVEFPAPR	sp|P19096|FAS_MOUSE	yes	yes	814	825	12	N	G	0	1339.729	2	6.86E-02	66.27	NaN	NaN	0
219	ALGAALTPFNPLAGLR	sp|Q9DBL9-2|ABHD5_MOUSE	yes	no	49	64	16	R	I	0	1580.904	2	1.31E-02	70.89	NaN	NaN	0
220	ALGAEIVR	sp|Q91WT9-2|CBS_MOUSE	yes	no	180	187	8	R	T	0	827.487	2	3.96E-02	106.36	NaN	NaN	0
221	ALGFPLER	sp|Q9CZU6|CISY_MOUSE	yes	yes	441	448	8	R	P	0	901.502	2	4.85E-02	98.93	NaN	NaN	0
222	ALGGFGSGAYVGLGASR	sp|Q8VED5|K2C79_MOUSE	yes	no	83	99	17	R	Q	0	1538.784	2	9.36E-04	101.90	NaN	NaN	0
223	ALHSLLLR	sp|Q61205|PA1B3_MOUSE	yes	no	208	215	8	R	L	0	921.576	3	3.00E-02	140.09	NaN	NaN	0
224	ALIAGGGAPEIELALR	sp|P80315|TCPD_MOUSE	yes	yes	420	435	16	R	L	0	1549.883	2	2.38E-03	93.91	NaN	NaN	0
225	ALKGAGTDEKVLTEIIASR	sp|P48036|ANXA5_MOUSE	yes	yes	97	115	19	H	T	0	1971.100	4	1.12E-03	72.36	0.92	0.90	2
226	ALKNNSNDIVNAIMELTM	sp|Q60817|NACA_MOUSE	yes	no	198	215	18	R	-	0	1989.986	2	4.96E-06	102.08	1.14	1.08	2
227	ALKQISSNR	sp|Q9R0P3|ESTD_MOUSE	yes	yes	2	10	9	M	C	0	1015.577	2	7.48E-06	167.93	1.13	0.98	4
228	ALKTVFGVEPDLTR	sp|Q9D1A2|CNDP2_MOUSE	yes	yes	400	413	14	R	E	0	1544.856	3	6.26E-03	66.39	1.03	0.88	4
229	ALLAEHLLKPLPADR	sp|Q9JL62|GLTP_MOUSE	yes	yes	2	16	15	M	Q	0	1655.972	3	4.02E-05	102.65	1.19	1.13	4
230	ALLANALTSALR	sp|Q9CR67|TMM33_MOUSE	yes	yes	58	69	12	R	L	0	1212.719	2	3.09E-03	120.57	NaN	NaN	0
231	ALLEDGTFR	sp|Q8K2T1-3|NMRL1_MOUSE	yes	no	23	31	9	R	I	0	1020.524	2	1.39E-02	136.57	NaN	NaN	0
232	ALLELQLEPEELYQTFQR	sp|P58252|EF2_MOUSE	yes	yes	163	180	18	R	I	0	2219.147	2;3	5.48E-03	83.76	NaN	NaN	0
233	ALLFIPR	sp|P11499|HS90B_MOUSE	yes	yes	331	337	7	R	R	0	828.522	2	5.46E-02	133.99	NaN	NaN	0
234	ALLFVPR	sp|P07901|HS90A_MOUSE	yes	yes	340	346	7	R	R	0	814.507	2	6.30E-02	118.06	NaN	NaN	0
235	ALLGYADNQCKLELQGIQGAVDH	sp|Q9CPV4-3|GLOD4_MOUSE	yes	no	154	182	29	R	I	0	3085.540	4	8.41E-04	89.27	1.11	1.05	1
236	ALLSAPWYLNR	sp|P29416|HEXA_MOUSE	yes	yes	413	423	11	R	V	0	1302.709	2	5.99E-02	76.23	NaN	NaN	0
237	ALLYFR	sp|Q6P253-4|DMKN_MOUSE	yes	no	405	410	6	R	K	0	781.449	2	6.53E-02	112.88	NaN	NaN	0
238	ALMGSPQLVAAVVR	sp|Q02257|PLAK_MOUSE	yes	yes	178	191	14	R	T	0	1410.802	2;3	2.96E-04	152.40	NaN	NaN	0
239	ALMLQGVDLLADAVAVTMGPKG	sp|P63038|CH60_MOUSE	yes	yes	38	60	23	R	T	0	2325.255	3	4.41E-04	72.57	1.25	1.14	6
240	ALNAQGQDLENPLELR	sp|Q61495|DSG1A_MOUSE	no	no	129	144	16	R	V	0	1779.912	2;3	1.45E-26	262.42	NaN	NaN	0
241	ALPFWNEEIVPQIKEGKR	sp|Q9DBJ1|PGAM1_MOUSE	yes	yes	163	180	18	R	V	0	2153.163	3;4	4.50E-05	92.26	1.24	1.01	7
242	ALQEASEAYLVGLFEDTNLCAIHAI	sp|P84244|H33_MOUSE	yes	no	92	117	26	G	V	0	2918.460	4	9.21E-04	65.43	1.76	1.18	1
243	ALQSVVQAVPLHELR	sp|Q8BJY1|PSMD5_MOUSE	yes	yes	24	38	15	R	E	0	1658.947	3	1.11E-03	101.01	NaN	NaN	0
244	ALSEIAGITLPYDTLDQVR	sp|Q91VD9|NDUS1_MOUSE	yes	yes	625	643	19	R	N	0	2074.095	2	5.88E-04	105.90	NaN	NaN	0
245	ALSNLESIPGGYNALR	sp|Q8R317-2|UBQL1_MOUSE	no	no	249	264	16	R	R	0	1673.874	2	3.52E-04	129.38	NaN	NaN	0
246	ALSTGEKGFGYKGSSFHR	sp|P17742|PPIA_MOUSE	yes	yes	38	55	18	R	I	0	1927.954	4;5	8.91E-04	74.14	1.22	0.96	10
247	ALTLGALTLPLAR	sp|Q3U7R1-2|ESYT1_MOUSE	yes	no	541	553	13	R	L	0	1308.813	2	8.45E-04	142.83	NaN	NaN	0
248	ALTNAIQDSLTR	sp|Q9Z1Q9|SYVC_MOUSE	yes	yes	354	365	12	H	W	0	1301.694	2	5.92E-04	152.38	NaN	NaN	0
249	ALTTEGIFR	sp|Q5FWK3|RHG01_MOUSE	yes	yes	274	282	9	H	R	0	1006.545	2	1.05E-02	143.28	NaN	NaN	0
250	ALTVPELTQQMFDAKNMMAACI	sp|P68372|TBB4B_MOUSE	no	no	283	306	24	R	H	0	2737.270	3	1.11E-03	63.87	1.23	1.09	5
251	ALTVPELTQQVFDAKNMMAACD	sp|P99024|TBB5_MOUSE	yes	yes	283	306	24	R	H	0	2705.298	3	9.19E-04	66.47	1.40	1.23	13
252	ALVADSHPESER	sp|Q62261|SPTB2_MOUSE	yes	no	1657	1668	12	R	I	0	1309.626	3	8.58E-02	52.25	NaN	NaN	0
253	ALVAGIDR	sp|P61358|RL27_MOUSE	yes	yes	41	48	8	H	Y	0	813.471	2	6.97E-02	81.64	NaN	NaN	0
254	ALVDELEWEIAR	sp|Q9QXT0|CNPY2_MOUSE	yes	yes	33	44	12	R	V	0	1442.741	2	1.38E-02	79.49	NaN	NaN	0
255	ALVDGPCTR	sp|Q9CR57|RL14_MOUSE	yes	yes	36	44	9	R	V	0	987.481	2	1.28E-02	120.99	NaN	NaN	0
256	ALVDHENVISCPHLGASTKEAQSR	sp|Q61753|SERA_MOUSE	yes	yes	271	294	24	R	C	0	2618.287	5	1.17E-01	31.36	1.45	1.10	3
257	ALVEEALAQR	sp|Q9JK81|MYG1_MOUSE	yes	yes	243	252	10	R	F	0	1098.603	2	3.27E-03	148.69	NaN	NaN	0
258	ALVPAAELLDSGVISHELYQQLQR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	2881	2904	24	R	G	0	2649.413	3	2.86E-04	87.32	NaN	NaN	0
259	ALVSAQWVAEALKAPR	sp|Q99J99|THTM_MOUSE	yes	yes	9	24	16	R	S	0	1708.962	3	1.22E-02	50.31	0.97	0.91	4
260	ALYKAISVPR	sp|E9Q557|DESP_MOUSE	yes	yes	163	172	10	R	V	0	1116.666	2;3	1.01E-03	120.06	1.47	0.97	7
261	ALYSLGSKEDPVLDP	sp|P54923|ADPRH_MOUSE	yes	no	348	362	15	R	-	0	1602.814	2	2.57E-02	64.10	1.56	1.25	1
262	ALYTFEPR	sp|Q62422|OSTF1_MOUSE	yes	yes	19	26	8	R	T	0	995.508	2	3.00E-02	140.09	NaN	NaN	0
263	AMADPEVQQIMSDPAMR	sp|Q60864|STIP1_MOUSE	yes	yes	489	505	17	R	L	0	1888.848	2	4.10E-03	87.43	NaN	NaN	0
264	AMGIMNSFVNDIFER	sp|Q9D2U9|H2B3A_MOUSE	yes	no	59	73	15	K	I	0	1742.812	2	6.08E-04	124.62	NaN	NaN	0
265	AMKFLR	sp|Q01768|NDKB_MOUSE	yes	yes	37	42	6	V	A	0	764.437	2	9.72E-03	126.07	1.05	0.94	4
266	AMVLDLR	sp|P97372|PSME2_MOUSE	yes	yes	204	210	7	R	A	0	816.453	2	1.10E-01	76.13	NaN	NaN	0
267	AMVSEFLKQAR	sp|P10107|ANXA1_MOUSE	yes	yes	2	12	11	M	F	0	1278.675	2	7.29E-17	220.10	1.10	0.93	15
268	ANELKATIDQNLEDLRR	sp|P06728|APOA4_MOUSE	yes	yes	205	221	17	R	S	1	1998.049	4	2.78E-02	55.55	0.95	0.90	1
269	ANHAPFETDISTLTR	sp|Q9QXD6|F16P1_MOUSE	yes	yes	2	16	15	M	F	0	1671.822	2	1.24E-04	95.66	0.04	0.03	2
270	ANILEDSYR	sp|P46935|NEDD4_MOUSE	yes	yes	537	545	9	R	R	0	1079.525	2	2.22E-03	168.83	NaN	NaN	0
271	ANKGPSYGMSR	sp|P37804|TAGL_MOUSE	yes	yes	2	12	11	M	E	0	1166.550	2	9.13E-04	110.80	1.24	1.02	3
272	ANLEKAQSELSGAADEAAR	sp|Q9D3D9|ATPD_MOUSE	yes	yes	132	150	19	R	A	0	1929.939	3	3.25E-08	113.86	1.23	0.91	9
273	ANLQNAIAEAEQR	sp|Q922U2|K2C5_MOUSE	yes	no	402	414	13	C	G	0	1426.717	2	4.93E-04	151.70	NaN	NaN	0
274	ANSPHELYR	sp|Q02788|CO6A2_MOUSE	yes	yes	220	228	9	I	N	0	1085.525	2	1.78E-02	128.60	NaN	NaN	0
275	ANTFVAELKGLDPAR	sp|P08249|MDHM_MOUSE	yes	yes	177	191	15	R	V	0	1600.857	2;3	5.83E-05	163.91	1.26	0.99	9
276	ANTVLSGGTTMYPGIADR	sp|P63260|ACTG_MOUSE	no	no	295	312	18	Y	M	0	1822.888	2	4.04E-06	166.60	NaN	NaN	0
277	ANVDKVFFDLMR	sp|Q9JIW9|RALB_MOUSE	yes	no	163	174	12	R	E	0	1453.739	3	1.82E-03	82.20	1.50	1.01	1
278	ANVKGYLGPEQLPDCLKGCDVVV	sp|P08249|MDHM_MOUSE	yes	yes	75	104	30	R	K	0	3220.674	4	6.66E-03	51.32	0.97	0.95	2
279	APAFLSAEEVQDHLR	sp|O54983|CRYM_MOUSE	yes	yes	4	18	15	R	S	0	1681.842	2;3	1.62E-07	194.48	NaN	NaN	0
280	APEEHPVLLTEAPLNPKANR	sp|P63260|ACTG_MOUSE	no	no	97	116	20	V	E	0	2195.170	3	2.04E-08	117.65	1.16	0.98	6
281	APFDLFENR	sp|P07901|HS90A_MOUSE	yes	yes	348	356	9	R	K	0	1107.535	2	7.25E-03	149.72	NaN	NaN	0
282	APIIAVTR	sp|P52480|KPYM_MOUSE	no	no	448	455	8	R	N	0	839.523	2	9.03E-04	153.71	0.02	0.01	1
283	APITGYIIR	sp|P11276|FINC_MOUSE	yes	yes	1473	1481	9	R	H	0	1002.586	2	1.68E-02	130.75	NaN	NaN	0
284	APLIPMEHCTTR	sp|P07214|SPRC_MOUSE	yes	yes	256	267	12	R	F	0	1424.690	3	1.95E-02	75.09	NaN	NaN	0
285	APLPYSDISGLNALLLR	sp|Q6PD26|PIGS_MOUSE	yes	yes	44	60	17	R	L	0	1812.015	2	2.52E-04	126.77	NaN	NaN	0
286	APQCLGKFIEIAAR	sp|Q8VEK3|HNRPU_MOUSE	yes	yes	535	548	14	R	K	0	1572.845	3	1.18E-08	169.04	1.18	0.87	10
287	APQLVGQFIAR	sp|Q61823|PDCD4_MOUSE	yes	yes	257	267	11	R	A	0	1198.682	2	3.22E-03	133.23	NaN	NaN	0
288	APQVLVLAPTR	sp|Q9JIK5|DDX21_MOUSE	yes	yes	332	342	11	R	E	0	1163.703	2	3.34E-03	132.32	NaN	NaN	0
289	APSLVGTVGSVSSFR	sp|B1AQ75|KRT36_MOUSE	yes	yes	39	53	15	R	T	0	1462.778	2	5.75E-05	164.15	NaN	NaN	0
290	APSTCGGMSVTSSR	sp|Q9Z2K1|K1C16_MOUSE	yes	no	38	51	14	R	F	0	1396.608	2	3.67E-06	180.85	NaN	NaN	0
291	APSTYGGMSVTSSR	sp|Q61781|K1C14_MOUSE	yes	yes	38	51	14	R	F	0	1399.640	2	5.43E-07	195.10	NaN	NaN	0
292	APTAQVESFR	sp|Q80YX1-5|TENA_MOUSE	yes	no	1096	1105	10	R	I	0	1104.556	2	1.31E-02	110.88	NaN	NaN	0
293	APVIDADKPVSSQLR	sp|Q9JHU4|DYHC1_MOUSE	yes	yes	120	134	15	R	V	0	1594.868	3	1.10E-02	52.53	1.62	0.97	6
294	APVPASELLDAKILSR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	3212	3227	16	R	A	0	1678.962	3	3.05E-02	57.29	0.46	0.28	2
295	AQAEAQQPVFNTLR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1040	1053	14	R	D	0	1571.806	2	8.05E-07	189.23	NaN	NaN	0
296	AQDFKTDLR	sp|P84244|H33_MOUSE	no	no	76	84	9	I	F	0	1092.556	2	7.94E-06	167.09	1.48	0.83	5
297	AQDQGEKENPMR	sp|Q9CXW4|RL11_MOUSE	yes	yes	2	13	12	M	E	0	1401.631	2	2.71E-05	148.41	1.34	0.96	13
298	AQEQLATALQNLEEAEKAADESEI	sp|Q6IRU2|TPM4_MOUSE	yes	yes	66	89	24	R	G	0	2643.262	3	1.02E-06	114.15	0.93	0.81	4
299	AQFEGIVTDLIKR	sp|P38647|GRP75_MOUSE	yes	yes	349	361	13	R	T	0	1488.830	2;3	2.65E-05	129.37	1.47	1.21	12
300	AQIGGPEAGKSEQSGAK	sp|P14602|HSPB1_MOUSE	yes	no	193	209	17	R	-	0	1613.801	2;3	7.86E-07	112.34	1.02	1.00	4
301	AQIHFPR	sp|Q00896|A1AT3_MOUSE	yes	no	302	308	7	L	L	0	867.472	2	4.27E-02	154.09	NaN	NaN	0
302	AQLADSFHLQQFFR	sp|P16546-2|SPTN1_MOUSE	yes	no	567	580	14	R	D	0	1706.853	3	4.62E-03	89.23	NaN	NaN	0
303	AQLLQPTLEINPR	sp|Q9CQN1|TRAP1_MOUSE	yes	yes	637	649	13	R	H	0	1491.841	2	2.85E-03	98.94	NaN	NaN	0
304	AQNLKDLAGR	sp|O35129|PHB2_MOUSE	yes	yes	2	11	10	M	L	0	1084.599	2	2.61E-04	150.46	1.73	1.63	7

305	AQPEHIISEGR	sp|Q99J99|THTM_MOUSE	yes	yes	283	293	11	R	G	0	1235.626	3	5.34E-02	67.39	NaN	NaN	0
306	AQSEAEKLAKER	sp|P26041|MOES_MOUSE	yes	yes	382	393	12	R	Q	0	1358.715	3	1.74E-02	58.17	0.99	0.70	4
307	AQSLLSTDR	sp|Q8BG32|PSD11_MOUSE	yes	yes	12	20	9	R	E	0	989.514	2	9.56E-02	67.33	NaN	NaN	0
308	AQVSLLIR	sp|O35129|PHB2_MOUSE	yes	yes	158	165	8	R	R	0	898.560	2	3.41E-02	133.12	NaN	NaN	0
309	AQYEEIALKSKAEAEALYQTKFQEI	sp|Q9R0H5|K2C71_MOUSE	yes	no	307	337	31	R	H	0	3496.820	5	1.96E-04	75.44	1.63	1.05	1
310	ARFEELNADLFR	sp|P63017|HSP7C_MOUSE	no	no	300	311	12	R	G	1	1479.747	2;3	4.04E-03	109.15	NaN	NaN	0
311	ARLECEINTYR	sp|Q61897|KT33B_MOUSE	no	no	347	357	11	K	G	1	1423.688	2;3	4.16E-03	127.17	NaN	NaN	0
312	ASALEQFVNSVR	sp|O88543|CSN3_MOUSE	yes	yes	2	13	12	M	Q	0	1319.683	2	3.72E-04	156.14	NaN	NaN	0
313	ASAPATPLSPTR	sp|P14733|LMNB1_MOUSE	yes	yes	16	27	12	R	L	0	1167.625	2	2.78E-03	124.21	NaN	NaN	0
314	ASAVSPANLPAVLLQPR	sp|Q61191|HCFC1_MOUSE	yes	yes	2	18	17	M	W	0	1702.973	3	5.34E-02	48.42	NaN	NaN	0
315	ASESGKLWGGR	sp|Q91YI0|ARLY_MOUSE	yes	yes	2	12	11	M	F	0	1146.578	2	1.35E-04	138.99	1.10	0.94	4
316	ASFLLNLR	sp|Q9WTI7-4|MYO1C_MOUSE	yes	no	814	821	8	R	R	0	932.544	2	1.59E-02	162.50	NaN	NaN	0
317	ASFTKSLQGIR	sp|Q02788|CO6A2_MOUSE	yes	yes	131	141	11	R	S	0	1206.672	2;3	8.16E-04	113.38	1.61	0.93	6
318	ASGIIDTLFQDR	sp|Q06890|CLUS_MOUSE	yes	yes	182	193	12	R	F	0	1334.683	2	3.95E-03	110.31	NaN	NaN	0
319	ASGNYATVISHNPETKKTR	sp|P62918|RL8_MOUSE	yes	yes	129	147	19	R	V	0	2073.060	4;5	6.38E-06	100.97	1.00	0.90	9
320	ASGPIRPIVR	sp|P47963|RL13_MOUSE	yes	yes	51	60	10	P	C	1	1064.646	2	2.75E-02	83.87	NaN	NaN	0
321	ASGVAVSDGVIKVFNDMKVR	sp|P18760|COF1_MOUSE	yes	yes	2	21	20	M	K	0	2091.115	2;3	1.99E-05	93.37	0.97	0.92	13
322	ASGVQVADEVCR	sp|Q9R0P5|DEST_MOUSE	yes	yes	2	13	12	M	I	0	1289.603	2	3.18E-04	159.77	NaN	NaN	0
323	ASIWVGPR	sp|O35639|ANXA3_MOUSE	yes	yes	2	9	8	M	G	0	884.487	2	4.17E-02	110.31	NaN	NaN	0
324	ASLIQKAKLAEQAER	sp|O70456|1433S_MOUSE	yes	yes	4	18	15	R	Y	0	1654.937	3;4	3.83E-06	128.64	1.04	0.92	8
325	ASLKDLEGKWR	sp|Q05816|FABP5_MOUSE	yes	yes	2	12	11	M	L	0	1301.709	2;3	1.47E-05	153.75	1.14	0.93	16
326	ASLPQVER	sp|O88342|WDR1_MOUSE	yes	yes	10	17	8	F	G	0	898.487	2	3.84E-02	122.19	NaN	NaN	0
327	ASLQNLLSASQAR	sp|P35505|FAAA_MOUSE	yes	yes	83	95	13	R	L	0	1357.731	2	1.93E-02	72.89	NaN	NaN	0
328	ASLSKLGDVYVNDAFGTAHR	sp|P09411|PGK1_MOUSE	yes	yes	152	171	20	R	A	0	2120.065	3;4	1.30E-16	178.72	1.19	0.98	11
329	ASLSLAPVNIFKAGADEER	sp|P80314|TCPB_MOUSE	yes	yes	2	20	19	M	A	0	1987.038	2	3.59E-12	145.02	1.21	0.95	7
330	ASNLNLKPGECLKVR	sp|P16045|LEG1_MOUSE	yes	yes	7	21	15	V	G	0	1697.925	2	3.39E-04	77.75	0.94	0.80	3
331	ASNVTNKTDPR	sp|Q9Z204-4|HNRPC_MOUSE	yes	no	2	12	11	M	S	0	1201.605	2	1.52E-04	137.01	1.11	0.79	9
332	ASSFVLALEPELESR	sp|Q91YQ5|RPN1_MOUSE	yes	yes	67	81	15	R	L	0	1646.852	2	1.01E-02	88.77	NaN	NaN	0
333	ASSKGAGGYTCQSGSGWDEFTKR	sp|E9Q557|DESP_MOUSE	yes	yes	176	198	23	R	L	0	2436.076	4	8.57E-04	67.56	1.86	1.08	2
334	ASVGTLAFDEYGRPFLIIKDQDR	sp|P80316|TCPE_MOUSE	yes	yes	2	24	23	M	K	1	2610.344	3	4.28E-07	114.46	1.24	0.97	6
335	ASYLDKVR	sp|Q9QWL7|K1C17_MOUSE	no	no	96	103	8	L	A	0	950.519	2	2.56E-03	141.48	1.62	1.02	6
336	ASYLEKVR	sp|Q497I4|KRT35_MOUSE	no	no	109	116	8	L	Q	0	964.534	2	2.69E-02	74.92	1.32	0.94	2
337	ASYMDKVR	sp|P02535-3|K1C10_MOUSE	yes	no	147	154	8	L	A	0	968.475	2	3.56E-05	180.34	1.52	1.04	8
338	ASYMEKVR	sp|Q61897|KT33B_MOUSE	no	no	68	75	8	L	Q	0	982.491	2	1.09E-03	152.34	1.84	1.20	6
339	ASYVAPLTAQPATYR	sp|Q8C2Q3-2|RBM14_MOUSE	yes	no	224	238	15	R	A	0	1607.831	2	1.94E-03	96.49	NaN	NaN	0
340	ATAENEFVVLKKDVDCAYLR	sp|Q9Z2T6|KRT85_MOUSE	no	no	219	238	20	R	K	0	2340.178	3;4	1.08E-08	123.19	2.17	1.21	3
341	ATATPVQQQR	sp|P14733|LMNB1_MOUSE	yes	yes	2	11	10	M	A	0	1098.578	2	9.27E-03	125.97	NaN	NaN	0
342	ATDELASKLSR	sp|Q9D8Y0|EFHD2_MOUSE	yes	yes	2	12	11	M	R	0	1189.630	2	8.37E-05	145.31	1.02	0.83	5
343	ATEKLLEYLR	sp|Q7TPV4|MBB1A_MOUSE	yes	yes	51	60	10	R	T	0	1234.692	3	9.82E-02	67.33	NaN	NaN	0
344	ATENDIYNFFSPLNPMR	sp|P70333|HNRH2_MOUSE	yes	yes	300	316	17	R	V	0	2027.941	2	5.93E-05	149.99	NaN	NaN	0
345	ATENDIYNFFSPLNPVR	sp|Q9Z2X1|HNRPF_MOUSE	no	no	300	316	17	K	V	0	1995.969	2;3	1.28E-05	166.92	NaN	NaN	0
346	ATESSPLTTHVLDTASGLPAQGLC	sp|Q9CRB3|HIUH_MOUSE	yes	yes	2	27	26	M	L	0	2694.365	2;3	2.32E-07	127.58	NaN	NaN	0
347	ATGANATPLDFPSKKR	sp|Q64213-2|SF01_MOUSE	yes	no	2	17	16	M	K	0	1672.890	3	1.57E-04	93.91	0.86	0.69	8
348	ATGGVLASSSLR	sp|Q99M73|KRT84_MOUSE	yes	yes	530	541	12	R	A	0	1117.609	2	1.04E-02	88.02	NaN	NaN	0
349	ATIATMPVPETR	sp|Q62189|SNRPA_MOUSE	yes	yes	2	13	12	M	A	0	1285.670	2	9.40E-03	90.61	16.13	12.97	1
350	ATKIDKEACR	sp|Q9CQI6|COTL1_MOUSE	yes	yes	2	11	10	M	A	0	1190.608	3	3.82E-02	54.49	1.26	1.01	5
351	ATKPLYVALAQR	sp|P29341|PABP1_MOUSE	yes	yes	359	370	12	V	K	0	1329.777	2	3.13E-04	119.25	1.15	1.08	4
352	ATLGINDTLIR	sp|Q8VCN5|CGL_MOUSE	yes	yes	364	374	11	R	L	0	1185.672	2	2.34E-03	139.86	NaN	NaN	0
353	ATNDAVLKR	sp|P31230|AIMP1_MOUSE	yes	yes	2	10	9	M	L	0	986.551	2	1.40E-04	151.22	1.21	0.97	7
354	ATNSELVQSGKSEISELR	sp|Q61781|K1C14_MOUSE	no	no	324	341	18	V	R	0	1946.991	2	7.34E-04	74.73	1.71	1.10	2
355	ATPLNCVVPLGSPLNHGCGTMYS	sp|Q9D3I6|KRA71_MOUSE	yes	yes	27	51	25	R	N	0	2687.262	3	8.68E-09	135.62	NaN	NaN	0
356	ATSENEFVALKKDVDCAYLR	sp|Q6IMF0|KRT83_MOUSE	yes	yes	207	226	20	R	K	0	2328.142	3;4	8.98E-09	124.20	1.98	1.18	6
357	ATTFLQTSSTFGGSSTR	sp|Q61414|K1C15_MOUSE	yes	no	2	18	17	M	G	0	1747.838	2	4.01E-04	119.46	NaN	NaN	0
358	ATVAATTKVPEIR	sp|Q9WTM5|RUVB2_MOUSE	yes	yes	2	14	13	M	D	0	1355.777	2	4.14E-08	157.86	1.33	1.03	8
359	ATVDLEKLR	sp|P12382|K6PL_MOUSE	yes	yes	2	10	9	M	M	0	1043.598	2	4.70E-04	140.16	1.09	1.03	6
360	ATVWDLR	sp|Q3UPL0-2|SC31A_MOUSE	yes	no	193	199	7	R	K	0	859.455	2	1.06E-01	77.06	NaN	NaN	0
361	ATYLDKVR	sp|Q61781|K1C14_MOUSE	no	no	133	140	8	L	A	0	964.534	2	2.41E-04	172.25	1.65	0.93	5
362	ATYLNSFSHVGTGIVHAINNVVR	sp|Q02788|CO6A2_MOUSE	yes	yes	923	945	23	R	G	0	2468.292	3;4	8.27E-12	158.37	NaN	NaN	0
363	AVAENQPFLIEAMTYR	sp|P50136|ODBA_MOUSE	yes	yes	314	329	16	R	I	0	1851.919	2	3.05E-03	90.35	NaN	NaN	0
364	AVAGDFMR	sp|Q61576|FKB10_MOUSE	yes	yes	282	289	8	R	Y	0	865.412	2	4.42E-02	102.41	NaN	NaN	0
365	AVAQALEVIPR	sp|P80318|TCPG_MOUSE	yes	yes	439	449	11	R	T	0	1165.682	2	1.72E-03	144.55	0.04	0.02	1
366	AVAVGRPSNEELR	sp|Q8C1B7-3|SEP11_MOUSE	yes	no	2	14	13	M	N	1	1396.742	2	1.57E-03	103.44	NaN	NaN	0
367	AVCMLSNTTAIAEAWAR	sp|P68373|TBA1C_MOUSE	no	no	374	390	17	R	L	0	1863.897	2	1.81E-04	132.81	NaN	NaN	0
368	AVDDGVNTFKVLTR	sp|P42932|TCPQ_MOUSE	yes	yes	391	404	14	R	D	0	1533.815	3	1.13E-02	56.57	1.35	0.99	10
369	AVDNQVYVATASPAR	sp|Q9JHW2|NIT2_MOUSE	yes	yes	196	210	15	R	D	0	1560.790	2	7.43E-04	107.50	NaN	NaN	0
370	AVEEVDEEGKFVR	sp|P48678|LMNA_MOUSE	yes	no	441	453	13	V	L	0	1505.736	2	6.32E-04	92.86	1.70	1.23	3
371	AVEFKVVETDPSPYCIVAPDTVIHC	sp|Q01853|TERA_MOUSE	yes	yes	160	191	32	R	E	0	3654.806	4;5	1.81E-03	88.40	1.09	0.99	4
372	AVEYLLMGIPGDR	sp|P54728|RD23B_MOUSE	yes	yes	221	233	13	R	E	0	1432.738	2	2.85E-03	98.94	NaN	NaN	0
373	AVFDETYPDPVR	sp|Q8BGQ7|SYAC_MOUSE	yes	yes	684	695	12	R	V	0	1407.667	2	6.49E-04	134.98	26.69	25.98	1
374	AVFPEGPWEEPLQLR	sp|Q4LDD4-3|ARAP1_MOUSE	yes	no	647	661	15	R	K	0	1766.899	2	3.00E-03	90.71	NaN	NaN	0
375	AVFPSIVGR	sp|P63260|ACTG_MOUSE	no	no	29	37	9	R	P	0	944.544	2	1.96E-02	118.33	NaN	NaN	0
376	AVFPSIVGRPR	sp|P63260|ACTG_MOUSE	no	no	29	39	11	R	H	1	1197.698	2;3	1.23E-04	171.85	NaN	NaN	0
377	AVFQANQENLPILKR	sp|Q8VDN2|AT1A1_MOUSE	yes	yes	431	445	15	R	A	0	1739.968	3	2.28E-05	112.42	1.11	1.00	9
378	AVFVDLEPTVIDEIR	sp|P68368|TBA4A_MOUSE	yes	yes	65	79	15	R	N	0	1714.914	2;3	3.71E-03	69.33	26.96	18.42	1
379	AVFVDLEPTVIDEVR	sp|P68373|TBA1C_MOUSE	no	no	65	79	15	R	T	0	1700.899	2;3	2.05E-05	175.15	NaN	NaN	0
380	AVGDIPGVR	sp|P62267|RS23_MOUSE	yes	yes	111	119	9	H	F	0	882.492	2	1.56E-02	133.23	NaN	NaN	0
381	AVLHVALR	sp|P06745|G6PI_MOUSE	yes	no	97	104	8	R	N	0	877.550	2	1.61E-01	70.00	NaN	NaN	0
382	AVLKFAAATGATPIAGR	sp|P14206|RSSA_MOUSE	yes	yes	86	102	17	R	F	0	1613.925	3	6.45E-07	115.56	1.13	0.99	6
383	AVLNPLCQVDYR	sp|Q01405|SC23A_MOUSE	yes	yes	68	79	12	R	A	0	1446.729	2	6.43E-03	98.11	NaN	NaN	0
384	AVLVDLEPGTMDSVR	sp|P68372|TBB4B_MOUSE	yes	no	63	77	15	R	S	0	1600.813	2	6.97E-04	113.40	NaN	NaN	0
385	AVNLLDVPVPVAR	sp|Q8K1M6-4|DNM1L_MOUSE	yes	no	498	510	13	H	K	0	1361.803	2	3.11E-02	68.00	NaN	NaN	0
386	AVNTQALSGAGILR	sp|Q9CWK8|SNX2_MOUSE	yes	yes	270	283	14	R	M	0	1369.768	2	5.39E-04	143.94	NaN	NaN	0
387	AVPLALALISVSNPR	sp|Q8VDM4|PSMD2_MOUSE	yes	yes	689	703	15	R	L	0	1519.909	2	3.66E-02	57.29	NaN	NaN	0
388	AVPPTYADLGKSAR	sp|Q60932-2|VDAC1_MOUSE	yes	no	2	15	14	M	D	0	1444.767	2	5.45E-04	85.84	1.27	0.93	11
389	AVPQLQGYLR	sp|P47911|RL6_MOUSE	yes	yes	271	280	10	K	S	0	1143.640	2	2.40E-02	83.95	0.06	0.06	1
390	AVQQNGAPATTKVKAN	sp|Q9JLJ5|ELOV1_MOUSE	yes	no	264	279	16	R	-	0	1596.858	3	3.90E-03	67.14	2.08	1.16	1
391	AVSDGVIKVFNDMKVR	sp|P18760|COF1_MOUSE	yes	yes	6	21	16	V	K	0	1776.956	2	8.93E-03	53.57	2.54	2.12	2
392	AVSTGVKVPR	sp|Q9D2M8-2|UB2V2_MOUSE	yes	no	2	11	10	M	N	0	1012.603	2	1.60E-04	145.99	1.24	1.01	5
393	AVTGYNDPETGNIISLFQAMNKEL	sp|E9Q557|DESP_MOUSE	yes	yes	2347	2378	32	R	L	0	3514.788	5	8.71E-16	157.82	1.73	0.95	1
394	AVTGYTDPYTGDQISLFQAMQR	sp|Q8R0W0|EPIPL_MOUSE	yes	no	2314	2335	22	R	D	0	2461.158	2	3.86E-04	95.50	NaN	NaN	0
395	AVTIFIR	sp|P80316|TCPE_MOUSE	yes	yes	382	388	7	R	G	0	818.501	2	5.78E-02	128.38	NaN	NaN	0
396	AVTLDKDAYYR	sp|Q920B9|SP16H_MOUSE	yes	yes	2	12	11	M	R	0	1313.662	2	4.01E-02	80.32	NaN	NaN	0
397	AVVGVVAGGGR	sp|P62918|RL8_MOUSE	yes	yes	164	174	11	R	I	0	940.545	2	3.21E-03	133.32	NaN	NaN	0
398	AWALDIAELR	sp|Q8QZR5|ALAT1_MOUSE	yes	yes	213	222	10	R	R	0	1156.624	2	8.13E-02	64.82	NaN	NaN	0
399	AWDDFFPGSDR	sp|Q8R5J9|PRAF3_MOUSE	yes	yes	10	20	11	R	F	0	1311.552	2	2.11E-02	77.06	NaN	NaN	0
400	AWGPGLHGGIVGR	sp|Q80X90|FLNB_MOUSE	yes	yes	554	566	13	R	S	0	1275.684	3	4.05E-02	64.12	NaN	NaN	0
401	AWIGGVGDCKLGGNYGPTVAVQ	sp|O35855|BCAT2_MOUSE	yes	yes	221	243	23	R	E	0	2374.185	3	1.15E-03	64.00	1.26	0.97	3
402	AWNPFR	sp|P35550|FBRL_MOUSE	yes	yes	142	147	6	R	S	0	789.392	2	4.87E-02	135.81	NaN	NaN	0
403	AYALAFAER	sp|P51660|DHB4_MOUSE	yes	yes	24	32	9	R	G	0	1010.519	2	3.53E-02	90.15	NaN	NaN	0
404	AYDPKGGLDNAR	sp|P15105|GLNA_MOUSE	yes	yes	287	298	12	R	R	0	1275.621	3	1.08E-02	66.27	0.77	0.72	3
405	AYEPQGGSGYDYSYAGGR	sp|P61979-3|HNRPK_MOUSE	yes	no	336	353	18	M	G	0	1896.792	2	1.45E-03	100.04	NaN	NaN	0
406	AYHSFLVEPISCHAWNKDR	sp|Q9WV32|ARC1B_MOUSE	yes	yes	2	20	19	M	T	0	2329.106	4	3.13E-02	42.07	1.16	0.94	4
407	AYICAHPLDR	sp|Q8JZN5|ACAD9_MOUSE	yes	yes	614	623	10	R	A	0	1214.587	3	5.59E-02	70.94	NaN	NaN	0

408	AYKLVLIR	sp|Q9DBJ1|PGAM1_MOUSE	yes	yes	3	10	8	A	H	0	974.628	2	1.40E-02	93.43	1.06	0.99	1
409	AYQKQPTIFQNKKR	sp|P62281|RS11_MOUSE	yes	yes	9	22	14	R	V	0	1748.969	4	1.82E-03	100.22	1.96	1.60	1
410	AYSAGAWAPAVALLR	sp|Q8CG70|P3H3_MOUSE	yes	yes	49	63	15	R	E	0	1515.820	2	3.89E-03	85.84	NaN	NaN	0
411	AYYNGISLFNNPVPYWEVQPATFI	sp|P28653|PGS1_MOUSE	yes	yes	331	354	24	R	C	0	2845.386	2;3	1.09E-05	108.96	NaN	NaN	0
412	CALGVFR	sp|Q8VDM4|PSMD2_MOUSE	yes	yes	251	257	7	R	K	0	821.422	2	6.62E-02	111.69	NaN	NaN	0
413	CALSSVDIYR	sp|Q91VH6|MEMO1_MOUSE	yes	yes	88	97	10	R	T	0	1182.570	2	2.85E-02	82.42	NaN	NaN	0
414	CANLFEALVGTLKAAKR	sp|Q4KML4|ABRAL_MOUSE	yes	yes	39	55	17	R	R	0	1861.024	4	2.37E-02	46.25	1.47	1.42	1
415	CCISAAPFR	sp|Q9Z2T6|KRT85_MOUSE	yes	yes	32	40	9	R	G	0	1080.485	2	2.18E-03	169.09	NaN	NaN	0
416	CCSVPTGPATTICSSDKSCR	sp|A2A591|KRA31_MOUSE	yes	no	8	27	20	R	C	0	2242.944	3	2.21E-05	92.26	1.98	1.27	4
417	CDSNILPLHDWLILNR	sp|Q80X72|LRC15_MOUSE	yes	yes	427	442	16	R	A	0	1978.010	3	3.41E-04	130.29	NaN	NaN	0
418	CDTVLGLLDSHLIKGAGDAESR	sp|O70456|1433S_MOUSE	yes	yes	96	117	22	V	V	0	2326.159	3	5.16E-03	67.93	NaN	NaN	0
419	CECFPGLAVGLDGR	sp|Q61554|FBN1_MOUSE	yes	yes	637	650	14	R	W	0	1549.702	2	1.10E-03	112.02	NaN	NaN	0
420	CEMEQQNQEYKILLDVKTR	sp|Q61781|K1C14_MOUSE	no	no	395	413	19	R	L	0	2424.178	4	5.82E-05	82.61	1.66	0.91	1
421	CGEEQGADAALHFNPR	sp|O54974|LEG7_MOUSE	yes	yes	39	54	16	L	L	0	1770.774	3	4.50E-03	82.65	NaN	NaN	0
422	CGPCNSFGC	sp|Q61897|KT33B_MOUSE	yes	no	396	404	9	R	-	0	1057.342	2	3.64E-02	89.05	NaN	NaN	0
423	CGPCNSFVR	sp|Q61765|K1H1_MOUSE	no	no	408	416	9	R	-	0	1095.459	2	1.39E-02	136.57	NaN	NaN	0
424	CGPCNTFVR	sp|Q8K0Y2|KT33A_MOUSE	yes	yes	396	404	9	R	-	0	1109.475	2	1.14E-02	141.48	NaN	NaN	0
425	CIALAQLLVEQNFPAIAIHR	sp|Q9Z1N5|DX39B_MOUSE	yes	yes	300	319	20	R	G	0	2276.246	3	9.01E-16	208.13	NaN	NaN	0
426	CIVTKEGIR	sp|O09061|PSB1_MOUSE	yes	yes	223	231	9	I	E	0	1074.586	2	5.65E-03	96.34	0.62	0.58	2
427	CKDISSAVQANPALTELSLR	sp|Q91VI7|RINI_MOUSE	yes	yes	40	59	20	R	T	0	2172.121	3	4.18E-03	62.85	1.08	0.88	5
428	CLASFTELVR	sp|Q9QXF8|GNMT_MOUSE	yes	yes	247	256	10	H	A	0	1194.607	2	1.61E-02	101.38	NaN	NaN	0
429	CLITNVESQLGEIR	sp|Q61897|KT33B_MOUSE	no	no	316	329	14	Q	A	0	1630.835	2	9.13E-13	182.33	0.07	0.05	1
430	CLYASVLTAQPR	sp|P58252|EF2_MOUSE	yes	yes	728	739	12	R	L	0	1377.708	2	1.35E-05	155.48	0.00	0.00	1
431	CNGVLEGIR	sp|Q8VDD5|MYH9_MOUSE	no	no	694	702	9	R	I	0	1016.507	2	1.49E-02	134.66	NaN	NaN	0
432	CPAYQAYFR	sp|Q61897|KT33B_MOUSE	no	no	100	108	9	V	T	0	1174.523	2	1.97E-02	117.40	NaN	NaN	0
433	CPTGYYLNEDTR	sp|Q61554|FBN1_MOUSE	yes	yes	1633	1644	12	R	V	0	1487.635	2	9.00E-03	91.62	NaN	NaN	0
434	CQDLSVNQDLADTDAR	sp|P10107|ANXA1_MOUSE	yes	yes	189	204	16	R	A	0	1819.801	2	4.08E-16	207.39	0.02	0.02	1
435	CQNAEYQQLLDIKTR	sp|P02535-3|K1C10_MOUSE	yes	no	416	430	15	E	L	0	1878.926	2	1.31E-05	120.70	1.31	0.89	3
436	CQSLTEDLEFR	sp|P14733|LMNB1_MOUSE	yes	yes	199	209	11	R	K	0	1396.629	2	8.14E-03	108.53	NaN	NaN	0
437	CQYEALVETNR	sp|Q61897|KT33B_MOUSE	no	no	230	240	11	R	R	0	1381.630	2	9.62E-07	196.16	NaN	NaN	0
438	CQYEALVETNRR	sp|Q61897|KT33B_MOUSE	no	no	230	241	12	R	E	1	1537.731	2;3	4.49E-04	154.23	NaN	NaN	0
439	CQYEAMVETNR	sp|Q61765|K1H1_MOUSE	yes	no	230	240	11	R	R	0	1399.586	2	1.69E-06	187.76	NaN	NaN	0
440	CQYEAMVETNRR	sp|Q61765|K1H1_MOUSE	yes	no	230	241	12	R	E	1	1555.687	3	5.53E-03	100.38	NaN	NaN	0
441	CSEGSFLLTTFPR	sp|Q99K48|NONO_MOUSE	yes	yes	210	222	13	R	P	0	1513.724	2	1.40E-03	127.71	NaN	NaN	0
442	CSPDPGLTALLSDHR	sp|Q91X72|HEMO_MOUSE	yes	yes	255	269	15	R	G	0	1637.783	3	2.88E-04	144.29	NaN	NaN	0
443	CSTFAAFFTR	sp|P40142|TKT_MOUSE	yes	yes	386	395	10	F	A	0	1206.549	2	4.54E-02	73.50	NaN	NaN	0
444	CSVLAAANPVYGR	sp|P25206|MCM3_MOUSE	yes	yes	446	458	13	R	Y	0	1376.687	2	1.80E-02	73.44	NaN	NaN	0
445	CTVVSVPDSLLWR	sp|Q6WVG3|KCD12_MOUSE	yes	yes	50	62	13	R	M	0	1530.786	2	8.05E-03	83.20	NaN	NaN	0
446	CVEDPETGLR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	2773	2782	10	R	L	0	1174.529	2	1.61E-02	101.38	NaN	NaN	0
447	CVESFSDYPPLGR	sp|P10126|EF1A1_MOUSE	yes	yes	411	423	13	M	F	0	1525.687	2	1.42E-03	125.82	NaN	NaN	0
448	CVLIFGVPSR	sp|P10518|HEM2_MOUSE	yes	yes	75	84	10	R	V	0	1146.622	2	2.05E-02	94.69	NaN	NaN	0
449	CVLKIGEHTPSALAIMENANVLAR	sp|P05064|ALDOA_MOUSE	yes	yes	150	173	24	R	Y	0	2606.367	4	9.19E-04	66.47	1.44	0.97	1
450	CYQLEFGR	sp|Q07076|ANXA7_MOUSE	yes	yes	273	280	8	R	D	0	1071.481	2	4.17E-02	110.12	NaN	NaN	0
451	DAAQSSPAFGDR	sp|P10518|HEM2_MOUSE	yes	yes	210	221	12	R	R	0	1220.542	2	1.19E-05	152.40	0.17	0.14	2
452	DADDAVYELDGKELCSER	sp|O35326|SRSF5_MOUSE	yes	yes	49	66	18	R	V	0	2083.900	3	7.42E-02	45.00	0.92	0.86	3
453	DADSIHQYLLQR	sp|Q11011|PSA_MOUSE	yes	yes	902	913	12	R	K	0	1457.726	3	6.43E-03	98.11	NaN	NaN	0
454	DAEAWFQEKSASLQQQISDDAGA	sp|Q9Z320|K1C27_MOUSE	yes	yes	264	291	28	R	N	0	3010.390	3	6.48E-24	206.48	1.58	0.96	2
455	DAEAWFQEKSASLQQQITEDVGA	sp|Q8VCW2|K1C25_MOUSE	yes	yes	265	292	28	R	N	0	3066.453	3	1.30E-15	169.26	1.25	0.95	2
456	DAEDAMDAMDGAVLDGR	sp|Q62093|SRSF2_MOUSE	yes	yes	67	83	17	R	E	0	1750.714	2	6.76E-04	105.89	NaN	NaN	0
457	DAEDAVYGR	sp|Q6PDM2-3|SRSF1_MOUSE	yes	no	66	74	9	R	D	0	994.436	2	3.97E-02	85.86	NaN	NaN	0
458	DAGHPLYPFNDPY	sp|Q9JII6|AK1A1_MOUSE	yes	no	313	325	13	R	-	0	1504.662	2	6.46E-03	88.02	NaN	NaN	0
459	DAGMQLQGYR	sp|P05202|AATM_MOUSE	yes	yes	171	180	10	R	Y	0	1137.524	2	4.93E-03	142.43	NaN	NaN	0
460	DAGVSTYMYEFR	sp|P23953|EST1C_MOUSE	yes	yes	426	437	12	R	Y	0	1437.624	2	1.67E-02	76.07	NaN	NaN	0
461	DAILFPSFIHSQKR	sp|P24270|CATA_MOUSE	yes	yes	157	170	14	R	N	0	1657.894	3	3.97E-02	44.51	0.86	0.69	2
462	DAISIFHYAKGQPYIDEVGAFKER	sp|P27573|MYP0_MOUSE	yes	yes	75	98	24	R	I	0	2753.381	4	1.20E-04	81.88	2.73	1.57	1
463	DAKGISQEQMQEFR	sp|P57780|ACTN4_MOUSE	yes	yes	759	772	14	R	A	0	1665.778	3	2.16E-04	100.40	1.27	0.96	7
464	DAKLDKSQIHDIVLVGGSTR	sp|P63017|HSP7C_MOUSE	yes	yes	323	342	20	R	I	0	2151.165	3;4	2.42E-03	63.87	1.22	0.95	18
465	DALDSTLAETEGR	sp|Q497I4|KRT35_MOUSE	yes	no	335	347	13	R	Y	0	1376.642	2	1.10E-03	136.30	NaN	NaN	0
466	DALGNAIDGKGPIGSKTR	sp|Q03265|ATPA_MOUSE	yes	yes	152	169	18	V	R	0	1768.943	3	5.50E-03	56.82	1.59	1.17	6
467	DALNIETAVKTKGVDEVTIVNILTN	sp|P07356|ANXA2_MOUSE	yes	yes	38	63	26	R	S	0	2825.550	4	8.26E-03	55.59	0.91	0.88	1
468	DATSLNQAALYR	sp|P51660|DHB4_MOUSE	yes	yes	494	505	12	R	L	0	1321.663	2	7.21E-05	176.42	NaN	NaN	0
469	DAVIYPILVEFTR	sp|Q9JKR6|HYOU1_MOUSE	yes	yes	439	451	13	R	E	0	1534.840	2	5.67E-03	90.41	NaN	NaN	0
470	DAYSGGAVNLYHVR	sp|O55234|PSB5_MOUSE	yes	yes	226	239	14	R	E	0	1520.737	2;3	1.60E-04	162.22	NaN	NaN	0
471	DCFILDHGR	sp|P13020-2|GELS_MOUSE	yes	no	279	287	9	E	D	0	1131.513	2	4.38E-02	81.95	NaN	NaN	0
472	DCGGAAAVLGAFR	sp|Q6NSR8|PEPL1_MOUSE	yes	yes	283	295	13	R	A	0	1263.603	2	3.12E-03	98.11	NaN	NaN	0
473	DCPVPLPGDGDLLVR	sp|Q8BGC4|ZADH2_MOUSE	yes	yes	54	68	15	R	N	0	1621.813	2	4.42E-02	52.50	NaN	NaN	0
474	DDDIAALVVDNGSGMCKAGFAG	sp|P60710|ACTB_MOUSE	yes	no	2	28	27	M	A	0	2736.212	2;3	2.69E-15	159.86	1.25	1.02	23
475	DDFLGQVDVPLYPLPTENPR	sp|P46935|NEDD4_MOUSE	yes	yes	159	178	20	R	M	0	2284.138	2	4.06E-02	48.05	NaN	NaN	0
476	DDGLADLLFVSSGPTNASAFTER	sp|P27546-3|MAP4_MOUSE	yes	no	146	168	23	R	D	0	2382.134	2	5.02E-04	81.14	NaN	NaN	0
477	DDGLFSGDPNWFPKKSKENPR	sp|Q9WVA4|TAGL2_MOUSE	yes	yes	140	160	21	R	N	0	2433.171	4	3.70E-03	50.96	0.85	0.78	1
478	DDGSWEVIEGYR	sp|P26443|DHE3_MOUSE	yes	yes	125	136	12	R	A	0	1424.621	2	9.92E-03	89.30	NaN	NaN	0
479	DDGVNTFKVLTR	sp|P42932|TCPQ_MOUSE	yes	yes	393	404	12	V	D	0	1363.710	2	6.34E-04	104.17	1.12	0.88	6
480	DDILPELGVR	sp|Q9ER72-2|SYCC_MOUSE	yes	no	619	628	10	R	F	0	1125.603	2	1.34E-02	83.87	NaN	NaN	0
481	DDLLLNNVR	sp|Q9CZ42-2|NNRD_MOUSE	yes	no	108	116	9	R	G	0	1070.572	2	5.75E-03	96.03	12.04	10.49	2
482	DDNGKPYVLPSVR	sp|P05202|AATM_MOUSE	yes	yes	69	81	13	R	K	0	1458.747	3	1.65E-04	115.10	1.25	0.97	7
483	DDPSGQMLLLLSDAR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	3769	3783	15	R	K	0	1629.803	2	4.36E-02	52.86	NaN	NaN	0
484	DDTKCFVKLPEGTTPEKYLGAEYN	sp|Q921I1|TRFE_MOUSE	yes	yes	651	681	31	R	K	0	3563.674	5	3.12E-02	40.46	1.04	0.95	2
485	DEATPAAGNHPDSLR	sp|Q921T2|TOIP1_MOUSE	yes	yes	260	274	15	R	G	0	1549.712	3	1.90E-03	96.67	NaN	NaN	0
486	DEELNKLLGR	sp|Q8CGP6|H2A1H_MOUSE	yes	no	91	100	10	N	V	0	1185.635	2	1.58E-04	146.11	1.28	0.84	4
487	DEESCPDLPR	sp|Q80X19-2|COEA1_MOUSE	yes	no	1441	1450	10	R	S	0	1216.503	2	7.97E-03	130.98	NaN	NaN	0
488	DEEVHTGLGELLR	sp|P19324|SERPH_MOUSE	yes	yes	103	115	13	R	S	0	1466.737	2;3	1.64E-06	186.51	0.11	0.09	1
489	DEFEGLFKQPAENVNQYLTDSKFV	sp|Q02053|UBA1_MOUSE	yes	yes	650	675	26	R	T	0	3102.493	4	6.74E-16	174.99	1.22	1.01	5
490	DEFLIQASPR	sp|P51150|RAB7A_MOUSE	yes	yes	104	113	10	R	D	0	1174.598	2	4.50E-02	117.71	NaN	NaN	0
491	DEFSYQEMIANLPLCSHPNPR	sp|Q64674|SPEE_MOUSE	yes	yes	75	95	21	R	K	0	2517.142	3	3.83E-03	74.78	NaN	NaN	0
492	DEFTNTCPSDKEVEIAYSDVAKR	sp|Q9QYB1|CLIC4_MOUSE	yes	yes	228	250	23	R	L	0	2673.223	4	2.65E-02	41.62	1.33	1.19	3
493	DEIQNMKEEMAR	sp|P20152|VIME_MOUSE	yes	yes	367	378	12	Q	H	0	1492.665	2	2.02E-04	124.51	1.08	0.85	6
494	DEKVQLYR	sp|P19783|COX41_MOUSE	yes	yes	76	83	8	R	I	0	1049.551	3	7.17E-02	67.90	1.71	1.16	5
495	DELADEIANSSGKGALALEEKR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	1704	1725	22	R	R	0	2315.161	3	2.67E-08	105.06	1.33	1.08	9
496	DESEAEKEKLQR	sp|Q8BK67|RCC2_MOUSE	yes	yes	500	511	12	R	L	0	1460.711	3	5.97E-02	42.84	1.01	0.82	6
497	DESSPYAAMLAAQDVAQR	sp|P62264|RS14_MOUSE	yes	yes	67	84	18	R	C	0	1921.884	2;3	3.24E-05	144.30	NaN	NaN	0
498	DETEFYLGKR	sp|O55142|RL35A_MOUSE	yes	yes	37	46	10	R	C	0	1256.604	2;3	2.48E-13	216.45	1.28	0.96	10
499	DETNYGIPQR	sp|P68040|GBLP_MOUSE	yes	yes	48	57	10	R	A	0	1191.552	2	3.19E-05	185.61	NaN	NaN	0
500	DEVQEVVFIPAGTHVPGSR	sp|Q8VCA8|SCRN2_MOUSE	yes	yes	38	56	19	R	L	0	2036.033	3	6.78E-02	45.35	NaN	NaN	0
501	DFAYGEADPLIR	sp|Q3UDE2|TTL12_MOUSE	yes	yes	236	247	12	R	K	0	1365.657	2	3.09E-02	71.18	NaN	NaN	0
502	DFFLANASR	sp|O35350|CAN1_MOUSE	yes	yes	462	470	9	R	A	0	1039.509	2	3.99E-02	85.72	NaN	NaN	0
503	DFGGITNGKPEDKLGIR	sp|Q8JZN5|ACAD9_MOUSE	yes	yes	254	270	17	R	G	0	1815.948	3	4.61E-02	39.34	0.82	0.79	5
504	DFKSPDDPSR	sp|P17182|ENOA_MOUSE	yes	yes	260	269	10	L	Y	0	1162.526	2	6.06E-02	69.82	1.22	1.16	1
505	DFKTDLR	sp|P84244|H33_MOUSE	no	no	78	84	7	Q	F	0	893.461	2	8.61E-03	130.27	1.16	0.80	3
506	DFLLKPELLR	sp|Q9Z1N5|DX39B_MOUSE	yes	no	49	58	10	R	A	0	1242.734	2;3	1.93E-04	143.97	1.30	1.01	13
507	DFLQLFAPR	sp|Q62219-7|TGFI1_MOUSE	yes	no	226	234	9	R	C	0	1105.592	2	3.99E-02	85.68	NaN	NaN	0
508	DFLTPPLLSVR	sp|P17426-2|AP2A1_MOUSE	yes	no	811	821	11	R	F	0	1256.713	2	1.77E-02	84.48	13.16	12.63	1
509	DFTPSGIAGAFR	sp|P56135|ATPK_MOUSE	yes	yes	28	39	12	R	R	0	1237.609	2	7.17E-03	96.24	NaN	NaN	0
510	DFTPVCTTELGR	sp|O08709|PRDX6_MOUSE	yes	yes	42	53	12	R	A	0	1394.650	2	2.94E-03	122.33	NaN	NaN	0

511	DFTSLENTVEER	sp|Q8BMK4|CKAP4_MOUSE	yes	yes	208	219	12	R	L	0	1438.658	2	2.54E-03	127.17	NaN	NaN	0
512	DFTVSAMHGDMDQKER	sp|P60843|IF4A1_MOUSE	yes	yes	296	311	16	R	D	0	1865.804	3	4.82E-04	76.34	1.43	1.03	5
513	DFVNYLVR	sp|O70133|DHX9_MOUSE	yes	no	64	71	8	R	I	0	1024.534	2	3.85E-02	121.74	NaN	NaN	0
514	DFWDNLEKETDWVR	sp|Q00623|APOA1_MOUSE	yes	yes	93	106	14	R	Q	0	1851.843	2;3	1.64E-08	164.15	1.28	1.16	9
515	DGDKLVVECVMKGVTSTR	sp|P04117|FABP4_MOUSE	yes	yes	110	127	18	R	V	0	1992.997	3;4	3.96E-03	62.62	0.77	0.75	7
516	DGDLENPVLYNGAVKVGAIQR	sp|P57759|ERP29_MOUSE	yes	yes	125	145	21	R	W	0	2227.160	3	3.50E-03	52.19	1.07	1.01	5
517	DGEAPDPEDPSR	sp|P24527|LKHA4_MOUSE	yes	yes	176	187	12	R	K	0	1283.527	2	5.43E-02	63.09	NaN	NaN	0
518	DGEEAGAYDGPR	sp|P27773|PDIA3_MOUSE	yes	yes	108	119	12	R	T	0	1235.506	2	1.92E-03	135.10	NaN	NaN	0
519	DGGQEYVVKEVLR	sp|Q9R269|PEPL_MOUSE	yes	yes	985	997	13	R	I	0	1490.773	3	1.09E-03	107.99	1.19	0.93	6
520	DGHFTLFAPTNEAFEKLPR	sp|Q62009-5|POSTN_MOUSE	yes	no	268	286	19	R	G	0	2189.091	3;4	9.31E-07	102.89	1.34	1.13	14
521	DGKALEQFLQEYFDGNLKR	sp|P27773|PDIA3_MOUSE	yes	yes	345	363	19	R	Y	0	2270.133	3;4	2.27E-05	95.21	1.34	1.04	9
522	DGLGGLPDIVR	sp|P56399|UBP5_MOUSE	yes	yes	134	144	11	R	D	0	1110.603	2	7.43E-03	111.86	NaN	NaN	0
523	DGLLPEDTFIVGYAR	sp|Q00612|G6PD1_MOUSE	yes	yes	58	72	15	R	S	0	1664.841	2	2.22E-02	66.25	NaN	NaN	0
524	DGQVINETSQHHDDLE	sp|P20152|VIME_MOUSE	yes	no	451	466	16	R	-	0	1835.792	2;3	2.60E-12	215.37	NaN	NaN	0
525	DGTGVVEFVR	sp|Q6PDM2-3|SRSF1_MOUSE	yes	no	155	164	10	R	K	0	1077.546	2	4.16E-04	145.25	0.52	0.41	5
526	DGVTGPGFTLSGSCCQGPR	sp|Q91YK8|LYPD3_MOUSE	yes	yes	204	222	19	R	C	0	1951.852	2	1.73E-02	58.85	NaN	NaN	0
527	DGYAQILR	sp|Q99KI0|ACON_MOUSE	yes	yes	430	437	8	R	D	0	934.487	2	3.11E-02	138.26	NaN	NaN	0
528	DHALLEEQSKQQSNEHLR	sp|P57780|ACTN4_MOUSE	yes	yes	635	652	18	R	R	0	2161.051	4	5.18E-02	44.39	1.18	1.13	3
529	DHINLPGFCGQNPLR	sp|P23492|PNPH_MOUSE	yes	yes	134	148	15	R	G	0	1736.842	3	7.25E-04	109.83	NaN	NaN	0
530	DHMKTVLPPDGPR	sp|Q921I1|TRFE_MOUSE	yes	yes	43	55	13	R	L	0	1461.740	3	8.70E-04	85.84	1.00	0.86	4
531	DIANSPHELYR	sp|Q02788|CO6A2_MOUSE	yes	yes	218	228	11	R	N	0	1313.636	2;3	2.13E-06	182.71	0.15	0.09	1
532	DIDSLAQR	sp|Q9D0F3|LMAN1_MOUSE	yes	yes	456	463	8	R	S	0	916.461	2	3.92E-02	119.17	NaN	NaN	0
533	DIERPTYTNLNR	sp|P68373|TBA1C_MOUSE	no	no	218	229	12	L	L	1	1490.748	2	1.18E-07	205.96	NaN	NaN	0
534	DIETSNFDEGYSVSR	sp|Q6P253-4|DMKN_MOUSE	yes	no	291	305	15	R	G	0	1717.743	2	1.31E-02	71.98	NaN	NaN	0
535	DIFPIAFPR	sp|Q8CGK3|LONM_MOUSE	yes	yes	930	938	9	R	R	0	1074.586	2	2.95E-02	95.74	NaN	NaN	0
536	DIIALNPLYR	sp|Q8CGK3|LONM_MOUSE	yes	yes	291	300	10	R	E	0	1186.671	2	9.25E-03	126.07	NaN	NaN	0
537	DIICQIAYAR	sp|P47962|RL5_MOUSE	yes	yes	59	68	10	R	I	0	1221.618	2	1.23E-02	113.93	NaN	NaN	0
538	DIKWEFIPSKNLR	sp|P50516-2|VATA_MOUSE	yes	no	130	142	13	R	V	0	1644.899	3	2.06E-02	50.09	0.98	0.93	4
539	DILDSALLRPGR	sp|P62196|PRS8_MOUSE	yes	yes	299	310	12	I	I	1	1324.746	2	7.43E-02	56.21	NaN	NaN	0
540	DIPVNPLCIYR	sp|P32261|ANT3_MOUSE	yes	yes	47	57	11	R	S	0	1358.702	2	1.23E-02	96.34	NaN	NaN	0
541	DISPLLKDPDSFR	sp|P08030|APT_MOUSE	yes	yes	28	40	13	R	A	0	1501.778	3	8.44E-03	65.04	1.20	1.05	5
542	DITQQLQSMCVALGASIQGLPSH\	sp|Q9DBG5|PLIN3_MOUSE	yes	yes	336	360	25	R	E	0	2708.374	3	3.48E-04	76.89	NaN	NaN	0
543	DITYFIQQLLR	sp|Q99JY9|ARP3_MOUSE	yes	no	199	209	11	R	D	0	1408.772	2	1.02E-02	100.88	NaN	NaN	0
544	DIVQFVPFR	sp|Q8BT60|CPNE3_MOUSE	yes	no	485	493	9	R	Q	0	1119.608	2	1.16E-02	141.20	NaN	NaN	0
545	DIVQFVPYR	sp|Q8C166|CPNE1_MOUSE	yes	yes	478	486	9	R	R	0	1135.603	2	1.56E-02	133.23	NaN	NaN	0
546	DKFASFIDKVR	sp|P04104|K2C1_MOUSE	no	no	197	207	11	N	F	0	1324.714	2;3	2.08E-03	92.86	1.70	1.03	8
547	DKGKSGFLLPESR	sp|P15089|CBPA3_MOUSE	yes	yes	381	393	13	R	I	0	1432.767	3	1.46E-02	54.90	1.33	0.72	1
548	DKILAATIDNSR	sp|Q61414|K1C15_MOUSE	yes	no	158	169	12	R	V	0	1315.710	2	7.79E-05	135.02	1.99	1.24	4
549	DKSYYTLSMANR	sp|Q9D7P9|SPB12_MOUSE	yes	yes	124	135	12	R	L	0	1447.677	3	1.65E-02	59.23	1.18	1.01	2
550	DKTPVQSQQPSATTPSGADEKSS\	sp|Q8VDM4|PSMD2_MOUSE	yes	yes	7	33	27	R	R	0	2815.358	4;5	4.84E-03	49.77	0.74	0.69	2
551	DKVVGKDYLLCDYNR	sp|P47757-2|CAPZB_MOUSE	yes	no	52	66	15	R	D	0	1856.909	3	1.16E-02	51.03	1.24	0.99	7
552	DKWLAPDGLIFPDR	sp|Q9JIF0-3|ANM1_MOUSE	yes	no	154	167	14	R	A	0	1641.852	3	8.83E-03	61.41	0.93	0.87	6
553	DLAALEDKVKALCAEADR	sp|P16546-2|SPTN1_MOUSE	yes	no	303	320	18	R	L	0	1987.004	3	3.30E-03	65.11	0.82	0.64	2
554	DLAALGDKVNSLGETAQR	sp|P16546-2|SPTN1_MOUSE	yes	no	1261	1278	18	R	L	0	1856.959	3	1.33E-07	121.26	1.31	0.81	2
555	DLAKDITSDTSGDFR	sp|P10107|ANXA1_MOUSE	yes	yes	163	177	15	R	K	0	1639.769	2;3	4.22E-09	160.04	1.10	1.01	10
556	DLALVNDQLLGFVR	sp|Q6A026|PDS5A_MOUSE	yes	yes	390	403	14	R	E	0	1571.867	2	5.20E-03	86.94	NaN	NaN	0
557	DLANGNITWADVEAR	sp|Q9CZD3|SYG_MOUSE	yes	yes	698	712	15	R	Y	0	1643.790	2	5.01E-02	50.31	NaN	NaN	0
558	DLASVQALLR	sp|P16546-2|SPTN1_MOUSE	yes	no	286	295	10	R	K	0	1084.624	2	7.11E-03	134.25	NaN	NaN	0
559	DLDDFQSWLSR	sp|Q62261|SPTB2_MOUSE	yes	no	1070	1080	11	R	T	0	1380.631	2	2.46E-03	138.99	NaN	NaN	0
560	DLDKPFLLPVESVYSIPGR	sp|Q8BFR5-2|EFTU_MOUSE	yes	no	253	271	19	R	G	0	2144.152	3	3.28E-08	113.73	1.13	0.92	7
561	DLDLKKPIYQR	sp|Q3THS6|METK2_MOUSE	yes	yes	363	373	11	R	T	0	1387.782	3	1.15E-02	69.72	1.12	0.98	4
562	DLDSLHSFVLR	sp|Q91W90|TXND5_MOUSE	yes	yes	401	411	11	R	Q	0	1300.678	2;3	1.12E-10	227.37	NaN	NaN	0
563	DLEVDTTLKSLSQQIENIR	sp|P11087|CO1A1_MOUSE	yes	no	1217	1235	19	R	S	0	2201.154	3	7.70E-13	153.21	1.13	0.98	2
564	DLFSDGHSEFLKAASNLR	sp|P27773|PDIA3_MOUSE	yes	yes	162	179	18	R	D	0	2005.986	3;4	3.30E-05	95.21	1.19	0.97	15
565	DLGEELEALR	sp|Q6URW6-2|MYH14_MOUSI	yes	no	1156	1165	10	R	G	0	1143.577	2	1.10E-02	119.22	NaN	NaN	0
566	DLGFNGAPYR	sp|Q920B9|SP16H_MOUSE	yes	yes	803	812	10	R	S	0	1108.530	2	2.23E-02	91.87	NaN	NaN	0
567	DLIDFDDR	sp|E9Q557|DESP_MOUSE	yes	yes	2088	2095	8	R	Q	0	1007.456	2	4.06E-02	114.28	NaN	NaN	0
568	DLIHDQDEEEEEEEGQR	sp|Q9CZ44|NSF1C_MOUSE	yes	no	77	93	17	R	F	0	2098.856	3	1.65E-05	162.81	NaN	NaN	0
569	DLINLAKKR	sp|P35550|FBRL_MOUSE	yes	yes	205	213	9	R	T	0	1069.661	3	4.11E-02	60.44	1.47	0.86	2
570	DLISHDELFSDIYKIR	sp|P63028|TCTP_MOUSE	yes	yes	6	21	16	R	E	0	1963.005	2;3;4	2.51E-11	169.92	0.99	0.88	17
571	DLKDEIVR	sp|E9Q557|DESP_MOUSE	yes	yes	1260	1267	8	R	L	0	986.540	2;3	1.54E-02	90.70	1.52	0.98	8
572	DLLDSVLPHLYNETKVR	sp|Q6ZQ38|CAND1_MOUSE	yes	yes	1043	1059	17	R	K	0	2011.074	3	6.13E-03	58.25	1.29	1.00	2
573	DLLFQALGR	sp|Q9WUA2|SYFB_MOUSE	yes	yes	9	17	9	R	T	0	1031.576	2	2.35E-02	101.54	NaN	NaN	0
574	DLLFQPVAELKKVTDFEHR	sp|Q9WUA3|K6PP_MOUSE	yes	yes	725	743	19	R	I	0	2284.222	4	4.83E-02	36.13	1.06	1.04	3
575	DLLLDPAWEKQQR	sp|P57780|ACTN4_MOUSE	no	no	42	54	13	R	K	0	1610.842	3	7.94E-04	88.10	1.42	1.11	8
576	DLLSSVSR	sp|Q07076|ANXA7_MOUSE	yes	yes	365	372	8	R	E	0	875.471	2	4.26E-02	107.01	NaN	NaN	0
577	DLLVQQASQCLSKLVQIASR	sp|Q00PI9|HNRL2_MOUSE	yes	yes	507	526	20	R	S	0	2256.226	3	6.52E-02	29.17	0.91	0.86	4
578	DLLYFDGLR	sp|Q9QY23|PKP3_MOUSE	yes	no	738	746	9	R	K	0	1110.571	2	2.08E-02	111.46	NaN	NaN	0
579	DLMADLKSEISGDLAR	sp|P14824|ANXA6_MOUSE	yes	yes	412	427	16	R	L	0	1732.867	2;3	1.42E-06	111.22	1.31	1.06	3
580	DLMSWINGIR	sp|P16546-2|SPTN1_MOUSE	yes	no	1330	1339	10	R	G	0	1203.607	2	3.00E-03	149.72	NaN	NaN	0
581	DLNMDCVVAEIKAQYDDVASR	sp|Q9Z2T6|KRT85_MOUSE	yes	yes	285	305	21	R	S	0	2411.110	2;3	7.07E-12	140.73	2.00	1.16	3
582	DLNYCFSGMSDHR	sp|O35737|HNRH1_MOUSE	no	no	263	275	13	R	Y	0	1600.640	3	7.18E-03	85.84	NaN	NaN	0
583	DLPAAAAPAGPASFAR	sp|Q9CQ60|6PGL_MOUSE	yes	yes	57	72	16	R	W	0	1481.763	2	6.39E-04	107.82	NaN	NaN	0
584	DLQLVLPDYFPER	sp|Q6WVG3|KCD12_MOUSE	yes	yes	98	110	13	R	S	0	1603.825	2	1.57E-03	103.76	NaN	NaN	0
585	DLQQYQSQAKQLFR	sp|O08547|SC22B_MOUSE	yes	yes	29	42	14	R	K	0	1751.896	3	2.39E-02	48.53	1.32	0.94	4
586	DLQSSNQLSNHISSLFR	sp|Q00612|G6PD1_MOUSE	yes	no	176	192	17	R	E	0	1944.965	3	4.71E-03	73.28	0.33	0.28	2
587	DLTDYLMKILTER	sp|P63260|ACTG_MOUSE	no	no	184	196	13	R	G	0	1609.839	2;3	4.34E-19	223.06	1.21	0.95	25
588	DLTGVQNLR	sp|P16546-2|SPTN1_MOUSE	yes	no	1775	1783	9	R	K	0	1014.546	2	1.54E-02	133.58	NaN	NaN	0
589	DLTPEHLPLLR	sp|Q9DAR7|DCPS_MOUSE	yes	yes	231	241	11	R	N	0	1302.730	3	1.99E-02	79.66	NaN	NaN	0
590	DLTTAGAVTQCYR	sp|P62717|RL18A_MOUSE	yes	yes	99	111	13	R	D	0	1454.682	2	1.81E-06	184.31	NaN	NaN	0
591	DMAETFDQGAHHAFGQGGR	sp|Q8CIT9|SBSN_MOUSE	yes	yes	398	416	19	R	E	0	2030.865	3	6.16E-04	104.76	NaN	NaN	0
592	DMLLANKVPAAAR	sp|P14869|RLA0_MOUSE	yes	yes	100	112	13	R	A	0	1368.755	2;3	7.86E-03	66.00	1.46	1.03	12
593	DMTDLTKELNR	sp|Q3UH93|PLXD1_MOUSE	yes	yes	1332	1342	11	T	S	0	1334.650	3	4.15E-02	49.00	1.61	1.03	4
594	DNGLLAKPTHGDIIR	sp|P29758|OAT_MOUSE	yes	yes	399	413	15	R	L	0	1618.879	3	2.47E-04	85.47	1.11	0.95	4
595	DNHCGLATAASYPVVN	sp|P06797|CATL1_MOUSE	yes	no	319	334	16	R	-	0	1687.762	2	1.19E-04	148.57	NaN	NaN	0
596	DNHLAPGQQTTLR	sp|P01027|CO3_MOUSE	yes	yes	571	583	13	R	I	0	1449.732	3	1.52E-03	110.44	NaN	NaN	0
597	DNIACVILTFKEPFGTEGR	sp|Q00612|G6PD1_MOUSE	yes	yes	228	246	19	R	G	0	2166.078	3	4.05E-02	38.88	2.30	1.99	2
598	DNIEVAYLKTLTKDDIIR	sp|Q9JHR7|IDE_MOUSE	yes	yes	921	938	18	R	F	0	2119.153	3	6.01E-02	33.36	1.11	1.07	3
599	DNIIKAAPR	sp|P80314|TCPB_MOUSE	yes	yes	518	526	9	V	K	0	996.572	2	2.95E-02	67.11	1.53	1.17	6
600	DNIQGITKPAIR	sp|P62806|H4_MOUSE	yes	yes	25	36	12	R	R	0	1324.746	2;3	1.52E-11	194.86	1.03	0.78	18
601	DNLAEDIMR	sp|P20152|VIME_MOUSE	yes	yes	176	184	9	R	L	0	1075.497	2	4.43E-03	155.84	NaN	NaN	0
602	DNMFSGSKINYTENR	sp|P06745|G6PI_MOUSE	yes	yes	82	96	15	R	A	0	1774.794	3	1.45E-04	93.91	1.07	1.01	1
603	DNQSGSLLFIGR	sp|P19324|SERPH_MOUSE	yes	yes	393	404	12	R	L	0	1305.668	2	1.71E-04	134.75	0.14	0.11	1
604	DNSTMGYMMAKKHLEINPDHPI\	sp|P11499|HS90B_MOUSE	yes	yes	613	639	27	R	Q	0	3139.525	5	1.98E-02	44.16	1.39	1.37	1
605	DPAGRPLLLTPVLSHPIFDNR	sp|Q04207-2|TF65_MOUSE	yes	no	167	187	21	R	A	1	2327.275	4	1.58E-02	50.96	NaN	NaN	0
606	DPDQTDGPGLGYLSSHIANVER	sp|P13020-2|GELS_MOUSE	yes	no	347	368	22	R	V	0	2340.098	3	4.56E-12	191.65	NaN	NaN	0
607	DPENFPFVVLGNKIDLENR	sp|P51150|RAB7A_MOUSE	yes	yes	114	132	19	R	Q	0	2215.127	3	2.53E-05	94.28	1.71	1.15	4
608	DPFTIKPLDR	sp|P40142|TKT_MOUSE	yes	yes	533	542	10	L	K	0	1200.650	2	2.30E-04	141.71	0.92	0.88	5
609	DPHLACVAYER	sp|Q68FD5|CLH1_MOUSE	yes	yes	913	923	11	R	G	0	1329.614	3	6.11E-02	65.18	NaN	NaN	0
610	DPHTEFTLKEFNR	sp|Q60847|COCA1_MOUSE	yes	no	487	499	13	R	V	0	1632.790	3	3.41E-02	46.88	2.37	1.56	3
611	DPLSPFAVGGDDLDPFGCQR	sp|Q8BHL8|PSMF1_MOUSE	yes	yes	186	205	20	R	G	0	2161.974	2	1.38E-02	60.06	NaN	NaN	0
612	DPNASPGDAGEQAIR	sp|Q64727|VINC_MOUSE	yes	yes	286	300	15	R	Q	0	1496.686	2	1.38E-04	152.34	NaN	NaN	0
613	DPSSPLYSVKSFEELR	sp|Q61655|DD19A_MOUSE	yes	yes	82	97	16	R	L	0	1852.921	3	6.96E-03	58.89	1.48	1.15	4

614	DPTNIKWGEAGAEYVVESTGVFT	sp|P16858|G3P_MOUSE	yes	yes	79	116	38	R	V	0	4005.005	5	5.34E-02	41.02	1.02	0.94	1
615	DPVQLNLLYVQAR	sp|P26039|TLN1_MOUSE	yes	no	208	220	13	R	D	0	1527.841	2	9.97E-05	174.05	NaN	NaN	0
616	DPYSGQSVSLFQALKKGLIPR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	3009	3029	21	R	E	0	2303.264	4	9.93E-03	62.62	1.30	0.88	1
617	DQEGQDVLLFIDNIFR	sp|P56480|ATPB_MOUSE	yes	yes	295	310	16	R	F	0	1920.958	2	1.51E-18	238.83	NaN	NaN	0
618	DQNTVETLQR	sp|Q62261|SPTB2_MOUSE	yes	no	1835	1844	10	R	M	0	1202.589	2	3.96E-03	146.11	NaN	NaN	0
619	DQPFTILYR	sp|Q9WVH9|FBLN5_MOUSE	yes	yes	343	351	9	R	D	0	1151.598	2	2.02E-02	114.89	NaN	NaN	0
620	DQYEKMAEKNR	sp|Q61781|K1C14_MOUSE	no	no	295	305	11	R	K	0	1410.656	3	1.19E-03	103.44	1.44	1.04	4
621	DQYELLCLDNTR	sp|Q921I1|TRFE_MOUSE	yes	yes	240	251	12	R	K	0	1538.704	2;3	1.86E-06	186.58	NaN	NaN	0
622	DREEALHQFR	sp|P16381|DDX3L_MOUSE	yes	no	478	487	10	R	S	1	1299.632	3	9.56E-02	61.34	NaN	NaN	0
623	DSCPLDCKVYVGNLGNNGNKTEL	sp|P84104-2|SRSF3_MOUSE	yes	no	4	28	25	R	A	0	2851.323	4	1.29E-04	88.24	1.07	0.95	2
624	DSDILGKYVD	sp|Q64433|CH10_MOUSE	yes	no	93	102	10	R	-	0	1123.540	2	1.42E-03	113.44	0.92	0.86	3
625	DSDSILETLQR	sp|Q9D6J6-2|NDUV2_MOUSE	yes	no	47	57	11	R	K	0	1275.631	2	1.30E-02	94.77	NaN	NaN	0
626	DSELDKHLESR	sp|P36993-2|PPM1B_MOUSE	yes	no	309	319	11	R	V	0	1327.637	3	1.39E-02	67.52	2.16	1.68	1
627	DSFPWEVPKKLKY	sp|Q3THS6|METK2_MOUSE	yes	no	383	395	13	R	-	0	1635.866	3;4	1.49E-02	54.34	1.15	1.17	9
628	DSLENTLGETEGR	sp|Q62168|K1H2_MOUSE	yes	no	293	305	13	R	F	0	1419.648	2	1.71E-06	153.81	0.07	0.05	1
629	DSLHSFVLR	sp|Q91W90|TXND5_MOUSE	yes	yes	403	411	9	L	Q	0	1072.567	2	7.48E-03	149.27	NaN	NaN	0
630	DSLLQDGEFTMDLR	sp|P62962|PROF1_MOUSE	yes	no	76	89	14	R	T	0	1638.756	2	1.04E-03	119.87	NaN	NaN	0
631	DSQVHSGVQVEGR	sp|P11088|FILA_MOUSE	yes	yes	24	36	13	S	R	0	1396.670	2	4.45E-03	94.09	NaN	NaN	0
632	DSVSAAWHTYDTDR	sp|Q8BH97|RCN3_MOUSE	yes	yes	116	129	14	R	D	0	1622.696	3	8.92E-04	131.66	NaN	NaN	0
633	DTAFDLDAFKKFS	sp|Q60597-2|ODO1_MOUSE	yes	no	1001	1013	13	L	-	0	1503.725	2	2.61E-02	70.09	NaN	NaN	0
634	DTANWLEINPETGAIFTR	sp|P09803|CADH1_MOUSE	yes	yes	530	547	18	R	A	0	2047.001	2	6.60E-05	130.01	NaN	NaN	0
635	DTDGKELLPKIR	sp|Q9DCD0|6PGD_MOUSE	yes	yes	244	255	12	R	D	0	1383.772	3	1.77E-03	83.18	1.15	1.00	5
636	DTDTGALLFIGR	sp|P97298|PEDF_MOUSE	yes	yes	399	410	12	R	I	0	1277.662	2	1.77E-03	136.96	NaN	NaN	0
637	DTFNHLTTWLEDAR	sp|P53994|RAB2A_MOUSE	yes	yes	92	105	14	R	Q	0	1717.806	3	1.12E-03	109.10	NaN	NaN	0
638	DTGVISVLTSGLDR	sp|P09803|CADH1_MOUSE	yes	yes	324	337	14	R	E	0	1431.757	2	2.03E-04	157.09	NaN	NaN	0
639	DTHSLFFR	sp|O54734|OST48_MOUSE	yes	yes	43	50	8	R	S	0	1021.498	2;3	1.48E-02	160.26	NaN	NaN	0
640	DTKNEIAELTR	sp|Q8VED5|K2C79_MOUSE	yes	no	353	363	11	R	T	0	1288.662	2;3	9.21E-07	155.66	1.35	0.80	8
641	DTLFTSDSGTR	sp|Q80X19-2|COEA1_MOUSE	yes	no	1122	1132	11	R	R	0	1198.547	2	5.12E-03	122.69	NaN	NaN	0
642	DTLYEAVR	sp|P53026|RL10A_MOUSE	yes	yes	8	15	8	R	E	0	965.482	2	3.62E-02	129.55	NaN	NaN	0
643	DTVTPGELLKAEIINQDLFEQLER	sp|Q8R0W0|EPIPL_MOUSE	yes	yes	573	596	24	R	G	0	2770.439	3	1.06E-05	101.60	1.81	1.24	1
644	DVAAVNGLYR	sp|Q3TAS6-2|EMC10_MOUSE	yes	no	100	109	10	R	V	0	1076.562	2	2.23E-02	91.87	NaN	NaN	0
645	DVAKEFDKLSPEESQAR	sp|Q8BH97|RCN3_MOUSE	yes	yes	63	79	17	R	L	0	1947.954	3;4	1.14E-06	104.20	1.11	1.05	9
646	DVAPQAPVHFLVIPR	sp|Q9D0S9|HINT2_MOUSE	yes	yes	80	94	15	R	K	0	1657.930	3	1.32E-02	71.88	NaN	NaN	0
647	DVAWAPSIGLPTSTIASCSQDGR	sp|Q9D1M0|SEC13_MOUSE	yes	yes	217	239	23	R	V	0	2388.138	2	5.94E-02	44.85	NaN	NaN	0
648	DVDEVSSLLR	sp|P42932|TCPQ_MOUSE	yes	yes	156	165	10	R	T	0	1131.577	2	1.83E-02	98.04	NaN	NaN	0
649	DVEAWFLR	sp|Q9Z2K1|K1C16_MOUSE	yes	no	299	306	8	R	K	0	1034.519	2	2.03E-02	136.11	NaN	NaN	0
650	DVEDEETWIR	sp|P16546-2|SPTN1_MOUSE	yes	no	792	801	10	R	E	0	1290.573	2	1.61E-02	101.38	NaN	NaN	0
651	DVEDEILWVGER	sp|Q62261|SPTB2_MOUSE	yes	no	1493	1504	12	R	M	0	1458.699	2	1.19E-02	84.37	NaN	NaN	0
652	DVFLPKPSWGNHTPIFR	sp|P05202|AATM_MOUSE	yes	yes	154	170	17	R	D	0	2010.048	3;4	4.23E-05	96.21	1.02	0.93	12
653	DVGGIVLANACGPCIGQWDR	sp|Q99KI0|ACON_MOUSE	yes	yes	438	457	20	R	K	0	2157.010	2	8.68E-03	69.36	NaN	NaN	0
654	DVILDNPALTLEVLEQAHVR	sp|Q08189|TGM3_MOUSE	yes	yes	589	608	20	R	K	0	2244.211	2;3	1.04E-04	123.19	NaN	NaN	0
655	DVQEIFR	sp|Q9Z1N5|DX39B_MOUSE	yes	no	210	216	7	R	M	0	905.461	2	5.81E-02	127.84	NaN	NaN	0
656	DVQIGDIVTVGECRPLSKTVR	sp|P62281|RS11_MOUSE	yes	yes	119	139	21	R	F	1	2341.242	3	1.73E-02	45.89	0.91	0.88	3
657	DVSELTGFPEMLGGR	sp|Q9CWJ9|PUR9_MOUSE	yes	yes	50	64	15	R	V	0	1606.766	2	3.70E-12	230.36	NaN	NaN	0
658	DVTHSTMNVVWEPVLGKVR	sp|Q60847|COCA1_MOUSE	yes	no	1576	1594	19	R	K	0	2166.126	3;4	1.88E-08	120.40	1.77	1.07	2
659	DVVEDYKKKYEEEINR	sp|Q9R0H5|K2C71_MOUSE	yes	no	212	227	16	R	R	0	2056.011	3	4.87E-03	64.52	1.69	1.12	2
660	DVVEDYKKKYEEEINRR	sp|Q9R0H5|K2C71_MOUSE	yes	no	212	228	17	R	T	1	2212.112	4	4.04E-02	41.09	1.76	1.17	2
661	DVVGKELQSQGR	sp|Q6P1B1|XPP1_MOUSE	yes	yes	594	605	12	R	Q	0	1314.689	3	4.66E-03	73.93	1.14	0.98	4
662	DVYESLCR	sp|Q60716-2|P4HA2_MOUSE	yes	no	290	297	8	R	G	0	1040.460	2	4.35E-02	103.74	NaN	NaN	0
663	DVYTGDALR	sp|O09061|PSB1_MOUSE	yes	yes	213	221	9	R	I	0	1008.488	2	4.11E-02	84.52	NaN	NaN	0
664	DWVLNEFKHGKAPILIATDVASR	sp|Q61656|DDX5_MOUSE	yes	yes	381	403	23	R	G	0	2579.386	4	2.38E-08	129.85	1.07	0.84	2
665	DWVLNEFR	sp|Q501J6-2|DDX17_MOUSE	yes	no	379	386	8	R	S	0	1077.524	2	3.99E-02	116.73	NaN	NaN	0
666	DWYPAHSR	sp|P14602|HSPB1_MOUSE	yes	no	21	28	8	R	L	0	1030.462	2;3	4.05E-02	114.50	NaN	NaN	0
667	DWYQKQAPGPAR	sp|Q9QWL7|K1C17_MOUSE	yes	no	118	129	12	R	D	0	1415.695	2;3	2.09E-07	168.02	1.61	0.96	9
668	DWYQKQSPASPDR	sp|Q61414|K1C15_MOUSE	yes	no	132	144	13	R	D	0	1576.727	3	1.91E-04	112.42	2.63	1.51	2
669	DYETATLSDIKALIR	sp|P57780|ACTN4_MOUSE	yes	yes	441	455	15	R	K	0	1707.904	2;3	1.92E-09	171.76	1.13	0.99	12
670	DYFEKYGKIETIEVMEDR	sp|Q8BG05-2|ROA3_MOUSE	no	no	122	139	18	R	Q	0	2264.067	4	2.95E-04	76.38	1.29	1.27	3
671	DYFVSCPGR	sp|Q91X72|HEMO_MOUSE	yes	yes	225	233	9	R	G	0	1099.476	2	2.21E-02	103.80	NaN	NaN	0
672	DYIWNTLNSGR	sp|Q9CZU6|CISY_MOUSE	yes	yes	330	340	11	R	V	0	1337.636	2	3.33E-04	126.19	0.03	0.02	1
673	DYLHLPPEIVPATLR	sp|P63325|RS10_MOUSE	yes	yes	81	95	15	R	R	0	1732.951	2;3	1.70E-03	97.80	NaN	NaN	0
674	DYLHYIR	sp|P62281|RS11_MOUSE	yes	yes	91	97	7	R	K	0	978.492	2	6.46E-02	114.72	NaN	NaN	0
675	DYLMKILTER	sp|P63260|ACTG_MOUSE	no	no	187	196	10	T	G	0	1280.680	2	1.33E-03	114.86	1.69	1.30	2
676	DYRPQVGVIADPSSKTLSFFNKDT	sp|Q60847|COCA1_MOUSE	yes	no	2605	2629	25	R	G	1	2840.446	5	2.46E-02	42.35	2.02	1.19	1
677	DYSDHPSGGSYR	sp|Q9WV02-2|RBMX_MOUSE	yes	no	271	282	12	R	D	0	1339.543	3	4.88E-02	45.28	1.33	0.92	1
678	DYTYEELLNR	sp|Q99L45|IF2B_MOUSE	yes	yes	171	180	10	R	V	0	1314.609	2	8.69E-03	128.27	NaN	NaN	0
679	EAAAPQPAASKPADR	sp|A2A5X5|KR161_MOUSE	yes	yes	488	502	15	R	-	0	1478.748	2;3	3.20E-05	104.55	1.61	1.17	5
680	EAAQMDMVNDGVEDLR	sp|P19157|GSTP1_MOUSE	yes	yes	86	101	16	R	G	0	1791.777	2	2.05E-03	95.66	NaN	NaN	0
681	EADDIVNWLKKR	sp|P09103|PDIA1_MOUSE	yes	yes	123	134	12	R	T	0	1485.794	3;4	5.45E-04	108.35	1.12	1.03	13
682	EADINGLRR	sp|P02535-3|K1C10_MOUSE	no	no	238	246	9	V	V	1	1042.552	2	2.11E-02	109.71	NaN	NaN	0
683	EADINSLRR	sp|Q9D646|KRT34_MOUSE	no	no	156	164	9	V	I	1	1072.563	2	3.17E-02	93.65	NaN	NaN	0
684	EAEAAIYHLQLFEELR	sp|P52480|KPYM_MOUSE	yes	yes	384	399	16	R	R	0	1930.979	3	4.36E-04	123.02	NaN	NaN	0
685	EAESLIAKKIHPQTIISGWR	sp|P80314|TCPB_MOUSE	yes	yes	112	131	20	R	E	0	2276.264	4	1.20E-03	98.18	1.03	1.00	1
686	EAEVLLLQQR	sp|Q9R269|PEPL_MOUSE	yes	yes	1026	1035	10	R	V	0	1197.672	2	1.12E-03	162.88	NaN	NaN	0
687	EAEYFELPELVR	sp|Q6WVG3|KCD12_MOUSE	yes	yes	116	127	12	R	R	0	1493.740	2	2.08E-03	128.85	0.25	0.18	3
688	EAGDHPVELLAR	sp|P07214|SPRC_MOUSE	yes	yes	206	217	12	L	D	0	1305.668	2	2.12E-03	132.50	NaN	NaN	0
689	EAGDVCYADVYR	sp|Q6PDM2-3|SRSF1_MOUSE	yes	no	143	154	12	R	D	0	1416.598	2	3.37E-03	117.20	NaN	NaN	0
690	EAGFLRPVTIFGPIADVAR	sp|P39447|ZO1_MOUSE	yes	yes	640	658	19	R	E	1	2028.116	3	1.98E-02	54.76	NaN	NaN	0
691	EAIICKNIPR	sp|O88844|IDHC_MOUSE	yes	yes	110	119	10	R	L	0	1212.665	3	2.32E-03	101.65	1.37	1.07	3
692	EAIIPGSVYDR	sp|Q9EPU0-2|RENT1_MOUSE	yes	no	934	944	11	R	S	0	1218.625	2	1.73E-02	85.36	NaN	NaN	0
693	EAILAIHKEAQR	sp|P57780|ACTN4_MOUSE	yes	yes	586	597	12	R	I	0	1377.773	3	4.88E-02	45.28	1.23	1.06	4
694	EALDCILPPTRPTDKPLR	sp|P10126|EF1A1_MOUSE	yes	yes	230	247	18	L	L	1	2091.115	3	4.87E-02	37.16	1.25	0.99	3
695	EALLSSAVDHGSDEAR	sp|P80314|TCPB_MOUSE	yes	yes	139	154	16	R	F	0	1655.775	3	6.44E-04	107.50	NaN	NaN	0
696	EANLAAAFGKPINF	sp|O08749|DLDH_MOUSE	yes	no	496	509	14	R	-	0	1461.762	2	3.26E-06	149.57	1.18	0.94	5
697	EANQAINPKLLQLVEDR	sp|Q61656|DDX5_MOUSE	yes	yes	462	478	17	R	G	0	1950.053	3	1.02E-06	106.93	1.20	1.13	7
698	EAPHIIVGTPGR	sp|P60843|IF4A1_MOUSE	yes	yes	150	161	12	M	V	0	1245.683	3	1.50E-03	140.57	NaN	NaN	0
699	EAPIDKKGNFNYIEFTR	sp|Q3THE2|ML12B_MOUSE	yes	yes	145	161	17	R	I	0	2041.027	4	6.89E-03	55.85	1.37	1.11	3
700	EAPLNPKANR	sp|P63260|ACTG_MOUSE	no	no	107	116	10	T	E	0	1108.599	2	4.50E-03	89.05	1.22	1.01	4
701	EAQDKVAVLSQNR	sp|Q8CAY6|THIC_MOUSE	yes	yes	176	188	13	R	A	0	1456.763	3	5.46E-06	150.11	1.06	0.90	3
702	EATESFASDPILYR	sp|P52480|KPYM_MOUSE	no	no	93	106	14	R	P	0	1597.762	2	5.38E-04	143.98	NaN	NaN	0
703	EATESFASDPILYRPVAVALDTKGF	sp|P52480|KPYM_MOUSE	no	no	93	120	28	R	T	1	3044.582	3;4	1.51E-06	123.29	1.11	1.02	8
704	EAVSLLR	sp|P97350|PKP1_MOUSE	yes	yes	334	340	7	R	R	0	786.460	2	1.02E-02	124.37	0.04	0.03	2
705	EAVTFLR	sp|Q9D2G2-2|ODO2_MOUSE	yes	no	179	185	7	R	K	0	834.460	2	6.30E-02	117.93	NaN	NaN	0
706	EAYPGDVFYLHSR	sp|Q03265|ATPA_MOUSE	yes	yes	335	347	13	R	L	0	1552.731	3	9.16E-03	79.88	NaN	NaN	0
707	ECLPLIIFLR	sp|P62702|RS4X_MOUSE	yes	yes	40	49	10	R	N	0	1272.726	2	7.81E-03	131.62	NaN	NaN	0
708	ECPSDECGAGVFMGSHFDR	sp|P62983|RS27A_MOUSE	yes	yes	120	138	19	R	H	0	2156.835	3	2.77E-03	93.37	NaN	NaN	0
709	ECQNAEYQQLLDIKTR	sp|P02535-3|K1C10_MOUSE	yes	no	415	430	16	T	L	0	2007.968	2	1.25E-06	113.47	1.89	1.30	3
710	EDAPVGPHLQSMPSEQIR	sp|P23116|EIF3A_MOUSE	yes	yes	503	520	18	R	N	0	1989.958	3	1.89E-02	61.10	NaN	NaN	0
711	EDDEDDDVDTKKQKTEEDD	sp|P26350|PTMA_MOUSE	yes	no	93	111	19	A	-	0	2267.904	3	2.64E-02	43.79	0.81	0.76	4
712	EDEEESLNEVGYDDIGGCR	sp|Q01853|TERA_MOUSE	yes	yes	192	210	19	R	K	0	2184.875	2	7.83E-05	126.07	NaN	NaN	0
713	EDGNEEDKENQGDETQGQQPPC	sp|P62960|YBOX1_MOUSE	yes	yes	255	277	23	R	R	0	2627.097	3	4.97E-24	205.02	1.14	1.05	5
714	EDINSLCLTVVQKLMER	sp|Q8JZK9|HMCS1_MOUSE	yes	yes	63	79	17	R	H	0	2047.044	3	4.05E-03	87.65	1.09	1.05	2
715	EDKNNLFSVQFR	sp|Q8K411-3|PREP_MOUSE	yes	no	81	92	12	R	T	0	1495.742	3	1.34E-01	59.98	NaN	NaN	0
716	EDLVVAPAGVTLKEANEILQR	sp|P24547|IMDH2_MOUSE	yes	yes	183	203	21	R	S	0	2264.238	3	2.96E-05	79.49	0.96	0.91	5

717	EDLVYQAKLAEQAER	sp|P62259|1433E_MOUSE	yes	yes	5	19	15	R	Y	0	1761.890	3	3.44E-04	77.32	1.09	0.95	4
718	EEAESTLQSFR	sp|P20152|VIME_MOUSE	yes	yes	197	207	11	R	Q	0	1295.599	2	2.24E-06	181.44	NaN	NaN	0
719	EEALLSVLTER	sp|Q8K010|OPLA_MOUSE	yes	yes	1188	1198	11	R	R	0	1258.677	2	3.65E-02	72.29	NaN	NaN	0
720	EEEAIQLDGLNASQIR	sp|P08113|ENPL_MOUSE	yes	yes	52	67	16	R	E	0	1784.891	2	6.25E-08	188.47	NaN	NaN	0
721	EEEEEAKR	sp|Q8VDD5|MYH9_MOUSE	yes	no	1346	1353	8	L	N	0	1018.457	2	7.58E-02	76.68	1.69	1.35	1
722	EEEIAALVIDNGSGMCKAGFAGDI	sp|P63260|ACTG_MOUSE	yes	yes	2	28	27	M	A	0	2792.275	2;3	1.49E-22	184.59	1.15	1.02	20
723	EEELGSKAKFAGR	sp|P17182|ENOA_MOUSE	yes	yes	414	426	13	I	S	0	1420.731	2;3	1.98E-02	72.71	0.99	0.95	3
724	EEELQQTLQQEQNMLDR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1965	1981	17	R	L	0	2130.985	2	1.41E-05	165.45	NaN	NaN	0
725	EEERAGLEQR	sp|P58660|CAR10_MOUSE	yes	yes	165	174	10	L	L	1	1215.584	2	2.19E-02	92.54	NaN	NaN	0
726	EEERPSLR	sp|Q91VI7|RINI_MOUSE	yes	yes	446	453	8	L	I	1	1014.509	2	2.03E-03	169.44	0.03	0.04	1
727	EEFASTCPDDEEIELAYEQVAR	sp|Q9Z1Q5|CLIC1_MOUSE	yes	yes	217	238	22	R	A	0	2600.122	2	8.77E-03	59.98	NaN	NaN	0
728	EEFKELKAR	sp|P48678|LMNA_MOUSE	yes	no	111	119	9	R	N	0	1148.619	3	2.68E-02	68.66	0.94	0.64	4
729	EEGLGFPSFLDPDR	sp|Q148V8|FA83H_MOUSE	yes	yes	335	348	14	R	H	0	1577.736	2	3.46E-02	63.19	NaN	NaN	0
730	EEIQPGDMVIIDQFIDR	sp|Q9CQ65|MTAP_MOUSE	yes	yes	100	116	17	R	T	0	2016.983	2	4.90E-03	83.76	NaN	NaN	0
731	EEIVYLPCIYR	sp|P17563|SBP1_MOUSE	yes	no	24	34	11	R	N	0	1453.728	2	3.49E-04	140.16	0.02	0.02	1
732	EEILFVTSKLWNTKHHPEDVEPALI	sp|Q9JII6|AK1A1_MOUSE	yes	yes	73	96	24	R	K	0	2874.466	4	1.29E-03	61.35	0.91	0.89	1
733	EEILTNWEQIR	sp|P16546-2|SPTN1_MOUSE	yes	no	337	347	11	R	T	0	1429.720	2	1.90E-03	143.24	NaN	NaN	0
734	EELLCLKKNHEEEVNTLR	sp|Q9D646|KRT34_MOUSE	yes	no	185	202	18	R	C	0	2253.142	4	2.79E-05	96.45	1.97	1.13	4
735	EELMAAVR	sp|Q99JI4|PSMD6_MOUSE	yes	yes	39	46	8	R	E	0	917.464	2	5.91E-02	90.31	NaN	NaN	0
736	EELNKLLGR	sp|Q8CGP6|H2A1H_MOUSE	yes	no	92	100	9	D	V	0	1070.608	2	6.56E-03	93.65	1.19	0.81	4
737	EELSSPKGAMR	sp|Q6EDY6-3|LR16A_MOUSE	yes	no	1098	1108	11	T	S	0	1203.592	2	1.80E-02	83.86	0.04	0.03	1
738	EELTAFLHPEEFPHMR	sp|Q8BH97|RCN3_MOUSE	yes	yes	186	201	16	R	D	0	1981.936	4	3.66E-03	87.14	NaN	NaN	0
739	EEVDEEGKFVR	sp|P48678|LMNA_MOUSE	yes	no	443	453	11	V	L	0	1335.631	2	2.91E-02	53.57	1.64	1.21	3
740	EEVITLIR	sp|Q9JKF1|IQGA1_MOUSE	yes	yes	894	901	8	R	S	0	971.565	2	3.13E-02	137.88	NaN	NaN	0
741	EEVQDGKVISSR	sp|Q9QWL7|K1C17_MOUSE	yes	no	414	425	12	V	E	0	1345.684	2	1.50E-03	88.10	1.59	0.99	2
742	EFDELSPSAQR	sp|O55143-2|AT2A2_MOUSE	yes	no	656	666	11	R	D	0	1277.589	2	1.39E-02	92.87	NaN	NaN	0
743	EFESVLVDAFSHVAR	sp|Q9CSU0-3|RPR1B_MOUSE	yes	no	80	94	15	R	E	0	1704.847	3	3.49E-02	58.32	NaN	NaN	0
744	EFFNFLPLSSQDPAPIR	sp|Q99MN9|PCCB_MOUSE	yes	yes	275	291	17	R	E	0	1977.000	2	1.90E-04	131.56	NaN	NaN	0
745	EFSITDVVPYPISLR	sp|Q61316|HSP74_MOUSE	yes	yes	391	405	15	R	W	0	1734.919	2	3.19E-05	171.76	NaN	NaN	0
746	EGAKYVSHGATGKGNDQVR	sp|P16460|ASSY_MOUSE	yes	yes	109	127	19	R	F	0	1972.972	4	8.08E-02	24.79	1.06	1.04	1
747	EGDVLTLLESER	sp|P62858|RS28_MOUSE	yes	yes	52	63	12	R	E	0	1359.688	2	1.96E-03	134.56	0.03	0.03	1
748	EGFIKEEER	sp|P16388|KCNA1_MOUSE	yes	yes	134	142	9	D	P	0	1135.551	2;3	3.85E-03	101.65	1.22	0.84	7
749	EGIDPAPYYWYTDQR	sp|Q8BP47|SYNC_MOUSE	yes	yes	503	517	15	R	K	0	1872.832	2	7.54E-04	106.14	NaN	NaN	0
750	EGLLAIFKSGGIPALVR	sp|Q02257|PLAK_MOUSE	yes	yes	217	233	17	R	M	0	1740.030	2;3	9.66E-09	149.52	1.67	1.13	6
751	EGSMLNEHVCSVIR	sp|P02772|FETA_MOUSE	yes	yes	211	224	14	R	K	0	1629.760	3	1.08E-03	113.53	NaN	NaN	0
752	EGSSIGAIDSR	sp|Q9CZU6|CISY_MOUSE	yes	yes	223	233	11	R	L	0	1090.526	2	3.09E-03	81.00	2.93	2.34	2
753	EGTGTETPMIGDR	sp|P30416|FKBP4_MOUSE	yes	yes	40	52	13	R	V	0	1362.609	2	9.42E-03	79.09	NaN	NaN	0
754	EHAFVPEPFTGTNLAPSLWLHR	sp|Q09PK2|APRV1_MOUSE	yes	yes	97	118	22	R	F	0	2518.276	3;4	1.14E-08	158.44	NaN	NaN	0
755	EHFEKWGTLTDCVVMR	sp|Q8BG05-2|ROA3_MOUSE	no	no	31	46	16	R	D	0	2006.934	3	1.70E-04	81.63	1.26	1.08	6
756	EHPWEVMPDLYFYR	sp|P14206|RSSA_MOUSE	yes	yes	192	205	14	R	D	0	1880.856	3	1.10E-03	110.92	NaN	NaN	0
757	EIADLGEALATAVIPQWQKDEQR	sp|Q8BGQ7|SYAC_MOUSE	yes	yes	794	816	23	R	E	0	2580.318	3	5.28E-16	160.30	1.23	1.13	3
758	EIAQDFKTDLR	sp|P84244|H33_MOUSE	no	no	74	84	11	R	F	0	1334.683	2;3	2.86E-11	198.32	1.19	0.81	16
759	EIDGGLETLR	sp|Q9DCW4|ETFB_MOUSE	yes	yes	165	174	10	R	L	0	1101.567	2	9.78E-03	123.96	NaN	NaN	0
760	EIGNLLHPSVPISNDEDADNKVER	sp|P26638|SYSC_MOUSE	yes	yes	134	157	24	R	I	0	2660.304	4	5.02E-02	32.55	1.64	1.23	5
761	EIGPNDGFLAQLCQLNDR	sp|Q9D7X3|DUS3_MOUSE	yes	yes	159	176	18	R	L	0	2058.979	2	7.34E-04	74.73	0.01	0.01	1
762	EIGQSVDEVEKLIKR	sp|Q62261|SPTB2_MOUSE	yes	no	2044	2058	15	R	H	0	1741.957	3	1.12E-04	96.71	1.34	0.82	3
763	EIKALTAEIDR	sp|Q9D0I9|SYRC_MOUSE	yes	yes	18	28	11	R	L	0	1257.693	3	1.02E-01	49.63	1.31	1.20	1
764	EILSPVDIIDR	sp|Q99JY8|LPP3_MOUSE	yes	yes	295	305	11	R	N	0	1268.698	2	1.30E-02	94.77	NaN	NaN	0
765	EISVPNLLCVGDTSQGPYSFLGDR	sp|Q8CE93|FA26D_MOUSE	yes	yes	275	298	24	R	V	0	2623.259	2	1.07E-05	109.41	NaN	NaN	0
766	EKDFDSLAQPSFFDR	sp|Q02788|CO6A2_MOUSE	yes	yes	1014	1028	15	R	F	0	1800.832	2;3	5.97E-14	199.65	1.46	0.93	7
767	EKETKALSLAR	sp|Q8VDD5|MYH9_MOUSE	no	no	1473	1483	11	R	A	0	1244.709	3	3.49E-02	50.35	1.33	1.09	2
768	EKFSPLTANLMNLLAENGR	sp|Q9DB20|ATPO_MOUSE	yes	yes	99	117	19	R	L	0	2117.094	3	1.06E-15	165.17	1.51	0.92	1
769	EKLQEEMLQR	sp|P20152|VIME_MOUSE	yes	yes	187	196	10	R	E	0	1302.660	2;3	3.68E-13	208.03	1.11	0.91	17
770	EKSAIYQLEEEYENLLKASFER	sp|E9Q557|DESP_MOUSE	yes	yes	256	277	22	R	M	0	2688.328	4	4.23E-12	147.67	1.98	1.15	1
771	ELAEDGYSGVEVR	sp|P62908|RS3_MOUSE	yes	yes	28	40	13	R	V	0	1422.663	2	1.41E-03	127.02	NaN	NaN	0
772	ELAFQISKEYER	sp|Q9Z1N5|DX39B_MOUSE	yes	no	124	135	12	R	F	0	1511.762	3	8.61E-03	69.03	1.53	0.95	5
773	ELAQQVQQVAAEYCR	sp|Q61656|DDX5_MOUSE	yes	yes	178	192	15	R	A	0	1791.857	2	3.66E-17	238.07	0.07	0.05	1
774	ELCAQPGQVVAPGALLVR	sp|Q7TSG2|CTDP1_MOUSE	yes	yes	93	110	18	R	L	0	1877.019	2	5.41E-02	47.55	NaN	NaN	0
775	ELDALDANDELTPLGR	sp|O70133|DHX9_MOUSE	yes	no	840	855	16	R	I	0	1740.853	2	7.38E-12	178.14	4.52	3.52	3
776	ELDDELMR	sp|O54983|CRYM_MOUSE	yes	yes	234	241	8	R	Q	0	1019.459	2	3.85E-02	121.85	NaN	NaN	0
777	ELDEYFTQANDQMEIIDGLIR	sp|E9Q557|DESP_MOUSE	yes	yes	118	138	21	R	E	0	2512.179	2	3.45E-03	75.53	NaN	NaN	0
778	ELDFWQEGWR	sp|Q8K411-3|PREP_MOUSE	yes	no	173	182	10	R	L	0	1364.615	2	1.94E-02	96.34	NaN	NaN	0
779	ELDLPEELVSR	sp|Q3THK7|GUAA_MOUSE	yes	yes	425	435	11	R	H	0	1298.672	2	8.53E-03	106.67	NaN	NaN	0
780	ELECKIQER	sp|Q61897|KT33B_MOUSE	yes	no	83	91	9	A	N	0	1203.592	2	7.22E-03	91.70	1.57	1.06	3
781	ELEDATETADAMNR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	1899	1912	14	R	E	0	1564.668	2	1.31E-10	208.27	0.09	0.07	3
782	ELELKVPLVVR	sp|Q9Z2I8-2|SUCB2_MOUSE	yes	no	334	344	11	R	L	0	1293.802	3	2.50E-02	57.35	1.23	1.09	5
783	ELEPGVEYFIR	sp|Q80YX1-5|TENA_MOUSE	yes	no	681	691	11	R	V	0	1350.682	2	6.63E-03	115.57	NaN	NaN	0
784	ELETQISELQEDLESER	sp|Q8VDD5|MYH9_MOUSE	yes	yes	1108	1124	17	R	A	0	2046.959	2	2.17E-08	195.92	NaN	NaN	0
785	ELFEADPER	sp|P06745|G6PI_MOUSE	yes	yes	28	36	9	R	F	0	1104.509	2	1.98E-02	117.31	NaN	NaN	0
786	ELFQETLESLR	sp|Q6URW6-2|MYH14_MOUSI	yes	no	339	349	11	R	V	0	1363.698	2	8.79E-03	105.46	NaN	NaN	0
787	ELFSPLHALNFGIGGDTTR	sp|Q61206|PA1B2_MOUSE	yes	yes	61	79	19	R	H	0	2044.038	2;3	3.48E-08	175.33	NaN	NaN	0
788	ELGGNLATPR	sp|Q91V98|CD248_MOUSE	yes	yes	53	62	10	R	T	0	1026.546	2	5.81E-02	70.41	NaN	NaN	0
789	ELHLDNNKLLR	sp|P28654|PGS2_MOUSE	yes	yes	268	278	11	R	V	0	1363.757	3	3.09E-03	81.02	1.55	1.06	5
790	ELHLDNNKLSR	sp|P28653|PGS1_MOUSE	yes	yes	282	292	11	R	V	0	1337.705	3	3.20E-03	79.66	1.89	1.05	5
791	ELIEQLQNKPSDLGTKLQDPR	sp|Q60864|STIP1_MOUSE	yes	yes	154	174	21	R	V	0	2421.286	4	6.98E-02	26.36	0.88	0.85	4
792	ELIIGDR	sp|Q03265|ATPA_MOUSE	yes	yes	208	214	7	R	Q	0	814.455	2	5.84E-02	127.12	NaN	NaN	0
793	ELILSSEPSPAVTPVTPTTLIAPR	sp|Q9CWK8|SNX2_MOUSE	yes	yes	89	112	24	R	I	0	2488.379	2	1.14E-03	75.06	NaN	NaN	0
794	ELIQTSALNFLTPLR	sp|Q9JK48|SHLB1_MOUSE	yes	no	134	148	15	R	N	0	1714.962	2	5.35E-05	165.34	NaN	NaN	0
795	ELISNASDALDKIR	sp|P11499|HS90B_MOUSE	no	no	42	55	14	R	Y	0	1543.821	2;3	4.08E-13	196.33	1.25	1.00	16
796	ELISNSSDALDKIR	sp|P07901|HS90A_MOUSE	yes	yes	47	60	14	R	Y	0	1559.816	3	8.23E-05	116.51	1.24	1.13	6
797	ELKQLYLER	sp|P61161|ARP2_MOUSE	yes	yes	320	328	9	R	V	0	1190.666	3	5.65E-03	96.34	1.33	1.16	8
798	ELLELASR	sp|Q8VDJ3|VIGLN_MOUSE	yes	yes	496	503	8	R	M	0	929.518	2	1.54E-02	163.20	NaN	NaN	0
799	ELLLTGPGLEER	sp|Q505F5|LRC47_MOUSE	yes	yes	25	36	12	R	V	0	1325.719	2	4.29E-03	106.26	NaN	NaN	0
800	ELLQQVDTTTR	sp|P04104|K2C1_MOUSE	yes	yes	221	231	11	W	T	0	1302.678	2	3.57E-03	130.56	NaN	NaN	0
801	ELLSVGLGFLR	sp|Q80WJ7|LYRIC_MOUSE	yes	yes	23	33	11	R	T	0	1202.702	2	3.68E-02	72.20	NaN	NaN	0
802	ELLTLDEKDPR	sp|Q6ZWN5|RS9_MOUSE	yes	yes	59	69	11	R	R	0	1327.698	2;3	1.90E-04	132.32	1.34	0.97	17
803	ELLTTMGDR	sp|Q3THE2|ML12B_MOUSE	yes	no	125	133	9	R	F	0	1034.507	2	1.19E-02	140.45	NaN	NaN	0
804	ELNDFISYLQR	sp|P27773|PDIA3_MOUSE	yes	yes	472	482	11	R	E	0	1396.699	2	6.58E-04	152.64	NaN	NaN	0
805	ELNKLLGR	sp|Q8CGP6|H2A1H_MOUSE	yes	no	93	100	8	E	V	0	941.566	2	2.10E-02	80.17	1.28	0.84	4
806	ELPPDQAEYCIAR	sp|P57780|ACTN4_MOUSE	no	no	871	883	13	R	M	0	1560.724	2	8.05E-03	83.20	NaN	NaN	0
807	ELPTAFDYVEFTR	sp|P16546-2|SPTN1_MOUSE	yes	no	2435	2447	13	R	S	0	1586.762	2	1.60E-01	43.03	NaN	NaN	0
808	ELSGTIKEILGTAQSVGCNVDGR	sp|P35979|RL12_MOUSE	yes	yes	124	146	23	R	H	0	2403.206	3	5.09E-07	111.66	1.76	1.40	2
809	ELSKTYIIGELHPDDR	sp|P56395|CYB5_MOUSE	yes	yes	74	89	16	R	S	0	1884.958	4	1.18E-04	88.39	1.35	1.02	4
810	ELSLDDPEVEQVR	sp|Q3THG9|AASD1_MOUSE	yes	yes	172	184	13	R	G	0	1527.742	2	7.69E-03	84.30	NaN	NaN	0
811	ELTAVVQKR	sp|P62908|RS3_MOUSE	yes	yes	68	76	9	R	F	0	1042.614	2	1.25E-05	158.76	0.78	0.59	2
812	ELTGLKALYETELADAR	sp|P14733|LMNB1_MOUSE	yes	yes	75	91	17	R	R	0	1891.989	3	1.68E-11	168.05	1.39	0.85	1
813	ELTPQVISAAR	sp|Q64727|VINC_MOUSE	yes	yes	670	680	11	R	I	0	1183.656	2	2.68E-03	103.08	1.05	0.96	7
814	ELVSLKQEQQAFKQAADSER	sp|Q8BMK4|CKAP4_MOUSE	yes	yes	307	326	20	R	L	0	2304.171	4	3.31E-04	75.53	0.70	0.49	3
815	ELWLGDCDVTNSGCSSLANVLLAI	sp|Q91VI7|RINI_MOUSE	yes	yes	369	393	25	R	S	0	2763.296	2	2.60E-03	70.99	NaN	NaN	0
816	ELYDAGVKR	sp|P07356|ANXA2_MOUSE	yes	yes	197	205	9	R	K	0	1049.551	2;3	5.12E-06	172.23	1.23	0.96	10
817	EMEAELEDER	sp|Q8VDD5|MYH9_MOUSE	yes	yes	1593	1602	10	R	K	0	1249.513	2	7.97E-03	130.98	NaN	NaN	0
818	EMEENFALEAANYQDTIGR	sp|P20152|VIME_MOUSE	yes	yes	346	364	19	R	L	0	2199.974	2	2.64E-04	118.72	NaN	NaN	0
819	EMLNISGPPLKAGKTR	sp|Q9CPY7-2|AMPL_MOUSE	yes	no	38	53	16	R	T	0	1710.945	4	6.08E-03	61.27	1.05	1.01	4

820	EMLQQSKILKVIR	sp|P11499|HS90B_MOUSE	no	no	393	405	13	R	K	0	1584.939	3	5.44E-02	66.99	1.36	1.32	2
821	ENAEKFASTVQGDVR	sp|O54983|CRYM_MOUSE	yes	yes	171	185	15	R	V	0	1649.801	3	3.07E-05	105.63	0.97	0.84	4
822	ENAELECKIQER	sp|Q61897|KT33B_MOUSE	yes	no	80	91	12	R	N	0	1517.714	2;3	5.49E-18	231.07	1.80	1.15	10
823	ENDKQETWLLMELQKIR	sp|E9Q557|DESP_MOUSE	yes	yes	672	688	17	R	R	0	2173.120	3;4	4.40E-03	63.69	1.53	0.93	2
824	ENECHFYAGGQVYPGEASR	sp|O08807|PRDX4_MOUSE	yes	yes	51	69	19	R	V	0	2169.917	3	1.78E-02	58.02	NaN	NaN	0
825	ENEFSFEDNAIR	sp|Q6PDQ2|CHD4_MOUSE	yes	yes	811	822	12	R	G	0	1469.642	2	1.47E-02	77.19	NaN	NaN	0
826	ENKTAVVVGTVTDDVR	sp|P35980|RL18_MOUSE	yes	yes	76	91	16	R	I	0	1701.890	3	1.78E-06	106.38	1.36	0.93	10
827	ENLSAAFSR	sp|Q8R050-2|ERF3A_MOUSE	yes	no	59	67	9	R	Q	0	993.488	2	4.87E-02	78.49	20.14	16.58	1
828	ENMAYTVEGIR	sp|Q9DB77|QCR2_MOUSE	yes	yes	117	127	11	R	S	0	1281.602	2	5.11E-03	122.70	NaN	NaN	0
829	ENVFKLLPQVMYLDGYDR	sp|O35381|AN32A_MOUSE	yes	yes	133	150	18	R	D	0	2199.103	3	2.92E-05	96.14	1.95	1.54	3
830	ENVFLTYQDKR	sp|Q6P3A4|VSIG8_MOUSE	yes	yes	73	83	11	R	I	0	1411.710	2;3	5.73E-11	188.91	2.32	1.47	9
831	ENYGELADCCTKQEPER	sp|P07724|ALBU_MOUSE	yes	yes	106	122	17	R	N	0	2097.873	2;3	1.64E-16	197.38	1.34	1.07	12
832	EPEKYIALDGDSLSTEDLVNLGKGI	sp|P35492|HUTH_MOUSE	yes	yes	109	133	25	R	Y	0	2718.371	4	5.23E-04	72.32	1.09	1.05	1
833	EPFIVPVEPER	sp|Q60847|COCA1_MOUSE	yes	no	3077	3087	11	R	T	0	1310.687	2	7.10E-03	113.38	NaN	NaN	0
834	EPIICKNIPR	sp|P54071|IDHP_MOUSE	yes	yes	150	159	10	R	L	0	1238.681	3	1.42E-02	71.61	1.02	0.87	6
835	EPMQTGIKAVDSLVPIGR	sp|Q03265|ATPA_MOUSE	yes	yes	187	204	18	R	G	0	1910.030	3	6.83E-09	141.60	1.09	0.86	12
836	EPVQLETLSIR	sp|P62315|SMD1_MOUSE	yes	yes	51	61	11	R	G	0	1283.709	2	2.02E-06	183.99	NaN	NaN	0
837	EPWDGKDGELPVEDDIDLSDVEL	sp|Q922R8|PDIA6_MOUSE	yes	no	410	440	31	R	-	0	3541.600	3	1.04E-03	68.96	0.81	0.79	1
838	EQAEAEVASLNR	sp|P21107-2|TPM3_MOUSE	yes	yes	43	54	12	R	R	0	1315.637	2	5.14E-05	177.83	NaN	NaN	0
839	EQAGGDATENFEDVGHSTDAR	sp|P56395|CYB5_MOUSE	yes	yes	53	73	21	R	E	0	2204.921	3	8.64E-03	65.18	NaN	NaN	0
840	EQCCYNCGKPGHLAR	sp|P53996-2|CNBP_MOUSE	yes	no	88	102	15	R	D	0	1848.782	4	6.94E-05	100.22	1.20	0.99	6
841	EQDAVDQVKVIVDALDER	sp|Q8R2Q0|TRI29_MOUSE	yes	yes	336	353	18	R	A	0	2041.033	3	9.54E-05	79.88	1.47	1.11	2
842	EQEIAAVQAR	sp|Q99PL5|RRBP1_MOUSE	yes	yes	955	964	10	R	M	0	1113.578	2	1.92E-02	96.62	NaN	NaN	0
843	EQENRLSEAR	sp|Q70FJ1-3|AKAP9_MOUSE	yes	no	532	541	10	A	K	1	1230.595	2	2.36E-02	89.91	NaN	NaN	0
844	EQFNDFR	sp|Q05186|RCN1_MOUSE	yes	yes	244	250	7	R	D	0	954.420	2	7.42E-02	100.19	NaN	NaN	0
845	EQFVEFR	sp|O35887|CALU_MOUSE	yes	yes	235	241	7	R	D	0	953.461	2	1.42E-02	172.03	0.13	0.12	3
846	EQIKALNNKFASFIDKVR	sp|Q9R0H5|K2C71_MOUSE	no	no	133	150	18	R	F	0	2120.174	5	1.91E-02	60.76	1.42	0.92	1
847	EQLAEKNR	sp|P02535-3|K1C10_MOUSE	yes	no	315	322	8	Y	K	0	986.515	2	8.16E-04	155.84	1.38	0.93	3
848	EQLAIAEFAR	sp|P11983|TCPA_MOUSE	yes	no	434	443	10	R	S	0	1146.603	2	6.35E-03	86.01	12.94	8.35	2
849	EQLEEEEEAKR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	1343	1353	11	R	N	0	1388.642	2;3	2.04E-04	130.56	1.36	1.15	14
850	EQTLSPTIINGLHSIAR	sp|Q3UPL0-2|SC31A_MOUSE	yes	no	1130	1146	17	R	S	0	1849.006	3	2.83E-02	54.96	NaN	NaN	0
851	EQVLAAIR	sp|Q571B6-2|WHAMM_MOUS	yes	no	426	433	8	N	Q	0	898.524	2	3.08E-02	138.83	NaN	NaN	0
852	EQWANLEQLSAIR	sp|Q62261|SPTB2_MOUSE	yes	no	724	736	13	R	K	0	1556.795	2	7.59E-04	145.00	NaN	NaN	0
853	EQWSNCPTIGQIR	sp|P10605|CATB_MOUSE	yes	yes	88	100	13	R	D	0	1587.746	2	1.36E-06	190.10	NaN	NaN	0
854	EQYEALAEKNR	sp|P08730|K1C13_MOUSE	yes	no	271	281	11	R	R	0	1349.658	2	1.20E-16	211.26	2.92	1.64	1
855	EQYLYYGDQLLSLNR	sp|P21845|TRYB2_MOUSE	yes	no	93	107	15	R	I	0	1873.921	2	7.25E-04	109.79	NaN	NaN	0
856	EQYSQYSLVVR	sp|Q61495|DSG1A_MOUSE	no	no	228	238	11	R	G	0	1370.683	2	2.75E-04	160.18	NaN	NaN	0
857	ERDFTSLENTVEER	sp|Q8BMK4|CKAP4_MOUSE	yes	yes	206	219	14	R	L	1	1723.801	3	6.84E-03	80.51	NaN	NaN	0
858	ESDLNGLRR	sp|Q61897|KT33B_MOUSE	yes	no	156	164	9	V	I	1	1058.547	2	2.38E-02	88.82	NaN	NaN	0
859	ESIESEIR	sp|Q01853|TERA_MOUSE	yes	yes	701	708	8	R	R	0	961.472	2	3.83E-02	122.52	NaN	NaN	0
860	ESIESEIRR	sp|Q01853|TERA_MOUSE	yes	yes	701	709	9	R	E	1	1117.573	3	4.77E-02	78.11	NaN	NaN	0
861	ESKINAMDTSPR	sp|Q9Z1T6-1|FYV1_MOUSE	yes	no	1489	1500	12	E	N	0	1347.645	2	3.17E-02	49.08	2.19	1.15	1
862	ESLIDGIKR	sp|P50247|SAHH_MOUSE	yes	yes	197	205	9	R	A	0	1029.582	2	2.88E-03	107.79	1.03	0.88	4
863	ESPENWEIVR	sp|P46935|NEDD4_MOUSE	yes	yes	319	328	10	R	E	0	1257.599	2	1.39E-02	107.55	NaN	NaN	0
864	ESPIFKQFFKNWK	sp|P24452|CAPG_MOUSE	yes	no	340	352	13	R	-	0	1697.893	4	8.35E-03	65.18	0.99	0.90	1
865	ESQQLEIENR	sp|Q9WVL2|STAT2_MOUSE	yes	yes	138	147	10	V	I	0	1244.600	2	5.76E-02	70.55	NaN	NaN	0
866	ESTGAQVQVAGDMLPNSTER	sp|P60335|PCBP1_MOUSE	yes	no	125	144	20	R	A	0	2088.975	2	3.43E-03	84.25	NaN	NaN	0
867	ETDLQELFRPFGSISR	sp|Q9Z1D1|EIF3G_MOUSE	yes	yes	252	267	16	R	I	1	1893.959	3	4.15E-04	124.62	NaN	NaN	0
868	ETGVDLTKDNMALQR	sp|P38647|GRP75_MOUSE	yes	yes	293	307	15	R	V	0	1689.836	3	1.99E-03	73.30	1.13	0.95	5
869	ETLEQAKVEVPVGSFKGR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	3134	3151	18	R	A	0	1973.058	3	6.05E-03	54.76	2.00	1.18	4
870	ETLIDVAR	sp|P80317|TCPZ_MOUSE	yes	yes	146	153	8	R	T	0	915.503	2	3.93E-02	118.74	NaN	NaN	0
871	ETMQFLNDR	sp|Q61897|KT33B_MOUSE	yes	no	58	66	9	R	L	0	1152.523	2	9.81E-03	144.65	NaN	NaN	0
872	ETNLESLPLVDTHSKR	sp|P20152|VIME_MOUSE	yes	yes	425	440	16	R	T	0	1837.953	4	1.41E-03	73.83	1.20	0.83	4
873	ETPPDALILESPFTNIR	sp|Q99LR1|ABD12_MOUSE	yes	yes	263	279	17	R	E	0	1911.994	2	8.72E-03	74.43	NaN	NaN	0
874	ETQALILAPTR	sp|Q91VC3|IF4A3_MOUSE	yes	yes	106	116	11	R	E	0	1211.687	2	1.24E-02	96.07	NaN	NaN	0
875	ETQSQLESER	sp|E9Q557|DESP_MOUSE	yes	yes	1935	1944	10	R	C	0	1205.552	2	3.83E-04	175.33	NaN	NaN	0
876	ETQTEYEWTVDSSKLVFDGLR	sp|E9Q557|DESP_MOUSE	yes	yes	1964	1984	21	R	K	0	2502.191	3	3.05E-08	107.78	1.73	1.13	1
877	ETSGNLEQLLLAVVKSIR	sp|P48036|ANXA5_MOUSE	yes	yes	226	243	18	R	S	0	1969.121	3	4.73E-03	59.73	1.24	0.98	1
878	ETVSEESNVLCLSKSPNKHNR	sp|P58252|EF2_MOUSE	yes	yes	581	601	21	R	L	0	2427.181	4	3.16E-05	77.87	1.13	0.94	3
879	ETVVEVPQVTWEDIGGLEDVKR	sp|Q01853|TERA_MOUSE	yes	yes	466	487	22	R	E	0	2497.270	2;3	6.09E-07	102.07	1.25	0.98	9
880	EVAGQVGVPLQDLMVR	sp|Q9Z2W0|DNPEP_MOUSE	yes	yes	391	406	16	R	N	0	1709.913	2	2.64E-04	136.63	NaN	NaN	0
881	EVATGDDKKR	sp|O70456|1433S_MOUSE	yes	yes	133	142	10	A	I	0	1117.573	2	1.84E-03	106.62	1.33	1.23	4
882	EVATNSELVQSGKSEISELR	sp|Q61781|K1C14_MOUSE	no	no	322	341	20	R	R	0	2175.102	2;3	1.47E-47	262.91	1.68	1.01	14
883	EVATNSELVQSGKSEISELRR	sp|Q61781|K1C14_MOUSE	no	no	322	342	21	R	T	1	2331.203	3;4	1.12E-08	121.44	1.61	0.98	13
884	EVCGFAPYER	sp|P47964|RL36_MOUSE	yes	yes	46	55	10	R	R	0	1226.539	2	8.75E-03	128.03	NaN	NaN	0
885	EVDDLEQWIAER	sp|Q62261|SPTB2_MOUSE	yes	no	1706	1717	12	R	E	0	1501.705	2	1.96E-04	168.02	NaN	NaN	0
886	EVDIGIPDATGR	sp|Q01853|TERA_MOUSE	yes	yes	366	377	12	R	L	0	1241.625	2	2.81E-03	123.95	NaN	NaN	0
887	EVEEWFTTQTEELNKQVVSSSEQI	sp|Q61897|KT33B_MOUSE	no	no	242	276	35	R	R	0	4166.995	3	1.72E-03	83.57	2.06	1.32	1
888	EVESQAQQQLER	sp|P54285|CACB3_MOUSE	yes	yes	43	54	12	R	A	0	1443.695	2	7.07E-03	70.94	12.11	7.41	1
889	EVFEMATR	sp|Q9QUI0|RHOA_MOUSE	yes	no	169	176	8	R	A	0	981.459	2	2.58E-02	147.36	NaN	NaN	0
890	EVGKALEGINNGITQAGR	sp|Q8CIT9|SBSN_MOUSE	yes	no	46	63	18	R	E	0	1825.965	3	6.99E-07	124.99	1.73	1.17	3
891	EVIELPLTNPELFQR	sp|P62334|PRS10_MOUSE	yes	yes	147	161	15	R	V	0	1796.967	2	4.66E-03	81.63	NaN	NaN	0
892	EVLEKQPVLSQTEAR	sp|P99026|PSB4_MOUSE	yes	yes	197	211	15	R	E	0	1725.926	3	7.30E-06	125.67	1.22	0.95	7
893	EVLINNINR	sp|Q6ZWX6|IF2A_MOUSE	yes	yes	174	182	9	R	R	0	1083.604	2	1.21E-02	140.09	NaN	NaN	0
894	EVQGNESDLFMSYFPR	sp|P24452|CAPG_MOUSE	yes	yes	97	112	16	R	G	0	1917.857	2	4.66E-04	120.77	NaN	NaN	0
895	EVQLPDR	sp|Q9JHR7|IDE_MOUSE	yes	yes	768	774	7	R	G	0	855.445	2	6.53E-02	113.50	NaN	NaN	0
896	EVQMGDFVR	sp|Q61576|FKB10_MOUSE	yes	yes	57	65	9	R	Y	0	1079.507	2	2.24E-02	102.62	NaN	NaN	0
897	EVSGIKAAYEAELGDAR	sp|P48678|LMNA_MOUSE	yes	no	73	89	17	R	K	0	1777.885	3	5.42E-03	76.05	1.24	0.83	3
898	EVVDPEVFFNATGCLR	sp|P97350|PKP1_MOUSE	yes	yes	397	412	16	R	N	0	1851.883	2	2.94E-04	134.14	NaN	NaN	0
899	EVVETPLLHPER	sp|P46471|PRS7_MOUSE	yes	yes	189	200	12	R	F	0	1417.757	3	7.50E-03	95.42	NaN	NaN	0
900	EVVKLQNDPQLEAEYR	sp|Q9R269|PEPL_MOUSE	yes	yes	1054	1069	16	R	R	0	1929.980	3	8.60E-05	92.44	1.33	0.81	3
901	EWTQKYAM	sp|Q6ZWY6|U2D2B_MOUSE	yes	no	140	147	8	R	-	0	1055.475	2	6.29E-03	117.40	1.62	1.44	4
902	EYENELAKVR	sp|E9Q557|DESP_MOUSE	yes	yes	1199	1208	10	R	N	0	1249.630	2	3.40E-06	164.31	1.92	1.13	1
903	EYFGQFGEIEAIELPIDPKLNKR	sp|Q99020|ROAA_MOUSE	yes	yes	177	199	23	R	R	0	2705.407	3;4	5.98E-11	146.19	0.93	0.91	7
904	EYQTQLIQR	sp|Q9JHU4|DYHC1_MOUSE	yes	yes	601	609	9	R	V	0	1177.609	2	1.01E-02	144.12	NaN	NaN	0
905	FACHSASLTVR	sp|Q99K48|NONO_MOUSE	yes	no	145	155	11	R	N	0	1247.608	3	9.01E-05	174.40	NaN	NaN	0
906	FAEFEDFPETSEPVWILGR	sp|Q8BGE6|ATG4B_MOUSE	yes	yes	13	31	19	R	K	0	2268.074	2	2.09E-04	120.90	NaN	NaN	0
907	FAELAQIYAQR	sp|Q9JHW2|NIT2_MOUSE	yes	yes	158	168	11	R	G	0	1308.683	2	3.66E-03	129.89	NaN	NaN	0
908	FAGKQLEDGR	sp|P62983|RS27A_MOUSE	yes	no	45	54	10	I	T	0	1119.567	2	6.28E-04	126.19	1.27	0.90	4
909	FAGVDIR	sp|P14131|RS16_MOUSE	yes	yes	63	69	7	R	V	0	776.418	2	5.17E-02	138.85	NaN	NaN	0
910	FANYIDKVR	sp|P20152|VIME_MOUSE	yes	yes	114	122	9	R	F	0	1124.598	2;3	1.92E-03	117.70	1.17	0.84	18
911	FAPPEAPEPWSGVR	sp|Q8BK48|EST2E_MOUSE	yes	no	73	86	14	R	D	0	1538.752	2	3.36E-02	63.73	NaN	NaN	0
912	FAQPGSFEYEYAMR	sp|Q99K48|NONO_MOUSE	yes	yes	259	272	14	R	W	0	1694.740	2	2.12E-02	69.92	NaN	NaN	0
913	FASFINKVR	sp|Q99M74|KRT82_MOUSE	yes	no	129	137	9	R	F	0	1080.608	3	8.35E-03	88.37	1.80	1.03	1
914	FATHAAALSVR	sp|Q8VIJ6|SFPQ_MOUSE	yes	yes	358	368	11	R	N	0	1142.620	3	7.05E-03	113.61	NaN	NaN	0
915	FAYDGLKR	sp|Q91VD9|NDUS1_MOUSE	yes	yes	292	299	8	R	Q	0	968.508	3	2.29E-01	63.57	NaN	NaN	0
916	FCIWTESAFR	sp|Q9D8E6|RL4_MOUSE	yes	yes	249	258	10	R	K	0	1315.602	2	6.79E-03	135.43	NaN	NaN	0
917	FCPFAQR	sp|O09131|GSTO1_MOUSE	yes	yes	31	37	7	R	T	0	924.428	2	9.64E-02	84.06	NaN	NaN	0
918	FCQLLWR	sp|Q8JZQ9|EIF3B_MOUSE	yes	yes	688	694	7	R	P	0	1021.517	2	5.76E-02	128.75	NaN	NaN	0
919	FDADEEFKKR	sp|Q9D0I9|SYRC_MOUSE	yes	yes	280	289	10	R	A	0	1283.615	3	3.40E-02	57.53	1.30	1.06	3
920	FDAGELITQR	sp|P67778|PHB_MOUSE	yes	yes	134	143	10	R	E	0	1148.583	2	5.08E-03	141.88	NaN	NaN	0
921	FDAMPFTLR	sp|P50580|PA2G4_MOUSE	yes	yes	273	281	9	R	A	0	1096.538	2	4.45E-02	81.26	NaN	NaN	0
922	FDDGAGGDNEVQR	sp|P46471|PRS7_MOUSE	yes	yes	285	297	13	R	T	0	1378.575	2	6.88E-04	146.79	NaN	NaN	0

923	FDDPLLGPR	sp|Q8BMJ2|SYLC_MOUSE	yes	yes	1120	1128	9	R	R	0	1028.529	2	1.31E-02	138.06	NaN	NaN	0
924	FDGALNVDLTEFQTNLVPYPR	sp|P68373|TBA1C_MOUSE	no	no	244	264	21	R	I	0	2408.201	2	1.86E-08	172.83	NaN	NaN	0
925	FDQQKNDYDQLQKAR	sp|E9Q557|DESP_MOUSE	yes	yes	1144	1158	15	R	Q	0	1895.913	3;4	9.85E-05	97.80	1.70	0.98	6
926	FDRPLPVSR	sp|Q9R1P4|PSA1_MOUSE	yes	yes	99	107	9	V	L	1	1085.598	2	1.24E-01	61.56	NaN	NaN	0
927	FDSPESHVGVAWR	sp|Q91WT9-2|CBS_MOUSE	yes	no	194	206	13	R	L	0	1485.700	3	4.01E-03	95.42	NaN	NaN	0
928	FDVQLKDLEKWQNNLLPSR	sp|P62245|RS15A_MOUSE	yes	yes	79	97	19	R	Q	0	2342.238	3;4	3.30E-12	145.88	1.27	1.10	9
929	FDVSGYPTLKIFR	sp|P08003|PDIA4_MOUSE	yes	yes	240	252	13	R	K	0	1541.824	3	1.19E-02	59.23	1.12	0.95	4
930	FEAPLFNAR	sp|Q91VD9|NDUS1_MOUSE	yes	yes	409	417	9	R	I	0	1063.545	2	2.18E-02	105.52	NaN	NaN	0
931	FEEFLQR	sp|Q60597-2|ODO1_MOUSE	yes	no	254	260	7	R	K	0	967.476	2	5.43E-02	134.44	NaN	NaN	0
932	FEELCSDLFR	sp|Q61696|HS71A_MOUSE	yes	no	302	311	10	R	G	0	1314.591	2	6.68E-03	135.86	NaN	NaN	0
933	FEELNADLFR	sp|P63017|HSP7C_MOUSE	no	no	302	311	10	R	G	0	1252.609	2	2.85E-05	187.97	NaN	NaN	0
934	FEELTNLIR	sp|Q8R1B4|EIF3C_MOUSE	yes	yes	57	65	9	R	T	0	1133.608	2	1.14E-02	141.48	NaN	NaN	0
935	FEGIVTDLIKR	sp|P38647|GRP75_MOUSE	yes	yes	351	361	11	Q	T	0	1289.734	2	5.28E-04	121.02	1.16	0.89	5
936	FEIFPTR	sp|Q08189|TGM3_MOUSE	yes	yes	659	665	7	R	S	0	908.476	2	5.96E-02	124.83	NaN	NaN	0
937	FELFADKVPKTAENFR	sp|P17742|PPIA_MOUSE	yes	yes	22	37	16	S	A	0	1910.989	3	7.69E-02	46.89	0.62	0.60	1
938	FELLAR	sp|P46471|PRS7_MOUSE	yes	no	370	375	6	R	L	0	747.428	2	5.58E-02	126.05	NaN	NaN	0
939	FEVIDDLNHWDHATKLR	sp|Q09PK2|APRV1_MOUSE	yes	yes	119	135	17	R	F	0	2108.044	4	3.63E-05	97.24	1.08	1.02	3
940	FFDEESYSLLR	sp|Q62186|SSRD_MOUSE	yes	yes	105	115	11	R	K	0	1404.656	2	4.37E-03	126.19	NaN	NaN	0
941	FFGAVLR	sp|Q3V1T4-2|P3H1_MOUSE	yes	no	112	118	7	R	R	0	808.460	2	5.87E-02	126.68	NaN	NaN	0
942	FFGNNWAETYR	sp|Q8CG76|ARK72_MOUSE	yes	yes	259	269	11	R	N	0	1403.626	2	5.92E-03	118.90	NaN	NaN	0
943	FFIQNVFR	sp|Q8BU30|SYIC_MOUSE	yes	yes	662	669	8	R	L	0	1069.571	2	4.00E-02	116.54	NaN	NaN	0
944	FFMPGFAPLTSR	sp|P99024|TBB5_MOUSE	no	no	265	276	12	H	G	0	1369.685	2	4.51E-02	66.27	NaN	NaN	0
945	FFQELPASDSAFKAVPVSNIAPAA	sp|Q99K01-3|PDXD1_MOUSE	yes	no	394	420	27	R	E	0	2788.455	3	4.14E-02	36.05	1.51	1.19	2
946	FFSDCKIQNGAQGIR	sp|O35737|HNRH1_MOUSE	yes	yes	30	44	15	R	F	0	1739.841	3	1.57E-05	118.52	1.41	1.19	4
947	FFSSDICR	sp|Q08857|CD36_MOUSE	yes	yes	266	273	8	R	S	0	1030.454	2	3.92E-02	119.41	NaN	NaN	0
948	FFTTSVEDLLR	sp|Q6ZWQ0-3|SYNE2_MOUSE	yes	no	697	707	11	R	F	0	1326.682	2	1.71E-02	85.81	NaN	NaN	0
949	FGDMQEIIQNFVR	sp|Q9QYG0-2|NDRG2_MOUSE	yes	no	71	83	13	R	V	0	1595.777	2	1.56E-03	105.03	NaN	NaN	0
950	FGEVVDCTIKTDPVTGR	sp|Q9Z130|HNRDL_MOUSE	yes	yes	52	68	17	R	S	0	1892.930	3	2.61E-03	69.33	1.32	1.18	6
951	FGFNPLEFENFSWR	sp|Q61001|LAMA5_MOUSE	yes	yes	896	909	14	R	G	0	1788.826	2	1.65E-02	72.32	NaN	NaN	0
952	FGFPEGSVELYAEKVATR	sp|P62908|RS3_MOUSE	yes	yes	77	94	18	R	G	0	1999.005	3	2.42E-03	68.41	1.34	1.02	7
953	FGGEHVPNSPFQVTALAGDQPTV	sp|Q8BTM8|FLNA_MOUSE	yes	yes	1726	1753	28	R	S	0	2962.494	3	2.85E-12	140.90	NaN	NaN	0
954	FGGGSGFGGGGFGGGSFGGGR	sp|Q3TTY5|K22E_MOUSE	yes	no	132	152	21	R	F	0	1734.750	2;3	3.96E-31	259.77	0.02	0.02	1
955	FGGGSVELLKQMVSKGFLGR	sp|Q8BMS1|ECHA_MOUSE	yes	yes	611	630	20	R	K	0	2109.141	3	5.24E-05	77.22	1.26	0.77	1
956	FGGNPGGFGNQGGFGNSR	sp|Q921F2|TADBP_MOUSE	yes	yes	276	293	18	R	G	0	1725.761	2	8.88E-07	178.00	NaN	NaN	0
957	FGKPQGTVAR	sp|Q6ZWV3|RL10_MOUSE	yes	no	119	128	10	A	V	0	1059.583	2	4.75E-03	87.57	1.04	0.96	5
958	FGNPLLVQDVESYDPVLNPVLNR	sp|Q9JHU4|DYHC1_MOUSE	yes	yes	3627	3649	23	R	E	0	2597.349	2;3	1.48E-12	177.08	NaN	NaN	0
959	FGQDIISPLLSVKELR	sp|Q8BRF7-2|SCFD1_MOUSE	yes	no	48	63	16	R	D	0	1814.030	3	4.85E-03	64.57	0.88	0.77	3
960	FGQGGAGPVGGQGPR	sp|Q8VIJ6|SFPQ_MOUSE	yes	yes	659	673	15	R	G	0	1340.659	2	2.28-05	174.46	NaN	NaN	0
961	FGSGSGGSSGFSQGR	sp|Q8VHD8|HORN_MOUSE	yes	no	795	809	15	R	S	0	1373.596	2	9.24E-18	254.10	NaN	NaN	0
962	FGSMGPVCPPGGIQEVTINQSLLC	sp|P04104|K2C1_MOUSE	yes	yes	148	189	42	R	E	0	4616.373	5	4.83E-04	59.93	0.93	0.64	1
963	FGTLFTMDR	sp|P82198|BGH3_MOUSE	yes	yes	488	496	9	R	M	0	1086.517	2	2.68E-03	166.16	NaN	NaN	0
964	FHPEPYGLEDDQR	sp|P30999-2|CTND1_MOUSE	yes	no	275	287	13	R	S	0	1601.711	3	1.70E-02	73.88	NaN	NaN	0
965	FHQLDIDNPQSIR	sp|P48758|CBR1_MOUSE	yes	yes	59	71	13	R	A	0	1581.790	3	4.83E-02	109.44	NaN	NaN	0
966	FHVNLLCGEEQGADAALHFNPR	sp|O54974|LEG7_MOUSE	yes	yes	33	54	22	R	L	0	2494.181	3;4	7.06E-12	183.09	NaN	NaN	0
967	FIAIKPDGVQR	sp|Q01768|NDKB_MOUSE	yes	no	8	18	11	T	G	0	1242.709	2	1.39E-03	100.93	1.06	0.88	4
968	FIDSDHTDNQR	sp|P09103|PDIA1_MOUSE	yes	yes	292	302	11	I	I	0	1346.585	2	3.48E-10	214.67	NaN	NaN	0
969	FIGYPITLYLEKER	sp|P11499|HS90B_MOUSE	yes	yes	208	221	14	Q	E	0	1740.945	3	2.41E-02	48.47	1.25	1.02	2
970	FIIDAKGVLR	sp|Q61171|PRDX2_MOUSE	yes	yes	130	139	10	L	Q	0	1130.681	2	2.02E-02	67.33	1.26	1.09	2
971	FIIDDKGILR	sp|P35700|PRDX1_MOUSE	yes	yes	131	140	10	L	Q	0	1188.687	2	4.76E-06	157.38	1.21	1.00	5
972	FIIDDKGVLR	sp|O08807|PRDX4_MOUSE	yes	yes	206	215	10	L	Q	0	1174.671	2	2.54E-02	63.62	1.38	1.10	3
973	FIKIDGKVR	sp|P62702|RS4X_MOUSE	yes	yes	69	77	9	R	T	0	1074.655	3	2.68E-02	68.66	1.11	0.96	4
974	FILNLPTFSVR	sp|Q9R1P3|PSB2_MOUSE	yes	yes	171	181	11	R	V	0	1305.745	2	2.18E-03	141.08	NaN	NaN	0
975	FINFFR	sp|Q8BGQ7|SYAC_MOUSE	yes	yes	14	19	6	R	R	0	842.444	2	3.50E-02	154.74	NaN	NaN	0
976	FINWDAINKGHAPSPSTR	sp|Q6P253-4|DMKN_MOUSE	yes	no	387	404	18	R	A	0	2010.007	4	3.67E-05	94.28	2.76	1.61	2
977	FIPLSEPAPVPPIPNEQQLAR	sp|Q8VBV7|CSN8_MOUSE	yes	yes	179	199	21	R	L	0	2312.253	2	1.22-02	58.12	NaN	NaN	0
978	FIYEVSR	sp|P02772|FETA_MOUSE	yes	yes	158	164	7	R	R	0	912.471	2	9.67E-03	126.20	0.11	0.09	1
979	FKASDLDGDLTATR	sp|Q05186|RCN1_MOUSE	yes	yes	169	182	14	R	E	0	1508.747	3	1.68E-02	60.55	1.08	0.92	4
980	FKAWAVAR	sp|P07724|ALBU_MOUSE	yes	no	235	242	8	A	L	0	947.534	2	4.52E-03	127.56	1.22	1.09	4
981	FKEANNFLWPFKLSSPR	sp|P14148|RL7_MOUSE	yes	yes	223	239	17	R	G	0	2080.089	4	2.27E-03	70.41	1.25	1.02	5
982	FKLPGQPPASMGR	sp|Q61598-2|GDIB_MOUSE	yes	no	20	32	13	R	G	0	1384.729	3	1.02E-03	81.57	1.32	1.22	4
983	FKSELR	sp|P27931|IL1R2_MOUSE	yes	no	49	54	6	E	L	0	778.434	2	3.33E-02	88.73	1.23	0.81	4
984	FLASEGAPDFLCPEELEHVSR	sp|Q148V8|FA83H_MOUSE	yes	yes	46	66	21	R	H	0	2402.121	3	8.52E-03	65.42	NaN	NaN	0
985	FLDDAFR	sp|Q9JHU4|DYHC1_MOUSE	yes	no	3612	3618	7	S	K	0	882.424	2	6.14E-02	121.29	NaN	NaN	0
986	FLDKAVELNMISLKGHR	sp|Q99K85|SERC_MOUSE	yes	yes	320	336	17	R	S	0	1970.077	4	7.36E-07	113.47	0.79	0.78	1
987	FLDTAFDLDAFKKFS	sp|Q60597-2|ODO1_MOUSE	yes	no	999	1013	15	R	-	0	1763.877	3	9.21E-04	75.76	1.94	1.38	3
988	FLEEYLSSTPQR	sp|P61804|DAD1_MOUSE	yes	yes	12	23	12	R	L	0	1468.720	2	9.92E-03	89.30	NaN	NaN	0
989	FLEFQFLTGGLVDPEVHGR	sp|E9Q557|DESP_MOUSE	yes	yes	2738	2756	19	R	I	0	2160.100	3	1.51E-06	149.53	NaN	NaN	0
990	FLEGVR	sp|P14869|RLA0_MOUSE	no	no	215	220	6	R	N	0	719.397	2	9.02E-03	154.44	NaN	NaN	0
991	FLEQQNKVLETKWNLLQEQGSR	sp|Q8BGZ7|K2C75_MOUSE	yes	no	170	191	22	R	T	0	2687.403	4	1.34E-11	130.83	1.41	0.93	3
992	FLEQQNQVLQTKWELLQQLDLSN	sp|Q6NXH9|K2C73_MOUSE	no	no	151	175	25	R	R	0	3130.587	3	1.52E-03	56.45	1.37	0.88	1
993	FLEQQNQVLQTKWELLQQVDTT	sp|P04104|K2C1_MOUSE	yes	yes	208	231	24	R	T	0	2945.525	2;3;4	7.38E-55	273.88	1.08	0.74	12
994	FLEQQNQVLR	sp|Q3TTY5|K22E_MOUSE	yes	no	219	228	10	R	T	0	1273.678	2	1.18E-04	179.80	NaN	NaN	0
995	FLHDPSATQGFVGCALSSNIQR	sp|P17563|SBP1_MOUSE	yes	no	255	276	22	R	F	0	2404.159	3	7.61E-08	152.13	NaN	NaN	0
996	FLLSLPEHR	sp|Q99JI4|PSMD6_MOUSE	yes	yes	24	32	9	R	G	0	1110.619	2;3	9.27E-03	145.72	NaN	NaN	0
997	FLLTQAVR	sp|P14685|PSMD3_MOUSE	yes	yes	357	364	8	Y	T	0	946.560	2	3.99E-02	116.90	NaN	NaN	0
998	FLNEQKNLHSEISGKR	sp|E9Q557|DESP_MOUSE	yes	yes	938	953	16	R	D	0	1898.996	4	6.18E-02	36.03	1.61	1.05	2
999	FLNKEPY	sp|P16675|PPGB_MOUSE	yes	no	468	474	7	R	-	0	909.460	2	2.94E-02	85.81	1.41	1.21	2
1000	FLSWILNR	sp|Q8BP47|SYNC_MOUSE	yes	yes	534	541	8	R	Y	0	1047.587	2	3.17E-02	137.18	NaN	NaN	0
1001	FLTTTPNSLLVSWQAPR	sp|P11276|FINC_MOUSE	yes	yes	2001	2017	17	R	A	0	1930.031	2	7.32E-04	103.13	NaN	NaN	0
1002	FLVDFGKEPLGPALAHELR	sp|P17563|SBP1_MOUSE	yes	no	442	460	19	N	Y	0	2108.142	3;4	7.70E-04	73.93	1.59	1.51	4
1003	FLVVAHDDGR	sp|Q61553|FSCN1_MOUSE	yes	yes	91	100	10	R	W	0	1127.572	3	5.07E-02	72.20	NaN	NaN	0
1004	FMAPDIEAAHR	sp|P35492|HUTH_MOUSE	yes	yes	595	605	11	R	L	0	1256.597	3	4.37E-03	126.19	NaN	NaN	0
1005	FMEQVIFKYLR	sp|Q99JY9|ARP3_MOUSE	yes	yes	92	102	11	R	A	0	1472.785	3	1.87E-02	63.07	1.41	0.91	1
1006	FMLQDVLDLR	sp|Q6NZJ6|IF4G1_MOUSE	yes	no	981	990	10	R	Q	0	1248.654	2	2.85E-02	82.42	NaN	NaN	0
1007	FNAHGDANTIVCNTKEDGTWGT	sp|P16045|LEG1_MOUSE	yes	yes	50	74	25	R	E	0	2829.253	4;5	5.19E-07	124.31	0.93	0.81	4
1008	FNGQFKTYGICGAIR	sp|Q9CQR2|RS21_MOUSE	yes	yes	46	60	15	R	R	0	1730.856	3	1.43E-01	32.15	0.87	0.83	1
1009	FNNLSQQVER	sp|Q9R269|PEPL_MOUSE	yes	yes	709	718	10	R	R	0	1233.610	2	7.02E-03	134.57	NaN	NaN	0
1010	FNPVTGEVPPR	sp|Q91X72|HEMO_MOUSE	yes	yes	208	218	11	R	Y	0	1211.630	2	7.35E-02	61.58	NaN	NaN	0
1011	FNQMLNQIPNDYHSSR	sp|Q60847|COCA1_MOUSE	yes	no	2925	2940	16	R	N	0	1962.901	3	8.04E-06	176.04	NaN	NaN	0
1012	FNSANEDNVTQVR	sp|P24270|CATA_MOUSE	yes	yes	432	444	13	R	T	0	1492.691	2	2.26E-03	100.73	NaN	NaN	0
1013	FNVLADTPSGLVPLHLR	sp|P97496-2|SMRC1_MOUSE	yes	no	555	571	17	H	S	0	1848.026	3	7.27E-04	103.39	NaN	NaN	0
1014	FPAMSDAYDR	sp|P23492|PNPH_MOUSE	yes	yes	159	168	10	R	D	0	1171.497	2	2.94E-02	81.02	NaN	NaN	0
1015	FPGQLNADLR	sp|P99024|TBB5_MOUSE	no	no	242	251	10	R	K	0	1129.588	2	3.46E-05	183.78	NaN	NaN	0
1016	FPGYDSESKEFNAEVHR	sp|P47962|RL5_MOUSE	yes	yes	180	196	17	R	K	0	2010.907	3;4	8.83E-07	110.12	1.14	0.94	15
1017	FPLDYYSIPFPTPTTPLTGR	sp|Q80X50-2|UBP2L_MOUSE	yes	no	861	880	20	R	D	0	2282.162	2	1.05E-03	99.09	NaN	NaN	0
1018	FPQLDDTSFANSR	sp|P19096|FAS_MOUSE	yes	yes	1705	1717	13	R	D	0	1496.690	2	1.54E-03	107.35	NaN	NaN	0
1019	FPQPLNMLEHLASKR	sp|Q8BHN3|GANAB_MOUSE	yes	no	446	460	15	R	R	0	1779.945	3;4	5.38E-02	39.63	0.99	0.94	2
1020	FPSHFSSDLKDLLR	sp|P68181-2|KAPCB_MOUSE	yes	no	245	258	14	R	N	0	1660.857	3	9.45E-03	60.20	1.38	0.86	1
1021	FPSIVGR	sp|P63260|ACTG_MOUSE	no	no	31	37	7	V	P	0	774.439	2	6.49E-02	114.19	NaN	NaN	0
1022	FPSIVGRPR	sp|P63260|ACTG_MOUSE	no	no	31	39	9	V	H	1	1027.593	2;3	7.25E-03	149.72	NaN	NaN	0
1023	FPSLHGDCVALPNGDDGECR	sp|O08677-2|KNG1_MOUSE	yes	no	210	229	20	R	G	0	2214.942	3	1.57E-02	56.72	NaN	NaN	0
1024	FQEHCPDLER	sp|Q9R269|PEPL_MOUSE	yes	yes	688	697	10	R	Q	0	1329.577	3	2.22E-02	91.96	NaN	NaN	0
1025	FQELIFEDFAR	sp|Q8R1F1|NIBL1_MOUSE	yes	yes	519	529	11	R	F	0	1413.693	2	3.25E-02	73.44	NaN	NaN	0

1026	FQPGETLTEILETPATNEQEAEHQ	sp|Q9JKF1|IQGA1_MOUSE	yes	yes	1398	1422	25	R	A	0	2867.357	3	2.08E-03	72.30	NaN	NaN	0
1027	FQQAVDAVEEFLR	sp|Q922P9|GLYR1_MOUSE	yes	yes	79	91	13	R	R	0	1550.773	2	3.82E-04	100.22	0.26	0.18	1
1028	FQQQLEQLSAMGFLNR	sp|Q8R317-2|UBQL1_MOUSE	yes	no	512	527	16	R	E	0	1908.952	2	3.01E-03	90.56	NaN	NaN	0
1029	FQSAAIGALQEASEAYLVGLFEDTI	sp|P84244|H33_MOUSE	yes	no	85	117	33	R	V	0	3592.798	4	3.03E-10	144.26	1.99	1.34	1
1030	FQSLGVAFYR	sp|P51150|RAB7A_MOUSE	yes	yes	70	79	10	R	G	0	1186.614	2	1.36E-04	179.51	NaN	NaN	0
1031	FQSLNAEVSKR	sp|Q9D154|ILEUA_MOUSE	yes	yes	70	80	11	R	G	0	1277.673	3	2.79E-03	84.48	1.46	1.26	6
1032	FQSSAVMALQEACEAYLVGLFEDT	sp|P68433|H31_MOUSE	yes	yes	85	117	33	R	V	0	3741.795	4	1.14E-10	151.23	1.74	1.13	2
1033	FQSSHHSTDITSLDQYVER	sp|P08113|ENPL_MOUSE	yes	yes	512	530	19	R	M	0	2249.035	3;4	3.30E-06	142.26	NaN	NaN	0
1034	FSGGGFCGSSGSGFGSKSLMNLG	sp|P04104|K2C1_MOUSE	yes	yes	50	75	26	R	S	0	2467.101	2;3	5.04E-23	198.47	1.75	0.98	17
1035	FSGVVSTGLKVR	sp|P58252|EF2_MOUSE	yes	yes	417	428	12	V	I	0	1248.719	2	9.38E-04	98.11	1.19	1.13	2
1036	FSGWYDADLSPAGHEEAKR	sp|Q9DBJ1|PGAM1_MOUSE	yes	yes	22	40	19	R	G	0	2134.971	3;4	4.19E-05	88.39	1.23	0.96	6
1037	FSHQGVQLIDFSPCER	sp|Q8JZQ9|EIF3B_MOUSE	yes	yes	360	375	16	R	Y	0	1918.900	3	2.58E-02	60.95	NaN	NaN	0
1038	FSNISAAKAVADAIR	sp|P80315|TCPD_MOUSE	yes	yes	35	49	15	R	T	0	1532.831	3	5.05E-03	66.25	1.22	0.87	9
1039	FSSETWQNLGTLQR	sp|Q8VCR7|ABHEB_MOUSE	yes	yes	43	56	14	R	L	0	1665.811	2	3.38E-03	94.09	NaN	NaN	0
1040	FSSGGACGIGGGYGGSFSSSSFGG	sp|Q61781|K1C14_MOUSE	yes	yes	52	84	33	R	F	0	2934.263	2;3	7.19E-16	140.55	NaN	NaN	0
1041	FSSVSVAR	sp|Q8BGZ7|K2C75_MOUSE	yes	no	32	39	8	R	S	0	851.450	2	4.13E-02	141.39	NaN	NaN	0
1042	FSSYSQMENWSR	sp|P97350|PKP1_MOUSE	yes	yes	118	129	12	R	H	0	1520.635	2	2.08E-03	132.99	NaN	NaN	0
1043	FSTPEQAAKNR	sp|Q8R081|HNRPL_MOUSE	yes	yes	482	492	11	R	I	0	1247.626	3	1.15E-02	69.72	1.08	0.68	6
1044	FSWNVWPSSR	sp|Q01405|SC23A_MOUSE	yes	no	19	28	10	R	L	0	1264.599	2	3.06E-02	79.23	NaN	NaN	0
1045	FTDEEVDELYR	sp|Q3THE2|ML12B_MOUSE	yes	yes	134	144	11	R	E	0	1414.625	2	2.07E-06	183.33	NaN	NaN	0
1046	FTDILVR	sp|O35286|DHX15_MOUSE	yes	yes	146	152	7	R	H	0	862.491	2	2.98E-02	163.84	NaN	NaN	0
1047	FTGLQYLR	sp|P51885|LUM_MOUSE	yes	yes	228	235	8	R	L	0	996.539	2	1.32E-02	166.17	NaN	NaN	0
1048	FTPGTFTNQIQAAFR	sp|P14206|RSSA_MOUSE	yes	yes	103	117	15	R	E	0	1697.853	2;3	3.16E-07	182.33	NaN	NaN	0
1049	FTQAGSEVSALLGR	sp|P56480|ATPB_MOUSE	yes	yes	311	324	14	R	I	0	1434.747	2	2.29E-04	154.72	NaN	NaN	0
1050	FTVLFPSGTPLPAR	sp|Q99M31|HSP7E_MOUSE	yes	no	412	425	14	R	R	0	1501.829	2	3.08E-03	95.26	NaN	NaN	0
1051	FVDLEPTVIDEVR	sp|P68373|TBA1C_MOUSE	no	no	67	79	13	V	T	0	1530.793	2	3.59E-02	66.00	NaN	NaN	0
1052	FVDLYGAQKVVDR	sp|Q8BMS1|ECHA_MOUSE	yes	yes	720	732	13	R	L	0	1508.799	3	2.37E-03	75.10	1.26	0.91	9
1053	FVEGGDAGNREDQINR	sp|P14148|RL7_MOUSE	yes	yes	249	264	16	H	L	1	1775.819	3	3.25E-02	56.51	NaN	NaN	0
1054	FVGINASDINYSAGR	sp|Q8BGC4|ZADH2_MOUSE	yes	yes	71	85	15	R	Y	0	1582.774	2	7.07E-02	48.41	NaN	NaN	0
1055	FVIGGPQGDAGLTGR	sp|Q3THS6|METK2_MOUSE	yes	yes	250	264	15	R	K	0	1443.747	2	5.87E-04	127.32	NaN	NaN	0
1056	FVKQDQVCIAR	sp|Q8R050-2|ERF3A_MOUSE	yes	no	582	592	11	R	L	0	1362.708	3	3.09E-03	81.02	2.89	2.29	1
1057	FVLPFPVNYIGECVR	sp|Q8K411-3|PREP_MOUSE	yes	no	817	831	15	H	T	0	1808.928	2	9.35E-02	46.32	NaN	NaN	0
1058	FVSILMESIPLPDR	sp|P23492|PNPH_MOUSE	yes	yes	274	287	14	R	G	0	1615.864	2	1.08E-03	113.76	NaN	NaN	0
1059	FVTGNKILR	sp|P62301|RS13_MOUSE	yes	yes	65	73	9	R	I	0	1046.624	3	4.04E-02	60.83	1.09	0.90	3
1060	FVTVQTISGTGALR	sp|P05202|AATM_MOUSE	yes	yes	126	139	14	R	V	0	1448.799	2	1.01E-03	124.07	NaN	NaN	0
1061	FWDNFLR	sp|Q3UIU2|NDUB6_MOUSE	yes	yes	46	52	7	R	D	0	996.482	2	3.11E-02	83.61	9.57	7.49	2
1062	FYADLAPEAR	sp|Q3TW96|UAP1L_MOUSE	yes	yes	22	31	10	R	A	0	1151.561	2	2.75E-02	83.86	NaN	NaN	0
1063	FYAFGR	sp|P58252|EF2_MOUSE	yes	yes	410	415	6	R	V	0	759.370	2	3.89E-02	149.33	NaN	NaN	0
1064	FYDMKVR	sp|Q9R0P5|DEST_MOUSE	yes	yes	15	21	7	I	K	0	957.474	2	9.44E-03	127.12	1.16	1.00	4
1065	FYEQMNGPVTSGSR	sp|P57776-2|EF1D_MOUSE	yes	no	25	38	14	R	Q	0	1571.704	2	7.58E-04	136.33	NaN	NaN	0
1066	FYQEMLAVDAPR	sp|Q9JHR7|IDE_MOUSE	yes	yes	939	950	12	R	R	0	1438.692	2	1.05E-03	96.06	0.10	0.08	1
1067	GAAGALLVYDITR	sp|P53994|RAB2A_MOUSE	yes	no	78	90	13	R	R	0	1318.725	2	8.05E-03	83.20	NaN	NaN	0
1068	GADFQCFQQAR	sp|P39061-2|COIA1_MOUSE	yes	no	1159	1169	11	R	A	0	1326.578	2	1.87E-02	82.42	NaN	NaN	0
1069	GADQEPLNWFFIER	sp|P55850-2|DSC3_MOUSE	yes	no	177	190	14	R	D	0	1720.821	2	1.10E-03	111.12	NaN	NaN	0
1070	GAEAEGRWRER	sp|Q8R4A3|DACT1_MOUSE	yes	yes	17	27	11	R	G	2	1315.638	2	1.36E-02	93.56	NaN	NaN	0
1071	GAEEQLKSYQSELEALR	sp|Q9R269|PEPL_MOUSE	yes	yes	1202	1218	17	R	N	0	1949.969	3	3.20E-11	155.79	1.92	1.20	1
1072	GAEYGAEALER	sp|P01942|HBA_MOUSE	yes	yes	22	32	11	H	M	0	1164.541	2	5.92E-03	118.90	NaN	NaN	0
1073	GAFGKPQGTVAR	sp|Q6ZWV3|RL10_MOUSE	yes	no	117	128	12	R	V	0	1187.641	3	6.49E-04	103.44	0.94	0.85	8
1074	GAFSNPETLDLYR	sp|Q9D2R0|AACS_MOUSE	yes	yes	652	664	13	R	D	0	1481.715	2	6.74E-04	91.62	1.05	0.82	3
1075	GAGKEAAGKSSGPTSLFAVTVAPF	sp|Q8VEK3|HNRPU_MOUSE	yes	yes	173	199	27	R	Q	0	2483.313	3;4	1.42E-03	55.59	1.20	1.10	10
1076	GAIILAKLSIVPVRR	sp|P25444|RS2_MOUSE	yes	yes	153	167	15	R	G	1	1605.045	3	3.61E-01	47.77	NaN	NaN	0
1077	GAMKGLGTDEDTLIEILTTR	sp|P10107|ANXA1_MOUSE	yes	yes	125	144	20	R	S	0	2133.099	2;3	2.60E-08	114.46	1.19	1.11	13
1078	GAPLAKVVFR	sp|P62918|RL8_MOUSE	yes	yes	55	64	10	R	D	0	1056.644	2	5.73E-09	182.76	1.11	0.84	8
1079	GASIVEDKLVEDLKTR	sp|P26443|DHE3_MOUSE	yes	yes	77	92	16	R	E	0	1771.968	4	4.18E-03	66.39	1.12	1.11	4
1080	GASKEILSEVER	sp|P80318|TCPG_MOUSE	yes	yes	378	389	12	R	N	0	1316.694	3	1.66E-02	59.16	1.25	1.02	8
1081	GATQQILDEAER	sp|P80314|TCPB_MOUSE	yes	yes	377	388	12	R	S	0	1329.653	2	1.26E-04	172.76	NaN	NaN	0
1082	GATTTFSAVER	sp|Q9QZZ6|DERM_MOUSE	yes	yes	170	180	11	R	D	0	1138.562	2	3.40E-03	131.83	NaN	NaN	0
1083	GAVLPIR	sp|Q3THS6|METK2_MOUSE	yes	yes	193	199	7	R	V	0	724.460	2	1.04E-01	78.45	NaN	NaN	0
1084	GCALQCAILSPAFKVR	sp|Q61316|HSP74_MOUSE	no	no	375	390	16	R	E	0	1789.933	3	6.22E-08	133.47	1.11	0.94	5
1085	GCHLLVATPGR	sp|P16381|DDX3L_MOUSE	yes	no	315	325	11	R	L	0	1179.618	3	2.53E-02	75.51	NaN	NaN	0
1086	GCICKGGSDKCSCCP	sp|P47945|MT4_MOUSE	yes	no	48	62	15	R	-	0	1744.646	3	4.64E-02	41.62	1.29	1.24	1
1087	GCILTLVER	sp|Q8R1B4|EIF3C_MOUSE	yes	yes	440	448	9	R	M	0	1059.575	2	3.99E-02	85.68	NaN	NaN	0
1088	GCTFLVGLIQKHR	sp|O08529|CAN2_MOUSE	yes	yes	404	416	13	R	R	0	1527.834	3;4	1.07E-04	121.02	1.75	1.65	2
1089	GDAAKNQLTSNPENTVFDAKR	sp|P20029|GRP78_MOUSE	yes	yes	78	98	21	I	L	0	2275.119	3	6.56E-02	27.92	1.12	1.09	2
1090	GDAAKNQVAMNPTNTVFDAKR	sp|P63017|HSP7C_MOUSE	yes	yes	52	72	21	I	L	0	2247.107	3	1.21E-05	93.50	1.24	1.04	5
1091	GDAKPPAVFTR	sp|P21812|MCPT4_MOUSE	yes	yes	221	231	11	R	I	0	1157.619	2;3	2.08E-04	130.10	1.64	0.93	6
1092	GDEGPPGPEGLR	sp|Q04857|CO6A1_MOUSE	yes	yes	478	489	12	R	G	0	1179.552	2	6.87E-04	151.13	NaN	NaN	0
1093	GDFCIQVGR	sp|Q01768|NDKB_MOUSE	yes	no	106	114	9	R	N	0	1050.492	2	2.08E-02	111.39	NaN	NaN	0
1094	GDGGPPGMTGFPGAAGR	sp|Q01149|CO1A2_MOUSE	yes	yes	784	800	17	R	T	0	1500.678	2	5.16E-03	82.59	NaN	NaN	0
1095	GDGPICLVLAPTR	sp|Q61656|DDX5_MOUSE	no	no	165	177	13	R	E	0	1367.723	2	1.15E-03	135.04	NaN	NaN	0
1096	GDGVVLVAPPLR	sp|P62311|LSM3_MOUSE	yes	yes	89	100	12	R	V	0	1191.698	2	9.28E-03	90.91	NaN	NaN	0
1097	GDIKNFLYAWCGKR	sp|O70133|DHX9_MOUSE	yes	no	2	15	14	M	K	0	1726.861	3	9.95E-03	59.23	1.16	0.90	7
1098	GDINILLIGDPSVAKSQLLR	sp|P25206|MCM3_MOUSE	yes	yes	337	356	20	R	Y	0	2121.216	3	3.11E-03	59.98	1.45	1.36	1
1099	GDLGIEIPAEKVFLAQKMMIGR	sp|P52480|KPYM_MOUSE	no	no	295	316	22	R	C	0	2415.302	4	6.96E-02	25.26	1.21	1.17	1
1100	GDLPFVVTR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	1924	1932	9	R	R	0	1002.550	2	2.76E-02	97.57	NaN	NaN	0
1101	GDLPLNINIQEPR	sp|Q91V61-2|SFXN3_MOUSE	yes	no	2	14	13	M	W	0	1477.789	2	2.65E-02	69.92	NaN	NaN	0
1102	GDLQSQAMVR	sp|Q80X19-2|COEA1_MOUSE	yes	no	1609	1618	10	R	A	0	1103.539	2	1.73E-02	99.57	NaN	NaN	0
1103	GDLTPLDSLIDFKR	sp|Q9EST1|GSDMA_MOUSE	yes	no	19	32	14	R	F	0	1588.846	3	5.45E-04	85.84	1.32	1.22	4
1104	GDNPFPKNADGTVR	sp|Q9JII6|AK1A1_MOUSE	yes	yes	121	134	14	R	Y	0	1486.717	3	3.59E-04	94.09	1.21	1.05	4
1105	GDREQLLQR	sp|P68510|1433F_MOUSE	yes	yes	2	10	9	M	A	1	1113.589	2	3.15E-03	163.38	NaN	NaN	0
1106	GDVVPKDVNAAIAAIKTKR	sp|P68368|TBA4A_MOUSE	yes	yes	321	339	19	R	S	0	1965.137	5	9.12E-03	72.36	NaN	NaN	0
1107	GDVVPKDVNAAIATIKTKR	sp|P68373|TBA1C_MOUSE	no	no	321	339	19	R	S	0	1995.148	4;5	6.19E-06	130.56	1.17	1.11	10
1108	GEAGAAGPSGPAGPR	sp|Q01149|CO1A2_MOUSE	yes	yes	700	714	15	R	G	0	1250.600	2	2.12E-05	174.95	NaN	NaN	0
1109	GEAGIPAEFSIWTR	sp|Q80X90|FLNB_MOUSE	yes	yes	2206	2219	14	R	E	0	1532.762	2	7.79E-03	76.76	NaN	NaN	0
1110	GEAHLAVNDFDLAR	sp|P30416|FKBP4_MOUSE	yes	yes	360	373	14	R	A	0	1526.748	3	1.15E-03	104.41	NaN	NaN	0
1111	GEATDLLR	sp|O54724|PTRF_MOUSE	yes	yes	358	365	8	R	G	0	873.456	2	1.47E-02	84.50	NaN	NaN	0
1112	GECQSEGVLFFQGNR	sp|Q91X72|HEMO_MOUSE	yes	yes	151	165	15	R	K	0	1726.773	2	4.09E-04	137.80	NaN	NaN	0
1113	GEEPGKSCGYSVR	sp|O70133|DHX9_MOUSE	yes	no	464	476	13	R	F	0	1424.635	3	4.08E-02	45.28	1.54	1.37	3
1114	GEEPGQDQDPVQLLSGFPR	sp|Q922Y1|UBXN1_MOUSE	yes	yes	248	266	19	R	R	0	2067.986	2	8.65E-03	73.14	NaN	NaN	0
1115	GEEQSAIPYFPFIPDQPFR	sp|Q8VED9|LEGL_MOUSE	yes	yes	107	125	19	R	V	0	2237.079	2	5.88E-03	79.49	NaN	NaN	0
1116	GEFCIAKFVDGEWYR	sp|Q78PY7|SND1_MOUSE	yes	yes	733	747	15	R	A	0	1875.861	3	2.46E-04	85.49	1.39	1.11	4
1117	GEFFNELVGGQR	sp|P09055|ITB1_MOUSE	yes	yes	229	240	12	R	I	0	1422.689	2	9.72E-03	89.81	NaN	NaN	0
1118	GEGGILINSQGER	sp|Q8K2B3|DHSA_MOUSE	yes	yes	313	325	13	R	F	0	1328.668	2	1.04E-03	138.02	NaN	NaN	0
1119	GEIAGPPDTPYEGGR	sp|P61087|UBE2K_MOUSE	yes	yes	41	55	15	R	Y	0	1514.700	2	5.73E-04	129.01	NaN	NaN	0
1120	GEIIAKQGGGGAGGSVPGIER	sp|Q9D0E1-2|HNRPM_MOUSE	yes	no	343	363	21	R	M	0	1909.002	3	1.00E-05	95.20	1.34	0.86	9
1121	GELADCCTKQEPER	sp|P07724|ALBU_MOUSE	yes	yes	109	122	14	Y	N	0	1691.724	2	1.44E-05	129.38	1.12	0.98	4
1122	GELALKDAR	sp|Q8BGZ7|K2C75_MOUSE	no	no	403	411	9	R	A	0	971.540	2;3	3.05E-03	105.98	1.65	1.08	4
1123	GENHCGIESEIVAGIPR	sp|P10605|CATB_MOUSE	yes	yes	315	331	17	R	T	0	1836.879	3	6.39E-04	107.73	NaN	NaN	0
1124	GEPGPAGSVGPVGAVGPR	sp|Q01149|CO1A2_MOUSE	yes	yes	985	1002	18	R	G	0	1559.806	2	1.75E-03	98.82	NaN	NaN	0
1125	GETGPAGPAGPIGPAGAR	sp|P11087|CO1A1_MOUSE	yes	no	1056	1073	18	R	G	0	1531.774	2	6.97E-06	156.00	NaN	NaN	0
1126	GETNPADSKPGTIR	sp|Q01768|NDKB_MOUSE	yes	no	92	105	14	L	G	0	1441.716	2	2.11E-08	159.22	1.11	0.96	4
1127	GEVASDAKSFVLNLGKDSNNLCLH	sp|P16045|LEG1_MOUSE	yes	yes	22	49	28	R	F	0	3101.535	5	5.21E-02	31.77	0.86	0.83	3
1128	GEYAGEVLR	sp|Q9D8C2|TSN13_MOUSE	yes	yes	159	167	9	I	F	0	992.493	2	2.07E-02	111.74	NaN	NaN	0

1129	GFAFVR	sp|Q62093|SRSF2_MOUSE	yes	yes	56	61	6	R	F	0	695.375	2	5.79E-02	123.07	NaN	NaN	0
1130	GFAFVTFESPADAKDAAR	sp|Q9WV02-2|RBMX_MOUSE	yes	no	50	67	18	R	D	0	1898.916	3	5.12E-03	58.25	1.45	0.95	7
1131	GFCFITYTDEEPVKKLLESR	sp|Q9Z130|HNRDL_MOUSE	yes	yes	156	175	20	R	Y	0	2431.209	4	2.97E-03	60.76	1.49	1.23	2
1132	GFFICDQPYEPVSPYSCR	sp|Q8CGC7|SYEP_MOUSE	yes	yes	676	693	18	R	E	0	2220.961	2	2.31E-02	55.44	NaN	NaN	0
1133	GFGFITFTNPEHASDAMR	sp|O89086|RBM3_MOUSE	yes	yes	48	65	18	R	A	0	1996.910	2;3	3.99E-05	141.13	NaN	NaN	0
1134	GFGFVEFEDPR	sp|O35326|SRSF5_MOUSE	yes	yes	38	48	11	R	D	0	1298.593	2	8.45E-03	107.06	NaN	NaN	0
1135	GFGGGQGFGGSGGFGGGSGFGG	sp|Q3TTY5|K22E_MOUSE	yes	no	101	131	31	R	F	0	2567.096	2;3	6.10E-28	222.47	NaN	NaN	0
1136	GFGHIGIAVPDVYSACKR	sp|Q9CPU0|LGUL_MOUSE	yes	yes	124	141	18	R	F	0	1945.983	4	6.19E-03	54.24	1.58	1.21	5
1137	GFGNLGYGYGCGCGFGGYGYGSC	sp|O08632|KR195_MOUSE	yes	yes	17	42	26	R	Y	0	2659.065	2;3	1.82E-12	158.94	NaN	NaN	0
1138	GFLDVVTR	sp|Q3TW96|UAP1L_MOUSE	yes	no	339	346	8	R	E	0	905.497	2	2.54E-02	93.43	NaN	NaN	0
1139	GFLLWYSGR	sp|Q61398|PCOC1_MOUSE	yes	yes	140	148	9	R	A	0	1097.566	2	1.47E-01	56.92	NaN	NaN	0
1140	GFNKETAAACGEK	sp|Q62348|TSN_MOUSE	yes	no	216	228	13	R	-	0	1381.630	3	7.87E-04	94.09	1.15	1.01	3
1141	GFPGYMYTDLATIYER	sp|P62814|VATB2_MOUSE	yes	yes	322	337	16	R	A	0	1895.876	2	3.28E-02	55.55	NaN	NaN	0
1142	GFQEVVTPNIFNSR	sp|Q9D0R2|SYTC_MOUSE	yes	yes	367	380	14	R	L	0	1606.810	2	2.97E-02	58.82	2.74	2.03	2
1143	GFQFVSSSLPDICYR	sp|P53996-2|CNBP_MOUSE	yes	no	35	49	15	R	C	0	1774.835	2	7.52E-04	106.42	NaN	NaN	0
1144	GFSGCSAVLSGGSSSSYR	sp|Q9R0H5|K2C71_MOUSE	no	no	15	32	18	R	A	0	1764.774	2	8.38E-09	192.85	NaN	NaN	0
1145	GFSLEELR	sp|P47963|RL13_MOUSE	yes	yes	75	82	8	R	V	0	949.487	2	3.74E-02	125.81	NaN	NaN	0
1146	GFSSGSAVVSGGSR	sp|Q3TTY5|K22E_MOUSE	no	no	23	36	14	R	R	0	1253.600	2	4.31E-04	147.70	NaN	NaN	0
1147	GFSTASATTPTAGR	sp|Q8BGZ7|K2C75_MOUSE	yes	no	16	29	14	R	S	0	1323.642	2	3.99E-05	135.81	NaN	NaN	0
1148	GFTATCGGFLITR	sp|P21812|MCPT4_MOUSE	yes	yes	45	57	13	R	Q	0	1399.692	2	6.02E-04	148.96	NaN	NaN	0
1149	GFTIPEAFR	sp|Q9Z1Q5|CLIC1_MOUSE	yes	yes	196	204	9	R	G	0	1036.534	2	1.20E-02	140.35	NaN	NaN	0
1150	GGAEGELQALR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1372	1382	11	R	A	0	1099.562	2	8.18E-03	108.31	NaN	NaN	0
1151	GGAEQFMEETER	sp|P80313|TCPH_MOUSE	yes	yes	376	387	12	R	S	0	1382.577	2	3.84E-05	178.71	NaN	NaN	0
1152	GGAGVGSMTKIYGGR	sp|Q9CZX8|RS19_MOUSE	yes	yes	68	82	15	R	Q	0	1409.709	3	9.21E-04	75.76	1.16	1.01	4
1153	GGANVIVTER	sp|Q61495|DSG1A_MOUSE	yes	yes	907	916	10	R	V	0	1014.546	2	9.34E-03	125.70	NaN	NaN	0
1154	GGDLMAYDR	sp|P61979-3|HNRPK_MOUSE	yes	no	293	301	9	R	R	0	996.433	2	4.67E-02	79.15	NaN	NaN	0
1155	GGDPTKEPEPVVHYDI	sp|Q9D6J5|NDUB8_MOUSE	yes	no	171	186	16	R	-	0	1751.837	3	6.35E-06	102.65	1.62	1.10	2
1156	GGGGFGGGPGPGGLQSGQTIALF	sp|O35295|PURB_MOUSE	yes	yes	165	195	31	R	D	0	2852.457	2	3.37E-05	76.84	NaN	NaN	0
1157	GGGGGGGGGGPGGFQPAPR	sp|O35295|PURB_MOUSE	yes	yes	11	28	18	R	G	0	1438.670	2	3.72E-03	90.85	NaN	NaN	0
1158	GGGGNFGPGPGSNFR	sp|O88569|ROA2_MOUSE	yes	no	214	228	15	R	G	0	1376.622	2	1.20E-04	153.32	NaN	NaN	0
1159	GGGQIIPTAR	sp|P58252|EF2_MOUSE	yes	no	717	726	10	R	R	0	968.540	2	1.72E-04	145.25	0.06	0.05	2
1160	GGGTGSGMGTLLISKIR	sp|P99024|TBB5_MOUSE	no	no	140	156	17	L	E	0	1603.872	2	3.06E-16	188.47	1.24	1.10	8
1161	GGGVGGFLPAMKQIGNVAALPGI	sp|Q99LF4|RTCB_MOUSE	yes	yes	56	81	26	R	S	0	2515.385	4	9.34E-05	95.20	1.22	1.14	2
1162	GGIKEDTEEHHLR	sp|O88569|ROA2_MOUSE	no	no	110	122	13	V	D	0	1519.738	3	1.19E-02	59.23	1.34	1.05	7
1163	GGIVDEGALLR	sp|Q61753|SERA_MOUSE	yes	yes	237	247	11	R	A	0	1098.603	2	1.02E-02	100.88	NaN	NaN	0
1164	GGLGKLAAEGLAHR	sp|Q8CF02|FM25C_MOUSE	yes	yes	3	16	14	L	T	0	1348.758	2	9.27E-03	60.55	1.29	1.11	2
1165	GGNFGFGDSR	sp|O88569|ROA2_MOUSE	yes	no	204	213	10	R	G	0	1012.436	2	9.34E-03	125.70	NaN	NaN	0
1166	GGPEAGKSEQSGAK	sp|P14602|HSPB1_MOUSE	yes	no	196	209	14	I	-	0	1301.621	2	1.27E-04	108.14	0.91	0.75	2
1167	GGPLSGPYR	sp|P16015|CAH3_MOUSE	yes	yes	81	89	9	R	L	0	902.461	2	1.96E-02	118.50	NaN	NaN	0
1168	GGPNIITLADIVKDPVSR	sp|Q60737|CSK21_MOUSE	yes	yes	90	107	18	R	T	0	1864.042	3	1.73E-05	99.04	1.08	1.02	4
1169	GGPNYQEGLR	sp|Q91V92|ACLY_MOUSE	yes	yes	380	389	10	R	V	0	1089.520	2	4.34E-03	144.65	NaN	NaN	0
1170	GGPPFAFVEFEDPR	sp|Q6PDM2-3|SRSF1_MOUSE	yes	no	52	65	14	R	D	0	1563.736	2	5.75E-03	84.75	NaN	NaN	0
1171	GGQQGSFSGQTSGR	sp|Q8VHD8|HORN_MOUSE	yes	no	647	660	14	R	S	0	1352.607	2	6.44E-05	173.59	NaN	NaN	0
1172	GGSGGGGGSSGGSYGGSSGGGR	sp|P04104|K2C1_MOUSE	yes	yes	586	607	22	R	G	0	1657.668	2	6.17E-09	168.81	NaN	NaN	0
1173	GGSGGSGGSGGGNKPECNNPGN	sp|Q6P253-4|DMKN_MOUSE	yes	no	311	335	25	R	M	0	2286.963	3	9.69E-24	205.43	1.08	0.83	7
1174	GGSSSGGAGSSSEKGGSGSGEGC	sp|Q3TTY5|K22E_MOUSE	yes	no	676	707	32	R	-	0	2840.190	3	4.61E-44	255.90	2.96	1.50	5
1175	GGSSSGGGGVKSSGSSTVKFVSTS	sp|P04104|K2C1_MOUSE	yes	yes	608	634	27	R	G	0	2509.205	4	1.73E-02	45.10	1.29	0.78	2
1176	GGSVQVLEDQELTCQPEPLVVKG	sp|P17563|SBP1_MOUSE	yes	no	358	382	25	R	I	0	2765.438	4	1.34E-15	164.27	0.98	0.96	4
1177	GGTGSVSGAGLEPVAR	sp|Q9QY23|PKP3_MOUSE	yes	no	262	277	16	R	A	0	1413.721	2	3.86E-04	126.77	NaN	NaN	0
1178	GGVIAGSPAPPELIR	sp|Q8VCW8|ACSF2_MOUSE	yes	yes	379	393	15	R	A	0	1432.804	2	5.97E-04	126.09	NaN	NaN	0
1179	GGVSEASR	sp|P35175|CYT1_MOUSE	yes	yes	4	11	8	L	A	0	761.367	1	3.88E-02	120.65	NaN	NaN	0
1180	GGVTCGGLTYGTTPGR	sp|Q6IMF0|KRT83_MOUSE	no	no	438	453	16	R	Q	0	1552.730	2	1.58E-05	171.08	NaN	NaN	0
1181	GGVVCGDLCVSGTAPAVNTR	sp|P97861|KRT86_MOUSE	yes	yes	433	452	20	R	V	0	1988.941	2	1.90E-06	144.33	NaN	NaN	0
1182	GGYFDEFGIIR	sp|Q00612|G6PD1_MOUSE	yes	no	247	257	11	R	D	0	1272.614	2	3.97E-03	128.03	NaN	NaN	0
1183	GGYIGSTYFER	sp|P61082|UBC12_MOUSE	yes	yes	170	180	11	R	C	0	1248.578	2	5.45E-02	67.08	NaN	NaN	0
1184	GHEVPVWDILTSNYVSR	sp|Q8R0W0|EPIPL_MOUSE	yes	yes	2531	2547	17	R	D	0	1970.985	3	4.70E-04	116.06	NaN	NaN	0
1185	GHPSAGAEEEGGSDGSAAEAEPR	sp|Q8JZQ9|EIF3B_MOUSE	yes	yes	108	130	23	R	A	0	2166.905	3	1.85E-15	183.09	NaN	NaN	0
1186	GHVVPVWDILTSNYVSR	sp|Q8R0W0|EPIPL_MOUSE	yes	yes	6136	6152	17	R	D	0	1941.011	3	1.43E-04	138.19	NaN	NaN	0
1187	GHYTIGKEIIDLVLDR	sp|P68373|TBA1C_MOUSE	no	no	106	121	16	R	I	0	1841.005	3	1.55E-08	149.97	0.80	0.64	3
1188	GHYTIGKEIIDPVLDR	sp|P68368|TBA4A_MOUSE	yes	yes	106	121	16	R	I	0	1824.973	3	5.37E-11	156.67	1.32	1.24	3
1189	GIAGLGDVAEVR	sp|Q8CI94|PYGB_MOUSE	yes	yes	18	29	12	R	K	0	1155.625	2	1.52E-03	140.24	NaN	NaN	0
1190	GIDIHGVPYVINVTLPDEKQNYVH	sp|Q91VR5|DDX1_MOUSE	yes	yes	578	602	25	R	I	0	2875.498	5	1.13E-02	47.37	1.46	1.37	1
1191	GIEIPEVR	sp|O08749|DLDH_MOUSE	yes	yes	110	117	8	R	L	0	911.508	2	5.53E-02	93.37	NaN	NaN	0
1192	GIFEPFGR	sp|Q8VH51-3|RBM39_MOUSE	yes	no	111	118	8	R	I	0	921.471	2	3.77E-02	124.83	NaN	NaN	0
1193	GIFPVLCKDAVLNAWAEDVDLR	sp|P52480|KPYM_MOUSE	no	no	468	489	22	R	V	0	2500.278	2;3	1.90E-16	162.81	1.09	0.98	9
1194	GIHVEIPGAQAESLGPLQVAR	sp|Q9DCW4|ETFB_MOUSE	yes	yes	86	106	21	R	V	0	2141.159	2;3	1.28E-04	116.39	NaN	NaN	0
1195	GIKLVVADTR	sp|Q02053|UBA1_MOUSE	yes	yes	183	192	10	R	G	0	1070.645	2	5.88E-02	61.34	1.14	1.06	1
1196	GILDGNSAPVFPQPFGVKER	sp|P54923|ADPRH_MOUSE	yes	yes	240	259	20	R	D	0	2127.111	3	3.10E-03	60.06	1.42	1.14	2
1197	GILLYGPPGTGKTLIAR	sp|Q01853|TERA_MOUSE	yes	yes	240	256	17	R	A	0	1726.014	2;3	1.87E-05	100.23	1.13	1.00	11
1198	GIMNSFVNDIFER	sp|Q9D2U9|H2B3A_MOUSE	yes	no	61	73	13	M	I	0	1540.734	2	3.37E-04	156.81	NaN	NaN	0
1199	GIPKVIVVITDGR	sp|Q80X19-2|COEA1_MOUSE	yes	no	1134	1146	13	R	S	0	1365.834	3	1.14E-03	77.89	2.00	1.23	1
1200	GIVDSITGQR	sp|E9Q557|DESP_MOUSE	yes	yes	2652	2661	10	R	L	0	1044.556	2	9.27E-03	125.97	NaN	NaN	0
1201	GIVEESVTGVHR	sp|Q80SW1|SAHH2_MOUSE	yes	yes	250	261	12	R	L	0	1281.668	3	4.48E-03	103.91	NaN	NaN	0
1202	GIVKQAGLDR	sp|Q9Z2X1|HNRPF_MOUSE	yes	no	221	230	10	I	M	0	1055.609	2	4.75E-03	87.57	1.38	1.02	7
1203	GIYAYGFEKPSAIQQR	sp|P60843|IF4A1_MOUSE	no	no	46	61	16	R	A	0	1826.932	2;3	1.29E-06	112.96	1.41	1.16	13
1204	GKFLEMCDDLLAR	sp|Q61316|HSP74_MOUSE	yes	yes	304	316	13	R	V	0	1566.753	3	6.06E-03	68.97	0.82	0.76	4
1205	GKGLLNAIVIR	sp|P29758|OAT_MOUSE	yes	yes	373	383	11	R	E	0	1152.734	3	1.51E-03	99.57	0.93	0.89	5
1206	GKIGGHGAEYGAEALER	sp|P01942|HBA_MOUSE	yes	yes	16	32	17	W	M	0	1713.843	3	1.41E-04	79.49	1.56	1.34	4
1207	GKLDGNQDLIR	sp|P54071|IDHP_MOUSE	yes	yes	383	393	11	R	F	0	1227.657	3	1.17E-03	103.91	1.04	0.97	5
1208	GKLTDLEEALQQCR	sp|Q3TTY5|K22E_MOUSE	yes	no	461	474	14	R	E	0	1659.825	2;3	3.86E-13	196.95	2.48	1.31	7
1209	GKVEIIANDQGNR	sp|P63017|HSP7C_MOUSE	no	no	24	36	13	H	T	0	1412.737	2;3	2.20E-04	109.44	1.24	0.97	14
1210	GLAPEQPVTLR	sp|Q32Q92-2|ACOT6_MOUSE	yes	no	25	35	11	R	S	0	1179.661	2	5.68E-03	120.06	NaN	NaN	0
1211	GLATFCLDKDALR	sp|Q80UU9|PGRC2_MOUSE	yes	yes	148	160	13	R	D	0	1478.755	3	4.73E-03	71.18	1.35	0.88	4
1212	GLAVFISDIR	sp|P17426-2|AP2A1_MOUSE	yes	no	12	21	10	R	N	0	1089.618	2	1.39E-02	107.79	NaN	NaN	0
1213	GLCAIAQAESLR	sp|P62908|RS3_MOUSE	yes	yes	95	106	12	R	Y	0	1287.661	2	4.71E-04	153.95	NaN	NaN	0
1214	GLCSGPGAGEESPAATLPR	sp|Q80UU9|PGRC2_MOUSE	yes	yes	73	91	19	R	M	0	1825.863	2	5.69E-03	80.32	NaN	NaN	0
1215	GLDGFQGPSGPR	sp|P08122|CO4A2_MOUSE	yes	yes	321	332	12	R	G	0	1186.573	2	2.78E-03	124.21	NaN	NaN	0
1216	GLDGKVICGSR	sp|Q8BL97-3|SRSF7_MOUSE	yes	no	66	76	11	R	V	0	1160.597	3	1.11E-02	70.09	1.75	1.23	3
1217	GLDISNVKHVINFDLPSDIEEYVHR	sp|P16381|DDX3L_MOUSE	yes	no	503	527	25	R	I	0	2908.472	4	9.91E-05	95.93	1.61	0.99	1
1218	GLDPVEILQER	sp|Q6DIC0|SMCA2_MOUSE	yes	no	341	351	11	Q	E	0	1267.677	2	8.44E-03	107.09	NaN	NaN	0
1219	GLENNVNVELLNALHSHMVNKR	sp|Q62009-5|POSTN_MOUSE	yes	no	154	175	22	R	M	0	2500.297	4;5	1.01E-05	83.40	1.59	0.97	2
1220	GLEVTAYSPLGSSDR	sp|Q9JII6|AK1A1_MOUSE	yes	yes	204	218	15	R	A	0	1550.758	2	5.19E-04	131.86	NaN	NaN	0
1221	GLFIIDAKGVLR	sp|Q61171|PRDX2_MOUSE	yes	yes	128	139	12	R	Q	0	1300.787	2;3	1.55E-03	87.18	1.25	1.10	10
1222	GLFIIDDKGILR	sp|P35700|PRDX1_MOUSE	yes	yes	129	140	12	R	Q	0	1358.792	2;3	2.19E-11	189.24	1.23	0.97	12
1223	GLFIIDDKGVLR	sp|O08807|PRDX4_MOUSE	yes	yes	204	215	12	R	Q	0	1344.777	2;3	6.61E-04	103.08	1.06	0.95	11
1224	GLFTGLTPR	sp|Q791V5|MTCH2_MOUSE	yes	yes	69	77	9	R	L	0	960.539	2	1.79E-02	128.12	NaN	NaN	0
1225	GLGCGYGYGCGYGSR	sp|Q925H3|KRA65_MOUSE	yes	no	43	57	15	R	S	0	1582.629	2	6.87E-04	114.64	NaN	NaN	0
1226	GLGGPDAISWISR	sp|Q99LN9-2|DOHH_MOUSE	yes	no	33	45	13	R	G	0	1327.688	2	2.85E-03	98.94	NaN	NaN	0
1227	GLGISVLEMSHR	sp|Q99K85|SERC_MOUSE	yes	yes	34	45	12	R	S	0	1297.681	2;3	7.50E-03	95.42	6.14	5.76	1
1228	GLGLDDALEPR	sp|Q9WTM5|RUVB2_MOUSE	yes	yes	30	40	11	R	Q	0	1154.593	2	6.43E-03	116.55	NaN	NaN	0
1229	GLGLSPDLVVCR	sp|P70698|PYRG1_MOUSE	yes	yes	206	217	12	R	C	0	1284.686	2	9.34E-04	147.91	NaN	NaN	0
1230	GLGMTLSYLFR	sp|Q8K3J1|NDUS8_MOUSE	yes	yes	69	79	11	R	E	0	1256.659	2	7.74E-03	110.39	NaN	NaN	0
1231	GLGTDEKTLINILTER	sp|O35639|ANXA3_MOUSE	yes	yes	33	48	16	R	S	0	1771.968	3	7.12E-08	130.29	0.78	0.73	1

1232	GLHQDFPSVVVVGLGKR	sp|Q9CPY7-2|AMPL_MOUSE	yes	no	57	73	17	Y	S	0	1807.011	3;4	9.78E-05	86.78	1.16	1.05	9
1233	GLIPVFALGR	sp|Q9QXK7|CPSF3_MOUSE	yes	yes	236	245	10	R	A	0	1041.634	2	1.99E-02	95.50	NaN	NaN	0
1234	GLIVYQLENQPSEFR	sp|Q8C570|RAE1L_MOUSE	yes	yes	191	205	15	R	R	0	1791.916	2	2.22E-02	66.25	NaN	NaN	0
1235	GLKAPGIIPR	sp|Q03265|ATPA_MOUSE	yes	yes	173	182	10	V	I	0	1020.644	2	4.31E-03	90.15	1.07	0.84	7
1236	GLKMAVTFIGNSTAIQELFKR	sp|P99024|TBB5_MOUSE	yes	yes	360	380	21	R	I	0	2323.272	4	2.50E-03	66.89	1.30	1.26	3
1237	GLKMSSTFIGNSTAIQELFKR	sp|Q9ERD7|TBB3_MOUSE	yes	yes	360	380	21	R	I	0	2327.231	4	1.98-05	87.35	1.13	1.10	2
1238	GLKTVFDEAIR	sp|Q05144|RAC2_MOUSE	yes	no	164	174	11	R	A	0	1247.687	2;3	1.63E-03	100.38	1.69	1.34	4
1239	GLLADNLIR	sp|P31428|DPEP1_MOUSE	yes	yes	340	348	9	R	V	0	983.576	2	1.96E-02	118.32	NaN	NaN	0
1240	GLLESEDCKLPCNPCATTNACDKP	sp|Q8K0Y2|KT33A_MOUSE	yes	yes	358	395	38	R	C	1	4352.989	5	1.49E-03	73.37	2.03	1.22	6
1241	GLLESEDCKLPCNPCATTNACDKP	sp|Q61897|KT33B_MOUSE	yes	no	358	393	36	R	S	0	4103.830	4	7.39E-07	126.68	1.83	1.21	5
1242	GLLESEDSKLPCNPCSTPSCQPCAI	sp|Q62168|K1H2_MOUSE	yes	no	357	387	31	R	T	0	3386.500	3	3.86E-06	120.93	1.30	0.80	1
1243	GLLGGVVHTVQNTLR	sp|Q8CGN5-2|PLIN1_MOUSE	yes	no	332	346	15	R	N	0	1562.889	3	6.64E-03	76.01	NaN	NaN	0
1244	GLLGTLNNNPR	sp|Q9DBX3-3|SUSD2_MOUSE	yes	no	189	199	11	R	D	0	1167.636	2	9.06E-03	104.22	NaN	NaN	0
1245	GLLSSLDHTSIR	sp|Q9D0M3-2|CY1_MOUSE	yes	no	41	52	12	R	R	0	1297.699	2;3	6.41E-06	182.35	NaN	NaN	0
1246	GLNISAVR	sp|Q8BGD9|IF4B_MOUSE	yes	yes	118	125	8	R	L	0	828.482	2	7.02E-02	81.22	NaN	NaN	0
1247	GLPLVDDGGWNTVPISKGSR	sp|Q6NZJ6|IF4G1_MOUSE	yes	yes	1047	1066	20	R	P	0	2067.075	3	2.62E-02	43.21	1.38	0.97	4
1248	GLPWQSSDQDIAR	sp|Q3US41-4|ESRP1_MOUSE	yes	no	231	243	13	R	F	0	1471.706	2	3.36E-02	66.99	NaN	NaN	0
1249	GLPWSCSADEVQR	sp|O35737|HNRH1_MOUSE	yes	yes	17	29	13	R	F	0	1503.678	2	1.23E-05	154.36	0.02	0.02	1
1250	GLPWSCSAEEVMR	sp|P70333|HNRH2_MOUSE	yes	yes	17	29	13	R	F	0	1520.675	2	8.05E-03	83.20	NaN	NaN	0
1251	GLPYKATENDIYNFFSPLNPVR	sp|Q9Z2X1|HNRPF_MOUSE	yes	no	295	316	22	R	V	0	2554.286	2;3	1.22E-04	76.02	1.23	0.96	8
1252	GLQDVLR	sp|P80317|TCPZ_MOUSE	yes	no	29	35	7	R	T	0	799.455	2	4.27E-02	119.57	NaN	NaN	0
1253	GLQGSFEELCR	sp|P41216|ACSL1_MOUSE	yes	yes	617	627	11	R	N	0	1294.598	2	1.09E-02	99.34	NaN	NaN	0
1254	GLSLGSAVNSPVLFSPAGR	sp|Q8R0G9|NU133_MOUSE	yes	yes	35	53	19	R	R	0	1827.984	2	2.05E-02	53.45	NaN	NaN	0
1255	GLSVLLFNDGTQGR	sp|Q9CYR6|AGM1_MOUSE	yes	yes	231	244	14	R	L	0	1475.773	2	4.91E-03	88.08	NaN	NaN	0
1256	GLVGEIIKR	sp|Q01768|NDKB_MOUSE	yes	no	19	27	9	R	F	0	983.613	2;3	3.93E-06	174.41	1.17	0.98	10
1257	GLVSSDELAKDVTGAEALLER	sp|P16546-2|SPTN1_MOUSE	yes	no	1340	1360	21	R	H	0	2172.127	3	2.92E-08	108.71	1.11	0.83	2
1258	GLVVPVIR	sp|Q9D2G2-2|ODO2_MOUSE	yes	no	74	81	8	R	N	0	851.559	2	3.91E-02	119.57	NaN	NaN	0
1259	GMAFLHTLEPLIPR	sp|O55222|ILK_MOUSE	yes	yes	304	317	14	R	H	0	1593.870	3	4.62E-03	89.23	NaN	NaN	0
1260	GMGTALKLLLGAGAVAYGVR	sp|O35129|PHB2_MOUSE	yes	yes	18	37	20	R	E	0	1917.087	3	4.28E-08	104.88	1.53	1.03	1
1261	GMKGLVYETSVLDPDEGIR	sp|Q9CZU6|CISY_MOUSE	yes	yes	74	92	19	R	F	0	2078.035	3	2.90E-03	64.26	1.79	1.07	5
1262	GMVFGIPDGVLELVPQR	sp|Q05793|PGBM_MOUSE	yes	yes	486	502	17	R	G	0	1825.976	2	2.68E-02	56.51	NaN	NaN	0
1263	GNDLLLKLLQFR	sp|Q9Z1Q2|ABHGA_MOUSE	yes	yes	446	457	12	R	Y	0	1428.845	3	4.28E-02	67.08	NaN	NaN	0
1264	GNDVAFHFNPR	sp|P16110|LEG3_MOUSE	yes	yes	166	176	11	R	F	0	1272.600	2;3	6.13E-03	117.94	NaN	NaN	0
1265	GNFGGSFAGSFGGAGGHAPGVAI	sp|Q9D0E1-2|HNRPM_MOUSE	yes	no	588	610	23	R	K	0	2033.946	3	1.56E-05	108.08	NaN	NaN	0
1266	GNGLIKVNGRPLEMIEPR	sp|P14131|RS16_MOUSE	yes	yes	28	45	18	R	T	1	1992.094	4	9.36E-05	80.32	1.07	0.72	3
1267	GNLANVIR	sp|P51881|ADT2_MOUSE	no	no	73	80	8	R	Y	0	855.493	2	2.29E-02	152.31	NaN	NaN	0
1268	GNLSWLR	sp|Q62422|OSTF1_MOUSE	yes	yes	84	90	7	R	E	0	844.456	2	6.27E-02	118.69	NaN	NaN	0
1269	GNPTVEVDLYTAKGLFR	sp|P17182|ENOA_MOUSE	yes	no	16	32	17	R	A	0	1878.984	2;3	1.43E-08	146.67	1.31	0.99	10
1270	GNSIIMLEALER	sp|P62309|RUXG_MOUSE	yes	yes	64	75	12	R	V	0	1344.707	2	2.59E-02	72.89	NaN	NaN	0
1271	GNVGFVFTKEDLTEIR	sp|P14869|RLA0_MOUSE	yes	yes	84	99	16	R	D	0	1823.942	3	1.40E-04	85.47	1.23	0.96	7
1272	GPAGPMGLTGR	sp|O88207|CO5A1_MOUSE	yes	yes	559	569	11	R	P	0	1012.512	2	2.06E-02	78.34	NaN	NaN	0
1273	GPAPESEKETKAVTNFIR	sp|P15089|CBPA3_MOUSE	yes	yes	274	291	18	R	S	0	1973.022	3	8.15E-04	74.43	1.62	0.89	3
1274	GPAPTPTVQACRRWR	sp|Q0PHV7|DACT3_MOUSE	yes	yes	441	455	15	R	S	2	1751.900	3	3.85E-02	43.76	1.22	0.84	7
1275	GPCIIYNEDNGIIKAFR	sp|Q9D8E6|RL4_MOUSE	yes	yes	206	222	17	R	N	0	1978.994	2;3	1.87E-05	100.23	1.26	0.93	11
1276	GPCRPCQSTFSGSLGFGSR	sp|O08640|KRA14_MOUSE	yes	yes	86	104	19	R	G	1	2056.921	3	7.22E-11	186.56	NaN	NaN	0
1277	GPGLGSTQGQTIALPAQGLIEFR	sp|P42669|PURA_MOUSE	yes	yes	176	198	23	R	D	0	2310.233	2	3.68E-10	154.65	NaN	NaN	0
1278	GPGLLESPSIFNFTADR	sp|Q6A0A2-3|LAR4B_MOUSE	yes	no	430	446	17	R	L	0	1819.911	2	1.48E-03	77.75	4.23	3.32	1
1279	GPGLYYVDSEGNR	sp|O55234|PSB5_MOUSE	yes	yes	167	179	13	R	I	0	1425.653	2	1.42E-03	125.82	NaN	NaN	0
1280	GPIKFNVWDTAGQEKFGGLR	sp|P62827|RAN_MOUSE	yes	no	57	76	20	R	D	0	2219.149	4	2.85E-08	113.05	1.01	0.86	6
1281	GPILPPESFVVLYR	sp|Q61398|PCOC1_MOUSE	yes	yes	432	445	14	R	S	0	1585.887	2	1.48E-03	101.53	NaN	NaN	0
1282	GPLPAAPPTAPER	sp|Q99P72|RTN4_MOUSE	yes	yes	90	102	13	R	Q	0	1272.683	2	3.34E-03	97.46	NaN	NaN	0
1283	GPPGPMGPPGLAGPPGESGR	sp|P11087|CO1A1_MOUSE	yes	yes	984	1003	20	R	E	0	1783.868	2	5.80E-11	182.76	NaN	NaN	0
1284	GPPGTGKTLLAR	sp|P62334|PRS10_MOUSE	yes	yes	174	185	12	Y	A	0	1166.677	2	3.88E-05	145.31	0.97	0.91	5
1285	GPQGALGEPGKQGSR	sp|Q02788|CO6A2_MOUSE	yes	yes	490	504	15	R	G	0	1437.732	3	5.64E-05	101.30	2.40	1.42	1
1286	GPQVQQPPPSNR	sp|Q01405|SC23A_MOUSE	yes	yes	217	228	12	R	F	0	1303.663	2	3.19E-03	119.39	NaN	NaN	0
1287	GPSCQDCDTGYTR	sp|Q05793|PGBM_MOUSE	yes	yes	1134	1146	13	R	V	0	1515.572	2	9.25E-04	140.82	NaN	NaN	0
1288	GPSLNPVLDYDHGSR	sp|Q8K310|MATR3_MOUSE	yes	yes	193	207	15	R	S	0	1625.780	3	6.87E-04	114.63	NaN	NaN	0
1289	GPSVTDKVFFDVR	sp|P30412|PPIC_MOUSE	yes	yes	33	45	13	R	I	0	1465.757	3	3.50E-03	73.22	1.30	1.06	3
1290	GPTEADELMKR	sp|Q00612|G6PD1_MOUSE	yes	yes	488	498	11	R	V	0	1245.602	3	1.15E-02	69.72	1.20	1.04	4
1291	GPVGSGSSIKFVSSTSSR	sp|Q8BGZ7|K2C75_MOUSE	yes	no	529	546	18	R	K	0	1738.885	3	1.54E-07	119.80	1.67	0.99	5
1292	GPVYIGELPQDFLR	sp|Q9QZ06|TOLIP_MOUSE	yes	yes	10	23	14	R	I	0	1602.841	2	1.18E-03	102.73	NaN	NaN	0
1293	GQCDLELINVCNENSLFKSLSR	sp|Q68FD5|CLH1_MOUSE	yes	yes	924	945	22	R	Y	0	2595.242	3	3.59E-06	96.23	1.38	1.17	5
1294	GQEFLRPCGTTEVD	sp|Q60716-2|P4HA2_MOUSE	yes	no	522	535	14	R	-	1	1607.725	2	7.99E-04	134.88	NaN	NaN	0
1295	GQIEVAFR	sp|P35492|HUTH_MOUSE	yes	yes	360	367	8	R	F	0	918.492	2	4.00E-02	116.37	NaN	NaN	0
1296	GQKVLDSGAPIKIPVGPETLGR	sp|P56480|ATPB_MOUSE	yes	yes	122	143	22	R	I	0	2231.264	3;4	5.70E-05	109.68	1.47	0.98	10
1297	GQNIQLYPEVPEVLGR	sp|Q9D967|MGDP1_MOUSE	yes	yes	42	57	16	R	L	0	1810.958	2	4.88E-03	80.63	NaN	NaN	0
1298	GQPLLVFR	sp|Q61753|SERA_MOUSE	yes	yes	462	469	8	R	A	0	928.549	2	4.33E-02	104.37	NaN	NaN	0
1299	GQPWEIILVCNR	sp|Q08189|TGM3_MOUSE	yes	yes	35	46	12	R	S	0	1483.761	2;3	3.89E-03	110.98	NaN	NaN	0
1300	GQTAVQKLQAEGLSPR	sp|P48758|CBR1_MOUSE	yes	yes	43	58	16	R	F	0	1681.911	3	1.88E-06	105.00	1.42	1.10	1
1301	GQTSGQIVMPR	sp|Q9D892|ITPA_MOUSE	yes	yes	134	144	11	R	G	0	1172.597	2	1.45E-06	190.57	NaN	NaN	0
1302	GQVFDVGPR	sp|P63085|MK01_MOUSE	yes	yes	14	22	9	R	Y	0	973.498	2	3.88E-02	86.74	NaN	NaN	0
1303	GQVGGDVNVEMDAAPGVDLSR	sp|Q61781|K1C14_MOUSE	no	no	268	288	21	R	I	0	2084.980	2	2.64E-11	187.07	NaN	NaN	0
1304	GSALRPSTSR	sp|P20152|VIME_MOUSE	yes	yes	41	50	10	L	S	1	1030.552	2	1.20E-01	55.47	NaN	NaN	0
1305	GSASDYKDTLTKGSSLSTPSKKGGI	sp|Q9R0H5|K2C71_MOUSE	yes	no	500	524	25	R	-	0	2527.288	5	2.41E-04	85.06	1.39	0.83	2
1306	GSGGSSAMCGGAGFGSR	sp|P50446|K2C6A_MOUSE	yes	no	41	57	17	R	S	0	1501.604	2	9.98E-06	170.09	NaN	NaN	0
1307	GSGSGSGGGGYSSGGGSR	sp|Q3TTY5|K22E_MOUSE	yes	no	576	593	18	R	G	0	1429.582	2	7.45E-03	76.38	NaN	NaN	0
1308	GSGSGSGGGGYSSGGGSRGGSGG	sp|Q3TTY5|K22E_MOUSE	yes	no	576	607	32	R	G	1	2523.036	3	1.64E-09	121.70	NaN	NaN	0
1309	GSGTSPDEGDAQDSSESAR	sp|Q8R0W0|EPIPL_MOUSE	yes	no	2602	2620	19	R	Q	0	1851.736	2	6.80E-11	187.75	NaN	NaN	0
1310	GSHCSGSGDPAEYNLR	sp|P48678|LMNA_MOUSE	yes	yes	569	584	16	R	S	0	1705.711	3	6.43E-05	153.09	NaN	NaN	0
1311	GSLGGGYSSGGFSGGSFSR	sp|P02535-3|K1C10_MOUSE	yes	no	33	51	19	R	G	0	1722.760	2	8.20E-17	231.83	NaN	NaN	0
1312	GSMYDGLADNYNNYGTTSR	sp|P97350|PKP1_MOUSE	yes	yes	68	86	19	R	S	0	2097.870	2	6.99E-08	169.43	NaN	NaN	0
1313	GSNTCEVHFENTR	sp|Q8JZN5|ACAD9_MOUSE	yes	yes	271	283	13	R	V	0	1549.658	3	1.45E-03	120.84	NaN	NaN	0
1314	GSPGAPSFAAGPPVSEGKYFSSNP	sp|Q7TPC1|CDSN_MOUSE	yes	yes	359	387	29	R	G	0	2873.435	3	1.54E-03	77.63	1.27	0.85	6
1315	GSPLLIGVR	sp|P47856-2|GFPT1_MOUSE	yes	no	204	212	9	R	S	0	910.560	2	2.15E-02	106.93	NaN	NaN	0
1316	GSQFFPGNNVIYEKTIR	sp|Q8K4L4|POF1B_MOUSE	yes	yes	156	172	17	R	K	0	1969.006	3	1.28E-04	81.66	1.92	1.10	5
1317	GSTAPVGGGSFPTITPR	sp|Q922R8|PDIA6_MOUSE	yes	yes	393	409	17	R	E	0	1600.821	2	4.23E-05	152.37	NaN	NaN	0
1318	GSTDNLMDDIER	sp|P42932|TCPQ_MOUSE	yes	yes	379	390	12	R	A	0	1364.588	2	2.77E-03	124.38	NaN	NaN	0
1319	GTEDITSPHGIPLDLLDR	sp|P60122|RUVB1_MOUSE	yes	yes	340	357	18	R	V	0	1947.990	3	7.45E-03	76.38	NaN	NaN	0
1320	GTFIEFR	sp|Q9Z2M7|PMM2_MOUSE	yes	no	113	119	7	R	N	0	868.444	2	6.67E-02	110.63	NaN	NaN	0
1321	GTGGVDTAATGSVFDISNLDR	sp|P30275|KCRU_MOUSE	yes	yes	355	375	21	R	L	0	2051.976	2	2.09E-06	133.21	NaN	NaN	0
1322	GTGGVDTAAVGGVFDVSNADR	sp|Q04447|KCRB_MOUSE	yes	yes	321	341	21	R	L	0	1963.924	2	2.44E-03	81.02	NaN	NaN	0
1323	GTINDISVLR	sp|Q3THG9|AASD1_MOUSE	yes	yes	62	71	10	R	V	0	1086.603	2	7.32E-03	133.44	NaN	NaN	0
1324	GTITAASGFDPLR	sp|P97384|ANX11_MOUSE	yes	yes	190	202	13	R	D	0	1304.673	2	5.98E-03	89.46	NaN	NaN	0
1325	GTKCCTLPEDQR	sp|P07724|ALBU_MOUSE	yes	yes	458	469	12	V	L	0	1463.650	2	2.96E-07	161.21	1.29	1.09	4
1326	GTLDPVEKALR	sp|P63017|HSP7C_MOUSE	yes	yes	312	322	11	R	D	0	1197.672	2;3	8.36E-07	158.04	1.28	0.94	19
1327	GTLEPVEKALR	sp|Q61696|HS71A_MOUSE	no	no	312	322	11	R	D	0	1211.687	3	9.85E-04	108.90	1.20	0.92	7
1328	GTPGESGAAGPSGPIGSR	sp|Q01149|CO1A2_MOUSE	yes	yes	598	615	18	R	G	0	1553.743	2	4.64E-03	60.06	0.21	0.12	1
1329	GTVLLSGPR	sp|P35980|RL18_MOUSE	yes	yes	135	143	9	R	K	0	898.524	2	5.32E-04	146.79	25.84	20.22	1
1330	GTVTDFPGFDGR	sp|P48036|ANXA5_MOUSE	yes	yes	5	16	12	R	A	0	1267.583	2	3.07E-04	160.52	NaN	NaN	0
1331	GTVVTGTLER	sp|Q8BFR5-2|EFTU_MOUSE	yes	no	272	281	10	R	G	0	1031.561	2	9.69E-03	124.33	NaN	NaN	0
1332	GTWDHGASDVSLYR	sp|Q60847|COCA1_MOUSE	yes	no	1673	1686	14	R	I	0	1562.711	2;3	3.57E-04	150.26	NaN	NaN	0
1333	GVCDTVLGLLDSHLIKGAGDAESR	sp|O70456|1433S_MOUSE	yes	yes	94	117	24	R	V	0	2482.249	2;3;4	1.30E-06	109.85	1.04	0.96	6
1334	GVDLQESNPASR	sp|P35278|RAB5C_MOUSE	yes	yes	199	210	12	R	S	0	1271.611	2	8.19E-04	149.41	NaN	NaN	0

1335	GVEICIATPGR	sp|Q61656|DDX5_MOUSE	no	no	217	227	11	R	L	0	1171.602	2	6.79E-03	114.86	NaN	NaN	0
1336	GVFIVAAKR	sp|Q8BWT1|THIM_MOUSE	yes	yes	6	14	9	R	T	0	959.592	2	9.63E-04	127.56	1.10	0.93	6
1337	GVIDMGNSLIER	sp|P16546-2|SPTN1_MOUSE	yes	no	1588	1599	12	R	G	0	1302.660	2	6.97E-03	96.75	NaN	NaN	0
1338	GVLKVFLENVIR	sp|P62806|H4_MOUSE	yes	yes	57	68	12	R	D	0	1385.840	2;3	1.09E-07	174.05	0.98	0.70	8
1339	GVLSSPSLAFTTPIR	sp|Q8R4R6|NUP53_MOUSE	yes	yes	254	268	15	R	T	0	1544.856	2	4.48E-03	82.65	NaN	NaN	0
1340	GVLYQTVSR	sp|Q04857|CO6A1_MOUSE	yes	yes	1012	1020	9	R	K	0	1021.556	2	1.87E-02	123.35	NaN	NaN	0
1341	GVNTFSPEGR	sp|Q9Z2U1|PSA5_MOUSE	yes	yes	11	20	10	R	L	0	1062.509	2	1.21E-02	114.89	NaN	NaN	0
1342	GVNWAAFHPTMPLIVSGADDR	sp|Q8CIE6|COPA_MOUSE	yes	yes	207	227	21	R	Q	0	2253.100	3	4.42E-07	150.91	NaN	NaN	0
1343	GVQDSIADAEQR	sp|Q3TTY5|K22E_MOUSE	yes	no	440	451	12	K	G	0	1287.606	2	1.32E-03	142.83	NaN	NaN	0
1344	GVQGPPGPAGPR	sp|P11087|CO1A1_MOUSE	yes	no	675	686	12	R	G	0	1088.573	2	1.55E-03	139.86	NaN	NaN	0
1345	GVTIKPTVDDD	sp|Q9Z0N1|IF2G_MOUSE	yes	no	462	472	11	R	-	0	1158.577	2	1.81E-06	155.33	1.58	1.37	6
1346	GVVDSEDLPLNISR	sp|P11499|HS90B_MOUSE	no	no	379	392	14	R	E	0	1512.778	2	8.61E-07	176.87	NaN	NaN	0
1347	GVVLFPWQAR	sp|Q91VA6|PDIP2_MOUSE	yes	yes	92	101	10	R	L	0	1171.650	2	3.48E-02	76.06	NaN	NaN	0
1348	GVVQDLQQAISKLEAR	sp|P57776-2|EF1D_MOUSE	yes	no	72	87	16	R	L	0	1753.969	3	1.07E-06	115.91	1.19	0.90	6
1349	GWEAFLNAPEASR	sp|Q8BGC0|HTSF1_MOUSE	yes	yes	369	381	13	R	G	0	1446.689	2	1.93E-02	72.89	NaN	NaN	0
1350	GWEEGVAQMSVGQR	sp|P26883|FKB1A_MOUSE	yes	yes	59	72	14	R	A	0	1532.704	2	1.82E-04	159.52	NaN	NaN	0
1351	GWFVYQQR	sp|Q9JHR7|IDE_MOUSE	yes	yes	775	782	8	R	N	0	1082.530	2	3.33E-03	135.87	0.08	0.07	1
1352	GWLKSNVNDGVAQSTR	sp|P17751|TPIS_MOUSE	yes	yes	241	256	16	R	I	0	1730.870	3	1.84E-09	154.81	1.09	0.94	4
1353	GYELLFQPEVVR	sp|P30999-2|CTND1_MOUSE	yes	no	649	660	12	R	I	0	1448.766	2	2.43E-02	73.44	NaN	NaN	0
1354	GYFDEEMNR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	2735	2743	9	R	I	0	1159.460	2	1.56E-02	133.23	NaN	NaN	0
1355	GYFEYIEENKYSR	sp|Q8VEK3|HNRPU_MOUSE	yes	yes	232	244	13	R	A	0	1696.773	2;3	1.65E-04	115.12	1.21	0.93	16
1356	GYGPDGHFGMFPANYVELIE	sp|Q62418-3|DBNL_MOUSE	yes	no	413	432	20	R	-	0	2211.994	2	1.84E-02	51.79	NaN	NaN	0
1357	GYPTLLLFR	sp|Q91W90|TXND5_MOUSE	yes	yes	380	388	9	R	G	0	1078.618	2	2.01E-02	115.49	NaN	NaN	0
1358	GYPTLLWFR	sp|Q91W90|TXND5_MOUSE	yes	yes	247	255	9	R	D	0	1151.613	2	1.81E-02	127.02	NaN	NaN	0
1359	GYSFTTTAER	sp|P63260|ACTG_MOUSE	no	no	197	206	10	R	E	0	1131.520	2	1.08E-03	147.78	0.00	0.00	1
1360	GYSFVTTAER	sp|P68134|ACTS_MOUSE	yes	no	199	208	10	R	E	0	1129.540	2	1.09E-02	119.53	NaN	NaN	0
1361	GYSNLLKR	sp|Q61656|DDX5_MOUSE	yes	yes	517	524	8	R	D	0	949.535	2	6.10E-03	118.50	1.25	0.92	6
1362	GYSSGGFSGGSFSR	sp|P02535-3|K1C10_MOUSE	yes	no	38	51	14	G	G	0	1351.579	2	1.10E-03	111.12	NaN	NaN	0
1363	GYTVLGVEGR	sp|P19096|FAS_MOUSE	yes	yes	469	478	10	R	V	0	1049.551	2	3.80E-03	120.45	1.13	0.69	1
1364	HCIDPALIAAIISR	sp|Q3V1I0|LYG2_MOUSE	yes	yes	92	105	14	R	E	0	1548.845	2;3	3.38E-03	94.09	NaN	NaN	0
1365	HGDDLKNTKNEITELTR	sp|Q9R0H5|K2C71_MOUSE	yes	no	338	354	17	R	F	0	1983.002	3	3.66E-03	66.02	1.27	0.93	5
1366	HGSLGFLPR	sp|P27659|RL3_MOUSE	yes	yes	11	19	9	R	K	0	982.535	2	2.68E-03	166.16	NaN	NaN	0
1367	HGYIKGIVKDIIHDPGR	sp|P62918|RL8_MOUSE	yes	yes	38	54	17	R	G	0	1917.059	4	3.54E-02	42.63	1.20	1.21	1
1368	HNPTQSLLFCGR	sp|Q9D7P9|SPB12_MOUSE	yes	yes	408	419	12	R	V	0	1428.693	2	4.08E-03	108.72	NaN	NaN	0
1369	HPDEPVLLEEPVVLALAEKHGR	sp|Q9JII6|AK1A1_MOUSE	yes	yes	222	243	22	R	S	0	2447.317	4	1.18E-05	80.24	1.06	1.00	1
1370	HPDYSVSLLLR	sp|P07724|ALBU_MOUSE	yes	yes	362	372	11	R	L	0	1298.698	2;3	2.40E-03	139.43	NaN	NaN	0
1371	HPGSFDVVHVKDANGNSFATR	sp|P62702|RS4X_MOUSE	yes	yes	201	221	21	R	L	0	2254.088	3;4	4.76E-06	99.41	1.18	1.07	4
1372	HPHDIIDDINSGAVECPAS	sp|P35979|RL12_MOUSE	yes	no	147	165	19	R	-	0	2045.911	3	3.95E-05	127.61	NaN	NaN	0
1373	HQEGEIFDTEKEKYEITEQR	sp|P47911|RL6_MOUSE	yes	yes	235	254	20	R	K	0	2508.177	3	3.10E-03	60.06	1.05	1.02	1
1374	HQGVMVGMGQKDSYVGDEAQS	sp|P63260|ACTG_MOUSE	no	no	40	62	23	R	G	0	2506.169	4;5	2.92E-04	74.36	1.05	0.99	5
1375	HSLSYDCIGR	sp|Q8JZK9|HMCS1_MOUSE	yes	yes	80	89	10	R	L	0	1206.545	2	2.17E-03	102.52	0.59	0.52	4
1376	HVAAGTQQPYTDGVR	sp|Q02257|PLAK_MOUSE	yes	yes	541	555	15	R	M	0	1598.780	3	3.45E-03	88.22	NaN	NaN	0
1377	HVGMAVAGLLADAR	sp|O70435|PSA3_MOUSE	yes	yes	73	86	14	R	S	0	1379.734	3	4.61E-02	57.43	NaN	NaN	0
1378	HVPVVYVDYPGPASLTQIYGTFNF	sp|Q9JHU4|DYHC1_MOUSE	yes	yes	2728	2751	24	R	A	0	2692.365	3	7.29E-03	60.13	NaN	NaN	0
1379	HYLFDVQR	sp|Q9CQQ7|AT5F1_MOUSE	yes	no	164	171	8	R	N	0	1076.540	2	2.10E-03	183.74	NaN	NaN	0
1380	IAAHGNSLR	sp|Q9DBJ1|PGAM1_MOUSE	yes	no	183	191	9	L	G	0	937.509	2	2.22E-02	103.01	NaN	NaN	0
1381	IAAQYSGAQVR	sp|Q9DBN0|EF1G_MOUSE	yes	yes	20	30	11	L	V	0	1162.610	2	8.17E-03	108.35	NaN	NaN	0
1382	IAATILTSPDLR	sp|P05202|AATM_MOUSE	yes	yes	326	337	12	R	K	0	1269.729	2	1.84E-06	186.81	9.22	5.53	1
1383	IADGYEQAAR	sp|P80316|TCPE_MOUSE	yes	yes	133	142	10	R	I	0	1092.520	2	5.31E-04	127.76	0.18	0.13	2
1384	IAEFAFEYAR	sp|Q9D6R2-2|IDH3A_MOUSE	yes	no	101	110	10	R	N	0	1215.592	2	5.59E-02	70.94	NaN	NaN	0
1385	IAIKPDGVQR	sp|Q01768|NDKB_MOUSE	yes	no	9	18	10	F	G	0	1095.640	2	2.17E-03	102.53	1.21	0.86	7
1386	IAIPGLAGAGNSVLLVSNLNPER	sp|P17225|PTBP1_MOUSE	yes	yes	324	346	23	R	V	0	2274.270	2;3	7.14E-12	161.47	NaN	NaN	0
1387	IALMPLFQAEKDR	sp|Q9ERS2|NDUAD_MOUSE	yes	yes	69	81	13	R	R	0	1530.823	3	3.07E-03	73.93	1.73	1.12	1
1388	IALTDNSLIAR	sp|P14148|RL7_MOUSE	yes	yes	189	199	11	R	S	0	1185.672	2	1.87E-04	166.97	NaN	NaN	0
1389	IALVITDGR	sp|Q04857|CO6A1_MOUSE	yes	yes	722	730	9	R	S	0	956.565	2	2.01E-03	128.36	67.42	45.63	1
1390	IANFKIEPPGLFR	sp|Q04750|TOP1_MOUSE	yes	yes	352	364	13	R	G	0	1500.845	3	7.73E-03	66.22	1.08	0.69	1
1391	IANLQTDLSDGLR	sp|Q8BTM8|FLNA_MOUSE	yes	no	64	76	13	R	L	0	1414.742	2	3.70E-08	192.15	22.46	20.09	2
1392	IAPLAEGALPYNLAELQR	sp|Q8BH59|CMC1_MOUSE	yes	yes	292	309	18	R	Q	0	1938.058	2	3.13E-04	119.80	NaN	NaN	0
1393	IAPLEEGMLPFNLAEAQR	sp|Q9QXX4|CMC2_MOUSE	yes	yes	293	310	18	R	Q	0	1998.024	2	2.18E-02	57.17	NaN	NaN	0
1394	IAQDFKTDLR	sp|P84244|H33_MOUSE	no	no	75	84	10	E	F	0	1205.640	2	1.43E-03	113.22	1.31	0.86	3
1395	IAQFLSGIPETVPLSTVNR	sp|Q921H8|THIKA_MOUSE	yes	no	103	121	19	R	Q	0	2041.121	2	2.81E-03	93.22	NaN	NaN	0
1396	IAQITGPPDR	sp|Q91WJ8|FUBP1_MOUSE	yes	no	318	327	10	R	C	0	1066.577	2	2.17E-03	102.52	1.97	1.61	3
1397	IAQPGDHVSVTGIFLPVLR	sp|Q61881|MCM7_MOUSE	yes	yes	264	282	19	R	T	0	2018.131	3	1.24E-02	66.89	NaN	NaN	0
1398	IAQSDYIPTQQDVLR	sp|P08752|GNAI2_MOUSE	yes	yes	163	177	15	R	T	0	1745.895	2	7.62E-04	105.17	NaN	NaN	0
1399	IATDALSTR	sp|P15089|CBPA3_MOUSE	yes	yes	333	341	9	R	Y	0	946.508	2	2.18E-02	105.52	NaN	NaN	0
1400	IAWGYPNLKSVNELIYKR	sp|P14148|RL7_MOUSE	yes	yes	162	179	18	Y	G	0	2163.184	4	3.86E-02	40.49	1.79	1.00	1
1401	ICIVTKEGIR	sp|O09061|PSB1_MOUSE	yes	yes	222	231	10	R	E	0	1187.670	3	6.46E-03	77.66	1.04	0.88	6
1402	ICKHPESNFCSR	sp|P00329|ADH1_MOUSE	yes	yes	103	114	12	R	S	0	1533.682	3	1.66E-02	59.16	1.15	1.00	4
1403	ICKNIPR	sp|P54071|IDHP_MOUSE	no	no	153	159	7	I	L	0	899.501	2	7.31E-02	56.12	0.91	0.85	1
1404	ICLDILKDKWSPALQIR	sp|P61089|UBE2N_MOUSE	yes	yes	86	102	17	R	T	0	2068.150	3	1.80E-02	65.23	0.57	0.42	2
1405	ICTVQPNPDYGGAITFLEER	sp|Q99JW2|ACY1_MOUSE	yes	yes	22	41	20	R	A	0	2279.089	2	1.00E-02	66.89	NaN	NaN	0
1406	IDDKGILR	sp|P35700|PRDX1_MOUSE	yes	yes	133	140	8	I	Q	0	928.534	2	8.36E-03	105.52	1.27	1.13	3
1407	IDEPGLR	sp|Q11136|PEPD_MOUSE	yes	yes	389	395	7	R	S	0	798.424	2	6.83E-02	107.43	NaN	NaN	0
1408	IDFSSIAVPGTSNPQQR	sp|A2ADY9|DDI2_MOUSE	yes	yes	94	110	17	R	Q	0	1815.912	2	4.92E-03	62.06	0.66	0.50	1
1409	IDGITIQAR	sp|P16546-2|SPTN1_MOUSE	yes	no	734	742	9	R	Q	0	985.556	2	2.15E-02	106.88	NaN	NaN	0
1410	IDILDSALLRPGR	sp|P62196|PRS8_MOUSE	yes	yes	298	310	13	R	I	1	1437.830	2;3	6.87E-03	86.77	NaN	NaN	0
1411	IDINMSGFNETDDLKR	sp|Q99K51|PLST_MOUSE	yes	yes	321	336	16	R	A	0	1866.878	3	1.32E-04	86.50	1.19	1.00	5
1412	IDKPILKAGR	sp|P62918|RL8_MOUSE	yes	yes	175	184	10	R	A	0	1109.692	3	4.00E-02	53.24	1.06	0.83	8
1413	IDNAKLAADDFR	sp|Q61897|KT33B_MOUSE	no	no	131	142	12	Q	T	0	1347.678	2	1.71E-03	84.30	1.63	1.12	1
1414	IDNLDVNR	sp|Q99JF8|PSIP1_MOUSE	yes	yes	363	370	8	K	C	0	957.488	2	6.08E-02	88.92	NaN	NaN	0
1415	IDSAEWGVDLPSVEAQLGSHR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	442	462	21	R	G	0	2265.103	3	3.26E-08	106.35	5.42	3.74	1
1416	IDSDHTDNQR	sp|P09103|PDIA1_MOUSE	yes	yes	293	302	10	F	I	0	1199.517	2	1.79E-03	154.24	NaN	NaN	0
1417	IDTQTPSVQER	sp|Q8K3I9-3|GLCI1_MOUSE	yes	no	149	159	11	S	S	0	1272.631	2	3.43E-02	72.92	NaN	NaN	0
1418	IEANEALVKALE	sp|Q9D3D9|ATPD_MOUSE	yes	no	157	168	12	R	-	0	1298.708	2	1.86E-07	168.76	0.99	0.78	9
1419	IEDQIVKSPEDKR	sp|Q9JHR7|IDE_MOUSE	yes	yes	50	62	13	R	E	0	1555.821	3;4	7.53E-04	89.30	1.05	0.96	6
1420	IEDVTPIPSDSTR	sp|P62264|RS14_MOUSE	yes	yes	129	141	13	R	R	0	1428.710	2	2.56E-04	162.72	NaN	NaN	0
1421	IEEELGSKAKFAGR	sp|P17182|ENOA_MOUSE	yes	yes	413	426	14	R	S	0	1533.815	3;4	9.11E-04	76.76	1.11	0.92	9
1422	IEENTLNAELLR	sp|O35902|DSG3_MOUSE	yes	no	276	287	12	R	F	0	1413.746	2	2.50E-03	127.56	NaN	NaN	0
1423	IEGDPQGVQQAKR	sp|Q8VDJ3|VIGLN_MOUSE	yes	yes	483	495	13	R	E	0	1424.737	3	4.07E-04	99.50	1.30	0.99	7
1424	IEGNTLVIPR	sp|Q05793|PGBM_MOUSE	yes	yes	2579	2588	10	R	V	0	1110.640	2	1.79E-03	154.24	NaN	NaN	0
1425	IEITSLLPSR	sp|P59235|NUP43_MOUSE	yes	yes	340	349	10	R	T	0	1127.655	2	2.51E-02	87.57	NaN	NaN	0
1426	IEPHTGLLLLSVQKR	sp|E9Q557|DESP_MOUSE	yes	yes	2204	2218	15	R	S	0	1703.009	4	6.13E-02	37.61	2.27	1.43	1
1427	IERPTYTNLNR	sp|P68373|TBA1C_MOUSE	no	no	219	229	11	D	L	1	1375.721	2	1.77E-02	84.48	NaN	NaN	0
1428	IESILMSLPLTAR	sp|P36552|HEM6_MOUSE	yes	yes	403	415	13	R	W	0	1442.817	2	3.82E-02	65.04	NaN	NaN	0
1429	IESKSISAPVIFDR	sp|Q9CWK8|SNX2_MOUSE	yes	yes	113	126	14	R	S	0	1560.851	3	4.78E-03	69.26	1.25	1.18	2
1430	IESLSSQLSNLQKESR	sp|P14733|LMNB1_MOUSE	yes	yes	301	316	16	R	A	0	1817.948	3	1.41E-03	73.83	1.31	0.83	6
1431	IETLDPALIRPGR	sp|P62192|PRS4_MOUSE	yes	yes	334	346	13	R	I	1	1449.830	2;3	9.67E-03	78.32	NaN	NaN	0
1432	IEWHLNAFNTKDEVIDAVR	sp|Q80X19-2|COEA1_MOUSE	yes	no	209	227	19	R	S	0	2269.149	4	5.12E-05	85.09	2.29	1.40	1
1433	IEYDCELVPR	sp|Q8BK67|RCC2_MOUSE	yes	yes	299	308	10	R	R	0	1292.607	2	1.42E-02	106.62	NaN	NaN	0
1434	IFAGKQLEDGR	sp|P62983|RS27A_MOUSE	yes	no	44	54	11	L	T	0	1232.651	2	2.27E-03	90.61	1.34	0.94	5
1435	IFAPNHVVAKSR	sp|P62717|RL18A_MOUSE	yes	yes	32	43	12	R	F	0	1337.757	3	1.03E-01	46.88	1.24	0.93	5
1436	IFEGANDILR	sp|P50544|ACADV_MOUSE	yes	yes	461	470	10	R	L	0	1146.603	2	2.85E-02	82.42	NaN	NaN	0
1437	IFEPKCLDAFPNLKDFMGR	sp|P15626|GSTM2_MOUSE	yes	yes	169	187	19	R	F	0	2297.134	4	6.05E-02	31.88	1.00	0.99	1

1438	IFGGLDR	sp|Q9EST5|AN32B_MOUSE	yes	no	76	82	7	R	L	0	776.418	2	4.55E-02	149.40	NaN	NaN	0
1439	IFGPIWNR	sp|Q00612|G6PD1_MOUSE	yes	yes	220	227	8	R	D	0	1001.545	2	4.25E-02	107.43	NaN	NaN	0
1440	IFHTVTTTDDPVIR	sp|O70194|EIF3D_MOUSE	yes	yes	223	236	14	R	K	0	1613.841	3	1.05E-03	117.70	NaN	NaN	0
1441	IFIDSDHTDNQR	sp|P09103|PDIA1_MOUSE	yes	yes	291	302	12	F	I	0	1459.669	3	4.09E-03	108.56	NaN	NaN	0
1442	IFQIHTSR	sp|P62192|PRS4_MOUSE	yes	yes	364	371	8	R	M	0	1000.545	3	1.05E-01	71.50	NaN	NaN	0
1443	IFSIVEQR	sp|Q61035|SYHC_MOUSE	yes	yes	389	396	8	R	L	0	990.550	2	4.00E-02	116.25	NaN	NaN	0
1444	IFSSEHDIFR	sp|P51174|ACADL_MOUSE	yes	yes	52	61	10	R	E	0	1249.609	3	1.14E-02	117.70	NaN	NaN	0
1445	IFTNLYGR	sp|Q91YT0|NDUV1_MOUSE	yes	yes	41	48	8	R	H	0	982.524	2	3.57E-02	130.27	NaN	NaN	0
1446	IFVWDWQR	sp|P17563|SBP1_MOUSE	yes	no	228	235	8	R	H	0	1148.577	2	3.92E-02	119.29	NaN	NaN	0
1447	IFYDMKVR	sp|Q9R0P5|DEST_MOUSE	yes	yes	14	21	8	R	K	0	1070.558	2;3	8.27E-03	106.04	1.11	1.04	8
1448	IGADFLGR	sp|P05201|AATC_MOUSE	yes	yes	115	122	8	R	W	0	847.455	2	1.94E-02	157.58	NaN	NaN	0
1449	IGASSLLSDIER	sp|Q91YP3|DEOC_MOUSE	yes	yes	288	299	12	R	Q	0	1259.672	2	3.72E-04	156.14	NaN	NaN	0
1450	IGCAMSGLIADAKTLIDKAR	sp|Q9Z2U1|PSA5_MOUSE	yes	yes	74	93	20	H	V	0	2103.118	4	4.04E-03	54.76	1.66	1.74	3
1451	IGDLQAFVGR	sp|P10852|4F2_MOUSE	yes	yes	120	129	10	R	D	0	1074.582	2	5.53E-03	140.17	NaN	NaN	0
1452	IGEWELIQESGVPLKPLFGPGYTGI	sp|P56399|UBP5_MOUSE	yes	yes	304	329	26	R	N	0	2855.522	3	5.58E-10	136.71	1.09	0.94	2
1453	IGFPWSEIR	sp|P26041|MOES_MOUSE	yes	yes	238	246	9	K	N	0	1103.576	2	4.51E-02	80.69	NaN	NaN	0
1454	IGGLNVQTSESGLR	sp|Q9CX86|ROA0_MOUSE	yes	yes	11	24	14	F	G	0	1429.753	2	2.67E-04	153.39	NaN	NaN	0
1455	IGGLSFETTDDSLR	sp|Q8BG05-2|ROA3_MOUSE	no	no	17	30	14	F	E	0	1509.731	2	1.74E-04	160.48	NaN	NaN	0
1456	IGGLSFETTDESLR	sp|P49312|ROA1_MOUSE	yes	no	18	31	14	F	S	0	1523.747	2	6.43E-04	140.31	NaN	NaN	0
1457	IGGLSFETTEESLR	sp|O88569|ROA2_MOUSE	yes	no	25	38	14	F	N	0	1537.762	2	2.93E-02	111.12	NaN	NaN	0
1458	IGGNEGIDVPIPR	sp|Q91WJ8|FUBP1_MOUSE	yes	no	268	280	13	R	F	0	1335.715	2	1.55E-04	170.00	NaN	NaN	0
1459	IGGPEAGKSEQSGAK	sp|P14602|HSPB1_MOUSE	yes	no	195	209	15	Q	-	0	1414.705	2	4.45E-05	102.29	0.82	0.68	2
1460	IGGVQQDTILAEGLHFR	sp|O35129|PHB2_MOUSE	yes	yes	55	71	17	R	I	0	1852.980	3	2.39E-08	194.77	NaN	NaN	0
1461	IGHGNLPHLQQR	sp|Q6P3A4|VSIG8_MOUSE	yes	yes	84	95	12	R	V	0	1368.738	3;4	3.90E-04	155.00	NaN	NaN	0
1462	IGIAVPDVYSACKR	sp|Q9CPU0|LGUL_MOUSE	yes	yes	128	141	14	H	F	0	1547.813	3	1.22E-02	54.90	1.39	1.32	4
1463	IGIFGQDEDVTSKAFTGR	sp|O55143-2|AT2A2_MOUSE	yes	no	638	655	18	R	E	0	1939.964	3	8.91E-04	74.14	1.35	0.97	6
1464	IGLAQYSGDPR	sp|Q80X19-2|COEA1_MOUSE	yes	no	198	208	11	R	I	0	1175.594	2	1.70E-04	168.30	NaN	NaN	0
1465	IGLINDMVR	sp|P23116|EIF3A_MOUSE	yes	yes	368	376	9	R	F	0	1029.564	2	4.17E-02	84.00	NaN	NaN	0
1466	IGLVYSGMGPDYR	sp|P49722|PSA2_MOUSE	yes	yes	72	84	13	H	V	0	1426.692	2	1.42E-03	125.82	NaN	NaN	0
1467	IGNAKGDEALEKR	sp|Q99K85|SERC_MOUSE	yes	yes	307	319	13	R	F	0	1399.742	4	6.82E-02	38.77	0.79	0.77	1
1468	IGNLQTDLSDGLR	sp|Q80X90|FLNB_MOUSE	yes	yes	37	49	13	R	L	0	1400.726	2	7.35E-04	145.60	NaN	NaN	0
1469	IGNSTAIQELFKR	sp|P99024|TBB5_MOUSE	no	no	368	380	13	F	I	0	1475.810	3	5.89E-04	94.12	1.39	1.25	5
1470	IGNVESQLGEIR	sp|Q497I4|KRT35_MOUSE	yes	no	359	370	12	M	A	0	1313.694	2	4.18E-03	107.53	NaN	NaN	0
1471	IGPGIDVPAPDMSTGER	sp|P26443|DHE3_MOUSE	yes	yes	215	231	17	F	E	0	1710.825	2	4.10E-03	87.43	NaN	NaN	0
1472	IGQSKVFFR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	756	764	9	R	A	0	1080.608	3	3.91E-02	61.56	1.31	0.75	2
1473	IGRPSETGIIGIIDPECR	sp|Q3U1J4|DDB1_MOUSE	yes	yes	112	129	18	R	M	1	1982.026	3	1.05E-02	72.36	NaN	NaN	0
1474	IGSVEEQLAQLR	sp|Q61781|K1C14_MOUSE	no	no	383	394	12	M	C	0	1341.725	2	6.77E-04	151.26	NaN	NaN	0
1475	IGTLLDAIICR	sp|Q8QZZ7|TPRKB_MOUSE	yes	yes	158	168	11	R	M	0	1243.696	2	1.11E-02	98.90	NaN	NaN	0
1476	IHDPQLLTER	sp|Q922B2|SYDC_MOUSE	yes	yes	432	441	10	R	A	0	1220.651	3	2.94E-02	81.02	NaN	NaN	0
1477	IIALDGDTKNSTFSELFKKEHPDR	sp|P40142|TKT_MOUSE	yes	yes	335	358	24	R	F	0	2760.408	5	4.81E-02	33.37	1.12	1.03	4
1478	IIAPPER	sp|P63260|ACTG_MOUSE	no	no	329	335	7	K	K	0	794.465	2	8.18E-02	94.66	NaN	NaN	0
1479	IIDDKGILR	sp|P35700|PRDX1_MOUSE	yes	yes	132	140	9	F	Q	0	1041.618	2	1.33E-03	123.75	1.28	1.01	3
1480	IIDVVYNASNNELVR	sp|P62242|RS8_MOUSE	yes	yes	78	92	15	R	T	0	1717.900	2	6.39E-04	120.70	NaN	NaN	0
1481	IIFDDFR	sp|P46978|STT3A_MOUSE	yes	yes	500	506	7	R	E	0	924.471	2	4.62E-02	148.21	NaN	NaN	0
1482	IIGATNRPDIIDPAILRPGR	sp|Q01853|TERA_MOUSE	yes	yes	619	638	20	F	L	2	2157.238	4	1.70E-02	54.29	NaN	NaN	0
1483	IIGDPYKVQQACEMVMDILR	sp|Q3U0V1|FUBP2_MOUSE	yes	yes	286	305	20	R	E	0	2378.180	3	3.61E-08	108.71	1.62	1.08	1
1484	IIGLDQVAGMSETALPGAFKTR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	618	639	22	R	K	0	2274.204	3	1.70E-06	99.93	1.31	0.96	11
1485	IIIQESALDYR	sp|Q61543|GSLG1_MOUSE	yes	yes	986	996	11	R	L	0	1319.709	2	1.17E-02	97.73	NaN	NaN	0
1486	IIKPCNHVLSLSFPIR	sp|P26443|DHE3_MOUSE	yes	yes	108	123	16	R	R	0	1893.066	4	4.23E-03	66.25	1.14	1.06	3
1487	IILLAEGR	sp|P50247|SAHH_MOUSE	yes	yes	336	343	8	R	L	0	883.549	2	2.75E-02	144.38	NaN	NaN	0
1488	IINDLLQSLR	sp|Q3U0V1|FUBP2_MOUSE	yes	yes	386	395	10	R	S	0	1183.693	2	1.33E-02	110.18	NaN	NaN	0
1489	IINEPTAAAIAYGLDKKVGAER	sp|P63017|HSP7C_MOUSE	yes	yes	172	193	22	R	N	0	2299.254	3;4	3.37E-09	126.26	1.22	1.00	9
1490	IINEPTAAAIAYGLDKR	sp|P20029|GRP78_MOUSE	yes	yes	199	215	17	R	E	0	1814.989	2;3	5.74E-07	117.18	1.22	0.96	10
1491	IINEPTAAAIAYGLDR	sp|Q61696|HS71A_MOUSE	yes	no	172	187	16	R	T	0	1686.894	2;3	6.42E-04	107.62	NaN	NaN	0
1492	IIPGFMCQGGDFTR	sp|P17742|PPIA_MOUSE	yes	yes	56	69	14	R	H	0	1597.738	2;3	6.80E-04	109.83	0.67	0.54	1
1493	IISLETYNLFR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	3559	3569	11	R	E	0	1367.745	2	4.56E-03	125.30	NaN	NaN	0
1494	IITGPAPVLPPAALR	sp|Q9QYS9-8|QKI_MOUSE	yes	no	228	242	15	R	T	0	1484.908	2	1.55E-02	70.44	NaN	NaN	0
1495	IITITGTQDQIQNAQYLLQNSVKQ	sp|P61979-3|HNRPK_MOUSE	yes	no	410	439	30	R	-	0	3445.788	3	3.67E-17	161.68	NaN	NaN	0
1496	IIVEKPFGR	sp|Q00612|G6PD1_MOUSE	yes	no	167	175	9	R	D	0	1057.628	3	3.52E-02	63.82	0.94	0.74	2
1497	IIVLGLLPR	sp|Q61206|PA1B2_MOUSE	yes	yes	134	142	9	K	G	0	992.675	2	2.18E-02	105.14	NaN	NaN	0
1498	IIYDDLSKQAVAYR	sp|Q03265|ATPA_MOUSE	yes	yes	309	322	14	L	Q	0	1653.873	3	1.26E-02	54.09	1.76	1.04	2
1499	IIYSPTVGDPIDEYTTVPGR	sp|Q60847|COCA1_MOUSE	yes	no	2059	2078	20	R	R	0	2192.100	2;3	4.85E-03	76.30	NaN	NaN	0
1500	IIYSPTVGDPIDEYTTVPGRR	sp|Q60847|COCA1_MOUSE	yes	no	2059	2079	21	R	N	1	2348.201	3	1.55E-02	51.57	NaN	NaN	0
1501	IKLYSESLAR	sp|Q61598-2|GDIB_MOUSE	yes	no	173	182	10	R	Y	0	1178.666	2;3	3.93E-04	131.82	1.17	1.02	10
1502	ILAKLPIEPR	sp|O70133|DHX9_MOUSE	yes	no	856	865	10	R	F	0	1148.728	3	1.01E-03	120.06	1.22	0.75	2
1503	ILAQATSDLVNAIKADAEGESDLEI	sp|P26039|TLN1_MOUSE	yes	yes	828	854	27	R	K	0	2829.399	3	6.61E-03	58.81	1.32	0.92	1
1504	ILATSFICTLPAGHR	sp|Q68FL6|SYMC_MOUSE	yes	yes	782	796	15	R	I	0	1655.882	3	6.35E-04	121.18	NaN	NaN	0
1505	ILCDVPCSGDGTMR	sp|Q1HFZ0-2|NSUN2_MOUSE	yes	no	199	212	14	R	K	0	1579.679	2	3.90E-03	92.04	NaN	NaN	0
1506	ILDDDTIITTLENLKR	sp|Q9JHU4|DYHC1_MOUSE	yes	yes	3758	3773	16	R	E	0	1872.020	3	7.55E-03	57.29	1.32	1.16	6
1507	ILDELTLCKSDLEAQVESLKEELLCL	sp|Q61765|K1H1_MOUSE	yes	no	165	192	28	R	N	0	3344.757	4	3.28E-02	47.33	3.15	2.03	1
1508	ILDELTLCKSDLEAQVESLR	sp|Q61897|KT33B_MOUSE	no	no	165	184	20	R	Q	0	2331.199	2;3	4.18E-28	213.15	1.97	1.26	12
1509	ILDGLADTTFR	sp|P47746|CNR1_MOUSE	yes	yes	4	14	11	S	T	0	1220.640	2	6.64E-02	63.62	NaN	NaN	0
1510	ILDGMFAVCGVPDSKFR	sp|Q61035|SYHC_MOUSE	yes	yes	216	232	17	R	T	0	1910.938	3	2.77E-02	58.25	1.29	0.87	1
1511	ILEDKEGTLPAALVQPR	sp|Q9CQ60|6PGL_MOUSE	yes	yes	215	231	17	R	T	0	1849.031	3	3.64E-07	121.99	1.17	1.08	5
1512	ILEFFGLKKEECPAVR	sp|P09103|PDIA1_MOUSE	yes	yes	303	318	16	R	L	0	1935.029	3;4	9.60E-03	51.77	1.17	1.05	11
1513	ILFRPVASQLPR	sp|P67778|PHB_MOUSE	yes	yes	94	105	12	R	I	1	1395.835	3	1.82E-03	136.38	NaN	NaN	0
1514	ILGADTSVDLEETGR	sp|Q03265|ATPA_MOUSE	yes	yes	59	73	15	R	V	0	1574.779	2	6.37E-04	120.92	NaN	NaN	0
1515	ILGALERDR	sp|Q80UF7|TCAM1_MOUSE	yes	yes	14	22	9	G	L	1	1041.593	2	4.56E-02	57.86	3.20	1.82	1
1516	ILGAVAKVR	sp|Q64727|VINC_MOUSE	yes	yes	824	832	9	R	E	0	925.607	3	2.76E-02	68.22	1.72	1.38	3
1517	ILGDPEALR	sp|P82198|BGH3_MOUSE	yes	yes	296	304	9	R	D	0	982.545	2	2.18E-02	105.52	NaN	NaN	0
1518	ILGLDFGYVTR	sp|Q9Z184|PADI3_MOUSE	yes	yes	384	394	11	R	E	0	1252.682	2	5.05E-03	123.01	NaN	NaN	0
1519	ILGLLDTHLKTR	sp|Q9D8N0|EF1G_MOUSE	yes	yes	138	149	12	R	T	0	1378.830	3;4	5.06E-03	73.44	1.79	1.20	5
1520	ILGPGAGEMVNEAALALEYGASCI	sp|O08749|DLDH_MOUSE	yes	yes	455	482	28	H	V	0	2876.368	3	4.04E-03	63.63	NaN	NaN	0
1521	ILHSHISDTSIVVKMDNSR	sp|P97861|KRT86_MOUSE	no	no	249	267	19	R	D	0	2151.111	4	5.75E-05	82.88	2.63	1.48	1
1522	ILIGGNLPGSR	sp|Q9Z184|PADI3_MOUSE	yes	yes	428	438	11	R	G	0	1095.640	2	3.38E-03	119.27	0.62	0.49	2
1523	ILISLATGNR	sp|P14824|ANXA6_MOUSE	yes	yes	500	509	10	R	E	0	1056.629	2	1.26E-02	112.71	NaN	NaN	0
1524	ILKSPEIQR	sp|Q9D8E6|RL4_MOUSE	yes	yes	292	300	9	R	A	0	1082.645	2;3	3.90E-04	142.83	1.20	0.88	12
1525	ILMGSTLR	sp|Q9DBC7|KAP0_MOUSE	yes	no	234	241	8	R	K	0	889.506	2	6.23E-02	87.70	NaN	NaN	0
1526	ILMWTELIR	sp|Q8K3J1|NDUS8_MOUSE	yes	yes	60	68	9	R	G	0	1173.658	2	3.17E-02	93.65	NaN	NaN	0
1527	ILNGRPPLGFLNPR	sp|O89023|TPP1_MOUSE	yes	yes	492	505	14	R	L	1	1562.905	3	5.04E-02	55.26	NaN	NaN	0
1528	ILNPLLDR	sp|Q9QY23|PKP3_MOUSE	yes	no	656	663	8	R	V	0	952.571	2	3.22E-02	136.27	NaN	NaN	0
1529	ILQEDFTCR	sp|Q91ZX7|LRP1_MOUSE	yes	yes	2511	2519	9	R	A	0	1180.555	2	2.08E-02	111.46	NaN	NaN	0
1530	ILQHKDEFNADHPFIYIIR	sp|P70124|SPB5_MOUSE	yes	yes	341	359	19	R	H	0	2368.233	4;5	3.69E-08	111.77	0.90	0.84	6
1531	ILQNIQVFDFTFSPEEMKQLDALN	sp|Q9JII6|AK1A1_MOUSE	yes	yes	270	297	28	R	Y	0	3423.729	4	2.47E-03	61.04	1.48	1.22	1
1532	ILSFVYPIR	sp|Q91VE0|S27A4_MOUSE	yes	yes	409	417	9	R	L	0	1106.649	2	1.89E-02	122.52	NaN	NaN	0
1533	ILTDYGFEGHPFR	sp|Q9DCT2|NDUS3_MOUSE	yes	yes	186	198	13	R	K	0	1550.752	3	9.20E-04	84.37	0.17	0.11	1
1534	ILVATNLFGR	sp|Q9Z1N5|DX39B_MOUSE	yes	no	340	349	10	R	G	0	1102.650	2	5.55E-03	140.11	NaN	NaN	0
1535	ILVCLLQGSR	sp|O35640|ANXA8_MOUSE	yes	yes	158	167	10	R	D	0	1157.659	2	8.62E-03	128.52	NaN	NaN	0
1536	ILVGTNLVR	sp|Q9EQH3|VPS35_MOUSE	yes	yes	218	226	9	R	L	0	983.613	2	1.90E-02	121.53	NaN	NaN	0
1537	ILVGTPGR	sp|Q9JIK5|DDX21_MOUSE	yes	no	383	390	8	D	I	0	811.492	2	6.61E-02	84.57	NaN	NaN	0
1538	ILVKYLR	sp|Q64481|CP3AG_MOUSE	yes	no	155	161	7	D	Q	0	903.591	3	1.57E-02	103.29	1.17	0.91	2
1539	ILVTGGSGLVGR	sp|P23591|FCL_MOUSE	yes	yes	10	21	12	R	A	0	1127.666	2	5.31E-03	100.93	NaN	NaN	0
1540	ILVTLLHTLER	sp|Q8CAY6|THIC_MOUSE	yes	yes	362	372	11	R	V	0	1306.797	2;3	3.10E-03	134.13	NaN	NaN	0

1541	IMDESNVLDSGFLER	sp|Q9JHU4|DYHC1_MOUSE	yes	yes	2991	3005	15	F	M	0	1723.809	2	1.89E-02	68.33	NaN	NaN	0
1542	IMDPNIVGNEHYDVAR	sp|P56480|ATPB_MOUSE	yes	yes	407	422	16	R	G	0	1841.873	3	4.99E-04	118.31	NaN	NaN	0
1543	IMEGPAFNFLDAPAVR	sp|Q9D051|ODPB_MOUSE	yes	yes	309	324	16	R	V	0	1746.876	2	6.13E-04	109.79	NaN	NaN	0
1544	IMGIPEDEQMGLLR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	328	341	14	R	V	0	1600.795	2	4.01E-03	91.62	NaN	NaN	0
1545	IMGPNYTPGKKEDLYLKPIQR	sp|P58252|EF2_MOUSE	yes	yes	429	449	21	R	T	0	2460.320	5	6.95E-02	44.24	1.14	0.93	2
1546	IMNVIGEPIDER	sp|P56480|ATPB_MOUSE	yes	yes	144	155	12	R	G	0	1384.702	2	2.41E-03	128.68	NaN	NaN	0
1547	IMPKDIQLAR	sp|P84244|H33_MOUSE	no	no	120	129	10	T	R	0	1183.675	2	4.21E-06	160.18	1.28	0.85	7
1548	IMVANIEEVLQR	sp|O08547|SC22B_MOUSE	yes	yes	148	159	12	R	G	0	1413.765	2	2.55E-04	164.04	NaN	NaN	0
1549	INAAEIESR	sp|P35235-2|PTN11_MOUSE	yes	no	221	229	9	R	V	0	1001.514	2	5.56E-02	75.39	NaN	NaN	0
1550	INALKQLQVR	sp|Q78ZA7|NP1L4_MOUSE	yes	yes	67	76	10	R	C	0	1181.724	3	4.59E-03	88.50	0.98	0.92	4
1551	INEILSNALKR	sp|Q9D0E1-2|HNRPM_MOUSE	yes	no	332	342	11	R	G	0	1269.741	2;3	8.61E-03	72.34	1.39	0.91	6
1552	INETSQHHDDLE	sp|P20152|VIME_MOUSE	yes	no	455	466	12	V	-	0	1436.617	2	1.89E-03	135.50	NaN	NaN	0
1553	INFMAAKL	sp|Q9JHR7|IDE_MOUSE	yes	no	1012	1019	8	H	-	0	906.500	2	1.63E-02	89.14	2.59	2.27	2
1554	INFYCPGSALGR	sp|Q920B9|SP16H_MOUSE	yes	yes	570	581	12	R	N	0	1353.650	2	3.12E-02	71.08	NaN	NaN	0
1555	INISEGNCPER	sp|P60335|PCBP1_MOUSE	yes	no	47	57	11	R	I	0	1287.588	2	4.74E-10	207.88	0.04	0.03	1
1556	INKMLSCAGADR	sp|Q6ZWV3|RL10_MOUSE	yes	no	99	110	12	R	L	0	1334.644	3	8.92E-04	98.94	1.11	0.96	8
1557	INLAQKAFCGFEDPR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	4251	4265	15	R	T	0	1764.862	3	2.87E-05	107.35	1.62	1.00	7
1558	INPDGSQSVVEVPYAR	sp|Q9QXT0|CNPY2_MOUSE	yes	yes	58	73	16	R	S	0	1729.864	2	6.59E-04	106.34	NaN	NaN	0
1559	INPVEFNPEFVAR	sp|Q9DCG9|TR112_MOUSE	yes	yes	32	44	13	R	M	0	1530.783	2	1.40E-03	127.78	0.22	0.22	1
1560	INQTYQQQYGR	sp|P97429|ANXA4_MOUSE	yes	yes	124	134	11	R	S	0	1397.669	2	1.14E-16	231.42	93.37	73.29	1
1561	INVLPLGSGAIAGNPLGVDR	sp|Q91YI0|ARLY_MOUSE	yes	yes	194	213	20	R	E	0	1932.079	2	9.20E-03	68.42	NaN	NaN	0
1562	INVYYNEAAGNKYVPR	sp|Q7TMM9|TBB2A_MOUSE	yes	yes	47	62	16	R	A	0	1869.937	3	1.97E-06	103.79	1.00	0.71	9
1563	INVYYNEATGGKYVPR	sp|P68372|TBB4B_MOUSE	yes	yes	47	62	16	R	A	0	1842.926	3	7.16E-07	120.70	1.19	0.93	10
1564	IPALLNTQPMLQLEYTATDR	sp|P19096|FAS_MOUSE	yes	yes	1251	1270	20	R	H	0	2287.188	2	7.45E-03	71.59	NaN	NaN	0
1565	IPAYFITVHDPAVPPGEDPDGR	sp|Q9Z1Q9|SYVC_MOUSE	yes	yes	730	751	22	R	Y	0	2362.159	3	7.57E-03	62.62	NaN	NaN	0
1566	IPGGPQMIQLSLDGKR	sp|P17563|SBP1_MOUSE	yes	no	383	398	16	R	L	0	1708.929	3	3.59E-07	125.50	1.01	0.95	9
1567	IPGMLIIDTPGHESFSNLR	sp|Q05D44|IF2P_MOUSE	yes	yes	691	709	19	R	N	0	2096.073	3	1.20E-02	67.65	NaN	NaN	0
1568	IPGSIIPPPLVR	sp|Q8CHY6|P66A_MOUSE	yes	yes	210	221	12	R	G	0	1257.781	2	4.48E-03	103.91	NaN	NaN	0
1569	IPKEQGFLSFWR	sp|P48962|ADT1_MOUSE	yes	yes	61	72	12	R	G	0	1506.798	3	3.71E-03	75.10	1.78	1.16	3
1570	IPKEQGVLSFWR	sp|P51881|ADT2_MOUSE	yes	yes	61	72	12	R	G	0	1458.798	2;3	2.71E-05	148.41	1.63	1.01	9
1571	IPKVQKLLQDFFNGR	sp|Q61696|HS71A_MOUSE	yes	no	343	357	15	R	D	0	1802.020	3;4	6.38E-03	63.19	0.95	0.92	3
1572	IPLENLQIIR	sp|Q01279|EGFR_MOUSE	yes	yes	99	108	10	R	G	0	1207.729	2	1.23E-02	113.93	NaN	NaN	0
1573	IPQSTLSEFYPR	sp|P62814|VATB2_MOUSE	yes	yes	495	506	12	R	D	0	1436.730	2	2.50E-03	127.56	NaN	NaN	0
1574	IPQTVLWR	sp|Q62452|UD19_MOUSE	yes	no	324	331	8	R	Y	0	1011.587	2	3.69E-02	127.56	NaN	NaN	0
1575	IPSAVGYQPTLATDMGTMQER	sp|P56480|ATPB_MOUSE	yes	yes	325	345	21	R	I	0	2265.077	2;3	2.30E-04	106.23	NaN	NaN	0
1576	IPVPILPGLPMNNHGNYIVR	sp|Q921G7|ETFD_MOUSE	yes	yes	155	174	20	R	L	0	2213.214	3	3.54E-03	83.54	NaN	NaN	0
1577	IPVQALLHLR	sp|P36916-2|GNL1_MOUSE	yes	no	274	283	10	R	H	0	1158.724	3	1.59E-02	101.65	NaN	NaN	0
1578	IPWFQYPIIYDIR	sp|O35129|PHB2_MOUSE	yes	yes	72	84	13	R	A	0	1722.913	3	1.00E-02	77.19	NaN	NaN	0
1579	IQELEDMLAKER	sp|P14733|LMNB1_MOUSE	yes	yes	322	333	12	R	D	0	1473.750	3	1.28E-03	91.96	1.28	0.83	5
1580	IQESKSQCTQVVQER	sp|E9Q557|DESP_MOUSE	yes	yes	1810	1824	15	R	E	0	1818.889	3	1.82E-10	180.64	1.81	1.05	5
1581	IQETQAELPR	sp|P97311|MCM6_MOUSE	yes	yes	208	217	10	R	G	0	1183.620	2	6.51E-03	136.49	NaN	NaN	0
1582	IQFNESFAEMNR	sp|P19783|COX41_MOUSE	yes	yes	84	95	12	R	G	0	1484.672	2	1.31E-06	192.68	NaN	NaN	0
1583	IQGITKPAIR	sp|P62806|H4_MOUSE	yes	yes	27	36	10	N	R	0	1095.676	2	4.24E-04	129.89	0.94	0.64	6
1584	IQKYSEGEIR	sp|Q9WUP7-2|UCHL5_MOUSE	yes	no	208	217	10	R	F	0	1221.635	3	3.01E-02	60.26	1.45	1.17	6
1585	IQLLEEELDR	sp|Q6IRU2|TPM4_MOUSE	yes	yes	56	65	10	R	A	0	1256.661	2	4.53E-03	143.96	NaN	NaN	0
1586	IQLVEEELDR	sp|P21107-2|TPM3_MOUSE	no	no	56	65	10	R	A	0	1242.646	2	7.36E-04	169.37	NaN	NaN	0
1587	IQNLLKITNLR	sp|P02469|LAMB1_MOUSE	yes	no	224	234	11	R	I	0	1324.819	3	2.44E-03	88.60	1.72	1.05	1
1588	IQNSVKLATEPLEQAVR	sp|Q9ER72-2|SYCC_MOUSE	yes	no	155	171	17	R	S	0	1895.048	3	3.63E-05	97.24	1.04	0.88	2
1589	IQQEIAVQNPLVSER	sp|Q7TQI3|OTUB1_MOUSE	yes	yes	37	51	15	R	L	0	1722.926	2	4.82E-05	166.92	NaN	NaN	0
1590	IQTQPGYANTLR	sp|Q8VEM8|MPCP_MOUSE	yes	yes	185	196	12	R	E	0	1360.710	2	1.32E-03	142.83	NaN	NaN	0
1591	IQVVGTYR	sp|P25206|MCM3_MOUSE	yes	yes	235	242	8	R	C	0	934.524	2	9.95E-04	153.04	0.23	0.22	3
1592	IQWVGDPR	sp|P27573|MYP0_MOUSE	yes	yes	99	106	8	R	W	0	969.503	2	4.18E-02	109.71	NaN	NaN	0
1593	IQYQLVDISQDNALR	sp|Q91VW3|SH3L3_MOUSE	yes	yes	33	47	15	R	D	0	1774.921	2	1.10E-02	73.30	NaN	NaN	0
1594	IRFEIFPTR	sp|Q08189|TGM3_MOUSE	yes	yes	657	665	9	R	S	1	1177.661	2;3	2.11E-02	109.66	NaN	NaN	0
1595	ISALEEQLQQIR	sp|P02535-3|K1C10_MOUSE	no	no	400	411	12	Q	A	0	1426.778	2	6.77E-23	269.81	NaN	NaN	0
1596	ISALNIVGDLLR	sp|Q9CZA6-4|NDE1_MOUSE	yes	no	119	130	12	R	K	0	1282.761	2	5.59E-03	100.22	NaN	NaN	0
1597	ISAVAVAER	sp|O70133|DHX9_MOUSE	yes	no	450	458	9	R	V	0	914.519	2	2.20E-02	104.42	NaN	NaN	0
1598	ISDTSIVVKMDNSR	sp|P97861|KRT86_MOUSE	no	no	254	267	14	H	D	0	1563.793	3	1.22E-02	54.90	2.10	1.18	1
1599	ISDTSVVLSMDNNR	sp|P50446|K2C6A_MOUSE	no	no	302	315	14	H	S	0	1549.741	2	1.06E-03	117.08	NaN	NaN	0
1600	ISDTSVVVKMDNSR	sp|Q6IMF0|KRT83_MOUSE	yes	yes	259	272	14	H	D	0	1549.777	3	1.11E-04	111.12	2.00	1.26	4
1601	ISEQFTAMFR	sp|P99024|TBB5_MOUSE	no	no	381	390	10	R	R	0	1228.591	2	1.76E-05	195.36	0.04	0.03	1
1602	ISGAGIDRPPYGVFTINPR	sp|Q7TMD7|DSG4_MOUSE	yes	yes	87	105	19	R	T	1	2029.075	3	1.37E-02	64.71	NaN	NaN	0
1603	ISGIGSGFGSR	sp|Q8BGZ7|K2C75_MOUSE	yes	no	50	60	11	R	S	0	1036.530	2	1.21E-06	193.30	NaN	NaN	0
1604	ISGLIYEETR	sp|P62806|H4_MOUSE	yes	yes	47	56	10	R	G	0	1179.614	2	4.12E-08	207.34	NaN	NaN	0
1605	ISIGGGSCGIGGGYGSR	sp|P50446|K2C6A_MOUSE	yes	no	68	84	17	R	F	0	1553.726	2	4.92E-04	114.96	NaN	NaN	0
1606	ISLGGACGAGGYGSR	sp|Q922U2|K2C5_MOUSE	yes	no	46	60	15	R	S	0	1381.641	2	2.67E-05	109.07	762.48	388.22	1
1607	ISLPLPTFSSLNLR	sp|P20152|VIME_MOUSE	yes	yes	411	424	14	R	E	0	1556.893	2;3	5.49E-07	194.98	NaN	NaN	0
1608	ISNASDALDKIR	sp|P11499|HS90B_MOUSE	no	no	44	55	12	L	Y	0	1301.694	2	7.31E-05	136.30	1.13	0.89	5
1609	ISPDLCGR	sp|Q61554|FBN1_MOUSE	yes	yes	1076	1083	8	R	G	0	916.444	2	6.59E-02	84.74	NaN	NaN	0
1610	ISPSETGNQVDR	sp|Q3V188|ENDOU_MOUSE	yes	no	170	181	12	R	S	0	1301.621	2	9.13E-04	148.18	NaN	NaN	0
1611	ISQCTPKVDFPQDQLATLTGR	sp|P08249|MDHM_MOUSE	yes	yes	209	229	21	L	I	0	2374.195	3	2.85E-28	208.27	1.21	1.00	8
1612	ISQLEMAR	sp|P26041|MOES_MOUSE	yes	yes	428	435	8	R	K	0	946.491	2	3.69E-02	127.46	NaN	NaN	0
1613	ISSIEQKTER	sp|Q9CQV8-2|1433B_MOUSE	yes	no	62	71	10	V	N	0	1189.630	2	3.24E-04	136.02	1.35	1.05	3
1614	ISSLQKQLDSLSGDR	sp|Q6NXH9|K2C73_MOUSE	yes	no	186	200	15	H	V	0	1645.864	3	1.77E-06	140.22	1.86	1.15	4
1615	ISSYVPWINR	sp|P21812|MCPT4_MOUSE	yes	yes	232	241	10	R	V	0	1233.651	2	5.46E-03	140.45	NaN	NaN	0
1616	ISVLEALR	sp|Q925I1-2|ATAD3_MOUSE	yes	no	290	297	8	R	H	0	899.544	2	4.75E-02	99.76	NaN	NaN	0
1617	ISVYYNEATGGKYVPR	sp|P99024|TBB5_MOUSE	yes	yes	47	62	16	R	A	0	1815.916	3	7.00E-05	94.49	1.25	1.00	10
1618	ISYFTFIGTPVQATNMNDFKR	sp|Q8CDN6|TXNL1_MOUSE	yes	yes	260	280	21	R	V	0	2449.210	3	1.42E-04	76.30	0.93	0.85	5
1619	ISYSSGGGSFR	sp|Q922U2|K2C5_MOUSE	yes	no	71	81	11	R	N	0	1116.520	2	6.58E-04	152.64	NaN	NaN	0
1620	ITAVCKVPDEAEVVVER	sp|Q08189|TGM3_MOUSE	yes	yes	572	588	17	R	D	0	1912.993	3	6.05E-12	176.69	1.19	0.97	6
1621	ITDAIQEWVMR	sp|P70698|PYRG1_MOUSE	yes	yes	117	127	11	H	Q	0	1360.681	2	6.50E-04	152.70	NaN	NaN	0
1622	ITDLYTDLR	sp|Q62261|SPTB2_MOUSE	yes	no	75	83	9	R	D	0	1108.576	2	1.69E-02	130.66	NaN	NaN	0
1623	ITDPEILESR	sp|Q8K010|OPLA_MOUSE	yes	yes	1145	1154	10	R	Y	0	1171.609	2	1.45E-02	105.46	NaN	NaN	0
1624	ITDPQYFLDTPR	sp|Q8R1F5|HYI_MOUSE	yes	yes	156	167	12	R	Q	0	1464.725	2	4.34E-03	105.65	NaN	NaN	0
1625	ITESEEVVSR	sp|P48678|LMNA_MOUSE	yes	no	63	72	10	R	E	0	1147.572	2	2.38E-03	152.04	NaN	NaN	0
1626	ITFTNPEHASDAMR	sp|O89086|RBM3_MOUSE	yes	yes	52	65	14	F	A	0	1588.730	2	3.82E-02	61.41	NaN	NaN	0
1627	ITGGGLLENIPR	sp|Q64737|PUR2_MOUSE	yes	yes	681	692	12	H	V	0	1238.698	2	3.94E-03	110.38	NaN	NaN	0
1628	ITGVEAENLLLTR	sp|P35235-2|PTN11_MOUSE	yes	no	11	23	13	N	G	0	1427.798	2	1.53E-03	109.07	NaN	NaN	0
1629	ITKYNTVQYSK	sp|Q61495|DSG1A_MOUSE	yes	no	1047	1057	11	R	-	0	1343.709	3	3.49E-02	50.35	1.50	0.92	3
1630	ITLNLPASTPVR	sp|Q8BY87-2|UBP47_MOUSE	yes	no	40	51	12	R	K	0	1280.745	2	1.46E-02	77.60	NaN	NaN	0
1631	ITNVESQLGEIR	sp|Q61897|KT33B_MOUSE	no	no	318	329	12	L	A	0	1357.720	2	2.23E-03	131.06	NaN	NaN	0
1632	ITNVLQNPDLALR	sp|Q68FD5|CLH1_MOUSE	yes	yes	338	350	13	Y	M	0	1465.825	2	2.47E-04	163.33	NaN	NaN	0
1633	ITPSYVAFTPEGER	sp|P20029|GRP78_MOUSE	yes	yes	62	75	14	R	L	0	1565.773	2	5.60E-04	122.78	42.56	33.37	2
1634	ITSLEVENQNLR	sp|P57776-2|EF1D_MOUSE	yes	no	60	71	12	R	G	0	1414.742	2	3.53E-12	233.13	NaN	NaN	0
1635	ITTMQLER	sp|P23116|EIF3A_MOUSE	yes	yes	733	740	8	R	E	0	990.517	2	3.08E-02	138.78	NaN	NaN	0
1636	ITWDPPSGPVKGYR	sp|Q80X19-2|COEA1_MOUSE	yes	no	848	861	14	R	I	0	1571.810	3	5.28E-03	68.28	2.10	1.20	2
1637	ITYQPSTGEGNEQTITVGGR	sp|Q60847|COCA1_MOUSE	yes	no	1787	1806	20	R	Q	0	2107.018	2	1.83E-06	144.75	NaN	NaN	0
1638	IVAEEFLKNF	sp|P59999|ARPC4_MOUSE	yes	no	159	168	10	R	-	0	1208.644	2	3.59E-03	94.31	1.28	1.05	7
1639	IVAPGKGILAADESTGSIAKR	sp|P05064|ALDOA_MOUSE	yes	yes	23	43	21	R	L	0	2053.153	3;4	7.53E-03	67.40	1.35	1.11	9
1640	IVATKPLYVALAQR	sp|P29341|PABP1_MOUSE	yes	yes	357	370	14	R	K	0	1541.929	2;3	9.50E-06	138.21	1.23	1.09	12
1641	IVAVTGAEAQKALR	sp|Q8BGQ7|SYAC_MOUSE	yes	yes	752	765	14	R	K	0	1425.830	3	7.22E-02	36.29	1.63	1.55	2
1642	IVEKPFGR	sp|Q00612|G6PD1_MOUSE	yes	no	168	175	8	I	D	0	944.544	2	2.63E-02	75.21	1.01	0.87	4
1643	IVEPYIAWGYPNLKSVNELIYKR	sp|P14148|RL7_MOUSE	yes	yes	157	179	23	R	G	0	2764.495	4	4.42E-03	67.76	1.56	1.00	1

1644	IVEVFEIGPKR	sp|Q60847|COCA1_MOUSE	yes	no	1225	1235	11	R	V	0	1285.739	2;3	6.01E-07	164.65	1.86	1.18	12
1645	IVQVVCKKYR	sp|Q9Z1Q5|CLIC1_MOUSE	yes	yes	186	195	10	H	G	0	1291.744	3	2.32E-02	65.22	0.92	0.75	3
1646	IVSQLLTLMDGLKQR	sp|Q01853|TERA_MOUSE	yes	yes	324	338	15	R	A	0	1713.981	2;3	8.55E-14	196.18	1.28	1.03	6
1647	IVSRPEELR	sp|P80318|TCPG_MOUSE	yes	yes	331	339	9	R	E	1	1097.619	3	3.45E-02	90.91	NaN	NaN	0
1648	IVYSPVAGTR	sp|Q60847|COCA1_MOUSE	yes	no	1968	1977	10	R	P	0	1061.587	2	1.61E-02	101.38	NaN	NaN	0
1649	IVYSPVAGTRPSESIVVPGNTR	sp|Q60847|COCA1_MOUSE	yes	no	1968	1989	22	R	T	1	2298.233	3	5.99E-04	90.46	NaN	NaN	0
1650	IWGDCTVR	sp|P26638|SYSC_MOUSE	yes	yes	158	165	8	R	K	0	1005.470	2	2.04E-02	81.30	0.08	0.07	1
1651	IWSVPNTSCVQVVR	sp|Q99KP6-3|PRP19_MOUSE	yes	no	205	218	14	R	A	0	1643.845	2	1.13E-03	107.65	NaN	NaN	0
1652	IYDDDFFQNLDGVANALDNIDAR	sp|Q02053|UBA1_MOUSE	yes	yes	559	581	23	R	M	0	2613.198	2;3	1.39E-15	189.11	NaN	NaN	0
1653	IYELAAGGTAVGTGLNTR	sp|P97807-2|FUMH_MOUSE	yes	no	226	243	18	R	I	0	1762.921	2	6.54E-03	79.49	NaN	NaN	0
1654	IYLYLTKVGISPDKLR	sp|Q9CZD3|SYG_MOUSE	yes	yes	403	418	16	R	F	0	1878.098	3	3.05E-02	57.29	1.03	0.99	1
1655	IYNEIPDINLDVPHSYSVLER	sp|Q61823|PDCD4_MOUSE	yes	yes	408	428	21	R	F	0	2485.249	3	2.74E-03	77.96	NaN	NaN	0
1656	IYSHSLLPIIR	sp|Q64737|PUR2_MOUSE	yes	yes	661	671	11	R	S	0	1310.771	3	1.52E-04	169.65	NaN	NaN	0
1657	IYVGNLPPDIR	sp|Q6PDM2-3|SRSF1_MOUSE	yes	no	18	28	11	R	T	0	1255.693	2	5.92E-03	118.90	NaN	NaN	0
1658	IYVVDVGSEPR	sp|P17563|SBP1_MOUSE	yes	no	104	114	11	R	A	0	1232.640	2	7.04E-03	113.67	NaN	NaN	0
1659	IYWNDGLDQYR	sp|Q60967|PAPS1_MOUSE	yes	yes	387	397	11	R	L	0	1441.663	2	1.28E-04	139.86	0.10	0.10	3
1660	KACGDSTLTQITAGLDPVGR	sp|P62880|GBB2_MOUSE	yes	yes	23	42	20	R	I	0	2059.037	3	3.25E-02	40.95	1.42	0.95	6
1661	KAEGAALAGR	sp|Q08AT1|RASLC_MOUSE	yes	yes	146	155	10	T	F	0	942.525	2	6.20E-03	79.16	4.26	2.64	2
1662	KAIFMDCGIHAR	sp|P15089|CBPA3_MOUSE	yes	yes	167	178	12	R	E	0	1417.696	3	1.26E-02	64.12	1.41	0.80	2
1663	KALLALAKGDR	sp|P10107|ANXA1_MOUSE	yes	yes	178	188	11	R	C	0	1154.714	3	1.11E-02	70.09	1.10	0.89	6
1664	KAMEAVAAQGKVKK	sp|Q9DBJ1|PGAM1_MOUSE	yes	no	241	254	14	R	-	0	1457.839	4	1.52E-01	42.32	1.01	0.95	1
1665	KAMKGIGTDEATIIDIVTHR	sp|P14824|ANXA6_MOUSE	yes	yes	374	393	20	R	S	0	2168.162	4	4.79E-05	79.47	1.00	0.98	4
1666	KAMKGLGTDEDSILNLLTSR	sp|P48036|ANXA5_MOUSE	yes	yes	24	43	20	R	S	0	2161.141	3;4	6.46E-06	100.02	0.96	0.92	14
1667	KAQPSQAAEEPAEKADEPMEH	sp|Q9R1P4|PSA1_MOUSE	yes	no	243	263	21	R	-	0	2292.033	4	4.63E-02	42.64	1.13	1.09	2
1668	KASGPPVSELITKAVAASKER	sp|P15864|H12_MOUSE	yes	no	34	54	21	R	S	0	2138.206	4	1.44E-02	53.63	1.51	0.98	1
1669	KASWVSSTLGFWFTELLER	sp|Q8VHE6|DYH5_MOUSE	yes	yes	4443	4461	19	K	N	0	2256.158	4	4.39E-02	37.69	4.30	3.48	1
1670	KASYSAVSLYGNPVR	sp|P28654|PGS2_MOUSE	yes	yes	316	330	15	R	Y	0	1610.842	3	7.15E-03	74.79	0.82	0.47	2
1671	KAYGLALAKLGHASDR	sp|P40142|TKT_MOUSE	yes	yes	319	334	16	R	I	0	1669.926	4	9.92E-02	40.86	1.40	1.29	3
1672	KCCESNLEPLFGGYIEALR	sp|Q9Z2T6|KRT85_MOUSE	yes	yes	162	180	19	R	R	0	2255.072	2;3	8.19E-12	131.67	1.77	1.12	4
1673	KCCESNMEPLFEGYIEALR	sp|P97861|KRT86_MOUSE	no	no	145	163	19	R	R	0	2345.049	2;3	2.27E-12	148.85	1.91	1.19	10
1674	KCCESNMEPLFEGYIEALRR	sp|P97861|KRT86_MOUSE	no	no	145	164	20	R	E	1	2501.150	4	2.69E-05	89.86	2.22	1.32	2
1675	KDAEDWFFSKTEELNR	sp|Q9QWL7|K1C17_MOUSE	yes	no	269	284	16	R	E	0	2013.943	3;4	1.77E-04	80.74	1.77	0.99	7
1676	KDAEEWFFSKTEELNR	sp|Q61781|K1C14_MOUSE	yes	yes	306	321	16	R	E	0	2027.959	3;4	1.70E-04	81.66	1.66	1.01	6
1677	KDAEEWFNQKSKELTTEIDSNIEQ	sp|P02535-3|K1C10_MOUSE	yes	no	323	359	37	R	T	1	4436.155	7	3.13E-02	44.90	2.20	1.32	1
1678	KDDPLTNLNTAFDVAER	sp|Q7TPR4|ACTN1_MOUSE	yes	yes	198	214	17	R	F	0	1917.943	3	1.36E-04	80.32	1.63	1.07	1
1679	KDGSASGTTLLEALDCILPPTRPTD	sp|P10126|EF1A1_MOUSE	yes	yes	219	247	29	R	L	1	3121.644	4;5	1.36E-08	119.35	1.16	0.96	7
1680	KDLYANTVLSGGTTMYPGIADR	sp|P63260|ACTG_MOUSE	no	no	291	312	22	R	M	0	2342.158	2;3	2.93E-12	150.06	1.22	0.99	30
1681	KDPELWGSVLLESNPYR	sp|Q68FD5|CLH1_MOUSE	yes	yes	951	967	17	R	R	0	2002.016	3	7.77E-06	102.08	1.10	0.86	4
1682	KEAESSPFVER	sp|P08113|ENPL_MOUSE	yes	yes	547	557	11	R	L	0	1277.625	3	1.45E-02	66.99	1.21	0.92	5
1683	KEIPAKIIFEDDR	sp|P70349|HINT1_MOUSE	yes	yes	25	37	13	R	C	0	1572.851	3	8.44E-03	65.04	1.22	1.03	5
1684	KELEEDFIR	sp|Q9CQJ6|COTL1_MOUSE	yes	yes	118	126	9	R	S	0	1177.598	2	2.50E-02	103.91	1.12	0.98	3
1685	KFAYLGR	sp|P19253|RL13A_MOUSE	yes	yes	134	140	7	R	L	0	853.481	2	2.29E-01	73.62	NaN	NaN	0
1686	KFDLNSPWEAFPAYR	sp|Q9DCT2|NDUS3_MOUSE	yes	yes	231	245	15	R	Q	0	1839.894	3	8.08E-03	59.25	0.97	0.80	3
1687	KFFDQYR	sp|E9Q557|DESP_MOUSE	yes	yes	2554	2560	7	R	S	0	1002.492	2	1.71E-02	101.43	1.56	0.88	2
1688	KFLPLFDR	sp|Q64433|CH10_MOUSE	yes	yes	8	15	8	R	V	0	1034.591	2	4.78E-03	126.07	1.08	1.02	4
1689	KFVADGIFKAELNEFLTR	sp|P62908|RS3_MOUSE	yes	yes	10	27	18	R	E	0	2097.126	4	5.02E-02	36.64	1.19	1.16	1
1690	KFYGPEGPYGVFAGR	sp|O55022|PGRC1_MOUSE	yes	yes	105	119	15	R	D	0	1643.810	3	3.20E-05	104.55	0.93	0.65	2
1691	KGDIFLVR	sp|Q01853|TERA_MOUSE	yes	yes	148	155	8	R	G	0	946.560	2	5.67E-03	120.99	1.20	1.06	4
1692	KGHAVGDIPGVR	sp|P62267|RS23_MOUSE	yes	yes	108	119	12	R	F	0	1204.668	3	7.76E-03	70.09	1.23	0.96	5
1693	KGLKEGIPALDNFLDKL	sp|P58252|EF2_MOUSE	yes	no	842	858	17	R	-	0	1870.056	3;4	4.10E-03	87.43	1.09	1.06	4
1694	KGTDIMYTGTLDCWR	sp|P51881|ADT2_MOUSE	yes	yes	245	259	15	R	K	0	1815.828	2;3	1.03E-05	123.08	1.21	0.80	8
1695	KGTDVNVFTTILTSR	sp|P10107|ANXA1_MOUSE	yes	yes	214	228	15	R	S	0	1650.894	2;3	3.28E-05	103.88	1.17	1.01	9
1696	KGTDVPKWISIMTER	sp|P07356|ANXA2_MOUSE	yes	yes	206	220	15	R	S	0	1759.929	3;4	7.21E-03	61.27	1.01	0.95	8
1697	KGVAINMVTEEDKR	sp|P60843|IF4A1_MOUSE	yes	yes	369	382	14	R	T	0	1588.824	3	2.27E-04	99.93	1.22	0.89	4
1698	KGVKIDKTDYMVGSYGPR	sp|Q99PT1|GDIR1_MOUSE	yes	yes	135	152	18	R	A	0	2013.035	4	5.02E-02	36.64	1.40	1.15	4
1699	KGVQDSIADAEQR	sp|Q3TTY5|K22E_MOUSE	yes	no	439	451	13	C	G	0	1415.701	3	3.40E-03	73.39	2.59	1.60	4
1700	KHEAFESDLAAHQDR	sp|P57780|ACTN4_MOUSE	no	no	456	470	15	R	V	0	1752.818	4	1.75E-04	91.40	1.16	0.99	8
1701	KIISLSQLLQEDSLNVADLSSLR	sp|P97372|PSME2_MOUSE	yes	yes	39	61	23	R	A	0	2541.401	3	1.59E-05	107.75	0.66	0.52	1
1702	KIQALQQQADDAEDR	sp|Q6IRU2|TPM4_MOUSE	yes	yes	13	27	15	R	A	0	1727.844	3	4.04E-07	152.00	1.01	0.82	4
1703	KIQVLQQQADDAEER	sp|P21107-2|TPM3_MOUSE	yes	yes	13	27	15	R	A	0	1769.891	3	1.24E-06	144.80	0.99	0.86	4
1704	KISSPTGSKDLQMVNISLR	sp|O35129|PHB2_MOUSE	yes	yes	89	107	19	R	V	0	2073.125	4	1.02E-02	70.56	1.80	1.02	1
1705	KITISDCGQL	sp|P17742|PPIA_MOUSE	yes	no	155	164	10	K	-	0	1133.575	2	4.31E-03	90.14	0.96	0.87	5
1706	KKCLGELICTLNAANVPAGTEVVC	sp|P17751|TPIS_MOUSE	yes	yes	69	103	35	R	Q	0	3818.916	4	4.38E-03	67.40	1.33	1.22	2
1707	KKFITPESTVMLLEAQAATGGIIDP	sp|E9Q557|DESP_MOUSE	yes	yes	2049	2075	27	R	N	0	2922.564	4;5	1.22E-05	100.24	1.77	1.22	2
1708	KKLLEGEEIR	sp|P04104|K2C1_MOUSE	yes	yes	491	500	10	Y	M	0	1213.703	3	3.70E-02	55.35	1.11	0.76	2
1709	KKTAPASVPPFQFPEPAESCKAHE	sp|P02772|FETA_MOUSE	yes	yes	125	151	27	R	A	0	3051.487	5	5.44E-02	31.17	1.11	1.02	1
1710	KKYNLGAPVAGTCYQAEWDDYV	sp|P70296|PEBP1_MOUSE	yes	no	156	187	32	R	-	0	3690.803	5	5.66E-04	69.49	0.96	0.89	1
1711	KLAQQYYLVYQEPIPTAQLVQR	sp|P49722|PSA2_MOUSE	yes	yes	92	113	22	R	V	0	2648.433	3	6.94E-06	89.66	1.37	0.97	5
1712	KLAVNMVPFPR	sp|P99024|TBB5_MOUSE	no	no	252	262	11	R	L	0	1270.722	2;3	1.12E-04	141.88	1.32	1.16	8
1713	KLDELYGTWR	sp|Q9D8E6|RL4_MOUSE	yes	yes	259	268	10	R	K	0	1279.656	2;3	1.61E-03	110.31	1.22	0.90	8
1714	KLDPGSEETQTLVR	sp|Q9D8N0|EF1G_MOUSE	yes	yes	401	414	14	R	E	0	1571.816	2;3	1.34E-08	167.32	1.28	0.95	16
1715	KLFIGGLSFETTDDSLR	sp|Q8BG05-2|ROA3_MOUSE	no	no	14	30	17	R	E	0	1897.979	3	5.29E-07	118.21	1.17	0.67	5
1716	KLFIGGLSFETTDESLR	sp|P49312|ROA1_MOUSE	yes	no	15	31	17	R	S	0	1911.994	3	2.34E-06	103.01	1.13	0.86	6
1717	KLFIGGLSFETTEESLR	sp|O88569|ROA2_MOUSE	yes	no	22	38	17	R	N	0	1926.010	3	1.98E-08	143.28	1.12	0.85	2
1718	KLFNLSKEDDVR	sp|P62754|RS6_MOUSE	yes	yes	143	154	12	R	Q	0	1462.778	3	1.42E-02	62.09	0.97	0.90	5
1719	KLKDGKMIVECVMNNATCTR	sp|Q05816|FABP5_MOUSE	yes	yes	110	129	20	R	V	0	2367.153	3;4	3.68E-05	84.95	1.15	0.96	7
1720	KLKEDKAPQVDVDR	sp|Q9CZD3|SYG_MOUSE	yes	yes	70	83	14	R	A	0	1639.889	4	8.19E-02	33.84	1.20	1.07	5
1721	KLLLAIVGQ	sp|Q07076|ANXA7_MOUSE	yes	no	455	463	9	R	-	0	953.627	2	1.18E-02	78.15	1.19	0.99	6
1722	KLMVALAKGR	sp|P07356|ANXA2_MOUSE	yes	yes	169	178	10	R	R	0	1085.674	3	2.83E-02	61.56	1.13	0.92	6
1723	KLPFQR	sp|P84244|H33_MOUSE	no	no	65	70	6	R	L	0	787.470	2	1.24E-02	114.67	1.52	0.92	2
1724	KLSSAMSAAKAIADHIR	sp|P14152|MDHC_MOUSE	yes	yes	239	255	17	R	D	0	1768.962	4	2.66E-03	69.19	0.95	0.95	1
1725	KLVIIEGDLER	sp|P21107-2|TPM3_MOUSE	yes	no	132	142	11	R	T	0	1283.745	3	8.66E-03	72.29	1.15	0.98	3
1726	KLVIIESDLER	sp|P58771-2|TPM1_MOUSE	yes	no	168	178	11	R	A	0	1313.756	2;3	1.45E-03	100.22	0.90	0.83	9
1727	KMCLFAGFQR	sp|Q8VEK3|HNRPU_MOUSE	yes	yes	568	577	10	R	K	0	1256.616	3	1.81E-02	68.85	1.52	1.32	3
1728	KNGFVVLKGR	sp|P63242|IF5A1_MOUSE	yes	no	27	36	10	R	P	0	1116.677	3	2.71E-02	62.46	0.77	0.76	1
1729	KNSATIPESDDL	sp|P35492|HUTH_MOUSE	yes	no	646	657	12	R	-	0	1288.615	2	1.60E-03	86.26	1.33	1.14	4
1730	KPAAGLSAAPVPPAAAPLLDFSSD	sp|Q99P72|RTN4_MOUSE	yes	yes	59	89	31	R	G	0	2966.587	3	2.39E-03	79.78	1.39	1.03	8
1731	KPPVLQPLALPPELSVR	sp|Q5SUR0|PUR4_MOUSE	yes	yes	645	661	17	R	Q	0	1853.114	3	6.36E-01	37.77	NaN	NaN	0
1732	KPTVTIVEPGEVR	sp|Q8R2Q0|TRI29_MOUSE	yes	yes	137	149	13	R	R	0	1423.804	3	4.91E-03	70.89	1.48	0.90	3
1733	KPVDQYEDCYLAR	sp|Q921I1|TRFE_MOUSE	yes	yes	252	264	13	R	I	0	1655.761	2;3	1.42E-08	173.44	1.00	0.87	8
1734	KPVKDFASCHLAQAPNHVVVSR	sp|Q921I1|TRFE_MOUSE	yes	yes	589	610	22	R	K	0	2459.286	5	2.36E-03	54.00	1.07	0.96	4
1735	KQGLEQFINKVAGHPLAQNER	sp|O70492|SNX3_MOUSE	yes	yes	119	139	21	R	C	0	2376.266	4	1.35E-01	27.93	1.28	1.26	1
1736	KQLAQIKEMVELPLR	sp|Q01853|TERA_MOUSE	yes	yes	211	225	15	R	H	0	1795.039	4	7.62E-04	105.14	0.95	0.93	1
1737	KQQLEIELR	sp|E9Q557|DESP_MOUSE	yes	yes	1456	1464	9	R	Q	0	1155.661	2	1.07E-02	81.53	1.40	1.01	2
1738	KQVVNIPSFIVR	sp|Q6ZWN5|RS9_MOUSE	yes	yes	139	150	12	R	L	0	1398.835	2;3	3.80E-03	74.99	1.13	0.99	11
1739	KRNSLSPPASPR	sp|Q5BKS4|ERI2_MOUSE	yes	yes	531	542	12	T	T	1	1308.726	2	1.91E-02	56.09	0.88	0.69	3
1740	KSATFQIQSFDIVCSPVWTSR	sp|Q60847|COCA1_MOUSE	yes	no	2699	2719	21	R	D	0	2456.216	3	8.62E-03	49.13	1.80	1.15	1
1741	KSDGIYIINLKR	sp|P14206|RSSA_MOUSE	yes	yes	42	53	12	R	T	0	1418.825	3	8.94E-04	98.90	1.01	0.94	6
1742	KSDLEANVEALVEESSFLKR	sp|Q9Z2T6|KRT85_MOUSE	yes	yes	239	258	20	R	L	0	2263.170	3;4	2.41E-05	91.28	1.83	1.10	5
1743	KTEELNKEVASNSDLIQSNR	sp|Q9Z2K1|K1C16_MOUSE	yes	no	307	326	20	R	S	0	2274.145	4	2.19E-02	44.79	1.73	1.07	4
1744	KTETVCTFQDGALVQHQQWDGK	sp|Q05816|FABP5_MOUSE	yes	yes	82	109	28	R	K	0	3262.568	4;5	1.29E-04	99.95	1.12	0.95	10
1745	KTFPTVNPSTGEVICQVAEGNKEL	sp|P47738|ALDH2_MOUSE	yes	yes	54	86	33	R	A	0	3557.815	5	2.14E-04	72.15	0.44	0.42	1
1746	KTFSHELSDFGLESTTGEVPVVAIR	sp|P27773|PDIA3_MOUSE	yes	yes	305	329	25	R	T	0	2718.387	4	1.12E-06	118.51	1.29	0.97	2

1747	KTGSQYDIQDAIDKGLVDR	sp|E9Q557|DESP_MOUSE	yes	yes	2535	2553	19	R	K	0	2121.070	3	4.83E-02	36.13	1.70	1.00	4
1748	KTVTAMDVVYALKR	sp|P62806|H4_MOUSE	yes	yes	80	93	14	R	Q	0	1593.891	3;4	1.37E-04	106.14	1.61	0.91	10
1749	KVACIGAWHPAR	sp|P27659|RL3_MOUSE	yes	yes	250	261	12	R	V	0	1364.714	3	9.01E-03	68.54	1.30	0.94	2
1750	KVGINYQPPTVVPGGDLAKVQR	sp|P68373|TBA1C_MOUSE	no	no	352	373	22	F	A	0	2335.301	4	8.77E-03	59.98	1.39	1.24	3
1751	KVGVNGFGR	sp|P16858|G3P_MOUSE	yes	yes	3	11	9	V	I	0	932.519	2	1.79E-03	119.07	1.26	1.05	4
1752	KVLDELTLSR	sp|Q9Z2K1|K1C16_MOUSE	yes	no	221	230	10	R	A	0	1172.677	2	2.49E-02	63.97	1.78	1.12	3
1753	KVLIIGGGDGGVLR	sp|Q64674|SPEE_MOUSE	yes	yes	96	109	14	R	E	0	1352.814	2;3	7.16E-05	118.52	1.13	0.95	7
1754	KVLQLLR	sp|P14148|RL7_MOUSE	yes	yes	129	135	7	R	L	0	868.586	2	6.52E-03	138.37	1.19	0.95	7
1755	KYAALYQPLFDKR	sp|Q78ZA7|NP1L4_MOUSE	yes	yes	94	106	13	R	R	0	1611.877	3	3.70E-03	72.89	1.36	1.20	2
1756	KYAPPPCGGPEDVALVPR	sp|Q6P3A4|VSIG8_MOUSE	yes	no	358	375	18	R	T	0	1921.972	3	2.17E-07	115.57	2.29	1.39	1
1757	KYAVLYQPLFDKR	sp|P28656|NP1L1_MOUSE	yes	yes	105	117	13	R	F	0	1639.909	3	8.70E-04	85.84	0.96	0.94	5
1758	KYEMFAQTLQQSR	sp|Q01853|TERA_MOUSE	yes	yes	754	766	13	R	G	0	1628.798	3	1.03E-04	121.45	1.20	1.00	5
1759	KYKEALLGR	sp|Q99PT1|GDIR1_MOUSE	yes	yes	50	58	9	R	V	0	1076.634	3	3.87E-02	61.78	0.97	0.94	2
1760	LAAAFAVSR	sp|Q99JY0|ECHB_MOUSE	yes	yes	231	239	9	R	M	0	904.513	2	3.42E-02	91.27	NaN	NaN	0
1761	LAADDFR	sp|Q61897|KT33B_MOUSE	no	no	136	142	7	K	T	0	806.392	2	2.02E-02	170.72	NaN	NaN	0
1762	LAADVGKAGAER	sp|P51881|ADT2_MOUSE	yes	yes	141	152	12	R	E	0	1156.620	2;3	8.61E-04	99.50	1.19	0.95	4
1763	LAAELNHVQEAMEGYKKKYEEEV	sp|Q9Z2T6|KRT85_MOUSE	yes	yes	193	218	26	R	A	0	3047.539	5	4.31E-02	35.36	2.34	1.51	1
1764	LAAELNHVQESMEGYKKR	sp|Q6IMF0|KRT83_MOUSE	yes	yes	181	198	18	R	Y	0	2102.058	3;4	3.83E-05	93.91	1.83	1.09	6
1765	LAAEQELIR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1612	1620	9	R	L	0	1041.582	2	1.56E-02	140.14	NaN	NaN	0
1766	LAAIQESGVER	sp|Q60692|PSB6_MOUSE	yes	yes	209	219	11	R	Q	0	1171.620	2	7.60E-04	147.91	0.44	0.35	1
1767	LAAIVAKQVLLGR	sp|P19253|RL13A_MOUSE	yes	yes	19	31	13	R	K	0	1350.871	2;3	9.46E-05	174.42	1.00	0.74	8
1768	LAALFPDLFSR	sp|Q9Z2L6|MINP1_MOUSE	yes	yes	155	165	11	R	E	0	1248.687	2	8.45E-03	107.06	NaN	NaN	0
1769	LAATLAQGPR	sp|Q6PGN1|F132B_MOUSE	yes	yes	175	184	10	L	A	0	996.572	2	1.19E-02	115.71	NaN	NaN	0
1770	LADALQELR	sp|P48678|LMNA_MOUSE	yes	no	241	249	9	R	A	0	1027.566	2	3.62E-03	160.59	NaN	NaN	0
1771	LADCCTKQEPER	sp|P07724|ALBU_MOUSE	yes	yes	111	122	12	E	N	0	1505.660	2	3.41E-04	117.93	1.19	1.05	4
1772	LADFGVLHR	sp|Q9D0R2|SYTC_MOUSE	yes	yes	433	441	9	R	N	0	1026.561	3	3.97E-02	85.86	NaN	NaN	0
1773	LAEDEAFQR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1772	1780	9	R	R	0	1077.509	2	3.33E-02	92.05	NaN	NaN	0
1774	LAELEEFINGPNNAHIQQVGDR	sp|Q68FD5|CLH1_MOUSE	yes	yes	1183	1204	22	R	C	0	2463.214	3	9.34E-03	58.71	NaN	NaN	0
1775	LAELEQEIR	sp|A6H6E2|MMRN2_MOUSE	yes	yes	698	706	9	T	R	0	1099.587	2	2.04E-02	113.71	NaN	NaN	0
1776	LAELKSNPTLNEYHTR	sp|Q00623|APOA1_MOUSE	yes	yes	201	216	16	R	A	0	1884.969	3;4	2.97E-08	144.97	1.45	1.10	14
1777	LAEMPADSGYPAYLGAR	sp|P50516-2|VATA_MOUSE	yes	no	365	381	17	R	L	0	1780.845	2	5.16E-03	82.59	NaN	NaN	0
1778	LAEPSQLLKSAIVHLINYQDDAELA	sp|Q02257|PLAK_MOUSE	yes	yes	116	142	27	R	A	0	3007.598	3;4	3.73E-10	145.20	1.90	1.16	2
1779	LAEVATGDDKKR	sp|O70456|1433S_MOUSE	yes	yes	131	142	12	Y	I	0	1301.694	2	2.01E-07	167.71	1.23	1.04	5
1780	LAEVEAALEKQR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1265	1276	12	R	Q	0	1355.741	3	5.21E-02	44.54	1.18	0.87	4
1781	LAGGDWFTSR	sp|Q76MZ3|2AAA_MOUSE	yes	yes	135	144	10	R	T	0	1108.530	2	5.45E-03	140.49	NaN	NaN	0
1782	LAGQIFLGGSIVR	sp|P17563|SBP1_MOUSE	yes	yes	345	357	13	R	G	0	1329.777	2	3.59E-02	66.00	NaN	NaN	0
1783	LAGTQPLEVLEAVQR	sp|Q02053|UBA1_MOUSE	yes	yes	679	693	15	R	S	0	1622.899	2;3	4.29E-05	168.50	NaN	NaN	0
1784	LAGVINFQR	sp|Q9D8W5|PSD12_MOUSE	yes	yes	409	417	9	R	P	0	1016.577	2	2.01E-03	159.04	9.99	9.79	1
1785	LAILYAKR	sp|Q99L47|F10A1_MOUSE	yes	yes	146	153	8	R	A	0	946.596	3	1.60E-02	89.55	0.97	0.94	3
1786	LAKADGIVSKNF	sp|Q9CQR2|RS21_MOUSE	yes	no	72	83	12	R	-	0	1261.703	2;3	1.62E-03	85.84	1.29	1.08	8
1787	LAKENAPAIIFIDEIDAIATKR	sp|P54775|PRS6B_MOUSE	yes	yes	253	274	22	R	F	0	2411.342	4	2.05E-02	49.66	NaN	NaN	0
1788	LAKLQDPFSVYR	sp|Q9CQA3|DHSB_MOUSE	yes	yes	233	244	12	R	C	0	1435.782	3	6.18E-04	104.94	1.96	1.21	1
1789	LAKVDATEESDLAQQYGVR	sp|P09103|PDIA1_MOUSE	yes	yes	81	99	19	R	G	0	2092.044	3	4.06E-21	196.65	1.21	1.00	4
1790	LAKYNQILR	sp|P17182|ENOA_MOUSE	yes	yes	404	412	9	R	I	0	1117.661	2;3	5.13E-06	172.21	1.25	0.96	10
1791	LALFNPDVSWDR	sp|Q62425|NDUA4_MOUSE	yes	yes	36	47	12	R	K	0	1431.715	2	3.62E-03	114.24	NaN	NaN	0
1792	LALIQPSR	sp|Q99LS3|SERB_MOUSE	yes	yes	66	73	8	R	D	0	896.544	2	3.85E-02	121.85	NaN	NaN	0
1793	LALQALTEKLLR	sp|Q8BMK4|CKAP4_MOUSE	yes	yes	327	338	12	R	S	0	1367.850	2;3	3.67E-04	116.71	1.54	0.90	4
1794	LAMLQEHVGNLGSSSDLASTVR	sp|Q8BMK4|CKAP4_MOUSE	yes	yes	428	449	22	R	S	0	2284.148	3	9.43E-13	204.04	NaN	NaN	0
1795	LANSAFAVDLFKQLCER	sp|P70124|SPB5_MOUSE	yes	yes	6	22	17	R	D	0	1981.009	2;3	3.18E-07	123.02	1.23	1.10	7
1796	LANYLEKVR	sp|Q62168|K1H2_MOUSE	no	no	66	74	9	R	Q	0	1104.629	3	1.09E-02	80.76	1.47	1.16	10
1797	LAPDYDALDVANKIGII	sp|P62751|RL23A_MOUSE	yes	no	140	156	17	R	-	0	1799.967	2	8.35E-07	111.22	0.90	0.85	6
1798	LAPEYEAAATR	sp|P27773|PDIA3_MOUSE	yes	yes	63	73	11	R	L	0	1190.593	2	7.20E-03	112.94	NaN	NaN	0
1799	LAPPLVIKEDEIR	sp|P29758|OAT_MOUSE	yes	yes	414	426	13	R	E	0	1491.866	3	1.49E-02	54.34	1.22	0.98	7
1800	LAQAPNHVVVSR	sp|Q921I1|TRFE_MOUSE	yes	yes	599	610	12	H	K	0	1289.720	3	3.37E-03	117.20	NaN	NaN	0
1801	LAQIHFPR	sp|Q00896|A1AT3_MOUSE	yes	no	301	308	8	R	L	0	980.556	3	4.56E-02	101.28	NaN	NaN	0
1802	LAQIHIPR	sp|Q00898|A1AT5_MOUSE	yes	yes	301	308	8	R	L	0	946.571	3	4.84E-02	99.00	NaN	NaN	0
1803	LAQQEKQEQVEMESLAKSLEDAL	sp|Q8CAQ8-2|IMMT_MOUSE	yes	no	194	218	25	R	T	0	2886.439	4	2.82E-02	40.99	2.91	2.04	1
1804	LAQQLTVER	sp|Q9D281|NXP20_MOUSE	yes	yes	278	286	9	R	T	0	1056.593	2	5.00E-02	76.94	0.57	0.45	2
1805	LASDLLEWIR	sp|P57780|ACTN4_MOUSE	no	no	302	311	10	R	R	0	1214.666	2	1.58E-04	159.83	0.02	0.02	1
1806	LASFYER	sp|P50516-2|VATA_MOUSE	yes	no	382	388	7	R	A	0	884.439	2	6.39E-02	116.30	NaN	NaN	0
1807	LASISLPR	sp|P11247|PERM_MOUSE	yes	yes	668	675	8	A	I	0	855.518	2	5.27E-02	95.53	NaN	NaN	0
1808	LASTLVHLGEYQAAVDGAR	sp|Q68FD5|CLH1_MOUSE	yes	yes	1227	1245	19	R	K	0	1970.022	3	9.95E-07	151.63	NaN	NaN	0
1809	LASVLNTDPALDSELTSKLKR	sp|Q99KK7|DPP3_MOUSE	yes	yes	216	236	21	R	Y	0	2270.248	4	4.93E-08	159.06	0.82	0.81	3
1810	LASYLDKVR	sp|Q9QWL7|K1C17_MOUSE	no	no	95	103	9	R	A	0	1063.603	2;3	2.88E-06	176.33	1.56	0.99	16
1811	LASYLDNVKALEEANSELER	sp|A6BLY7|K1C28_MOUSE	yes	yes	95	114	20	R	K	0	2263.133	3	1.48E-12	151.87	1.19	0.82	3
1812	LASYLDNVQALQEANADLEQKIKC	sp|Q8VCW2|K1C25_MOUSE	yes	yes	86	120	35	R	G	0	3997.963	4;5	4.71E-03	65.88	1.65	1.07	2
1813	LASYLEKVR	sp|Q4974|KRT35_MOUSE	no	no	108	116	9	R	Q	0	1077.618	3	1.09E-02	80.76	1.58	1.00	4
1814	LASYMDKVR	sp|P02535-3|K1C10_MOUSE	yes	no	146	154	9	R	A	0	1081.559	2;3	1.92E-08	182.39	1.47	1.09	16
1815	LASYMEKVR	sp|Q61897|KT33B_MOUSE	no	no	67	75	9	R	Q	0	1095.575	2;3	1.66E-04	150.35	1.60	1.14	17
1816	LATALQKLEEAEKAADESER	sp|P21107-2|TPM3_MOUSE	no	no	70	89	20	R	G	0	2201.118	3;4	4.28E-08	104.88	1.04	0.94	6
1817	LATLLGLQAPPTR	sp|P23116|EIF3A_MOUSE	yes	yes	355	367	13	R	I	0	1349.803	2	3.56E-04	155.39	NaN	NaN	0
1818	LATTVSAPDLKSVR	sp|P27546-3|MAP4_MOUSE	yes	no	896	909	14	R	S	0	1456.825	3	6.80E-04	79.88	1.24	1.05	4
1819	LATYLDKVR	sp|Q61781|K1C14_MOUSE	no	no	132	140	9	R	A	0	1077.618	2;3	8.47E-13	216.12	1.57	0.96	12
1820	LAVCGNPATSQPVTSSNHSSR	sp|P46935|NEDD4_MOUSE	yes	yes	362	382	21	R	G	0	2169.023	3	6.34E-09	178.32	NaN	NaN	0
1821	LAVSQVPR	sp|P40142|TKT_MOUSE	yes	yes	587	594	8	R	S	0	868.513	2	2.69E-02	145.34	NaN	NaN	0
1822	LAVVDPLFGMQPIR	sp|Q61024|ASNS_MOUSE	yes	yes	50	63	14	R	V	0	1554.859	2	3.69E-03	92.86	NaN	NaN	0
1823	LAVYIDKVR	sp|P14733|LMNB1_MOUSE	yes	yes	44	52	9	R	S	0	1075.639	2;3	2.20E-02	71.45	1.07	0.70	5
1824	LAWINTPR	sp|O08807|PRDX4_MOUSE	no	no	160	167	8	H	R	0	969.540	2	3.92E-02	119.41	NaN	NaN	0
1825	LCAATATILDKPEDR	sp|O35215|DOPD_MOUSE	yes	yes	23	37	15	R	V	0	1672.845	3	1.56E-03	88.56	1.10	0.94	2
1826	LCAEAALR	sp|P50580|PA2G4_MOUSE	yes	yes	148	155	8	H	L	0	902.464	2	3.98E-02	117.10	NaN	NaN	0
1827	LCDLLR	sp|Q61140-2|BCAR1_MOUSE	yes	no	823	828	6	L	G	0	788.421	2	6.40E-02	114.67	NaN	NaN	0
1828	LCEGVGSVNVCVSSSR	sp|P97861|KRT86_MOUSE	no	no	417	432	16	R	G	0	1708.787	2	4.63E-08	193.32	0.99	0.79	1
1829	LCELLTDPR	sp|Q0VGB7|PP4R2_MOUSE	yes	yes	104	112	9	R	R	0	1115.565	2	3.87E-02	86.90	NaN	NaN	0
1830	LCITSFLR	sp|P02772|FETA_MOUSE	yes	yes	506	513	8	R	D	0	1008.543	2	5.44E-02	94.11	NaN	NaN	0
1831	LCLDLR	sp|P35802|GPM6A_MOUSE	yes	no	173	178	6	N	Q	0	788.421	2	4.39E-02	142.53	NaN	NaN	0
1832	LCLISTFLEDGIR	sp|Q64310|SURF4_MOUSE	yes	yes	31	43	13	R	M	0	1535.802	2	4.44E-03	94.12	NaN	NaN	0
1833	LCTSATESEVTR	sp|Q9CZ13|QCR1_MOUSE	yes	yes	379	390	12	R	G	0	1352.624	2	3.40E-02	70.09	NaN	NaN	0
1834	LDAEVPTR	sp|P97350|PKP1_MOUSE	yes	yes	466	473	8	R	Y	0	899.471	2	3.95E-02	118.33	NaN	NaN	0
1835	LDCLKSLDLFGCEVTNR	sp|Q9EST5|AN32B_MOUSE	yes	no	112	128	17	R	S	0	2038.982	3	8.94E-07	109.87	1.48	1.08	7
1836	LDDCGLTEVR	sp|Q91VI7|RINI_MOUSE	yes	yes	30	39	10	R	C	0	1176.545	2	1.50E-03	156.48	NaN	NaN	0
1837	LDFIGVEGSNYPR	sp|Q80X50-2|UBP2L_MOUSE	yes	no	247	259	13	R	K	0	1465.720	2	7.19E-02	51.09	NaN	NaN	0
1838	LDFNLVR	sp|Q9CWJ9|PUR9_MOUSE	yes	yes	91	97	7	R	V	0	875.487	2	5.14E-02	139.31	NaN	NaN	0
1839	LDGLCIPLR	sp|Q91ZX7|LRP1_MOUSE	yes	yes	1072	1080	9	R	W	0	1055.580	2	1.89E-02	122.44	NaN	NaN	0
1840	LDGLVDTPTGYIESLPKVVKR	sp|P28656|NP1L1_MOUSE	yes	yes	56	76	21	R	R	0	2299.279	3;4	8.70E-12	200.60	1.16	0.96	7
1841	LDGNPLTQSSLPPDMYECLR	sp|P51885|LUM_MOUSE	yes	yes	311	330	20	R	V	0	2305.072	2	5.31E-08	168.05	NaN	NaN	0
1842	LDHKFDLMYAKR	sp|P68373|TBA1C_MOUSE	no	no	391	402	12	R	A	0	1535.792	3;4	8.92E-04	98.94	1.27	1.19	8
1843	LDHLAEKFR	sp|P57780|ACTN4_MOUSE	no	no	412	420	9	R	Q	0	1127.609	3	1.09E-02	80.76	1.27	0.96	6
1844	LDIDPETITWQR	sp|Q922D8|C1TC_MOUSE	yes	yes	521	532	12	R	V	0	1485.746	2	3.70E-03	113.24	NaN	NaN	0
1845	LDIDSAPITAR	sp|P52480|KPYM_MOUSE	no	no	33	43	11	R	N	0	1170.625	2	3.51E-03	131.02	NaN	NaN	0
1846	LDIERPTYTNLNR	sp|P68373|TBA1C_MOUSE	no	no	217	229	13	N	L	1	1603.832	2	4.77E-02	61.11	NaN	NaN	0
1847	LDILAQEVNFLR	sp|Q3TTY5|K22E_MOUSE	yes	no	324	335	12	R	T	0	1429.793	2;3	1.90E-06	186.17	NaN	NaN	0
1848	LDKIIDLIIPR	sp|Q9Z110-2|P5CS_MOUSE	yes	no	546	556	11	R	G	0	1307.818	3	2.60E-03	86.77	1.32	1.11	4
1849	LDLIAQQMMPEVR	sp|P50518|VATE1_MOUSE	yes	yes	200	212	13	R	G	0	1542.790	2	1.45E-03	121.24	NaN	NaN	0

1850	LDLLEDR	sp|Q8BHN3|GANAB_MOUSE	yes	no	158	164	7	R	S	0	872.460	2	5.04E-02	140.98	NaN	NaN	0
1851	LDPAWEKQQR	sp|P57780|ACTN4_MOUSE	no	no	45	54	10	L	K	0	1269.647	2	4.10E-02	52.49	1.40	1.08	2
1852	LDPFTIKPLDR	sp|P40142|TKT_MOUSE	yes	yes	532	542	11	V	K	0	1313.734	2	1.75E-03	96.75	1.13	0.99	4
1853	LDPVEKALR	sp|P63017|HSP7C_MOUSE	yes	yes	314	322	9	T	D	0	1039.603	2	3.13E-03	105.20	1.27	0.96	7
1854	LDQELKLIGEYGLR	sp|Q6ZWN5|RS9_MOUSE	yes	yes	25	38	14	R	N	0	1645.904	3	1.36E-05	130.72	1.25	0.98	8
1855	LDQETAQWLR	sp|Q7TSV4|PGM2_MOUSE	yes	yes	23	32	10	R	W	0	1258.631	2	6.15E-02	113.93	0.16	0.15	3
1856	LDQLIYIPLPDEKSR	sp|Q01853|TERA_MOUSE	yes	yes	639	653	15	R	V	0	1798.983	2;3	2.93E-06	130.23	1.20	1.03	12
1857	LDQPMTEIVSR	sp|Q02053|UBA1_MOUSE	yes	yes	1011	1021	11	R	V	0	1287.649	2	3.80E-03	128.85	NaN	NaN	0
1858	LDQWLTTMLLR	sp|Q9DB05|SNAA_MOUSE	yes	no	272	282	11	R	I	0	1388.749	2	3.57E-03	130.56	NaN	NaN	0
1859	LDSQKHIDFSLR	sp|Q6ZWN5|RS9_MOUSE	yes	yes	151	162	12	R	S	0	1457.763	3;4	4.32E-04	113.69	1.25	1.04	10
1860	LDVGNFSWGSECCTR	sp|P62242|RS8_MOUSE	yes	yes	60	74	15	R	K	0	1786.740	2	2.62E-04	145.69	NaN	NaN	0
1861	LDYHISVQNMMR	sp|Q9CQQ7|AT5F1_MOUSE	yes	yes	197	208	12	R	R	0	1505.712	3	3.38E-07	203.51	NaN	NaN	0
1862	LEACTFHKH	sp|Q921I1|TRFE_MOUSE	yes	no	689	697	9	L	-	0	1141.534	2	8.30E-03	88.50	0.90	0.85	3
1863	LEAGDHPVELLAR	sp|P07214|SPRC_MOUSE	yes	yes	205	217	13	R	D	0	1418.752	2	8.28E-03	82.52	NaN	NaN	0
1864	LEAPCQQWMELR	sp|Q9CRB3|HIUH_MOUSE	yes	yes	31	42	12	R	T	0	1559.723	2	6.97E-03	96.75	NaN	NaN	0
1865	LEAPLEELR	sp|Q8BJY1|PSMD5_MOUSE	yes	yes	15	23	9	R	A	0	1068.582	2	4.82E-02	77.66	NaN	NaN	0
1866	LEAQLASLR	sp|Q8BJS4-3|SUN2_MOUSE	yes	no	396	404	9	R	Q	0	999.571	2	1.21E-02	140.16	NaN	NaN	0
1867	LEAYHTQTTPLVEYYR	sp|Q9WTP6-2|KAD2_MOUSE	yes	no	187	202	16	R	K	0	1982.974	3	4.20E-04	124.25	NaN	NaN	0
1868	LECEIDTYR	sp|Q62168|K1H2_MOUSE	yes	no	348	356	9	R	G	0	1197.534	2	3.62E-03	160.59	NaN	NaN	0
1869	LECEINTYR	sp|Q61897|KT33B_MOUSE	no	no	349	357	9	R	G	0	1196.550	2	8.49E-05	189.38	NaN	NaN	0
1870	LECKIQER	sp|Q61897|KT33B_MOUSE	yes	no	84	91	8	E	N	0	1074.549	2	8.42E-03	105.20	2.10	1.31	2
1871	LECVEPNCR	sp|P83882|RL36A_MOUSE	yes	yes	70	78	9	R	S	0	1175.506	2	2.34E-02	101.65	0.65	0.53	1
1872	LEDKDDLDVTELSNEELLDQLVR	sp|Q61029-2|LAP2B_MOUSE	no	no	103	125	23	R	Y	0	2700.334	3	7.52E-09	129.07	1.24	0.76	1
1873	LEDLFEVLNNKNCKALR	sp|O89094-2|CASPE_MOUSE	yes	no	109	125	17	R	G	0	2075.083	4	6.21E-02	34.40	0.96	0.93	3
1874	LEDWLGKTVPGSDWTPNAR	sp|Q68FL6|SYMC_MOUSE	yes	yes	463	481	19	R	F	0	2141.054	3	1.97E-04	76.53	1.60	1.43	3
1875	LEEEEEAKR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	1345	1353	9	Q	N	0	1131.541	2	2.14E-02	107.79	1.69	1.36	3
1876	LEEERPSLR	sp|Q91VI7|RINI_MOUSE	yes	yes	445	453	9	A	I	1	1127.594	2	1.26E-01	61.16	NaN	NaN	0
1877	LEEGPPVTTVLTR	sp|P35486|ODPA_MOUSE	yes	yes	46	58	13	R	E	0	1410.772	2	2.04E-04	121.45	25.28	20.66	1
1878	LEEIPLIKSAYEEQR	sp|P23116|EIF3A_MOUSE	yes	yes	704	718	15	R	V	0	1816.957	3	8.59E-03	58.08	1.28	1.01	8
1879	LEELELLVSSLR	sp|Q80YX1-5|TENA_MOUSE	yes	no	126	137	12	R	E	0	1399.792	2	1.96E-03	134.56	NaN	NaN	0
1880	LEEVSPNLVR	sp|Q91VD9|NDUS1_MOUSE	yes	yes	646	655	10	R	Y	0	1154.630	2	1.39E-03	113.93	5.59	3.39	1
1881	LEFLYDKLR	sp|Q3UPL0-2|SC31A_MOUSE	yes	no	1121	1129	9	R	E	0	1195.660	3	5.07E-03	98.05	1.51	1.18	2
1882	LEGEGSSSGGGGGR	sp|P02535-3|K1C10_MOUSE	yes	no	442	455	14	L	P	0	1205.527	2	1.06E-03	116.19	NaN	NaN	0
1883	LEGIVNKMFQR	sp|Q3TXS7|PSMD1_MOUSE	yes	yes	130	140	11	R	C	0	1333.718	3	2.48E-02	57.53	1.29	1.12	2
1884	LEGNTVGVEAAR	sp|P46061|RAGP1_MOUSE	yes	yes	56	67	12	R	V	0	1214.626	2	4.46E-03	104.17	NaN	NaN	0
1885	LEKELGSPPGISLETIDAAFSCPGSS	sp|Q91X72|HEMO_MOUSE	yes	yes	343	369	27	R	L	0	2817.386	3	5.60E-04	73.68	1.00	0.95	4
1886	LEKLFVTNDAATILR	sp|P42932|TCPQ_MOUSE	yes	yes	60	74	15	R	E	0	1702.962	3	2.78E-05	108.14	1.13	0.94	5
1887	LEKLQLEYCNLTATSCEPLASVLR	sp|Q91VI7|RINI_MOUSE	yes	yes	139	162	24	R	V	0	2807.420	3	1.14E-04	82.89	0.99	0.92	2
1888	LELQQKFR	sp|P48758|CBR1_MOUSE	yes	yes	152	159	8	R	S	0	1060.603	3	1.72E-02	87.32	0.99	0.93	3
1889	LELSKVR	sp|P48678|LMNA_MOUSE	yes	no	104	110	7	Q	E	0	843.518	2	2.17E-02	95.53	1.11	0.81	3
1890	LELVEQER	sp|Q9R269|PEPL_MOUSE	yes	yes	1191	1198	8	R	K	0	1014.535	2	3.72E-02	126.62	NaN	NaN	0
1891	LENEIQTYR	sp|P02535-3|K1C10_MOUSE	no	no	431	439	9	R	S	0	1164.578	2	3.19E-05	200.56	NaN	NaN	0
1892	LENWITSLAESQLQTR	sp|P42227-2|STAT3_MOUSE	yes	no	263	278	16	R	Q	0	1887.969	2	4.70E-03	81.59	NaN	NaN	0
1893	LEQEIATYR	sp|Q61781|K1C14_MOUSE	no	no	414	422	9	R	R	0	1121.572	2	1.58E-03	172.59	NaN	NaN	0
1894	LEQEIATYRR	sp|Q61781|K1C14_MOUSE	no	no	414	423	10	R	L	1	1277.673	3	9.82E-03	123.79	NaN	NaN	0
1895	LEQQVPVNQVFGQDEMIDVIGVT	sp|P27659|RL3_MOUSE	yes	yes	201	234	34	R	W	0	3718.935	5	9.54E-03	48.85	0.74	0.68	1
1896	LERRFEEELR	sp|Q3UHD3-3|MTUS2_MOUSE	yes	no	57	66	10	T	R	2	1375.721	2	5.97E-02	70.03	NaN	NaN	0
1897	LESEIATYR	sp|B1AQ75|KRT36_MOUSE	yes	yes	386	394	9	R	R	0	1080.545	2	2.11E-02	109.66	NaN	NaN	0
1898	LESLNIQR	sp|P23116|EIF3A_MOUSE	yes	yes	582	589	8	R	E	0	971.540	2	1.59E-02	162.50	NaN	NaN	0
1899	LETCFLKYDDEECTLPIAGR	sp|Q61554|FBN1_MOUSE	yes	yes	955	974	20	R	H	0	2429.124	3	2.71E-08	113.88	1.26	0.86	2
1900	LETPSAKKLTDVGIR	sp|P51174|ACADL_MOUSE	yes	yes	36	50	15	R	R	0	1626.931	3	9.97E-03	54.90	1.10	1.05	1
1901	LETVALPLQGLEDLAADR	sp|Q9QXZ0-3|MACF1_MOUSE	yes	no	2647	2664	18	R	M	0	1923.031	2	3.10E-03	93.38	NaN	NaN	0
1902	LETYYNATEPVISFYDKR	sp|Q9R0Y5|KAD1_MOUSE	yes	no	150	167	18	R	G	0	2208.074	3	6.85E-05	86.49	1.43	1.14	1
1903	LEVAQHLGESTVR	sp|P56480|ATPB_MOUSE	yes	yes	97	109	13	V	T	0	1437.758	2	2.79E-02	69.35	NaN	NaN	0
1904	LEVNLQAMKAQFER	sp|Q8VDD5|MYH9_MOUSE	yes	yes	1558	1571	14	R	D	0	1675.872	3	9.22E-05	114.64	1.88	1.46	5
1905	LEYCEALAMLR	sp|Q922B2|SYDC_MOUSE	yes	yes	346	356	11	R	E	0	1367.658	2	7.43E-03	111.86	NaN	NaN	0
1906	LFAFVR	sp|Q9CQJ6|COTL1_MOUSE	yes	no	58	63	6	R	F	0	751.438	2	5.25E-02	130.51	NaN	NaN	0
1907	LFAVAPNR	sp|Q02788|CO6A2_MOUSE	yes	yes	202	209	8	R	N	0	886.502	2	2.64E-02	125.62	NaN	NaN	0
1908	LFAYPDTHR	sp|P24270|CATA_MOUSE	yes	yes	355	363	9	R	H	0	1118.551	3	3.35E-02	91.87	NaN	NaN	0
1909	LFCNINNVCNFASR	sp|Q9QZS0|CO4A3_MOUSE	yes	no	1502	1515	14	F	N	0	1727.787	2	4.24E-03	90.71	NaN	NaN	0
1910	LFDQAFGVPR	sp|P14602|HSPB1_MOUSE	yes	no	29	38	10	R	L	0	1148.598	2	2.13E-03	152.97	NaN	NaN	0
1911	LFEAEAQDLFR	sp|Q9EQP2|EHD4_MOUSE	yes	yes	273	283	11	R	D	0	1337.662	2	9.54E-03	102.40	NaN	NaN	0
1912	LFEFAGYDVLR	sp|Q9D0I9|SYRC_MOUSE	yes	yes	224	234	11	R	L	0	1328.677	2	7.41E-03	96.23	0.06	0.05	1
1913	LFEGNALLR	sp|Q6ZWN5|RS9_MOUSE	yes	yes	71	79	9	R	R	0	1031.576	2	4.08E-03	157.91	NaN	NaN	0
1914	LFELEEQDLFR	sp|Q8BH64|EHD2_MOUSE	yes	yes	270	280	11	R	D	0	1437.714	2	1.28E-03	147.91	NaN	NaN	0
1915	LFEQNVQR	sp|P61082|UBC12_MOUSE	yes	yes	159	166	8	R	S	0	1032.535	2	3.75E-02	125.25	NaN	NaN	0
1916	LFGSVLR	sp|Q9CYD3|CRTAP_MOUSE	yes	no	107	113	7	R	R	0	790.470	2	4.90E-02	143.37	NaN	NaN	0
1917	LFIVDAR	sp|Q9CZ44|NSF1C_MOUSE	yes	no	323	329	7	R	P	0	832.481	2	5.78E-02	128.48	NaN	NaN	0
1918	LFLAGYDPTPTMR	sp|P40336|VP26A_MOUSE	yes	no	250	262	13	R	D	0	1480.738	2	5.00E-02	60.16	NaN	NaN	0
1919	LFNLDR	sp|Q07105|GDF9_MOUSE	yes	no	141	146	6	L	V	0	776.418	2	6.31E-02	116.00	NaN	NaN	0
1920	LFNVDR	sp|O70435|PSA3_MOUSE	yes	yes	67	72	6	R	H	0	762.402	2	6.16E-02	118.06	NaN	NaN	0
1921	LFQDSTEPR	sp|P58871|TB182_MOUSE	yes	yes	1597	1605	9	R	A	0	1091.525	2	4.20E-02	59.91	35.54	27.96	1
1922	LFQLNR	sp|Q62261|SPTB2_MOUSE	yes	no	1700	1705	6	R	E	0	789.450	2	7.93E-02	99.23	NaN	NaN	0
1923	LFQQSCPPGLVFR	sp|Q9D7Q1|CHIT1_MOUSE	yes	yes	443	455	13	R	A	0	1547.792	2	1.46E-03	119.39	NaN	NaN	0
1924	LFSSHDYEAPQEITLGANKVIEGLD	sp|Q61576|FKB10_MOUSE	yes	yes	415	440	26	R	G	0	2901.451	4	2.85E-04	78.10	1.36	1.08	2
1925	LFVGNLPADITEDEFKR	sp|Q8VIJ6|SFPQ_MOUSE	yes	yes	291	307	17	R	L	0	1963.005	3	7.61E-03	53.57	1.43	1.20	4
1926	LFVGNLPPDITEEEMR	sp|Q99K48|NONO_MOUSE	yes	no	78	93	16	R	K	0	1858.914	2	1.75E-03	97.24	NaN	NaN	0
1927	LFVPSTIGAFGPTSPR	sp|Q8K3F7|TDH_MOUSE	yes	yes	165	180	16	R	N	0	1645.883	2;3	3.25E-02	55.76	NaN	NaN	0
1928	LFVSEGSPGSLPVLAAAAR	sp|Q68FL6|SYMC_MOUSE	yes	yes	3	21	19	R	A	0	1841.005	2	6.13E-04	104.88	NaN	NaN	0
1929	LGAAPEEESAYVAGER	sp|Q9CZ44|NSF1C_MOUSE	yes	no	157	172	16	R	R	0	1647.774	2	4.13E-04	124.78	NaN	NaN	0
1930	LGADMEDLR	sp|P08226|APOE_MOUSE	yes	yes	114	122	9	R	N	0	1018.475	2	1.69E-02	130.66	NaN	NaN	0
1931	LGAHLPQDTVCLDTLPALR	sp|Q9R1A9|TREX2_MOUSE	yes	yes	134	152	19	R	G	0	2089.099	3	5.15E-04	108.75	NaN	NaN	0
1932	LGAIAKDPKSETGTR	sp|Q02788|CO6A2_MOUSE	yes	yes	660	674	15	R	V	0	1542.837	4	1.13E-02	51.77	1.60	1.02	4
1933	LGANSLLDLVVFGR	sp|Q8K2B3|DHSA_MOUSE	yes	yes	452	465	14	R	A	0	1472.835	2	8.61E-07	187.97	NaN	NaN	0
1934	LGCPYLLDPEDLGTNSLDIEWMQ	sp|Q6P3A4|VSIG8_MOUSE	yes	yes	42	72	31	R	E	0	3584.655	3	1.23E-08	108.72	NaN	NaN	0
1935	LGDAVEQGVINNSVLGYFIGR	sp|Q9CZD3|SYG_MOUSE	yes	yes	382	402	21	R	I	0	2220.154	2;3	2.19E-08	171.35	NaN	NaN	0
1936	LGDDPLSR	sp|P23116|EIF3A_MOUSE	yes	yes	878	885	8	R	K	0	871.440	2	2.81E-02	143.28	NaN	NaN	0
1937	LGDLYEEEMR	sp|P20152|VIME_MOUSE	yes	yes	146	155	10	R	E	0	1253.560	2	1.17E-03	160.53	0.04	0.04	2
1938	LGDVISIQPCPDVKYGKR	sp|Q01853|TERA_MOUSE	yes	yes	96	113	18	R	I	0	2044.078	3;4	3.85E-09	147.64	1.19	0.91	15
1939	LGEKDTSLYRPALEELR	sp|Q8VDM4|PSMD2_MOUSE	yes	yes	63	79	17	R	R	1	1989.053	4	1.41E-04	79.39	1.29	1.22	4
1940	LGELVLGPYDNTVVLEELR	sp|Q60847|COCA1_MOUSE	yes	no	1130	1148	19	R	A	0	2128.142	2;3	1.36E-02	65.02	NaN	NaN	0
1941	LGEQNFHKVR	sp|Q02788|CO6A2_MOUSE	yes	yes	859	868	10	R	R	0	1226.652	3	1.24E-02	72.93	1.52	1.03	2
1942	LGETGKEKLPR	sp|P62281|RS11_MOUSE	yes	yes	25	35	11	L	Y	0	1226.698	2	1.76E-02	64.12	0.78	0.76	3
1943	LGETNPADSKPGTIR	sp|Q01768|NDKB_MOUSE	yes	no	91	105	15	M	G	0	1554.800	2	4.07E-09	160.81	1.09	0.96	6
1944	LGFHLPLEVAYQR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	3716	3728	13	R	G	0	1541.835	3	1.43E-03	124.60	NaN	NaN	0
1945	LGFSGCSAVISGR	sp|Q6IME9|K2C72_MOUSE	yes	no	14	26	13	R	L	0	1309.645	2	6.44E-03	88.09	NaN	NaN	0
1946	LGGTALAQCFSQLGEHPPDLDLPE	sp|Q55UR0|PUR4_MOUSE	yes	yes	862	889	28	R	A	0	3046.518	3	9.47E-05	78.10	NaN	NaN	0
1947	LGGVSEASR	sp|P35175|CYT1_MOUSE	yes	yes	3	11	9	S	A	0	874.451	2	8.73E-03	146.79	NaN	NaN	0
1948	LGHNYVTAIR	sp|Q921I1|TRFE_MOUSE	yes	yes	334	343	10	Y	N	0	1142.620	2	1.12E-02	118.28	NaN	NaN	0
1949	LGIEKTDPTTLTDDEINR	sp|Q922D8|C1TC_MOUSE	yes	yes	500	517	18	R	F	0	2030.017	3	6.46E-05	87.43	1.13	0.99	4
1950	LGIPVKLEPR	sp|Q05793|PGBM_MOUSE	yes	yes	2471	2480	10	R	M	0	1120.697	3	9.71E-03	74.84	1.37	0.84	2
1951	LGIVVEGFMKRIEEKGVPEDMR	sp|A2CG49-4|KALRN_MOUSE	yes	no	219	240	22	D	G	1	2531.324	4	6.05E-02	28.75	1.14	0.92	3
1952	LGLDYEER	sp|O35129|PHB2_MOUSE	yes	yes	124	131	8	R	V	0	993.477	2	2.84E-02	142.79	NaN	NaN	0

1953	LGLGEGAEEKSIPTLISR	sp|Q8VE37|RCC1_MOUSE	yes	yes	326	343	18	R	L	0	1869.021	3	2.53E-05	97.10	1.42	0.91	4
1954	LGLGHNQIR	sp|P28653|PGS1_MOUSE	yes	yes	259	267	9	R	M	0	1006.567	3	2.25E-02	102.51	NaN	NaN	0
1955	LGLIQEDVASSCIPR	sp|Q8BTI8-3|SRRM2_MOUSE	yes	no	1133	1147	15	R	D	0	1656.851	2	1.09E-01	44.93	NaN	NaN	0
1956	LGLLVDTVGPR	sp|Q9WVJ3-2|CBPQ_MOUSE	yes	no	65	75	11	R	L	0	1138.671	2	7.71E-03	110.54	NaN	NaN	0
1957	LGLPLLLLPEEAR	sp|Q8BMZ5-2|SEN34_MOUSE	yes	no	46	58	13	R	L	0	1432.865	2	3.11E-02	68.00	NaN	NaN	0
1958	LGLQNDLFSLAR	sp|Q11011|PSA_MOUSE	yes	yes	617	628	12	R	A	0	1345.735	2	1.31E-03	142.97	NaN	NaN	0
1959	LGLSTLGELKQNLSR	sp|Q9CYZ2|TPD54_MOUSE	yes	yes	81	95	15	R	S	0	1627.926	3	2.42E-04	85.84	1.15	0.88	2
1960	LGNTQGIISAFSTIMSVHR	sp|Q9DB20|ATPO_MOUSE	yes	yes	118	136	19	R	G	0	2031.057	3	4.48E-03	85.74	NaN	NaN	0
1961	LGPLLDVLADSR	sp|Q80UM7|MOGS_MOUSE	yes	yes	706	717	12	R	H	0	1267.714	2	1.23E-02	83.20	NaN	NaN	0
1962	LGPLVEQGR	sp|P08226|APOE_MOUSE	yes	yes	191	199	9	R	Q	0	967.545	2	1.75E-02	129.42	NaN	NaN	0
1963	LGPNYLQIPVNCPYR	sp|P24270|CATA_MOUSE	yes	yes	366	380	15	R	A	0	1802.914	2	5.29E-04	131.32	NaN	NaN	0
1964	LGPSDYFGEIALLMNRPR	sp|Q9DBC7|KAP0_MOUSE	yes	yes	318	335	18	R	A	1	2048.051	3	5.77E-03	82.59	NaN	NaN	0
1965	LGQEDPPQHGLPR	sp|P19096|FAS_MOUSE	yes	yes	1163	1175	13	M	L	0	1442.727	3	8.45E-04	142.83	NaN	NaN	0
1966	LGQSDPAPLQHQVDIYQKR	sp|P40142|TKT_MOUSE	yes	yes	187	205	19	R	C	0	2192.134	3;4	5.51E-12	139.46	1.12	0.93	6
1967	LGTDTLPVCSSPASVR	sp|Q80X72|LRC15_MOUSE	yes	yes	445	460	16	R	G	0	1658.830	2	5.33E-04	115.80	NaN	NaN	0
1968	LGTLPPAFSTR	sp|Q78PY7|SND1_MOUSE	yes	yes	777	787	11	R	V	0	1158.640	2	1.97E-02	80.25	NaN	NaN	0
1969	LGTPALTSR	sp|P50431|GLYC_MOUSE	yes	yes	397	405	9	R	G	0	914.519	2	3.47E-02	90.70	NaN	NaN	0
1970	LGTVPQFPR	sp|Q05793|PGBM_MOUSE	yes	yes	189	197	9	R	V	0	1013.566	2	3.17E-02	93.65	NaN	NaN	0
1971	LGYILTCPSNLGTGLR	sp|P30275|KCRU_MOUSE	no	no	311	326	16	R	A	0	1733.913	2	3.02E-04	133.48	NaN	NaN	0
1972	LGYKAKQGYVIYR	sp|Q9CZM2|RL15_MOUSE	yes	yes	51	63	13	R	I	0	1557.867	4	1.32E-02	57.18	1.18	0.95	3
1973	LHFFMPGFAPLTAR	sp|Q922F4|TBB6_MOUSE	no	no	263	276	14	R	G	0	1603.833	3	1.09E-03	113.24	NaN	NaN	0
1974	LHFFMPGFAPLTSR	sp|P99024|TBB5_MOUSE	no	no	263	276	14	R	G	0	1619.828	2;3	1.48E-04	104.17	25.15	24.21	2
1975	LHPFHVIR	sp|Q6ZWV3|RL10_MOUSE	yes	no	91	98	8	R	I	0	1017.587	3	5.75E-02	91.63	NaN	NaN	0
1976	LHPVILASIVDSYER	sp|Q9DCH4|EIF3F_MOUSE	yes	yes	98	112	15	R	R	0	1710.931	3	7.62E-04	105.19	NaN	NaN	0
1977	LHVALR	sp|P06745|G6PI_MOUSE	yes	no	99	104	6	V	N	0	707.444	2	7.69E-02	100.52	NaN	NaN	0
1978	LIAAHGNSLR	sp|Q9DBJ1|PGAM1_MOUSE	yes	no	182	191	10	V	G	0	1050.593	2	1.27E-02	112.36	NaN	NaN	0
1979	LIALLEVLSQKKMHR	sp|Q8BTM8|FLNA_MOUSE	yes	no	77	91	15	R	K	0	1778.060	4	4.54E-02	51.77	0.75	0.73	1
1980	LIALLEVLSQKR	sp|Q80X90|FLNB_MOUSE	yes	no	50	61	12	R	M	0	1381.866	3	7.81E-04	100.93	1.25	0.94	2
1981	LIDFLECGKTNLR	sp|Q61656|DDX5_MOUSE	yes	yes	228	240	13	R	R	0	1577.824	3	1.60E-02	52.58	1.17	1.02	6
1982	LIDGDEGSCVKAKGQGR	sp|Q9Z320|K1C27_MOUSE	yes	yes	381	397	17	R	P	0	1788.879	4	1.48E-03	72.90	1.12	0.89	7
1983	LIDKEVISPDTR	sp|Q9DCN2-2|NB5R3_MOUSE	yes	no	24	35	12	R	R	0	1384.756	3	6.31E-03	71.88	1.84	1.09	2
1984	LIDWGLAEFYHPGQEYNVR	sp|Q60737|CSK21_MOUSE	yes	yes	173	191	19	R	V	0	2306.112	3	1.24E-02	66.89	NaN	NaN	0
1985	LIELYKEAGVGKDR	sp|Q93092|TALDO_MOUSE	yes	yes	125	138	14	R	I	0	1589.878	3;4	5.94E-04	83.69	1.02	0.94	10
1986	LIFAGKQLEDGR	sp|P62983|RS27A_MOUSE	yes	no	43	54	12	R	T	0	1345.735	2;3	1.19E-05	152.40	1.29	0.85	9
1987	LIFFDEIDAIGGAR	sp|P46471|PRS7_MOUSE	yes	yes	271	284	14	C	F	0	1535.798	2	3.28E-02	64.10	NaN	NaN	0
1988	LIGDAAKNQLTSNPENTVFDAKR	sp|P20029|GRP78_MOUSE	yes	yes	76	98	23	R	L	0	2501.287	4	6.62E-07	106.35	1.51	1.01	12
1989	LIGDAAKNQVALNPQNTVFDAKR	sp|Q61696|HS71A_MOUSE	yes	no	50	72	23	R	L	0	2482.329	3;4	2.48E-05	93.58	1.13	0.94	13
1990	LIGDAAKNQVAMNPTNTVFDAKI	sp|P63017|HSP7C_MOUSE	yes	yes	50	72	23	R	L	0	2473.275	3;4	1.30E-05	98.30	1.14	1.00	15
1991	LIGGKPDR	sp|P61979-3|HNRPK_MOUSE	yes	no	170	177	8	V	V	0	854.497	2	1.41E-01	65.22	1.02	0.79	1
1992	LIGQIVSSITASLR	sp|P68369|TBA1A_MOUSE	yes	no	230	243	14	R	F	0	1456.861	2;3	9.72E-04	128.76	NaN	NaN	0
1993	LIKTVETR	sp|P20152|VIME_MOUSE	yes	yes	443	450	8	L	D	0	958.581	2	4.87E-03	125.57	1.03	0.96	6
1994	LILCDCDEFR	sp|P27048|RSMB_MOUSE	yes	no	40	49	10	N	K	0	1339.590	2	1.48E-02	104.22	NaN	NaN	0
1995	LILHTSSCDAER	sp|Q9Z184|PADI3_MOUSE	yes	yes	199	210	12	R	A	0	1400.672	3	1.32E-03	142.83	NaN	NaN	0
1996	LILQIDNAKLAADDFR	sp|B1AQ75|KRT36_MOUSE	yes	yes	164	179	16	R	T	0	1814.989	3	6.08E-03	61.27	4.97	3.22	1
1997	LINLVGESLR	sp|Q9Z1R2|BAG6_MOUSE	yes	yes	323	332	10	R	L	0	1112.655	2	2.51E-02	87.57	NaN	NaN	0
1998	LIPDELAPTYSLDTR	sp|Q7TNG5|EMAL2_MOUSE	yes	no	33	47	15	M	S	0	1702.878	2	3.78E-02	56.51	NaN	NaN	0
1999	LIPDGCGVKYIPNR	sp|Q6ZWV3|RL10_MOUSE	yes	yes	190	203	14	R	G	0	1600.840	3	3.36E-02	46.07	1.31	0.95	9
2000	LISEILSESVVPDVR	sp|O54941|SMCE1_MOUSE	yes	yes	202	216	15	R	S	0	1654.914	2	4.54E-02	51.77	NaN	NaN	0
2001	LISQIVSSITASLR	sp|P68373|TBA1C_MOUSE	no	no	230	243	14	R	F	0	1486.872	2;3	4.96E-04	145.43	NaN	NaN	0
2002	LITGLGVGR	sp|Q7TPV4|MBB1A_MOUSE	yes	yes	75	83	9	R	E	0	884.544	2	1.33E-02	137.84	NaN	NaN	0
2003	LITLEEEMTKYKPESDELTAEKITEF	sp|P09103|PDIA1_MOUSE	yes	yes	319	347	29	R	F	0	3539.716	5;6	2.80E-02	41.48	0.97	0.73	3
2004	LITNVESQLGEIR	sp|Q61897|KT33B_MOUSE	no	no	317	329	13	C	A	0	1470.804	2	1.97E-06	182.37	NaN	NaN	0
2005	LIVENLSSR	sp|O35326|SRSF5_MOUSE	no	no	110	118	9	R	V	0	1029.582	2	4.37E-03	156.18	NaN	NaN	0
2006	LIVNLMR	sp|P14824|ANXA6_MOUSE	yes	yes	85	91	7	R	P	0	857.516	2	5.52E-02	132.94	NaN	NaN	0
2007	LIVSVNDLR	sp|P25206|MCM3_MOUSE	yes	yes	47	55	9	R	R	0	1027.603	2	3.42E-03	161.79	NaN	NaN	0
2008	LIYIPLPDEKSR	sp|Q01853|TERA_MOUSE	yes	yes	642	653	12	Q	V	0	1442.813	2	7.42E-02	39.63	1.23	1.10	4
2009	LKAFIPQLLSR	sp|Q9JHR7|IDE_MOUSE	yes	yes	712	722	11	R	L	0	1284.792	3	2.68E-03	85.81	1.06	0.95	5
2010	LKAGVGAPVTQVTLQSTQR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	398	416	19	R	R	0	1953.101	3	1.43E-05	98.18	1.60	1.00	5
2011	LKEDQTEYLEER	sp|P11499|HS90B_MOUSE	no	no	185	196	12	H	R	0	1551.742	2;3	1.13E-03	94.69	1.27	1.04	11
2012	LKEGVEYR	sp|Q99PT1|GDIR1_MOUSE	yes	yes	104	111	8	V	I	0	992.529	2	3.63E-02	70.06	0.95	0.91	1
2013	LKKQAGPASVPLR	sp|P27773|PDIA3_MOUSE	yes	yes	128	140	13	H	T	0	1363.830	3	8.05E-03	83.20	1.06	0.95	4
2014	LKKSADTLWGIQKELQF	sp|P06151|LDHA_MOUSE	yes	no	316	332	17	R	-	0	2004.104	3	1.56E-03	99.04	0.91	0.88	4
2015	LKLLLPWLEAR	sp|Q68FD5|CLH1_MOUSE	yes	yes	855	865	11	R	I	0	1350.839	2;3	2.08E-03	92.87	1.34	0.90	3
2016	LKLPAVVTADLR	sp|Q9DCW4|ETFB_MOUSE	yes	yes	175	186	12	R	L	0	1294.797	3	3.72E-03	75.09	1.01	0.95	3
2017	LKLSPADGTR	sp|Q60847|COCA1_MOUSE	yes	no	2237	2246	10	R	G	0	1056.593	3	1.82E-03	107.03	2.90	1.82	2
2018	LKNTLAQTTENLR	sp|E9Q557|DESP_MOUSE	yes	yes	1424	1436	13	R	R	0	1500.826	2;3	5.77E-03	69.46	1.65	0.95	2
2019	LKNTSEQDQPMGGWEMIR	sp|P14733|LMNB1_MOUSE	yes	yes	457	474	18	R	K	0	2118.983	3	9.25E-05	80.59	1.55	0.94	1
2020	LKPWALTFSYGR	sp|P05064|ALDOA_MOUSE	yes	yes	293	304	12	L	A	0	1437.777	3	1.56E-03	86.91	1.11	0.84	4
2021	LKQIGALQL	sp|Q9QUH0|GLRX1_MOUSE	yes	no	99	107	9	R	-	0	982.618	2	1.04E-02	82.28	1.13	1.06	5
2022	LKQLVDKETNER	sp|E9Q557|DESP_MOUSE	yes	yes	1498	1509	12	R	K	0	1471.800	4	1.77E-03	83.20	1.52	0.93	3
2023	LKQQSELQSQVR	sp|Q61792|LASP1_MOUSE	yes	yes	74	85	12	R	Y	0	1442.784	3	3.72E-03	75.09	0.79	0.69	3
2024	LKSPEIQR	sp|Q9D8E6|RL4_MOUSE	yes	yes	293	300	8	I	A	0	969.561	2	1.32E-02	94.85	1.25	0.95	7
2025	LKTPAQFDADELR	sp|P10107|ANXA1_MOUSE	yes	yes	112	124	13	M	G	0	1502.773	3	9.27E-04	84.17	1.08	0.89	4
2026	LKTVLELQYVLDKLGDDDVR	sp|Q60865|CAPR1_MOUSE	yes	yes	144	163	20	R	T	0	2331.269	4	3.86E-02	48.29	NaN	NaN	0
2027	LKVGLQVVAVKAPGFGDNR	sp|P63038|CH60_MOUSE	yes	yes	291	309	19	R	K	0	1967.132	4	1.59E-02	61.10	1.07	1.06	1
2028	LKVPPAINQFTQALDR	sp|P12970|RL7A_MOUSE	yes	yes	74	89	16	R	Q	0	1810.010	3	3.16E-11	166.90	1.26	0.90	8
2029	LKVTEGGEPYR	sp|Q8BHN3|GANAB_MOUSE	yes	no	268	278	11	R	L	0	1247.651	3	1.12E-03	105.25	1.11	1.02	5
2030	LKYENELTLR	sp|Q61414|K1C15_MOUSE	no	no	186	195	10	R	Q	0	1277.698	3	1.15E-01	49.47	2.43	1.36	2
2031	LKYENEVTLR	sp|P02535-3|K1C10_MOUSE	yes	no	225	234	10	R	Q	0	1263.682	2;3	5.66E-07	178.71	1.56	1.08	11
2032	LLAEPVPGIKAEPDESNAR	sp|P61089|UBE2N_MOUSE	yes	yes	15	33	19	R	Y	0	2005.048	3	1.65E-03	69.94	1.42	1.08	8
2033	LLANKVPAAAR	sp|P14869|RLA0_MOUSE	yes	yes	102	112	11	M	A	0	1122.687	2	3.88E-02	73.89	1.19	0.99	4
2034	LLASKSLLNR	sp|Q9CPW5|SSRB_MOUSE	yes	yes	23	32	10	R	Y	0	1113.687	3	4.96E-03	86.34	0.98	0.80	5
2035	LLCGEEQGADAALHFNPR	sp|O54974|LEG7_MOUSE	yes	yes	37	54	18	N	L	0	1996.943	2;3	2.26E-06	173.03	NaN	NaN	0
2036	LLCNFMR	sp|Q9R1P4|PSA1_MOUSE	yes	yes	83	89	7	R	Q	0	952.462	2	5.25E-02	137.50	NaN	NaN	0
2037	LLDAQLSTGGIVDPSKSHR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	3035	3053	19	R	V	0	1993.059	4	1.62E-03	70.09	1.16	0.91	5
2038	LLDEFVSLHGPTLR	sp|Q3UDE2|TTL12_MOUSE	yes	yes	22	35	14	R	A	0	1595.867	3	4.48E-02	58.08	NaN	NaN	0
2039	LLDMDGIIVEKQR	sp|P23116|EIF3A_MOUSE	yes	yes	341	353	13	R	R	0	1528.828	3	2.72E-02	48.53	1.45	1.21	6
2040	LLDNLLALVR	sp|Q924C1-2|XPO5_MOUSE	yes	no	52	61	10	R	T	0	1138.707	2	1.61E-02	101.38	NaN	NaN	0
2041	LLDPAWEKQQR	sp|P57780|ACTN4_MOUSE	no	no	44	54	11	L	K	0	1382.731	2	3.09E-03	81.02	1.41	1.10	6
2042	LLDSEIKIMKSEVLR	sp|O88685|PRS6A_MOUSE	yes	yes	50	64	15	R	V	0	1773.007	3;4	5.14E-02	40.28	1.55	1.49	2
2043	LLDTEETDLMLAALR	sp|Q99KD5|UN45A_MOUSE	yes	yes	203	217	15	R	T	0	1702.881	2	4.66E-02	51.03	NaN	NaN	0
2044	LLEAASVSSKGLPSPYNMSAPGSR	sp|E9Q557|DESP_MOUSE	yes	yes	2814	2837	24	R	S	0	2418.221	3	3.53E-02	38.27	1.68	1.09	4
2045	LLEACTFHKH	sp|Q921I1|TRFE_MOUSE	yes	no	688	697	10	R	-	0	1254.618	3	3.24E-03	96.34	1.02	0.88	4
2046	LLEAQACTGGIIHPTTGQKLSLQD	sp|E9Q557|DESP_MOUSE	yes	yes	2662	2699	38	R	L	0	4063.047	4	7.13E-04	83.29	2.21	1.35	1
2047	LLEAQIATGGIIDPKESHR	sp|E9Q557|DESP_MOUSE	yes	yes	2379	2397	19	R	L	0	2047.106	3	8.93E-13	152.86	1.79	1.09	3
2048	LLEAQIATGGIIDPVHSHR	sp|Q9QXS1-15|PLEC_MOUSE	no	no	2707	2725	19	R	V	0	2026.096	4	3.17E-03	91.59	NaN	NaN	0
2049	LLEAQIATGGVIDPVHSHR	sp|Q8R0W0|EPIPL_MOUSE	yes	no	727	745	19	R	V	0	2012.080	3;4	1.70E-03	98.18	NaN	NaN	0
2050	LLEAQVATGGIIDPVHSHR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	3366	3384	19	R	L	0	2012.080	3	5.41E-04	107.72	NaN	NaN	0
2051	LLEEAFNCR	sp|Q8C1A5|THOP1_MOUSE	yes	yes	239	247	9	R	C	0	1150.544	2	1.16E-02	141.20	NaN	NaN	0
2052	LLEFQNDR	sp|P29391|FRIL1_MOUSE	yes	yes	66	73	8	R	G	0	1033.519	2	4.12E-02	111.95	NaN	NaN	0
2053	LLEGEDAHLSSSQFSSSSQFSSGSQ	sp|Q61781|K1C14_MOUSE	yes	yes	424	451	28	R	D	0	2931.312	3	1.24E-34	236.05	NaN	NaN	0
2054	LLEGEDAHLTQYKPKEPVTTR	sp|Q9QWL7|K1C17_MOUSE	yes	no	387	407	21	R	Q	0	2424.265	4;5	3.04E-03	55.45	1.71	1.10	13
2055	LLELFPVNR	sp|Q91VK1|BZW2_MOUSE	yes	yes	216	224	9	R	Q	0	1099.639	2	2.14E-02	107.57	NaN	NaN	0

2056	LLELGPKPEVAQQTR	sp|Q8CIE6|COPA_MOUSE	yes	yes	1128	1142	15	R	K	0	1677.941	3	1.07E-02	53.30	1.79	1.00	5
2057	LLELLPR	sp|P20782|ACHE_MOUSE	yes	yes	346	352	7	I	L	0	852.543	2	6.79E-02	108.24	NaN	NaN	0
2058	LLELQYFISR	sp|Q61543|GSLG1_MOUSE	yes	yes	542	551	10	R	D	0	1280.713	2	8.26E-03	129.89	NaN	NaN	0
2059	LLEPEEPGLSRPPLPR	sp|Q9QZQ1-2|AFAD_MOUSE	yes	no	1658	1673	16	R	D	1	1798.994	3	2.95E-02	58.08	NaN	NaN	0
2060	LLFEELVR	sp|P52480-2|KPYM_MOUSE	yes	yes	393	400	8	R	A	0	1017.586	2	7.21E-02	79.71	NaN	NaN	0
2061	LLFNDVQTLKDGR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	357	369	13	R	H	0	1517.820	3	3.41E-02	46.88	1.43	1.02	5
2062	LLGADGGCITR	sp|Q91VD9|NDUS1_MOUSE	yes	yes	547	557	11	F	Q	0	1131.571	2	2.31E-02	76.17	NaN	NaN	0
2063	LLGANIR	sp|Q8CGC7|SYEP_MOUSE	yes	yes	1334	1340	7	R	V	0	755.465	2	6.24E-02	119.22	NaN	NaN	0
2064	LLGINVTDFTR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	377	387	11	H	G	0	1247.687	2	1.41E-03	146.90	14.57	11.88	1
2065	LLGLGVTDFSR	sp|Q6URW6-2|MYH14_MOUSI	yes	no	399	409	11	R	A	0	1176.650	2	1.53E-02	89.81	NaN	NaN	0
2066	LLGMNVMEFTR	sp|Q61879|MYH10_MOUSE	yes	yes	384	394	11	H	A	0	1309.652	2	9.54E-03	102.40	NaN	NaN	0
2067	LLGNTFVALSDLR	sp|Q9Z1R2|BAG6_MOUSE	yes	yes	333	345	13	R	C	0	1417.793	2	4.06E-03	95.26	NaN	NaN	0
2068	LLGVEGTTLR	sp|Q9WTI7-4|MYO1C_MOUSE	yes	no	341	350	10	R	E	0	1057.613	2	6.76E-03	135.55	NaN	NaN	0
2069	LLHSHISDTSVVVKMDNSR	sp|Q6IMF0|KRT83_MOUSE	yes	yes	254	272	19	R	D	0	2137.095	4	2.00E-05	96.14	1.94	1.12	1
2070	LLIDEAIQKCDGER	sp|P26638|SYSC_MOUSE	yes	yes	108	121	14	R	V	0	1658.830	3	7.98E-02	48.53	1.15	0.99	3
2071	LLIEDLEAR	sp|Q9ERS2|NDUAD_MOUSE	yes	yes	60	68	9	R	I	0	1070.597	2	2.21E-02	103.55	NaN	NaN	0
2072	LLIKTVETR	sp|P20152|VIME_MOUSE	yes	yes	442	450	9	T	D	0	1071.665	2	2.81E-03	108.47	0.98	0.94	2
2073	LLKKGYEVIYLTEPVDEYCIQALPEI	sp|P08113|ENPL_MOUSE	yes	yes	558	587	30	R	F	0	3585.843	5	4.23E-03	54.17	0.99	0.90	1
2074	LLKPELLR	sp|Q9Z1N5|DX39B_MOUSE	yes	no	51	58	8	F	A	0	980.638	2	2.69E-02	74.92	1.43	1.07	6
2075	LLLAGYDDFNCNIWDAMKGDR	sp|P62880|GBB2_MOUSE	yes	yes	284	304	21	R	A	0	2486.136	3	3.13E-03	54.83	1.69	1.14	1
2076	LLLAGYDDFNCNVWDALKADR	sp|P62874|GBB1_MOUSE	yes	yes	284	304	21	R	A	0	2468.179	3	2.64E-05	82.01	1.34	0.90	1
2077	LLLASPGACFR	sp|Q9Z184|PADI3_MOUSE	yes	yes	488	498	11	R	L	0	1203.643	2	1.23E-04	146.11	8.71	7.12	1
2078	LLLNNDNLLR	sp|P47754|CAZA2_MOUSE	yes	no	38	47	10	R	E	0	1196.688	2	7.70E-03	132.01	NaN	NaN	0
2079	LLLSDMWASKELQSVLR	sp|P97350|PKP1_MOUSE	yes	yes	687	703	17	R	Q	0	1988.077	2;3	3.13E-07	123.14	1.76	1.09	4
2080	LLLSELR	sp|Q9QZ25|VNN3_MOUSE	yes	yes	300	306	7	Q	S	0	842.523	2	6.22E-02	119.57	NaN	NaN	0
2081	LLLTAAVPSDR	sp|Q9D7Q1|CHIT1_MOUSE	yes	no	178	188	11	R	G	0	1154.666	2	1.53E-02	89.90	NaN	NaN	0
2082	LLLVGAPR	sp|Q61739-2|ITA6_MOUSE	yes	no	61	68	8	R	A	0	837.544	2	4.33E-02	104.45	NaN	NaN	0
2083	LLNFPTIVER	sp|O54984|ASNA_MOUSE	yes	yes	176	185	10	R	G	0	1200.687	2	7.22E-03	133.81	NaN	NaN	0
2084	LLNLKNDSLR	sp|Q62348|TSN_MOUSE	yes	yes	183	192	10	R	K	0	1184.688	3	1.16E-02	73.50	1.26	1.09	4
2085	LLNNAFEELVAFQR	sp|P25206|MCM3_MOUSE	yes	yes	65	78	14	R	A	0	1662.873	2	1.07E-03	115.12	NaN	NaN	0
2086	LLPASFPCIFGPGEDQPLSPEASR	sp|Q8K010|OPLA_MOUSE	yes	yes	401	424	24	R	K	0	2584.263	2	1.08E-02	51.55	NaN	NaN	0
2087	LLPETPSDPFAIWQITDR	sp|Q60847|COCA1_MOUSE	yes	no	2587	2604	18	R	D	0	2098.074	2;3	3.10E-03	93.37	NaN	NaN	0
2088	LLPLTDKAAKGGELVYTDTEAR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	2783	2804	22	R	D	0	2360.259	4	4.16E-02	35.99	2.08	1.24	2
2089	LLPQLSYLDGYDR	sp|Q9EST5|AN32B_MOUSE	yes	no	138	150	13	R	E	0	1551.793	2	3.26E-03	97.69	NaN	NaN	0
2090	LLQAFLER	sp|Q9ERK4|XPO2_MOUSE	yes	yes	707	714	8	R	G	0	988.571	2	3.83E-02	122.52	NaN	NaN	0
2091	LLQAGFR	sp|Q9Z2W0|DNPEP_MOUSE	yes	yes	40	46	7	R	E	0	803.465	2	4.81E-02	119.22	NaN	NaN	0
2092	LLQAVEPIHLAR	sp|Q8BJY1|PSMD5_MOUSE	yes	yes	71	82	12	R	N	0	1358.803	3	4.35E-03	105.46	NaN	NaN	0
2093	LLQDSVDFSLADAINTEFKNTR	sp|P20152|VIME_MOUSE	yes	yes	79	100	22	R	T	0	2496.250	3	2.57E-08	105.96	1.16	0.93	5
2094	LLQFYAETCPAPER	sp|Q9WTI7-4|MYO1C_MOUSE	yes	no	153	166	14	R	G	0	1693.813	2	2.12E-02	69.92	NaN	NaN	0
2095	LLQLGQQSR	sp|Q9QY23|PKP3_MOUSE	yes	no	54	62	9	R	H	0	1041.593	2	2.46E-03	123.86	0.89	0.60	1
2096	LLQLQEQMR	sp|E9Q557|DESP_MOUSE	yes	yes	154	162	9	R	A	0	1157.623	2	3.79E-03	159.58	NaN	NaN	0
2097	LLQNLR	sp|Q8K3W2|LRC10_MOUSE	yes	no	119	124	6	S	T	0	755.465	2	6.38E-02	115.01	NaN	NaN	0
2098	LLQSGNSDVVR	sp|P97350|PKP1_MOUSE	yes	yes	583	593	11	R	S	0	1186.631	2	1.23E-03	148.28	NaN	NaN	0
2099	LLSPGSVMLVSAR	sp|Q64105|SPRE_MOUSE	yes	yes	31	43	13	R	S	0	1328.749	2	6.44E-03	88.08	NaN	NaN	0
2100	LLSWSDNWR	sp|Q9JM14|NT5C_MOUSE	yes	yes	182	190	9	R	G	0	1175.572	2	2.04E-02	113.66	NaN	NaN	0
2101	LLTAFR	sp|P28658|ATX10_MOUSE	yes	no	128	133	6	S	C	0	719.433	2	5.96E-02	120.76	NaN	NaN	0
2102	LLTEAPLNPKANR	sp|P63260|ACTG_MOUSE	no	no	104	116	13	V	E	0	1435.815	2	2.53E-05	130.56	1.07	0.97	3
2103	LLTSGYLQR	sp|Q7TQI3|OTUB1_MOUSE	yes	yes	177	185	9	R	E	0	1049.587	2	3.74E-02	88.14	NaN	NaN	0
2104	LLTSHTGNTSNSEDILSSACYTVR	sp|P97350|PKP1_MOUSE	yes	yes	623	646	24	R	N	0	2625.234	3	4.07E-06	121.50	NaN	NaN	0
2105	LLVACCLADIFR	sp|Q6A026|PDS5A_MOUSE	yes	no	87	98	12	R	I	0	1449.747	2	9.40E-03	90.61	NaN	NaN	0
2106	LLVKLYR	sp|P35980|RL18_MOUSE	yes	yes	27	33	7	R	F	0	903.591	2;3	1.81E-03	159.19	0.94	0.90	6
2107	LLVPLVPDLQDVAQLR	sp|Q3U7R1-2|ESYT1_MOUSE	yes	no	298	313	16	R	S	0	1788.051	2;3	3.59E-03	87.52	NaN	NaN	0
2108	LLVPYLIEAVR	sp|Q61425|HCDH_MOUSE	yes	yes	222	232	11	R	L	0	1284.781	2	1.93E-02	81.02	NaN	NaN	0
2109	LLVVTDPR	sp|P14206|RSSA_MOUSE	yes	yes	121	128	8	R	A	0	911.544	2	4.29E-02	105.81	NaN	NaN	0
2110	LLVVYPWTQR	sp|P02104|HBE_MOUSE	yes	no	32	41	10	R	F	0	1273.718	2	1.03E-02	121.80	NaN	NaN	0
2111	LLWENGNLLR	sp|P01027|CO3_MOUSE	yes	no	1311	1320	10	R	S	0	1226.677	2	1.40E-04	147.20	0.18	0.18	1
2112	LLWTLESLVTGR	sp|Q571I9|A16A1_MOUSE	yes	yes	118	129	12	R	A	0	1386.787	2	3.40E-02	70.09	NaN	NaN	0
2113	LLYEANLPENFR	sp|Q91VZ6|SMAP1_MOUSE	yes	yes	96	107	12	R	R	0	1477.757	2	2.62E-02	125.54	NaN	NaN	0
2114	LLYPPETGLFLVR	sp|P41241|CSK_MOUSE	yes	yes	95	107	13	R	E	0	1516.865	2	4.29E-02	63.09	NaN	NaN	0
2115	LMADFQAGR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	3506	3514	9	R	V	0	1007.486	2	3.22E-02	93.17	NaN	NaN	0
2116	LMEPIYLVEIQCPEQVVGGIYGVLI	sp|P58252|EF2_MOUSE	yes	yes	740	765	26	R	K	0	2988.545	2;3	4.34E-09	134.66	NaN	NaN	0
2117	LMESHGFEEYMKELGVGLALR	sp|Q05816|FABP5_MOUSE	yes	yes	13	33	21	R	K	0	2408.187	3;4	1.56E-05	90.72	1.11	1.06	10
2118	LMMDPLTGLNR	sp|Q7TMK9-2|HNRPQ_MOUSE	yes	no	193	203	11	R	G	0	1259.637	2	6.43E-03	116.55	NaN	NaN	0
2119	LMNETTAVALAYGIYKQDLPALEE	sp|Q61316|HSP74_MOUSE	yes	yes	170	196	27	R	N	0	3033.585	4	7.38E-03	56.69	1.60	1.56	1
2120	LMTDTINEPILLCR	sp|Q8BP47|SYNC_MOUSE	yes	yes	437	450	14	R	F	0	1687.864	2	4.64E-05	175.74	NaN	NaN	0
2121	LNDLLVKVLEKH	sp|Q9CQN1|TRAP1_MOUSE	yes	no	695	706	12	R	-	0	1419.845	3	1.83E-03	82.07	1.50	1.37	2
2122	LNDSILQATEQR	sp|E9Q557|DESP_MOUSE	yes	yes	1268	1279	12	R	R	0	1386.710	2	1.62E-10	221.75	32.68	22.33	1
2123	LNEAAAGLNQAATELVQASR	sp|P26039|TLN1_MOUSE	yes	yes	1242	1261	20	R	G	0	2026.044	2	8.91E-08	159.14	NaN	NaN	0
2124	LNFLSPELPAVAEFSTNETMGHSA	sp|Q99JY0|ECHB_MOUSE	yes	yes	205	230	26	R	L	0	2832.339	3	7.76E-03	56.91	NaN	NaN	0
2125	LNGEYKGTVLSIDDSLQR	sp|Q61495|DSG1A_MOUSE	no	no	456	473	18	R	T	0	2007.027	3	7.37E-05	85.20	1.50	0.94	4
2126	LNIEVDAAPPVDLTR	sp|Q62168|K1H2_MOUSE	no	no	208	222	15	R	M	0	1621.868	2	7.69E-04	104.26	NaN	NaN	0
2127	LNIISNLDCVNEVIGIR	sp|Q76MZ3|2AAA_MOUSE	yes	no	382	398	17	R	Q	0	1941.035	2	8.54E-05	146.30	NaN	NaN	0
2128	LNIPVNQVNPR	sp|Q8VDN2|AT1A1_MOUSE	yes	yes	648	658	11	R	D	0	1262.710	2	7.74E-03	110.38	NaN	NaN	0
2129	LNKCGVISPR	sp|P62245|RS15A_MOUSE	yes	yes	69	78	10	R	F	0	1142.623	3	5.46E-04	127.51	1.30	1.05	2
2130	LNLNNTVLSKR	sp|Q8CGC7|SYEP_MOUSE	yes	yes	426	436	11	R	K	0	1270.736	3	2.90E-03	83.18	1.57	1.36	4
2131	LNLVLSR	sp|Q91WT4|DJC17_MOUSE	yes	yes	205	211	7	V	K	0	813.507	2	1.83E-02	172.03	NaN	NaN	0
2132	LNLYELKEGR	sp|Q9R1P1|PSB3_MOUSE	yes	yes	71	80	10	R	Q	0	1233.672	2;3	1.71E-03	108.70	1.21	0.95	12
2133	LNPGGYFIGTTPNSFELIR	sp|Q9D0L8-2|MCES_MOUSE	yes	no	297	315	19	R	R	0	2095.074	2	6.13E-04	104.88	NaN	NaN	0
2134	LNPQEYLTSTACR	sp|P97496-2|SMRC1_MOUSE	yes	no	499	511	13	R	R	0	1551.735	2	1.51E-03	111.88	NaN	NaN	0
2135	LNPTWNQPNQDTEAGFR	sp|Q9JK81|MYG1_MOUSE	yes	yes	201	217	17	R	R	0	1986.918	2	5.36E-03	81.66	NaN	NaN	0
2136	LNQDQLDAVSKYQEVTNNLEFAK	sp|Q60865|CAPR1_MOUSE	yes	yes	86	112	27	R	S	0	3192.605	4	7.75E-02	23.28	1.50	1.44	1
2137	LNQLVDSLQQLR	sp|Q80U93|NU214_MOUSE	yes	yes	869	880	12	R	L	0	1425.794	2	6.56E-03	97.78	NaN	NaN	0
2138	LNQWCNVVR	sp|Q8CGC7|SYEP_MOUSE	yes	yes	1144	1152	9	R	W	0	1187.587	2	7.62E-03	148.99	NaN	NaN	0
2139	LNSAIIYDR	sp|P07742|RIR1_MOUSE	yes	yes	131	139	9	R	D	0	1063.566	2	8.25E-03	147.75	NaN	NaN	0
2140	LNVEVDAAPPVDLNR	sp|Q497I4|KRT35_MOUSE	no	no	250	264	15	R	V	0	1620.847	2	7.25E-04	109.79	NaN	NaN	0
2141	LNVEVDAAPTVDLNR	sp|Q61897|KT33B_MOUSE	no	no	209	223	15	R	V	0	1624.842	2	3.79E-05	169.98	NaN	NaN	0
2142	LNVFKNDQDTWDYTNPNLSGQG	sp|Q8R081|HNRPL_MOUSE	yes	yes	270	300	31	R	Q	0	3490.614	4	2.10E-02	45.14	1.14	0.88	6
2143	LNVLANVIR	sp|Q60597-2|ODO1_MOUSE	yes	no	305	313	9	R	K	0	1010.624	2	1.44E-01	57.59	NaN	NaN	0
2144	LPAAGVGDMVMATVKKGKPELR	sp|P62830|RL23_MOUSE	yes	yes	52	73	22	R	K	0	2267.249	5	5.27E-06	127.32	0.83	0.76	1
2145	LPAIEPSDQGQYLCR	sp|Q05793|PGBM_MOUSE	yes	yes	1919	1933	15	R	A	0	1745.841	2	1.80E-04	150.11	NaN	NaN	0
2146	LPAKPEVSSDEDVQYR	sp|Q8BMS1|ECHA_MOUSE	yes	yes	661	676	16	R	V	0	1831.895	3	7.02E-04	103.13	1.72	0.97	1
2147	LPATSAESESAVISNGEH	sp|Q8JZK9|HMCS1_MOUSE	yes	no	503	520	18	R	-	0	1797.838	2;3	2.26E-19	241.68	NaN	NaN	0
2148	LPAYLTIQMVR	sp|Q9JMA1|UBP14_MOUSE	yes	yes	320	330	11	R	F	0	1303.732	2	7.81E-02	60.26	NaN	NaN	0
2149	LPCVEDYLSAILNR	sp|P07724|ALBU_MOUSE	yes	yes	470	483	14	R	V	0	1661.845	2;3	1.03E-06	184.21	22.70	18.44	1
2150	LPDGTSLTQTFR	sp|Q922Y1|UBXN1_MOUSE	yes	yes	220	231	12	R	A	0	1334.683	2	1.47E-03	140.91	NaN	NaN	0
2151	LPEAAFLAR	sp|O55029|COPB2_MOUSE	yes	yes	751	759	9	R	T	0	986.555	2	1.84E-02	125.04	NaN	NaN	0
2152	LPEYTPR	sp|Q8BK67|RCC2_MOUSE	yes	yes	512	518	7	R	T	0	874.455	2	6.65E-02	111.04	NaN	NaN	0
2153	LPFLDIAPLDIGGADQEFR	sp|Q01149|CO1A2_MOUSE	yes	yes	1345	1363	19	R	V	0	2086.074	2	1.82E-06	148.26	NaN	NaN	0
2154	LPFLPSSNLSLDILR	sp|Q9CQT5|POMP_MOUSE	yes	yes	92	106	15	R	G	0	1683.956	2	5.24E-02	50.09	NaN	NaN	0
2155	LPFSGFR	sp|Q9DAR7|DCPS_MOUSE	yes	yes	41	47	7	R	V	0	822.439	2	5.76E-02	128.75	NaN	NaN	0
2156	LPFSLR	sp|Q9WVB6|LENEP_MOUSE	yes	no	12	17	6	A	D	0	731.433	2	2.82E-02	105.42	NaN	NaN	0
2157	LPGAIDVIGQTITISR	sp|Q9D824-4|FIP1_MOUSE	yes	no	309	324	16	R	V	0	1652.946	2	6.88E-04	104.21	NaN	NaN	0
2158	LPGINCGPDFTPSFANLGR	sp|Q6NZJ6|IF4G1_MOUSE	yes	no	661	679	19	R	P	0	2031.984	2	1.24E-15	209.70	NaN	NaN	0

2159	LPKMVGVPAAFDMMLTGR	sp|Q8BMS1|ECHA_MOUSE	yes	yes	188	205	18	R	N	0	1932.999	3	7.96E-05	83.76	1.33	0.89	1
2160	LPLEAALR	sp|Q8R0W0|EPIPL_MOUSE	yes	yes	420	427	8	R	F	0	881.533	2	7.56E-03	110.12	2.41	1.56	1
2161	LPLLQPETPVSLR	sp|Q80U72|SCRIB_MOUSE	yes	no	832	844	13	R	Q	0	1461.856	2	1.00E-02	77.19	NaN	NaN	0
2162	LPLPEPWR	sp|Q9JK81|MYG1_MOUSE	yes	yes	316	323	8	R	G	0	1006.560	2	3.85E-02	121.99	NaN	NaN	0
2163	LPLPYGFSAMQGWR	sp|Q61074|PPM1G_MOUSE	yes	yes	23	36	14	R	V	0	1621.808	2	1.82E-03	100.22	NaN	NaN	0
2164	LPLQDVYKIGGIGTVPVGR	sp|P10126|EF1A1_MOUSE	yes	no	248	266	19	R	V	0	1981.136	2;3	7.18E-21	188.19	1.33	1.00	20
2165	LPLQLDDAIRPEVEGEEDGR	sp|Q922B2|SYDC_MOUSE	yes	yes	152	171	20	R	A	1	2250.113	3	6.00E-04	101.92	NaN	NaN	0
2166	LPMDYYGIPFAAPTALASR	sp|Q91VX2|UBAP2_MOUSE	yes	yes	849	867	19	R	D	0	2053.034	2	1.14E-02	68.64	NaN	NaN	0
2167	LPNNHIGISFIPR	sp|Q80X90|FLNB_MOUSE	yes	yes	1957	1969	13	R	E	0	1476.820	3	1.17E-03	134.68	NaN	NaN	0
2168	LPPGEYIVVPSTFEPNKEGDFLLR	sp|O35350|CAN1_MOUSE	yes	yes	488	511	24	R	F	0	2716.411	3	1.11E-04	83.40	1.27	1.08	6
2169	LPPLPLHIR	sp|Q501J7-2|PHAR4_MOUSE	yes	no	378	386	9	R	I	0	1054.665	3	2.21E-02	103.83	NaN	NaN	0
2170	LPSEGPQPAHVVVGDVR	sp|Q923D2|BLVRB_MOUSE	yes	yes	40	56	17	R	Q	0	1755.927	3	8.81E-05	145.91	NaN	NaN	0
2171	LPVDMAYKR	sp|E9Q557|DESP_MOUSE	yes	yes	2398	2406	9	R	G	0	1091.580	2;3	2.31E-02	70.82	1.62	1.02	8
2172	LPVDVAYQR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	3385	3393	9	R	G	0	1059.571	2	1.71E-02	130.31	NaN	NaN	0
2173	LPVEEAYKR	sp|E9Q557|DESP_MOUSE	yes	yes	2322	2330	9	R	G	0	1103.598	2;3	2.31E-03	113.62	2.34	1.31	2
2174	LPVEVAYKR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	3963	3971	9	R	G	0	1073.623	3	5.06E-02	54.98	1.40	1.01	9
2175	LQAALDNEAGGR	sp|Q8VEK3|HNRPU_MOUSE	yes	yes	38	49	12	R	P	0	1213.605	2	4.39E-03	105.03	NaN	NaN	0
2176	LQAALDNEAGGRPAMEPGNGSL	sp|Q8VEK3|HNRPU_MOUSE	yes	yes	38	68	31	R	S	1	2979.411	3	6.05E-06	98.15	NaN	NaN	0
2177	LQAEIFQAR	sp|P08226|APOE_MOUSE	yes	yes	262	270	9	R	L	0	1074.582	2	3.85E-03	159.28	NaN	NaN	0
2178	LQDEIQNMKEEMAR	sp|P20152|VIME_MOUSE	yes	yes	365	378	14	R	H	0	1733.808	2;3	9.89E-09	171.08	1.20	0.98	27
2179	LQDLYSIVR	sp|P39061-2|COIA1_MOUSE	yes	no	1185	1193	9	R	R	0	1105.613	2	2.07E-02	111.61	NaN	NaN	0
2180	LQDSGAFQCVAR	sp|Q8BKG3|PTK7_MOUSE	yes	yes	85	96	12	R	D	0	1350.635	2	4.00E-03	109.72	NaN	NaN	0
2181	LQDVTDDHIR	sp|Q923D2|BLVRB_MOUSE	yes	yes	125	134	10	R	M	0	1210.594	3	1.19E-02	115.57	NaN	NaN	0
2182	LQDVYKIGGIGTVPVGR	sp|P10126|EF1A1_MOUSE	yes	no	250	266	17	P	V	0	1770.999	2	2.57E-05	99.04	1.36	0.99	7
2183	LQEKEDLQELNDR	sp|P48678|LMNA_MOUSE	yes	no	29	41	13	R	L	0	1628.801	2;3	1.24E-12	189.10	1.15	0.65	8
2184	LQEKLSPPYSSPQEFAQDVGR	sp|Q62318|TIF1B_MOUSE	yes	yes	747	767	21	R	M	0	2375.176	3	8.98E-06	96.02	1.39	1.10	2
2185	LQENGKPLDEVLR	sp|P10107|ANXA1_MOUSE	yes	yes	85	97	13	Y	K	0	1509.815	3	1.78E-03	76.07	0.96	0.85	4
2186	LQEPQACKHFTSFR	sp|P21844|CMA1_MOUSE	yes	yes	169	182	14	R	H	0	1747.846	4	3.44E-02	63.29	NaN	NaN	0
2187	LQEVFGCAIR	sp|Q9D0I9|SYRC_MOUSE	yes	yes	80	89	10	R	A	0	1191.607	2	7.83E-03	131.52	NaN	NaN	0
2188	LQEVIETLLSLEKQTR	sp|Q9D8W5|PSD12_MOUSE	yes	yes	40	55	16	R	T	0	1899.068	3	2.61E-05	100.11	1.11	1.02	5
2189	LQEVPHEGPMCDLLWSDPDDR	sp|P63330|PP2AA_MOUSE	yes	no	186	206	21	R	G	0	2508.105	3	1.16E-03	93.78	NaN	NaN	0
2190	LQGEISHVKKQCKGVQDSIADAEC	sp|Q3TTY5|K22E_MOUSE	yes	no	427	451	25	R	G	0	2823.430	4;5	1.23E-04	88.98	2.85	1.83	9
2191	LQIDEQLR	sp|P35922-9|FMR1_MOUSE	yes	no	413	420	8	R	Q	0	1013.551	2	2.96E-02	127.02	NaN	NaN	0
2192	LQIDQINTDLNLER	sp|Q8VDD5|MYH9_MOUSE	yes	yes	1757	1770	14	N	S	0	1683.879	2	1.45E-04	163.99	NaN	NaN	0
2193	LQKDLEGLSQR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	1390	1400	11	R	L	0	1285.699	3	3.51E-05	151.26	1.42	0.94	9
2194	LQLEACETR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	897	905	9	R	T	0	1118.539	2	1.51E-02	134.25	NaN	NaN	0
2195	LQLELSKVR	sp|P48678|LMNA_MOUSE	yes	no	102	110	9	R	E	0	1084.660	2;3	1.58E-04	150.61	1.38	0.83	11
2196	LQLETTER	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1362	1369	8	R	Q	0	988.519	2	3.69E-02	127.68	NaN	NaN	0
2197	LQLGPRPPPVAVAVIPR	sp|P49919-2|CDN1C_MOUSE	yes	no	91	107	17	R	S	1	1779.088	3	2.81E-04	125.36	NaN	NaN	0
2198	LQLWDTAGQER	sp|P35279-2|RAB6A_MOUSE	yes	no	64	74	11	R	F	0	1315.652	2	2.43E-02	75.82	NaN	NaN	0
2199	LQNAIAEAEQR	sp|Q922U2|K2C5_MOUSE	yes	no	404	414	11	N	G	0	1241.636	2	1.22E-04	171.92	NaN	NaN	0
2200	LQNLEFALNLLR	sp|Q9R269|PEPL_MOUSE	yes	yes	855	866	12	R	Q	0	1442.825	2	2.13E-03	132.32	NaN	NaN	0
2201	LQNVAITGPAVPYSR	sp|P46935|NEDD4_MOUSE	yes	yes	493	507	15	R	D	0	1584.862	2	6.80E-04	115.56	NaN	NaN	0
2202	LQPALTSR	sp|Q8C7B8|ZSWM4_MOUSE	yes	yes	380	387	8	S	T	0	884.508	2	6.42E-02	86.14	NaN	NaN	0
2203	LQQDIEAVKGQR	sp|Q99M74|KRT82_MOUSE	yes	yes	344	355	12	R	C	0	1383.747	3	1.32E-03	91.31	1.67	1.02	8
2204	LQQELDDLLVDLDHQR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	1418	1433	16	R	Q	0	1948.985	2;3	3.67E-08	196.22	NaN	NaN	0
2205	LQQENSILR	sp|Q99PL5|RRBP1_MOUSE	yes	yes	1001	1009	9	R	D	0	1099.599	2	6.04E-03	152.11	NaN	NaN	0
2206	LQQLFR	sp|P16546-2|SPTN1_MOUSE	yes	no	786	791	6	R	D	0	803.465	2	6.19E-02	117.54	NaN	NaN	0
2207	LQSEPESIR	sp|O08585|CLCA_MOUSE	yes	yes	102	110	9	R	K	0	1057.540	2	1.51E-02	134.23	NaN	NaN	0
2208	LQSIGTENTEENR	sp|P05064|ALDOA_MOUSE	yes	yes	44	56	13	R	R	0	1489.701	2	1.67E-06	186.13	NaN	NaN	0
2209	LQSIGTENTEENRR	sp|P05064|ALDOA_MOUSE	yes	yes	44	57	14	R	F	1	1645.802	3	1.36E-04	124.07	0.05	0.04	3
2210	LQSLGVPVAAASR	sp|Q9D967|MGDP1_MOUSE	yes	yes	58	70	13	R	T	0	1267.725	2	1.71E-02	73.83	NaN	NaN	0
2211	LQTLKEELDFQKNIYSEELR	sp|P48678|LMNA_MOUSE	yes	no	197	216	20	R	E	0	2495.291	4	2.60E-08	114.46	1.32	0.77	3
2212	LQVLKSTGDVVAGR	sp|Q99KK7|DPP3_MOUSE	yes	yes	625	638	14	R	A	0	1441.825	3	3.62E-05	125.22	1.06	0.98	5
2213	LQVVDRPLPVR	sp|P19096|FAS_MOUSE	yes	yes	374	384	11	R	G	1	1290.777	2;3	3.40E-03	102.52	0.03	0.02	1
2214	LREAGPELSSER	sp|Q3UPH7-3|ARH40_MOUSE	yes	no	1220	1231	12	L	Q	1	1342.684	2	2.29E-02	51.29	34.42	23.58	1
2215	LRSEIDGCKKQISQIQQNINDAEQ	sp|P04104|K2C1_MOUSE	yes	yes	416	440	25	R	G	1	2970.494	4;5	5.63E-04	71.68	1.62	0.88	5
2216	LSAEAEKVLALPEPSPAAPTLR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	946	967	22	R	S	0	2259.247	3	4.29E-04	72.99	1.33	0.94	6
2217	LSAEDLVLEGAGLR	sp|P02468|LAMC1_MOUSE	yes	yes	588	601	14	R	V	0	1441.778	2	9.82E-04	127.36	NaN	NaN	0
2218	LSDKGLKADLMDR	sp|Q8VEK3|HNRPU_MOUSE	yes	yes	25	37	13	R	L	0	1460.766	4	7.86E-03	66.00	1.23	0.98	6
2219	LSDQDSPDEKER	sp|Q80W04|TMCC2_MOUSE	yes	yes	114	125	12	G	S	0	1417.632	2	2.24E-02	51.98	0.22	0.17	1
2220	LSDQFHDILIR	sp|P12815-2|PDCD6_MOUSE	yes	no	124	134	11	R	K	0	1355.720	3	1.02E-02	100.93	NaN	NaN	0
2221	LSEEKAQASAISVGSR	sp|Q9D1E6|TBCB_MOUSE	yes	yes	149	164	16	R	C	0	1631.848	3	2.67E-05	100.04	0.97	0.87	3
2222	LSELLR	sp|P11499|HS90B_MOUSE	no	no	451	456	6	R	Y	0	729.438	2	2.03E-02	168.62	NaN	NaN	0
2223	LSENVIDR	sp|Q9CRB9|CHCH3_MOUSE	yes	yes	28	35	8	R	M	0	944.493	2	4.87E-02	126.07	NaN	NaN	0
2224	LSFDKDAMVAR	sp|Q93092|TALDO_MOUSE	yes	yes	111	121	11	R	A	0	1251.628	3	1.51E-03	99.50	1.06	1.00	5
2225	LSFQHDPETSVLILR	sp|Q8BHN3|GANAB_MOUSE	yes	no	915	929	15	R	K	0	1753.936	3	6.88E-05	160.78	NaN	NaN	0
2226	LSFYETGEIPR	sp|Q9D6Z1|NOP56_MOUSE	yes	yes	405	415	11	R	K	0	1310.651	2	5.52E-03	120.77	NaN	NaN	0
2227	LSGIMVPAPIQDLEALR	sp|P28658|ATX10_MOUSE	yes	yes	11	27	17	R	A	0	1822.002	2	2.35E-02	59.73	NaN	NaN	0
2228	LSGSLGAGSCR	sp|Q9QWL7|K1C17_MOUSE	yes	no	31	41	11	R	L	0	1063.508	2	9.94E-04	150.09	NaN	NaN	0
2229	LSIIATDHTYR	sp|Q04857|CO6A1_MOUSE	yes	yes	199	209	11	R	R	0	1288.678	2;3	4.75E-03	124.42	NaN	NaN	0
2230	LSISGDYNLKTLMSPLGITR	sp|P22599|A1AT2_MOUSE	yes	yes	309	328	20	R	I	0	2178.172	3	3.48E-05	85.94	1.31	1.04	3
2231	LSKEDIER	sp|P63017|HSP7C_MOUSE	yes	yes	510	517	8	R	M	0	988.519	2;3	6.45E-03	116.52	1.02	0.89	14
2232	LSKVSFPGLR	sp|Q8R0W0|EPIPL_MOUSE	yes	no	2692	2701	10	R	R	0	1102.650	3	1.71E-03	108.70	1.33	0.89	9
2233	LSLDVEALR	sp|E9Q557|DESP_MOUSE	yes	yes	1669	1677	9	R	R	0	1014.571	2	4.00E-03	158.37	NaN	NaN	0
2234	LSNIFVIGKGNKPWISLPR	sp|P62702|RS4X_MOUSE	yes	yes	222	240	19	R	G	0	2138.236	3	9.71E-03	71.38	1.04	1.00	1
2235	LSNRPAFMPSEGR	sp|P57780|ACTN4_MOUSE	no	no	367	379	13	R	M	1	1460.719	3	1.66E-03	102.52	NaN	NaN	0
2236	LSPLQFR	sp|Q6GQT6|SCAP_MOUSE	yes	yes	1037	1043	7	S	G	0	859.492	2	5.52E-02	132.96	NaN	NaN	0
2237	LSPVAEEFR	sp|Q00623|APOA1_MOUSE	yes	yes	164	172	9	R	D	0	1046.540	2	2.11E-02	109.29	NaN	NaN	0
2238	LSQETEALGR	sp|Q02819|NUCB1_MOUSE	yes	yes	367	376	10	R	S	0	1102.562	2	8.55E-03	128.81	NaN	NaN	0
2239	LSQTFPNADFAEITKLATDLTKVN	sp|P07724|ALBU_MOUSE	yes	yes	243	281	39	R	A	0	4495.109	5;6	5.01E-04	77.53	1.19	1.12	6
2240	LSSEMNTSTVNSAR	sp|P14733|LMNB1_MOUSE	yes	yes	278	291	14	R	E	0	1495.694	2	1.00E-10	214.14	NaN	NaN	0
2241	LSSLDNLKSSVSQVESDLKMLR	sp|Q8BMK4|CKAP4_MOUSE	yes	yes	506	527	22	R	T	0	2448.289	4	4.40E-06	94.63	2.29	1.30	1
2242	LSSLEKSSPTPR	sp|P57776-2|EF1D_MOUSE	yes	no	88	99	12	R	A	0	1300.699	3	7.37E-04	104.24	1.19	1.11	5
2243	LSSSQFSSSSQFSSGSQSSR	sp|Q61781|K1C14_MOUSE	yes	yes	432	451	20	H	D	0	2066.914	2	5.01E-08	168.79	NaN	NaN	0
2244	LSVAYKNVIGAR	sp|P62259|1433E_MOUSE	yes	yes	45	56	12	L	R	0	1289.746	2	9.21E-03	91.09	1.42	1.37	1
2245	LSVAYKNVVGAR	sp|Q9CQV8-2|1433B_MOUSE	no	no	44	55	12	L	R	0	1275.730	2	3.49E-05	146.36	1.02	0.99	5
2246	LSVAYKNVVGGQR	sp|O70456|1433S_MOUSE	yes	yes	44	56	13	L	A	0	1389.773	2	1.29E-05	142.83	1.15	0.97	4
2247	LSVLGAITSVQQR	sp|Q8BWY3|ERF1_MOUSE	yes	yes	69	81	13	R	L	0	1370.788	2	9.89E-04	139.19	NaN	NaN	0
2248	LSYLLMCLESAVHR	sp|Q61543|GSLG1_MOUSE	yes	yes	394	407	14	R	G	0	1690.854	3	1.11E-03	109.83	NaN	NaN	0
2249	LSYQKTADVQIYNVPVTVKDR	sp|P55850-2|DSC3_MOUSE	yes	no	636	656	21	R	A	0	2436.301	4	1.07E-11	133.21	1.81	1.01	3
2250	LSYTQLLKR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	3757	3765	9	R	C	0	1120.660	3	3.37E-02	64.71	1.80	1.19	3
2251	LTADDFR	sp|Q9Z320|K1C27_MOUSE	no	no	158	164	7	R	M	0	836.403	2	4.30E-03	146.94	0.01	0.01	2
2252	LTAEDLYEAR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	3549	3558	10	R	I	0	1179.577	2	3.09E-02	78.68	NaN	NaN	0
2253	LTAEIENAKCQNTKLEAAVTQSEQ	sp|Q6IMF0|KRT83_MOUSE	yes	yes	337	370	34	R	C	0	3687.801	4	3.19E-16	166.74	1.82	1.10	4
2254	LTAEIENAKCQR	sp|Q9Z2T6|KRT85_MOUSE	no	no	349	360	12	R	A	0	1431.714	2;3	1.92E-17	224.24	1.65	1.06	13
2255	LTAKKQELEEICHDLEAR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	906	923	18	R	V	0	2182.105	4	5.99E-02	48.91	1.58	1.39	4
2256	LTASESSLQR	sp|Q8BL66|EEA1_MOUSE	yes	yes	353	362	10	R	A	0	1090.562	2	2.42E-05	190.88	NaN	NaN	0
2257	LTEAPLNPKANR	sp|P63260|ACTG_MOUSE	no	no	105	116	12	L	E	0	1322.731	2	9.77E-05	129.82	1.19	1.05	4
2258	LTEEETVCLDLDKVEAYR	sp|E9Q557|DESP_MOUSE	yes	yes	803	820	18	R	C	0	2182.046	3	3.14E-07	109.04	1.58	0.96	1
2259	LTEGCSFR	sp|Q6ZWY3|RS27L_MOUSE	yes	no	73	80	8	R	R	0	968.439	2	4.53E-02	101.54	NaN	NaN	0
2260	LTELEATVR	sp|Q99KJ8|DCTN2_MOUSE	yes	yes	232	240	9	R	C	0	1030.566	2	2.53E-02	99.86	NaN	NaN	0
2261	LTELLKQGQYSPMAIEEQVAVIYA	sp|Q03265|ATPA_MOUSE	yes	yes	467	493	27	R	G	0	3005.590	3	1.53E-15	169.26	1.65	1.03	1

2262	LTESPCALVASQYGWSGNMER	sp|P08113|ENPL_MOUSE	yes	yes	640	660	21	R	I	0	2355.062	2	5.29E-03	71.85	NaN	NaN	0
2263	LTFIPGFIGSLR	sp|Q80TH2-1|LAP2_MOUSE	yes	no	219	230	12	R	Q	0	1319.760	2	1.33E-02	80.69	NaN	NaN	0
2264	LTGECLGWMR	sp|E9Q557|DESP_MOUSE	yes	yes	199	208	10	R	Q	0	1221.563	2	1.70E-05	195.79	NaN	NaN	0
2265	LTGINVNPNALFPPVEFPAPR	sp|P19096|FAS_MOUSE	yes	yes	805	825	21	H	G	0	2262.216	2;3	2.92E-07	152.51	NaN	NaN	0
2266	LTILQPLRASPVFR	sp|Q3UH93|PLXD1_MOUSE	yes	yes	456	469	14	P	A	1	1609.967	2	8.98E-03	61.11	1.45	0.99	3
2267	LTLEDLEDSWDR	sp|Q99PV0|PRP8_MOUSE	yes	yes	1403	1414	12	R	G	0	1490.689	2	3.51E-03	115.57	NaN	NaN	0
2268	LTLPFLLLQGSADR	sp|O35678|MGLL_MOUSE	yes	yes	227	240	14	R	L	0	1542.877	2	1.05E-03	118.52	NaN	NaN	0
2269	LTLPQLEIR	sp|P11859|ANGT_MOUSE	yes	yes	370	378	9	R	G	0	1081.650	2	4.67E-02	79.15	NaN	NaN	0
2270	LTLYDIAHTPGVAADLSHIETR	sp|P08249|MDHM_MOUSE	yes	yes	53	74	22	R	A	0	2392.239	3;4	3.56E-17	225.30	NaN	NaN	0
2271	LTNAAATSGDGYR	sp|Q3V1T4-2|P3H1_MOUSE	yes	no	492	504	13	R	G	0	1295.611	2	1.10E-06	192.14	NaN	NaN	0
2272	LTPEEIER	sp|P20029|GRP78_MOUSE	yes	yes	534	541	8	R	M	0	985.508	2	5.01E-02	97.64	NaN	NaN	0
2273	LTPKIGFPWSEIR	sp|P26041|MOES_MOUSE	yes	yes	234	246	13	R	N	0	1542.856	3	5.50E-04	95.26	1.24	0.97	10
2274	LTQGEVYKELR	sp|P19096|FAS_MOUSE	yes	yes	986	996	11	R	L	0	1334.719	3	3.09E-03	81.02	1.36	1.08	4
2275	LTQYKPKEPVTTR	sp|Q9QWL7|K1C17_MOUSE	yes	no	395	407	13	H	Q	0	1559.867	4	5.90E-04	94.09	1.53	1.04	5
2276	LTSLVPFVDAFQLER	sp|P23116|EIF3A_MOUSE	yes	yes	455	469	15	R	A	0	1733.935	2	3.20E-03	89.62	NaN	NaN	0
2277	LTTIIEEAEETQESKPKPR	sp|Q8R0W0|EPIPL_MOUSE	yes	no	2571	2589	19	R	D	0	2198.143	3;4	6.13E-06	101.05	1.52	1.01	5
2278	LTTLELLEVR	sp|Q62261|SPTB2_MOUSE	yes	no	2079	2088	10	R	R	0	1185.697	2	1.30E-03	159.83	NaN	NaN	0
2279	LTVDDIR	sp|Q00612|G6PD1_MOUSE	yes	yes	75	81	7	R	K	0	830.450	2	6.75E-02	108.92	NaN	NaN	0
2280	LTVDEAVR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	2978	2985	8	R	A	0	901.487	2	3.34E-02	134.30	NaN	NaN	0
2281	LTVDVDGR	sp|Q1HFZ0-2|NSUN2_MOUSE	yes	no	183	190	8	R	K	0	873.456	2	4.80E-02	99.31	NaN	NaN	0
2282	LTVEDPVTVEYITR	sp|Q9Z2U0|PSA7_MOUSE	yes	no	96	109	14	R	Y	0	1633.856	2	4.96E-04	145.43	NaN	NaN	0
2283	LTVVDTPGYGDAINCR	sp|P42208|SEPT2_MOUSE	yes	yes	97	112	16	R	D	0	1749.836	2	2.28E-04	139.58	NaN	NaN	0
2284	LTWDPASGKISGYR	sp|Q80X19-2|COEA1_MOUSE	yes	no	554	567	14	R	I	0	1549.789	3	7.44E-03	64.10	1.95	1.22	5
2285	LTYEIEDEKR	sp|E9Q557|DESP_MOUSE	yes	yes	1126	1135	10	R	R	0	1294.641	3	6.45E-03	77.74	1.92	1.08	3
2286	LVAMKFLR	sp|Q01768|NDKB_MOUSE	yes	yes	35	42	8	R	A	0	976.589	2;3	1.23E-03	151.29	1.16	1.02	10
2287	LVARPEPATGFTLEFR	sp|Q61553|FSCN1_MOUSE	yes	yes	202	217	16	R	S	1	1802.968	3	3.85E-05	156.49	NaN	NaN	0
2288	LVEGILHAPDAGWGNLVYVVNYF	sp|Q921F2|TADBP_MOUSE	yes	yes	56	83	28	R	K	0	3136.646	4;5	3.49E-08	110.01	1.37	0.77	1
2289	LVEIPPNLPSSLVELR	sp|P28653|PGS1_MOUSE	yes	yes	151	166	16	H	I	0	1775.019	2	3.66E-02	52.53	NaN	NaN	0
2290	LVEPGSPAEKSGLLAGDR	sp|P70441|NHRF1_MOUSE	yes	yes	41	58	18	R	L	0	1794.948	3	2.00E-03	69.98	0.88	0.70	2
2291	LVEWIVVQCGPDVGRPDR	sp|P37804|TAGL_MOUSE	yes	yes	30	47	18	R	G	1	2094.068	3	2.26E-02	56.12	NaN	NaN	0
2292	LVFGLLNGR	sp|P23492|PNPH_MOUSE	yes	yes	68	76	9	R	C	0	987.587	2	2.10E-02	110.12	NaN	NaN	0
2293	LVGEIMQETGTR	sp|Q8VDJ3|VIGLN_MOUSE	yes	yes	244	255	12	R	I	0	1332.671	2	4.56E-03	102.97	NaN	NaN	0
2294	LVGGKDFEQPLAISR	sp|O70400|PDLI1_MOUSE	yes	yes	18	32	15	R	V	0	1628.889	3	9.37E-02	43.59	1.06	0.92	2
2295	LVGIISSR	sp|P24547|IMDH2_MOUSE	yes	yes	154	161	8	R	D	0	843.518	2	7.15E-02	80.17	NaN	NaN	0
2296	LVGSQEELASWGHEYVR	sp|Q8VDM4|PSMD2_MOUSE	yes	yes	144	160	17	R	H	0	1958.949	3	2.31E-04	127.83	NaN	NaN	0
2297	LVIGQNGILSTPAVSCIIR	sp|Q9D0F9|PGM1_MOUSE	yes	yes	86	104	19	R	K	0	2010.130	2	4.87E-04	109.87	NaN	NaN	0
2298	LVINTVEPSAVR	sp|Q8R5F8|ES8L1_MOUSE	yes	yes	198	209	12	R	G	0	1296.740	2	1.29E-02	81.71	NaN	NaN	0
2299	LVKLFDFPGR	sp|Q8BK67|RCC2_MOUSE	yes	yes	373	382	10	R	G	0	1190.681	3	4.07E-03	91.55	0.98	0.95	5
2300	LVLDQLR	sp|Q8VDD5|MYH9_MOUSE	no	no	687	693	7	H	C	0	855.518	2	4.08E-02	110.61	NaN	NaN	0
2301	LVLEVAQHLGESTVR	sp|P56480|ATPB_MOUSE	yes	yes	95	109	15	R	T	0	1649.910	2;3	1.48E-04	151.80	NaN	NaN	0
2302	LVLSTFSNIR	sp|Q8K4L4|POF1B_MOUSE	yes	yes	328	337	10	R	E	0	1148.655	2	6.76E-03	135.55	NaN	NaN	0
2303	LVNLQHLDLLNNR	sp|Q922Q8|LRC59_MOUSE	yes	yes	84	96	13	R	L	0	1560.874	3	1.43E-03	124.07	NaN	NaN	0
2304	LVPFDHAESTYGLYR	sp|Q9CQ60|6PGL_MOUSE	yes	yes	82	96	15	R	T	0	1766.863	3	1.16E-02	72.90	NaN	NaN	0
2305	LVPSVNGIR	sp|Q922D8|C1TC_MOUSE	yes	yes	479	487	9	R	K	0	953.566	2	9.12E-02	68.22	NaN	NaN	0
2306	LVQIHIPR	sp|P22599|A1AT2_MOUSE	yes	yes	301	308	8	R	L	0	974.603	3	4.56E-02	101.33	NaN	NaN	0
2307	LVQLADMLLNHNR	sp|Q7TPV4|MBB1A_MOUSE	yes	yes	543	555	13	R	N	0	1535.824	3	1.45E-03	120.87	NaN	NaN	0
2308	LVQLLVKAHQDAQR	sp|Q02257|PLAK_MOUSE	yes	yes	527	540	14	R	H	0	1617.932	3	1.38E-02	51.73	2.00	1.12	1
2309	LVQLLVR	sp|Q02248|CTNB1_MOUSE	yes	yes	536	542	7	R	A	0	839.559	2	6.05E-02	122.98	NaN	NaN	0
2310	LVQNCLWTLR	sp|Q02257|PLAK_MOUSE	no	no	368	377	10	R	N	0	1301.691	2	3.30E-03	148.56	NaN	NaN	0
2311	LVQTIIENPFLNGEVIR	sp|O08756|HCD2_MOUSE	yes	yes	236	252	17	H	L	0	1954.089	2	8.95E-04	102.08	NaN	NaN	0
2312	LVSDGNINSDR	sp|Q62261|SPTB2_MOUSE	yes	no	1235	1245	11	R	I	0	1188.574	2	8.17E-02	59.20	NaN	NaN	0
2313	LVSLIGSKTQIPTQR	sp|Q9R1P4|PSA1_MOUSE	yes	yes	108	122	15	R	Y	0	1639.962	2;3	1.31E-05	120.70	1.21	1.05	12
2314	LVSPGSANETSSILVESVTR	sp|Q80X90|FLNB_MOUSE	yes	yes	2476	2495	20	R	S	0	2045.064	2	6.91E-03	72.57	NaN	NaN	0
2315	LVSQIDNTKLAADDLR	sp|Q6IFX4|K1C39_MOUSE	yes	no	162	177	16	R	A	0	1770.948	3	1.70E-06	107.50	2.11	1.26	2
2316	LVSSPCCIVTSTYGWTANMER	sp|P11499|HS90B_MOUSE	yes	yes	584	604	21	R	I	0	2431.097	2	2.38E-06	130.05	NaN	NaN	0
2317	LVSYPYDMAR	sp|Q640N1-2|AEBP1_MOUSE	yes	no	379	388	10	R	T	0	1213.580	2	2.30E-02	90.83	NaN	NaN	0
2318	LVTGWVKPIIIGR	sp|O88844|IDHC_MOUSE	yes	yes	120	132	13	R	H	0	1450.902	2;3	4.07E-04	99.50	1.17	0.91	9
2319	LVTLEEFLASTQR	sp|Q02819|NUCB1_MOUSE	yes	yes	310	322	13	R	K	0	1505.809	2	9.16E-03	79.88	NaN	NaN	0
2320	LVTLEEFLR	sp|P81117|NUCB2_MOUSE	yes	yes	312	320	9	R	A	0	1118.634	2	1.82E-02	126.07	NaN	NaN	0
2321	LVVLGIRPIR	sp|Q9EPU0-2|RENT1_MOUSE	yes	no	683	692	10	R	L	1	1134.760	3	2.04E-02	94.85	NaN	NaN	0
2322	LVVQIDNAKLAADDFR	sp|Q61897|KT33B_MOUSE	no	no	127	142	16	R	T	0	1786.958	2;3	3.26E-16	195.92	1.78	1.09	11
2323	LVVQIDNAKLASDDFR	sp|Q9D646|KRT34_MOUSE	no	no	127	142	16	R	T	0	1802.953	2;3	2.13E-11	171.71	1.61	1.13	13
2324	LWADHGVQACFGR	sp|P08752|GNAI2_MOUSE	yes	yes	131	143	13	R	S	0	1515.704	3	1.52E-03	110.80	NaN	NaN	0
2325	LWDLTTGTTTR	sp|P68040|GBLP_MOUSE	yes	yes	89	99	11	R	R	0	1263.646	2	7.50E-03	111.52	NaN	NaN	0
2326	LWGLTEMFPER	sp|Q9CPQ3|TOM22_MOUSE	yes	yes	48	58	11	R	V	0	1377.675	2	1.57E-03	98.90	2.25	1.55	2
2327	LYDASFETKESR	sp|Q9R0P5|DEST_MOUSE	yes	yes	84	95	12	A	K	0	1444.683	2	2.19E-02	52.58	1.04	0.97	2
2328	LYDLNHNEIGELIR	sp|Q6P4T2|U520_MOUSE	yes	yes	1153	1166	14	R	M	0	1697.874	3	3.10E-02	65.04	NaN	NaN	0
2329	LYDLYWQAMR	sp|Q7TPV4|MBB1A_MOUSE	yes	yes	1132	1141	10	R	M	0	1357.649	2	3.41E-02	76.23	NaN	NaN	0
2330	LYELDGLR	sp|Q9WUP7-2|UCHL5_MOUSE	yes	no	175	182	8	R	E	0	977.518	2	5.78E-02	91.32	NaN	NaN	0
2331	LYGEQEFPICSEYSDDVTEFFHTTV	sp|Q9D7P9|SPB12_MOUSE	yes	yes	136	173	38	R	Q	0	4548.023	5	1.98E-02	47.13	1.48	1.20	1
2332	LYGPSSVSFADDFVR	sp|P19324|SERPH_MOUSE	yes	yes	133	147	15	R	S	0	1658.794	2	1.92E-09	171.76	1.44	0.95	2
2333	LYGPTNFAPIINHVAR	sp|Q8C166|CPNE1_MOUSE	yes	yes	384	399	16	R	F	0	1781.958	3	6.16E-05	103.88	15.35	12.36	1
2334	LYGPTNFSPIINHVAR	sp|Q8BT60|CPNE3_MOUSE	yes	yes	391	406	16	R	F	0	1797.953	3	9.66E-04	101.42	NaN	NaN	0
2335	LYLGHNYVTAIR	sp|Q921I1|TRFE_MOUSE	yes	yes	332	343	12	R	N	0	1418.767	2;3	2.08E-04	167.20	NaN	NaN	0
2336	LYLINSPVVR	sp|Q8BU30|SYIC_MOUSE	yes	yes	625	634	10	R	A	0	1172.692	2	4.31E-03	144.77	NaN	NaN	0
2337	LYPLYGLGELPQGFAR	sp|Q61598-2|GDIB_MOUSE	yes	no	189	204	16	Y	L	0	1792.951	2;3	3.22E-04	131.86	NaN	NaN	0
2338	LYPPSAEYPDLR	sp|P30275|KCRU_MOUSE	yes	yes	47	58	12	R	K	0	1419.703	2	2.76E-02	72.29	NaN	NaN	0
2339	LYSGPGIVGNVLVDPSAR	sp|Q8BTZ7|GMPPB_MOUSE	yes	yes	244	261	18	R	I	0	1812.973	2	3.99E-04	116.60	NaN	NaN	0
2340	LYSLLFR	sp|Q8R1I1|QCR9_MOUSE	yes	yes	10	16	7	R	R	0	910.528	2	4.12E-02	155.73	NaN	NaN	0
2341	MAGGTFTGEALQYTR	sp|Q04857|CO6A1_MOUSE	yes	yes	696	710	15	W	D	0	1601.751	2	1.85E-07	192.65	NaN	NaN	0
2342	MAGIDDCYTSAR	sp|P25444|RS2_MOUSE	yes	yes	216	227	12	M	G	0	1358.560	2	1.32E-03	142.89	0.37	0.25	1
2343	MASGSGKNGGFGFGR	sp|Q9R0H5|K2C71_MOUSE	yes	no	60	74	15	N	N	0	1428.657	3	9.21E-04	75.76	1.42	0.94	12
2344	MCPDYQSYFR	sp|Q497I4|KRT35_MOUSE	no	no	140	149	10	Y	T	0	1365.548	2	1.50E-02	103.26	NaN	NaN	0
2345	MDGIVPDIAVGTKR	sp|P17225|PTBP1_MOUSE	yes	yes	1	14	14	-	G	0	1470.786	2	1.04E-04	112.42	1.38	0.80	9
2346	MDLAAAAEPGAGSQHPEVR	sp|P97311|MCM6_MOUSE	yes	yes	1	19	19	-	D	0	1905.900	2	2.83E-06	144.17	NaN	NaN	0
2347	MDLAGDSDGWVSLAELR	sp|Q8BH97|RCN3_MOUSE	yes	yes	87	103	17	R	A	0	1833.857	2	2.65E-02	56.82	NaN	NaN	0
2348	MDSAEELLAPLR	sp|Q9CZD3|SYG_MOUSE	yes	yes	47	58	12	S	L	0	1343.676	2	3.81E-03	111.94	NaN	NaN	0
2349	MDSELKNMQDLVEEYR	sp|P04104|K2C1_MOUSE	yes	yes	260	275	16	R	T	0	1998.903	2;3	3.79E-11	164.01	1.83	1.10	7
2350	MDSLTAANNKFCFDFFR	sp|Q9D7P9|SPB12_MOUSE	yes	yes	1	17	17	-	E	0	2082.929	2	7.36E-07	113.47	1.26	1.09	6
2351	MDVNLAPLR	sp|Q8R5J9|PRAF3_MOUSE	yes	yes	1	9	9	-	A	0	1027.549	2	4.55E-02	80.23	NaN	NaN	0
2352	MEEIVEGCTGALHILAR	sp|Q02257|PLAK_MOUSE	no	no	556	572	17	R	D	0	1897.939	3	3.18E-03	91.66	NaN	NaN	0
2353	MEFAELIKTPR	sp|Q9Z2D0|MTMR9_MOUSE	yes	yes	1	11	11	-	V	0	1333.706	2	3.01E-03	83.18	0.78	0.62	1
2354	MEGHDPKEPEQLR	sp|Q8BG05-2|ROA3_MOUSE	yes	yes	1	13	13	-	K	0	1564.730	3	1.38E-03	76.73	1.18	0.67	10
2355	MEGMKGCPAVMPIDHVYGTLGI	sp|Q62009-5|POSTN_MOUSE	yes	no	88	125	38	R	E	0	4119.005	5	4.87E-02	31.29	2.04	1.38	1
2356	MEGPLSVFGDR	sp|P11983|TCPA_MOUSE	yes	yes	1	11	11	-	S	0	1206.570	2	1.95E-02	80.69	NaN	NaN	0
2357	MEKPSPLLVGR	sp|P97855|G3BP1_MOUSE	no	no	3	13	11	V	E	0	1225.685	2	1.87E-02	63.09	1.42	1.09	3
2358	MEKTLETVPLER	sp|O88569|ROA2_MOUSE	yes	yes	1	12	12	-	K	0	1444.760	2	5.59E-05	140.82	1.26	0.79	1
2359	MELKPGDNLNVNFHLR	sp|P01027|CO3_MOUSE	yes	yes	463	478	16	R	T	0	1895.968	4	8.32E-03	67.14	0.97	0.93	1
2360	MELVEVLKR	sp|Q7TMF3|NDUAC_MOUSE	yes	yes	1	9	9	-	G	0	1115.637	2	6.99E-06	168.83	1.62	1.26	3
2361	MENQLTKSVEER	sp|Q9DC50|OCTC_MOUSE	yes	yes	1	12	12	-	T	0	1462.709	2	1.20E-03	93.35	1.42	1.07	3
2362	MFAPTKTWR	sp|Q9D8E6|RL4_MOUSE	yes	yes	101	109	9	R	R	0	1136.580	3	1.99E-02	72.61	1.51	0.87	1
2363	MFLNDFLNDQNR	sp|Q8JZK9|HMCS1_MOUSE	yes	yes	278	289	12	R	D	0	1525.698	2	1.36E-04	172.11	NaN	NaN	0
2364	MFSWVSKDAR	sp|Q9WVK4|EHD1_MOUSE	yes	yes	1	10	10	-	R	0	1225.591	2	5.39E-03	83.86	1.62	1.28	2

2365	MGHYLHEVAR	sp|P07724|ALBU_MOUSE	yes	yes	159	168	10	F	R	0	1211.587	4	4.54E-02	73.50	NaN	NaN	0
2366	MGPAMGPALGAGIER	sp|Q9D0E1-2|HNRPM_MOUSE	yes	no	552	566	15	R	M	0	1426.706	2	2.09E-02	67.10	NaN	NaN	0
2367	MGPLGLDHMASSIER	sp|Q9D0E1-2|HNRPM_MOUSE	yes	no	417	431	15	R	M	0	1612.770	3	4.31E-03	83.54	NaN	NaN	0
2368	MGPLINAPHLER	sp|Q9JLJ2|AL9A1_MOUSE	yes	yes	327	338	12	R	V	0	1346.713	3	1.14E-02	85.55	NaN	NaN	0
2369	MGPSGGEGVEPER	sp|Q61792|LASP1_MOUSE	yes	yes	131	143	13	R	R	0	1300.572	2	7.86E-02	50.09	NaN	NaN	0
2370	MIAGQVLDINLAAEPKVNR	sp|Q9Z204-4|HNRPC_MOUSE	yes	no	74	92	19	R	G	0	2051.120	3	1.93E-05	96.38	1.40	0.82	3
2371	MIISVNGDLVTIR	sp|P04117|FABP4_MOUSE	yes	yes	41	53	13	N	S	0	1429.796	2	1.49E-03	114.72	NaN	NaN	0
2372	MIVHIDNAKLAADDFR	sp|Q62168|K1H2_MOUSE	yes	no	126	141	16	R	T	0	1827.930	3;4	1.98E-03	72.32	1.85	1.15	2
2373	MKCSSMQKFGER	sp|P07724|ALBU_MOUSE	yes	yes	222	233	12	R	A	0	1487.668	4	1.70E-03	84.37	1.23	1.19	1
2374	MKSAVEKGEELSCEER	sp|O70456|1433S_MOUSE	yes	yes	26	41	16	F	N	0	1880.861	4	4.87E-03	64.52	0.95	0.90	5
2375	MKSVTEQGAELSNEER	sp|P63101|1433Z_MOUSE	yes	yes	26	41	16	C	N	0	1806.842	3	1.12E-01	37.69	1.37	1.17	4
2376	MLDMGFEPQIR	sp|Q61656|DDX5_MOUSE	no	no	253	263	11	R	K	0	1335.632	2	1.00E-02	101.39	NaN	NaN	0
2377	MLGGLGKLAAEGLAHR	sp|Q8CF02|FM25C_MOUSE	yes	yes	1	16	16	-	T	0	1592.882	2;3	6.41E-08	132.81	1.45	1.38	9
2378	MLGPEGGEGYVVKLR	sp|Q9Z2X1|HNRPF_MOUSE	yes	yes	2	16	15	M	G	0	1603.839	2	8.09E-07	148.52	1.14	0.91	14
2379	MLITIMGTVKPNANR	sp|P16110|LEG3_MOUSE	yes	yes	144	158	15	R	I	0	1657.901	3	4.31E-02	55.72	2.05	1.26	1
2380	MLSAVSQQVQCIQEALR	sp|Q9JHU4|DYHC1_MOUSE	yes	yes	1965	1981	17	R	E	0	1959.987	2	4.23E-06	176.49	NaN	NaN	0
2381	MLSFQYPDVYR	sp|Q9QUR6|PPCE_MOUSE	yes	yes	1	11	11	-	D	0	1417.670	2	3.45E-03	120.06	0.09	0.07	1
2382	MLSNTTAIAEAWAR	sp|P68373|TBA1C_MOUSE	no	no	377	390	14	C	L	0	1533.761	2	3.82E-02	61.41	NaN	NaN	0
2383	MNAGSDPVVIVSAAR	sp|Q8CAY6|THIC_MOUSE	yes	yes	1	15	15	-	T	0	1485.761	2	3.44E-03	88.31	NaN	NaN	0
2384	MNIPFR	sp|Q99K85|SERC_MOUSE	yes	yes	301	306	6	R	I	0	776.400	2	4.98E-02	134.24	NaN	NaN	0
2385	MNVEHEVNLLVEEIHR	sp|Q4KML4|ABRAL_MOUSE	yes	yes	1	16	16	-	L	0	1959.984	3	5.63E-05	153.75	NaN	NaN	0
2386	MNVLADALKSINNAEKR	sp|P62245|RS15A_MOUSE	yes	yes	4	20	17	R	G	0	1886.004	3	8.84E-05	88.39	0.89	0.85	3
2387	MPEFYNR	sp|P16460|ASSY_MOUSE	yes	yes	147	153	7	R	F	0	955.422	2	6.27E-02	118.69	NaN	NaN	0
2388	MPELIDIR	sp|P41216|ACSL1_MOUSE	yes	yes	12	19	8	R	Q	0	985.527	2	3.88E-02	120.87	NaN	NaN	0
2389	MPIPVIQAFGILKR	sp|P97807-2|FUMH_MOUSE	yes	no	45	58	14	R	A	0	1581.943	3	3.22E-03	72.29	1.09	1.02	6
2390	MPKDIQLAR	sp|P84244|H33_MOUSE	no	no	121	129	9	I	R	0	1070.591	2	3.22E-03	104.22	1.02	0.82	4
2391	MPKVQQTVQDLFGR	sp|P38647|GRP75_MOUSE	yes	yes	392	405	14	R	A	0	1645.861	3	9.83E-04	127.30	1.17	1.11	1
2392	MPLFEHYTR	sp|Q9CPY7-2|AMPL_MOUSE	yes	no	401	409	9	R	Q	0	1192.570	3	3.83E-02	87.26	NaN	NaN	0
2393	MPTPPSYKVGDKIATR	sp|P40142|TKT_MOUSE	yes	yes	303	318	16	R	K	0	1759.929	3;4	6.65E-03	59.71	1.18	0.99	6
2394	MQPASAKWYDR	sp|Q9R0Q7|TEBP_MOUSE	yes	yes	1	11	11	-	R	0	1351.634	2	3.47E-04	125.82	1.18	1.00	6
2395	MSGECTPNVSVSVSTSHTSMSGS	sp|P04104|K2C1_MOUSE	yes	yes	501	526	26	R	G	0	2658.132	3	4.13E-09	135.62	NaN	NaN	0
2396	MSSILAGGSCR	sp|Q61781|K1C14_MOUSE	no	no	27	37	11	R	A	0	1137.527	2	2.00E-04	131.12	0.37	0.29	4
2397	MSVEADINGLR	sp|Q61781|K1C14_MOUSE	no	no	218	228	11	R	R	0	1203.592	2	1.44E-03	146.71	0.32	0.22	1
2398	MTDQEAIQDLWQWR	sp|Q61937|NPM_MOUSE	yes	yes	276	289	14	R	K	0	1818.836	2	1.87E-04	159.00	NaN	NaN	0
2399	MVNHFIAEFKR	sp|P63017|HSP7C_MOUSE	yes	yes	237	247	11	R	K	0	1390.718	3	6.49E-04	117.79	1.11	0.94	3
2400	MVPFPR	sp|P99024|TBB5_MOUSE	no	no	257	262	6	N	L	0	745.395	2	8.46E-02	96.34	NaN	NaN	0
2401	MVPTGMGASLER	sp|Q9D0E1-2|HNRPM_MOUSE	yes	no	492	503	12	R	M	0	1247.600	2	1.30E-02	81.57	NaN	NaN	0
2402	MVQEAEKYKAEDEKQR	sp|P63017|HSP7C_MOUSE	yes	yes	518	533	16	R	D	0	1980.958	3;4	3.09E-02	44.93	1.15	0.99	7
2403	MVSDEYEQLSSEALEAAR	sp|Q6ZWV3|RL10_MOUSE	yes	no	52	69	18	H	I	0	2026.915	2	3.27E-03	92.67	NaN	NaN	0
2404	MVVPAALKVVR	sp|P19253|RL13A_MOUSE	yes	yes	118	128	11	R	L	0	1181.732	3	1.96E-03	94.31	1.01	0.95	12
2405	MVWVPSELHGFEAAALR	sp|Q6URW6-2|MYH14_MOUSI	yes	no	51	67	17	R	D	0	1911.967	3	4.21E-02	49.60	NaN	NaN	0
2406	MYSYVTEELPQLINANFPVDPQR	sp|Q9R0P3|ESTD_MOUSE	yes	yes	120	142	23	R	M	0	2723.327	2	1.61E-08	138.03	NaN	NaN	0
2407	MYTPIPQSGSPFPASVQDPGLHIV	sp|P24452|CAPG_MOUSE	yes	yes	1	25	25	-	V	0	2780.375	2;3	3.06E-06	120.32	NaN	NaN	0
2408	NAAPGVDLTQLLNNMR	sp|P02535-3|K1C10_MOUSE	no	no	296	311	16	M	N	0	1725.883	2	3.19E-03	89.62	NaN	NaN	0
2409	NAEQFKDQADKASTR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	1857	1871	15	R	L	0	1707.818	3	3.05E-04	80.63	1.36	0.76	7
2410	NAEYQQLLDIKTR	sp|P02535-3|K1C10_MOUSE	yes	no	418	430	13	Q	L	0	1590.837	2	1.18E-05	143.93	1.89	1.25	2
2411	NAFDLLLPKLAR	sp|P54822|PUR8_MOUSE	yes	yes	126	137	12	R	V	0	1369.808	3	1.82E-02	57.18	1.22	1.14	4
2412	NALCAPEVISLINSR	sp|Q3TDN2-2|FAF2_MOUSE	yes	no	172	186	15	R	M	0	1655.867	2	1.22E-03	100.43	NaN	NaN	0
2413	NALEIELQAQHCMR	sp|Q9D646|KRT34_MOUSE	no	no	280	293	14	V	N	0	1711.813	2	1.23E-03	102.52	NaN	NaN	0
2414	NALEIELQAQHELR	sp|Q8K0Y2|KT33A_MOUSE	yes	yes	280	293	14	V	N	0	1662.869	2	9.46E-04	129.77	NaN	NaN	0
2415	NALGPGLSPELGPLPALR	sp|Q505F5|LRC47_MOUSE	yes	yes	87	104	18	R	V	0	1770.999	2	2.46E-05	147.64	NaN	NaN	0
2416	NALLQLTDSQIADVAR	sp|Q6P4T2|U520_MOUSE	yes	yes	1994	2009	16	R	F	0	1726.921	2	1.52E-05	171.46	NaN	NaN	0
2417	NALVSHLDGTTPVCEDIGR	sp|Q9CZ13|QCR1_MOUSE	yes	yes	397	415	19	R	S	0	2052.990	3	6.19E-06	137.61	NaN	NaN	0
2418	NAMLKSICEVLDLER	sp|Q7TNV0|DEK_MOUSE	yes	yes	158	172	15	R	S	0	1789.907	3	6.01E-03	64.04	1.79	1.22	1
2419	NANIILQNDNAR	sp|Q9Z320|K1C27_MOUSE	yes	yes	146	157	12	H	L	0	1354.695	2	3.74E-04	155.99	NaN	NaN	0
2420	NANNGNLLLR	sp|P32067|LA_MOUSE	yes	yes	287	296	10	R	N	0	1097.594	2	6.19E-03	137.69	NaN	NaN	0
2421	NAPWTLTPEFLAEHR	sp|P49586|PCY1A_MOUSE	yes	yes	148	162	15	R	I	0	1780.890	3	1.01E-02	73.83	NaN	NaN	0
2422	NAVTQEFGPVPDTAR	sp|Q99KI0|ACON_MOUSE	yes	yes	634	648	15	R	Y	0	1600.785	2	3.26E-07	181.58	NaN	NaN	0
2423	NAYTEKSSTGCFSNR	sp|P97350|PKP1_MOUSE	yes	yes	483	497	15	R	G	0	1720.748	3	5.57E-03	65.04	1.75	1.00	5
2424	NDEELNKLLGR	sp|Q8CGP6|H2A1H_MOUSE	yes	no	90	100	11	R	V	0	1299.678	2;3	2.64E-17	228.83	1.26	0.82	15
2425	NDFQLIGIQDGYLSLLQDSGEVR	sp|P63242|IF5A1_MOUSE	yes	yes	87	109	23	R	E	0	2579.287	2	1.66E-08	137.52	NaN	NaN	0
2426	NDGVLLLQALTR	sp|Q9Z1Z0-3|USO1_MOUSE	yes	no	184	195	12	R	S	0	1311.751	2	3.77E-03	112.42	NaN	NaN	0
2427	NDISSHPPVEGSYAPR	sp|Q78PY7|SND1_MOUSE	yes	yes	716	731	16	R	R	0	1724.812	3	1.42E-02	69.98	NaN	NaN	0
2428	NEEDATELVGLAQAVNAR	sp|Q02053|UBA1_MOUSE	yes	yes	351	368	18	R	S	0	1898.933	2;3	1.18E-08	186.94	NaN	NaN	0
2429	NEGNIFPNPEATFVKEITYR	sp|Q920B9|SP16H_MOUSE	yes	yes	582	601	20	R	A	0	2338.159	3	1.04E-03	71.59	1.35	0.98	3
2430	NEGTATYAAAVLFR	sp|Q02257|PLAK_MOUSE	yes	yes	638	651	14	R	I	0	1482.747	2;3	1.16E-03	103.76	NaN	NaN	0
2431	NEGVATYAAAVLFR	sp|Q02248|CTNB1_MOUSE	yes	yes	648	661	14	R	M	0	1480.767	2	8.54E-04	132.97	NaN	NaN	0
2432	NEKLTVDNAVAR	sp|E9Q557|DESP_MOUSE	yes	yes	2076	2087	12	R	D	0	1328.705	3	2.20E-07	166.45	1.53	0.97	4
2433	NELSGALTGLTR	sp|Q9D0R2|SYTC_MOUSE	yes	yes	442	453	12	R	V	0	1230.657	2	1.04E-02	88.10	NaN	NaN	0
2434	NEPTAAAIAYGLDKKVGAER	sp|P63017|HSP7C_MOUSE	yes	yes	174	193	20	I	N	0	2073.086	3	3.58E-03	57.37	1.08	0.99	4
2435	NEPTAAAIAYGLDKR	sp|P20029|GRP78_MOUSE	yes	yes	201	215	15	I	E	0	1588.821	2	4.51E-06	128.06	1.45	1.03	6
2436	NFDEILR	sp|O08709|PRDX6_MOUSE	yes	yes	156	162	7	R	V	0	905.461	2	5.93E-02	125.50	NaN	NaN	0
2437	NFDFEDVFVNIPR	sp|Q9DC69|NDUA9_MOUSE	yes	yes	138	150	13	R	A	0	1610.773	2	4.78E-02	91.62	NaN	NaN	0
2438	NFDVSWDSSPNTNKPCLNVYR	sp|P15089|CBPA3_MOUSE	yes	yes	253	273	21	R	G	0	2512.144	3	2.80E-16	171.35	1.68	0.98	3
2439	NFILDQCNVYNSGQR	sp|Q00PI9|HNRL2_MOUSE	yes	yes	530	544	15	R	R	0	1826.837	2	8.07E-04	102.65	NaN	NaN	0
2440	NFILDQTNVSAAAQR	sp|Q8VEK3|HNRPU_MOUSE	yes	yes	552	566	15	R	R	0	1646.838	2	1.81E-04	150.05	NaN	NaN	0
2441	NFLASQVPFPSR	sp|O08756|HCD2_MOUSE	yes	yes	215	226	12	R	L	0	1361.709	2	2.54E-04	164.11	NaN	NaN	0
2442	NFLENLVTAFNVGSEKTR	sp|Q80X19-2|COEA1_MOUSE	yes	no	180	197	18	R	I	0	2038.048	3	1.60E-08	129.11	1.97	1.17	1
2443	NFLGEKYIR	sp|P51410|RL9_MOUSE	yes	yes	116	124	9	R	R	0	1138.614	2;3	4.11E-03	100.88	1.43	0.82	3
2444	NFSDNQLQEGKNVIGLQMGTNR	sp|Q9WVA4|TAGL2_MOUSE	yes	yes	161	182	22	R	G	0	2462.197	3	2.88E-12	150.14	0.67	0.64	3
2445	NFSSCSAVAPKTGNR	sp|Q9Z2T6|KRT85_MOUSE	no	no	17	31	15	R	C	0	1594.752	2;3	1.54E-13	187.00	1.72	1.06	11
2446	NFSSGSAGLVSFQR	sp|P04104|K2C1_MOUSE	yes	yes	19	32	14	R	R	0	1455.711	2	3.20E-04	151.56	NaN	NaN	0
2447	NFTAEEKTLINGLWSKVNVEEVG	sp|P02104|HBE_MOUSE	yes	yes	3	31	29	V	L	0	3159.620	5	1.40E-02	47.29	1.48	1.13	2
2448	NFVLTAAHCAGR	sp|P21844|CMA1_MOUSE	yes	yes	59	70	12	R	S	0	1315.646	2	3.97E-03	110.08	NaN	NaN	0
2449	NGGQILIADLR	sp|Q9D1M0|SEC13_MOUSE	yes	yes	44	54	11	R	G	0	1168.656	2	2.73E-03	136.96	NaN	NaN	0
2450	NGKTIQVDNTDAEGR	sp|Q9CPY7-2|AMPL_MOUSE	yes	no	323	337	15	R	L	0	1616.775	3	8.78E-04	151.41	0.28	0.25	2
2451	NGKTSKKITISDCGQL	sp|P17742|PPIA_MOUSE	yes	no	149	164	16	R	-	0	1748.909	3	1.70E-04	81.63	0.94	0.96	5
2452	NGLAAEPGPTGPR	sp|Q9JI99|SGPP1_MOUSE	yes	yes	80	92	13	R	R	0	1235.626	2	5.52E-03	90.86	NaN	NaN	0
2453	NGLTLGGQKCSVIR	sp|P62962|PROF1_MOUSE	yes	no	62	75	14	V	D	0	1501.804	2	6.95E-03	65.04	1.11	0.93	4
2454	NGWVTQIATTPQFPDMILSASR	sp|P68040|GBLP_MOUSE	yes	yes	15	36	22	H	D	0	2432.216	2	9.34E-03	58.71	NaN	NaN	0
2455	NGYELSPTAAANFTR	sp|Q9R1P3|PSB2_MOUSE	yes	yes	71	85	15	R	R	0	1610.769	2	2.35E-04	147.12	NaN	NaN	0
2456	NGYGFINR	sp|P62960|YBOX1_MOUSE	no	no	68	75	8	R	N	0	939.456	2	3.61E-02	129.68	NaN	NaN	0
2457	NHEEEVGVLR	sp|Q62168|K1H2_MOUSE	yes	no	192	201	10	R	Q	0	1180.584	2	3.20E-02	77.06	NaN	NaN	0
2458	NIDEHANEDVER	sp|P61027|RAB10_MOUSE	yes	yes	106	117	12	R	M	0	1439.628	3	4.59E-02	66.00	NaN	NaN	0
2459	NIGVVVVGFPATPIIESR	sp|P97363|SPTC2_MOUSE	yes	yes	488	505	18	R	A	0	1867.057	2	6.45E-03	79.84	NaN	NaN	0
2460	NIIFFGKFCSP	sp|P70124|SPB5_MOUSE	yes	no	365	375	11	R	-	0	1328.659	2	1.83E-02	63.47	1.00	0.84	4
2461	NILGGTVFR	sp|P54071|IDHP_MOUSE	no	no	141	149	9	R	E	0	975.550	2	1.82E-02	126.07	NaN	NaN	0
2462	NIQACKELAQTTR	sp|P42932|TCPQ_MOUSE	yes	yes	32	44	13	R	T	0	1531.778	3	3.45E-04	101.32	1.34	0.97	7
2463	NIQVYNPTPNSLDVR	sp|Q60847|COCA1_MOUSE	yes	no	1941	1955	15	R	W	0	1728.880	2	8.67E-06	178.67	NaN	NaN	0
2464	NITEDELKEVFEDAMEIR	sp|P09405|NUCL_MOUSE	yes	yes	405	422	18	F	L	0	2180.031	3	2.21E-03	69.19	0.97	0.91	1
2465	NIVEAAAVR	sp|P62855|RS26_MOUSE	yes	yes	43	51	9	R	D	0	941.529	2	2.71E-02	98.06	NaN	NaN	0
2466	NKCGVISPR	sp|P62245|RS15A_MOUSE	yes	yes	70	78	9	L	F	0	1029.539	2	5.45E-01	44.86	NaN	NaN	0
2467	NKFASFIDKVR	sp|Q3TTY5|K22E_MOUSE	no	no	208	218	11	N	F	0	1323.730	2;3;4	8.76E-04	111.79	1.80	1.15	20

2468	NKLILPGLISSR	sp|P17563|SBP1_MOUSE	yes	no	92	103	12	R	I	0	1309.808	2;3	1.84E-03	81.92	1.15	1.02	12
2469	NKLKYLAFLR	sp|P19253|RL13A_MOUSE	yes	yes	50	59	10	R	K	0	1264.766	3	2.45E-02	88.50	0.91	0.89	1
2470	NKLTELEEALQKAKQDMAR	sp|Q922U2|K2C5_MOUSE	yes	no	424	442	19	R	L	0	2215.163	5	3.89E-05	89.47	1.27	0.82	1
2471	NKSNEDQSMGNWQIR	sp|P48678|LMNA_MOUSE	yes	no	456	470	15	R	R	0	1805.812	2	2.87E-09	166.92	1.56	0.93	1
2472	NKSTESLQANVQR	sp|P47963|RL13_MOUSE	yes	yes	104	116	13	R	L	0	1473.754	3	2.29E-05	132.97	1.05	0.90	4
2473	NLADCLR	sp|Q9R1P3|PSB2_MOUSE	yes	yes	87	93	7	R	S	0	860.417	2	6.17E-02	120.52	NaN	NaN	0
2474	NLALCPANHAPLQEAAVIPR	sp|Q02257|PLAK_MOUSE	yes	yes	507	526	20	R	L	0	2154.137	2;3	2.57E-06	140.35	NaN	NaN	0
2475	NLAMDVGKAR	sp|P52480|KPYM_MOUSE	no	no	491	500	10	V	G	0	1073.565	2	6.52E-03	90.91	1.07	1.01	3
2476	NLANTVTEEILEKSFSQFGKLER	sp|Q7TMK9-2|HNRPQ_MOUSE	yes	no	344	366	23	R	V	0	2652.376	4	4.34E-02	35.09	1.13	1.00	2
2477	NLCSDDTPMVR	sp|Q76MZ3|2AAA_MOUSE	yes	yes	172	182	11	R	R	0	1306.565	2	8.79E-03	105.46	NaN	NaN	0
2478	NLDIERPTYTNLNR	sp|P68373|TBA1C_MOUSE	no	no	216	229	14	R	L	1	1717.875	2;3	4.00E-18	259.00	NaN	NaN	0
2479	NLDLDSIIAEVR	sp|Q6NXH9|K2C73_MOUSE	yes	no	295	306	12	R	A	0	1356.725	2	3.07E-03	120.84	NaN	NaN	0
2480	NLDLDSIIDEVR	sp|Q9R0H5|K2C71_MOUSE	no	no	295	306	12	R	A	0	1400.715	2	1.86E-06	186.58	NaN	NaN	0
2481	NLETAIADAEQR	sp|Q9R0H5|K2C71_MOUSE	no	no	372	383	12	S	G	0	1329.653	2	1.14E-02	85.54	NaN	NaN	0
2482	NLGQNLWGPHR	sp|Q8BK67|RCC2_MOUSE	yes	yes	129	139	11	R	Y	0	1290.658	3	1.27E-02	95.48	NaN	NaN	0
2483	NLGSINTELQDVQR	sp|O08547|SC22B_MOUSE	yes	yes	134	147	14	R	I	0	1585.806	2	1.85E-03	100.11	NaN	NaN	0
2484	NLHQSGFSLSGAQIDDNIPR	sp|O08553|DPYL2_MOUSE	yes	yes	533	552	20	R	R	0	2168.061	3	4.44E-06	129.20	NaN	NaN	0
2485	NLKQLDNPAR	sp|P56399|UBP5_MOUSE	yes	yes	182	191	10	F	I	0	1167.636	3	3.60E-02	56.04	1.11	1.03	3
2486	NLKYLPFVPSR	sp|P50608|FMOD_MOUSE	yes	yes	96	106	11	R	M	0	1332.755	3	6.08E-04	118.90	3.02	2.03	1
2487	NLLEGQDAKMAGIGVR	sp|Q61414|K1C15_MOUSE	yes	no	401	416	16	R	E	0	1670.877	3	1.93E-04	78.69	2.06	1.17	8
2488	NLLSSPNPEGINIYQPAPPTGPTR	sp|G3X9C2|FBX50_MOUSE	yes	yes	95	118	24	R	K	0	2532.297	3	7.04E-03	60.74	NaN	NaN	0
2489	NLLSVAYKNVIGAR	sp|P62259|1433E_MOUSE	yes	yes	43	56	14	R	R	0	1516.873	2;3	5.59E-19	208.15	1.12	0.99	11
2490	NLLSVAYKNVVGAR	sp|Q9CQV8-2|1433B_MOUSE	no	no	42	55	14	R	R	0	1502.857	2;3	2.84E-10	181.26	1.19	1.01	12
2491	NLLSVAYKNVVGGQR	sp|O70456|1433S_MOUSE	yes	yes	42	56	15	R	A	0	1616.900	2;3	3.42E-09	164.15	1.05	0.96	10
2492	NLLSVAYKNVVGGR	sp|P68254-2|1433T_MOUSE	yes	no	42	55	14	R	R	0	1488.841	2;3	2.49E-04	98.94	1.03	0.97	10
2493	NLMTSQPQMAKQYFSNSMLNN	sp|P97350|PKP1_MOUSE	yes	yes	647	673	27	R	N	0	3235.504	3	2.52E-04	86.79	1.55	0.98	1
2494	NLPGLVQEGEPFSEEATLFTKELVL	sp|Q78PY7|SND1_MOUSE	yes	yes	566	592	27	R	E	0	3043.587	3	3.30E-02	39.21	1.57	1.02	1
2495	NLPLPPPPPPR	sp|P61979-3|HNRPK_MOUSE	yes	no	282	292	11	R	G	0	1193.692	2;3	7.32E-03	112.36	0.03	0.03	1
2496	NLQDAMQVCR	sp|P80318|TCPG_MOUSE	yes	yes	390	399	10	R	N	0	1233.559	2	7.85E-03	131.46	NaN	NaN	0
2497	NLQEILIGAVR	sp|Q01279|EGFR_MOUSE	yes	yes	139	149	11	R	F	0	1224.719	2	2.60E-03	137.89	NaN	NaN	0
2498	NLQNLLILTAIKADR	sp|Q68FD5|CLH1_MOUSE	yes	yes	1023	1037	15	R	T	0	1695.004	3	3.15E-05	104.95	1.14	0.84	3
2499	NLQPDTPYTITVVPVYTEGDGGR	sp|Q60847|COCA1_MOUSE	yes	no	1904	1926	23	R	T	0	2491.223	2	8.19E-03	58.95	NaN	NaN	0
2500	NLVDNITGQR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	4203	4212	10	R	L	0	1128.589	2	1.30E-02	111.27	NaN	NaN	0
2501	NLVDSYVAIINKSIR	sp|P39054-2|DYN2_MOUSE	yes	no	654	668	15	R	D	0	1703.957	3	4.38E-02	42.32	1.36	0.93	1
2502	NLVVIPKSVTPVR	sp|P45376|ALDR_MOUSE	yes	yes	257	269	13	R	I	0	1420.877	2	4.18E-04	99.16	1.11	0.94	5
2503	NLYELKEGR	sp|Q9R1P1|PSB3_MOUSE	yes	yes	72	80	9	L	Q	0	1120.588	2	9.61E-02	56.40	1.08	0.94	4
2504	NMGGPYGGGNYGPGGSGGSGG	sp|O88569|ROA2_MOUSE	yes	no	326	350	25	R	S	0	2188.898	2	5.31E-16	192.58	NaN	NaN	0
2505	NMMGNIAGANNLR	sp|P97350|PKP1_MOUSE	yes	yes	710	722	13	R	N	0	1374.650	2	5.81E-04	149.49	NaN	NaN	0
2506	NMNCIEMGGNPLENSGFEPGAFI	sp|P28653|PGS1_MOUSE	yes	yes	185	215	31	R	I	0	3456.590	3	5.83E-10	136.66	1.50	0.96	1
2507	NMQEVVEDFKVR	sp|Q8BGZ7|K2C75_MOUSE	yes	no	228	239	12	R	Y	0	1492.734	3	4.69E-04	111.94	1.86	1.24	3
2508	NNEDVSIIPPLFTVSVDHR	sp|Q62186|SSRD_MOUSE	yes	yes	120	138	19	R	G	0	2151.096	3	5.91E-06	131.67	NaN	NaN	0
2509	NNLAGAEELFAR	sp|Q68FD5|CLH1_MOUSE	yes	yes	355	366	12	R	K	0	1303.652	2	4.09E-03	108.56	NaN	NaN	0
2510	NNTCFVEAVEELAR	sp|Q9Z184|PADI3_MOUSE	yes	yes	315	328	14	R	K	0	1650.767	2	1.18E-04	117.08	0.46	0.38	2
2511	NNYATMRPDSTEIDQDTINR	sp|Q02788|CO6A2_MOUSE	yes	yes	229	248	20	R	I	1	2353.061	3	4.36E-11	188.84	NaN	NaN	0
2512	NPAVLSAASFDGR	sp|Q3UPL0-2|SC31A_MOUSE	yes	no	315	327	13	R	I	0	1303.652	2	1.50E-03	113.76	NaN	NaN	0
2513	NPDELAEALDER	sp|Q9Z0G0|GIPC1_MOUSE	yes	yes	296	307	12	R	L	0	1370.631	2	3.43E-03	116.51	NaN	NaN	0
2514	NPDTQWITKPVHKHR	sp|Q9CZM2|RL15_MOUSE	yes	yes	145	159	15	R	E	0	1855.981	4	2.63E-02	47.04	1.00	0.96	1
2515	NPLQKDPQYR	sp|Q3UM45|PP1R7_MOUSE	yes	yes	332	341	10	R	R	0	1257.647	3	4.27E-02	51.28	1.23	1.10	4
2516	NPNPSALPQLQEQR	sp|Q61247|A2AP_MOUSE	yes	yes	435	448	14	R	D	0	1590.811	2	3.34E-04	151.07	NaN	NaN	0
2517	NPPGFAFVEFEDPR	sp|Q8BL97-3|SRSF7_MOUSE	no	no	45	58	14	R	D	0	1620.757	2;3	9.84E-04	127.07	NaN	NaN	0
2518	NPPTFTELQLPR	sp|Q3TIU4|PDE12_MOUSE	yes	yes	159	170	12	R	Y	0	1411.746	2	1.04E-02	88.02	NaN	NaN	0
2519	NPQFQKLLEWHR	sp|P06745|G6PI_MOUSE	yes	yes	7	18	12	R	A	0	1594.837	3	3.15E-05	147.24	1.00	0.96	1
2520	NPSVLLTLR	sp|Q11136|PEPD_MOUSE	yes	yes	140	148	9	R	G	0	1011.608	2	2.09E-02	110.38	NaN	NaN	0
2521	NQEQMKPLEEKQEEER	sp|P62192|PRS4_MOUSE	yes	yes	81	96	16	R	S	0	2043.953	4	9.60E-03	51.77	1.31	1.26	1
2522	NQGGYGGSSSSSSYGSGR	sp|P49312|ROA1_MOUSE	yes	yes	301	318	18	R	R	0	1693.693	2	4.33E-13	216.17	NaN	NaN	0
2523	NQPQFQQMR	sp|P54728|RD23B_MOUSE	yes	yes	281	289	9	R	Q	0	1175.551	2	2.26E-02	102.46	NaN	NaN	0
2524	NQQEGVCPEGSIDNSPVKWCALS	sp|Q921I1|TRFE_MOUSE	yes	yes	344	370	27	R	T	0	3109.435	4	8.63E-07	124.39	1.01	0.88	4
2525	NQQQDPLVCPAYQAYFR	sp|Q61897|KT33B_MOUSE	no	no	92	108	17	R	T	0	2096.974	2;3	9.68E-06	170.42	NaN	NaN	0
2526	NQSFCPTVNLDKLWTLVSEQTR	sp|P14115|RL27A_MOUSE	yes	yes	66	87	22	R	V	0	2635.306	3	1.28E-11	131.82	1.03	0.71	3
2527	NQYDNDVTVWSPQGR	sp|Q9R1P4|PSA1_MOUSE	yes	yes	4	18	15	R	I	0	1777.802	2	3.42E-05	171.08	NaN	NaN	0
2528	NQYEQLAEKNR	sp|P02535-3|K1C10_MOUSE	yes	no	312	322	11	R	K	0	1391.679	2;3	1.42E-32	262.56	1.52	1.11	18
2529	NSLENTLAESEAR	sp|Q61897|KT33B_MOUSE	yes	no	294	306	13	R	Y	0	1432.679	2	4.35E-11	228.80	NaN	NaN	0
2530	NSLENTLTESEAR	sp|Q9D646|KRT34_MOUSE	no	no	294	306	13	R	Y	0	1462.690	2	7.05E-19	225.79	0.01	0.00	1
2531	NSLESTLAETEAR	sp|B1AQ75|KRT36_MOUSE	no	no	331	343	13	R	Y	0	1419.684	2	1.53E-03	109.44	NaN	NaN	0
2532	NSLPDSVQIR	sp|O55135|IF6_MOUSE	yes	yes	86	95	10	R	R	0	1127.594	2	7.75E-03	131.82	NaN	NaN	0
2533	NSNLVGAAHEELQQSR	sp|P48678|LMNA_MOUSE	yes	no	281	296	16	R	I	0	1751.855	2;3	3.91E-14	206.63	NaN	NaN	0
2534	NTDEMVELR	sp|P61979-3|HNRPK_MOUSE	yes	no	38	46	9	R	I	0	1105.507	2	4.26E-03	156.83	NaN	NaN	0
2535	NTEDLTEEWLR	sp|Q9CQI3|GMFB_MOUSE	yes	yes	125	135	11	R	E	0	1404.652	2	3.03E-04	158.05	NaN	NaN	0
2536	NTGIICTIGPASR	sp|P52480|KPYM_MOUSE	no	no	44	56	13	R	S	0	1358.698	2	1.58E-04	169.79	NaN	NaN	0
2537	NTIEETGILAER	sp|P02468|LAMC1_MOUSE	yes	yes	1120	1131	12	R	A	0	1344.689	2	5.59E-03	100.22	0.02	0.01	1
2538	NTIQWLENELNR	sp|Q61768|KINH_MOUSE	yes	yes	356	367	12	R	W	0	1528.763	2	1.32E-03	142.83	NaN	NaN	0
2539	NTISAVTWAPAAVLGTVGR	sp|Q8CGN5-2|PLIN1_MOUSE	yes	no	347	365	19	R	I	0	1883.027	2	1.46E-07	156.73	NaN	NaN	0
2540	NTKKEGDLLAAQAR	sp|P48678|LMNA_MOUSE	yes	no	120	133	14	R	L	0	1513.821	3	6.17E-04	82.65	1.33	0.90	6
2541	NTKMEISELNR	sp|P04104|K2C1_MOUSE	yes	yes	401	411	11	R	M	0	1333.666	2;3	7.85E-08	179.35	1.38	0.90	19
2542	NTKQEIAEINR	sp|P50446|K2C6A_MOUSE	no	no	365	375	11	R	M	0	1314.689	3	1.19E-03	103.44	1.83	1.03	3
2543	NTLLIAGLQAR	sp|O54734|OST48_MOUSE	yes	yes	225	235	11	R	N	0	1168.693	2	9.30E-03	103.08	NaN	NaN	0
2544	NTMSLLAANNLLAGLR	sp|Q91Z53|GRHPR_MOUSE	yes	yes	303	318	16	R	G	0	1670.914	2	2.57E-06	179.56	NaN	NaN	0
2545	NTTIPTKQTQTFTTYSDNQPGVLH	sp|P63017|HSP7C_MOUSE	yes	yes	417	447	31	R	A	0	3528.737	3	2.83E-07	128.71	1.27	0.78	3
2546	NTVEITELPVR	sp|Q64511|TOP2B_MOUSE	yes	yes	928	938	11	R	T	0	1269.693	2	1.83E-02	83.18	NaN	NaN	0
2547	NVCTEAGMFAIR	sp|P62334|PRS10_MOUSE	yes	yes	345	356	12	R	A	0	1367.633	2	4.48E-03	103.91	NaN	NaN	0
2548	NVHSYFAER	sp|O35640|ANXA8_MOUSE	yes	yes	253	261	9	R	L	0	1121.525	3	9.18E-02	68.11	NaN	NaN	0
2549	NVKSLEKVCADLIR	sp|P60867|RS20_MOUSE	yes	yes	28	41	14	R	G	0	1643.903	3;4	9.70E-03	59.71	1.20	1.12	4
2550	NVLDTSWPTPPPALR	sp|Q9WTI7-4|MYO1C_MOUSE	yes	no	827	841	15	R	E	0	1662.873	2	8.07E-04	102.65	NaN	NaN	0
2551	NVPVITGSKDLQNVNITLR	sp|P67778|PHB_MOUSE	yes	yes	75	93	19	R	I	0	2080.164	3	2.55E-03	65.86	1.59	0.93	3
2552	NVQGVNYVSPVR	sp|P97821|CATC_MOUSE	yes	yes	238	249	12	R	N	0	1330.699	2	3.40E-04	158.30	NaN	NaN	0
2553	NVTSVTSLTTQQR	sp|Q7TPV4|MBB1A_MOUSE	yes	yes	556	568	13	R	Q	0	1433.747	2	3.40E-03	97.27	NaN	NaN	0
2554	NVVTIFSAPNYCYR	sp|P63330|PP2AA_MOUSE	yes	no	255	268	14	R	C	0	1702.814	2	1.54E-03	101.30	NaN	NaN	0
2555	NWNLYPACLR	sp|P97770-2|THUM3_MOUSE	yes	no	420	429	10	R	E	0	1305.629	2	1.99E-02	95.50	NaN	NaN	0
2556	NWQWWR	sp|Q8VDD5|MYH9_MOUSE	no	no	824	829	6	R	L	0	974.451	2	6.46E-02	113.82	NaN	NaN	0
2557	NYSKLLCGLLSDR	sp|P34884|MIF_MOUSE	yes	yes	75	87	13	R	L	0	1537.792	2;3	3.10E-08	163.80	1.16	1.03	9
2558	PAAAAAAATPAVR	sp|P29341|PABP1_MOUSE	yes	yes	494	506	13	R	T	0	1136.630	2	1.49E-03	114.72	NaN	NaN	0
2559	PAICIPVR	sp|Q9Z287|KR121_MOUSE	yes	yes	57	64	8	R	Y	0	924.522	2	8.03E-03	146.21	24.33	16.58	1
2560	PALEDLR	sp|Q00623|APOA1_MOUSE	yes	yes	230	236	7	R	H	0	812.439	2	4.99E-03	183.89	NaN	NaN	0
2561	PAPAIGEAEDKENQQAANGPNQ	sp|Q9JKB3-2|YBOX3_MOUSE	yes	no	221	246	26	R	R	0	2659.259	3	7.60E-10	129.90	1.32	1.06	3
2562	PAPVPLANAVVQ	sp|Q9JK81|MYG1_MOUSE	no	no	369	380	12	R	-	0	1174.671	2	4.31E-03	105.98	NaN	NaN	0
2563	PAPVVAPGNQVTLR	sp|Q61398|PCOC1_MOUSE	yes	yes	116	129	14	R	M	0	1417.804	2	1.23E-03	102.52	NaN	NaN	0
2564	PASGPIRPIVR	sp|P47963|RL13_MOUSE	yes	yes	50	60	11	R	C	1	1161.698	3	3.97E-03	128.03	NaN	NaN	0
2565	PATAEVQEIADR	sp|P56567|CYTA_MOUSE	yes	yes	11	22	12	R	V	0	1298.647	2	1.86E-06	186.58	NaN	NaN	0
2566	PATPEIQMIADKVR	sp|P35173|CYT3_MOUSE	yes	yes	17	30	14	R	P	0	1567.839	3	1.35E-04	106.58	1.18	1.10	5
2567	PATSEIQEIADKVR	sp|P35174-2|CYT2_MOUSE	yes	no	17	30	14	R	P	0	1555.821	3	1.69E-02	63.19	1.23	1.17	1
2568	PAVPPAPGPGQLTLR	sp|Q62465|VAT1_MOUSE	yes	yes	81	95	15	R	V	0	1469.835	2;3	6.80E-03	75.91	NaN	NaN	0
2569	PAVQFSNLPR	sp|A2ADY9|DDI2_MOUSE	yes	yes	84	93	10	R	I	0	1127.609	2	7.83E-03	131.52	NaN	NaN	0
2570	PCPDVKYGKR	sp|Q01853|TERA_MOUSE	yes	yes	104	113	10	Q	I	0	1218.618	2	2.17E-03	102.52	0.90	0.87	5

2571	PCQRPFYSQR	sp|O08640|KRA14_MOUSE	yes	yes	74	83	10	R	I	1	1337.630	3	2.25E-02	91.55	NaN	NaN	0
2572	PCVEDYLSAILNR	sp|P07724|ALBU_MOUSE	yes	yes	471	483	13	L	V	0	1548.761	2	6.06E-03	89.23	NaN	NaN	0
2573	PCVPPSCHGCTLPGACNIPANVGI	sp|Q61897|KT33B_MOUSE	yes	no	20	57	38	R	E	0	4305.775	3	6.55E-05	74.87	NaN	NaN	0
2574	PDGCGVKYIPNR	sp|Q6ZWV3|RL10_MOUSE	yes	yes	192	203	12	I	G	0	1374.671	2	3.42E-07	158.04	1.09	0.90	4
2575	PDGLAEDIDKGEVSAR	sp|P58252|EF2_MOUSE	yes	yes	610	625	16	F	Q	0	1670.811	2	3.08E-03	77.75	1.08	0.94	4
2576	PEEHPVLLTEAPLNPKANR	sp|P63260|ACTG_MOUSE	no	no	98	116	19	A	E	0	2124.133	3;4	2.06E-12	149.47	1.31	1.03	15
2577	PEHIISEGR	sp|Q99J99|THTM_MOUSE	yes	yes	285	293	9	Q	G	0	1036.530	2	1.61E-02	74.84	11.30	11.52	1
2578	PEYEAAATR	sp|P27773|PDIA3_MOUSE	yes	yes	65	73	9	A	L	0	1006.472	2	4.66E-03	154.85	NaN	NaN	0
2579	PFCSTFAAFFTR	sp|P40142|TKT_MOUSE	yes	yes	384	395	12	V	A	0	1450.670	2	3.71E-02	69.03	NaN	NaN	0
2580	PFFENYISILR	sp|P04104|K2C1_MOUSE	yes	yes	237	247	11	D	R	0	1397.734	2	2.04E-04	165.63	NaN	NaN	0
2581	PFPDGLAEDIDKGEVSAR	sp|P58252|EF2_MOUSE	yes	yes	608	625	18	R	Q	0	1914.932	3	1.35E-03	72.43	1.24	0.98	7
2582	PFTIKPLDR	sp|P40142|TKT_MOUSE	yes	yes	534	542	9	D	K	0	1085.623	2	8.84E-03	86.90	1.14	0.98	4
2583	PFTLEYR	sp|Q9D819|IPYR_MOUSE	yes	yes	12	18	7	A	V	0	924.471	2	7.66E-02	98.42	NaN	NaN	0
2584	PFWNEEIVPQIKEGKR	sp|Q9DBJ1|PGAM1_MOUSE	yes	yes	165	180	16	L	V	0	1969.042	3	3.05E-04	76.82	1.25	1.11	4
2585	PGDVFYLHSR	sp|Q03265|ATPA_MOUSE	yes	yes	338	347	10	Y	L	0	1189.588	2	2.80E-02	83.08	NaN	NaN	0
2586	PGFMCQGGDFTR	sp|P17742|PPIA_MOUSE	yes	yes	58	69	12	I	H	0	1371.570	2	3.59E-04	157.03	NaN	NaN	0
2587	PGGDTIFGKIIR	sp|P70349|HINT1_MOUSE	yes	yes	13	24	12	Q	K	0	1272.719	2	1.17E-02	65.18	1.53	1.51	3
2588	PGGYGYGYGR	sp|O89086|RBM3_MOUSE	yes	yes	119	128	10	R	S	0	1045.462	2	1.42E-07	180.87	0.16	0.13	7
2589	PGLISSR	sp|P17563|SBP1_MOUSE	no	no	97	103	7	L	I	0	728.418	2	1.59E-01	67.98	NaN	NaN	0
2590	PGPDGPAAPGPAAIR	sp|Q64674|SPEE_MOUSE	yes	yes	3	17	15	E	E	0	1342.699	2	3.81E-02	56.29	NaN	NaN	0
2591	PGPIGPAGPR	sp|Q01149|CO1A2_MOUSE	yes	yes	483	492	10	R	G	0	917.508	2	3.98E-03	146.03	NaN	NaN	0
2592	PGPNIYELR	sp|O55126|NIPS2_MOUSE	yes	yes	177	185	9	R	S	0	1057.556	2	2.11E-02	109.44	NaN	NaN	0
2593	PGQLNADLR	sp|P99024|TBB5_MOUSE	no	no	243	251	9	F	K	0	982.520	2	4.18E-02	83.87	NaN	NaN	0
2594	PGQQIATCVR	sp|Q91W50|CSDE1_MOUSE	yes	yes	499	508	10	R	L	0	1128.571	2	9.92E-03	123.42	NaN	NaN	0
2595	PGTFTNQIQAAFR	sp|P14206|RSSA_MOUSE	yes	yes	105	117	13	T	E	0	1449.737	2	1.51E-03	112.44	NaN	NaN	0
2596	PGWTKPITIGR	sp|P54071|IDHP_MOUSE	yes	yes	162	172	11	V	H	0	1224.698	2	1.83E-02	63.47	1.06	0.91	4
2597	PHPGEGASAAQAGGAAPPTR	sp|Q9JHH9|COPZ2_MOUSE	yes	yes	10	29	20	R	A	0	1798.871	3	1.06E-02	65.86	NaN	NaN	0
2598	PICRPICSGPITFR	sp|A2A5X5|KR161_MOUSE	yes	yes	384	397	14	R	Q	1	1672.854	3	1.00E-03	124.62	NaN	NaN	0
2599	PICSGPITFR	sp|A2A5X5|KR161_MOUSE	yes	yes	388	397	10	R	Q	0	1146.586	2	1.20E-03	146.11	0.63	0.35	3
2600	PIFQAYIGMLKKQVDR	sp|Q3TTY5|K22E_MOUSE	yes	no	248	263	16	D	L	0	1906.050	4	1.78E-04	80.63	2.64	1.58	1
2601	PIIAVTR	sp|P52480|KPYM_MOUSE	no	no	449	455	7	A	N	0	768.486	2	7.34E-02	100.75	NaN	NaN	0
2602	PIKPSPPYFGLLLASVGR	sp|P70698|PYRG1_MOUSE	yes	yes	533	550	18	R	L	0	1911.098	3	9.56E-05	79.84	1.09	1.03	3
2603	PKDIQLAR	sp|P84244|H33_MOUSE	no	no	122	129	8	M	R	0	939.550	2	5.67E-03	120.99	1.41	0.95	6
2604	PKEPEQLR	sp|Q8BG05-2|ROA3_MOUSE	no	no	7	14	8	S	K	0	995.540	2	1.49E-01	63.82	1.24	1.16	1
2605	PKLEEFFAR	sp|Q00612|G6PD1_MOUSE	yes	yes	96	104	9	R	N	0	1135.603	3	2.04E-02	72.33	1.04	0.92	4
2606	PKNFGIGQDIQPKR	sp|P12970|RL7A_MOUSE	yes	yes	36	49	14	R	D	0	1596.874	4	1.07E-04	111.83	1.12	0.86	7
2607	PKQYFSSPCQGGFTGSFGYGNTGI	sp|Q9QZU5|KR151_MOUSE	yes	yes	79	113	35	R	S	0	3626.631	3	3.35E-06	119.99	1.84	1.19	2
2608	PLALALISVSNPR	sp|Q8VDM4|PSMD2_MOUSE	yes	yes	691	703	13	V	L	0	1349.803	2	6.40E-02	54.34	NaN	NaN	0
2609	PLELSDFR	sp|Q61029-2|LAP2B_MOUSE	yes	no	301	308	8	R	M	0	975.503	2	1.60E-02	162.25	NaN	NaN	0
2610	PLEMIEPR	sp|P14131|RS16_MOUSE	yes	yes	38	45	8	R	T	0	983.511	2	3.92E-02	119.21	NaN	NaN	0
2611	PLFEHYTR	sp|Q9CPY7-2|AMPL_MOUSE	yes	no	402	409	8	M	Q	0	1061.529	2	4.18E-02	109.71	NaN	NaN	0
2612	PLFEQYINNLR	sp|Q922U2|K2C5_MOUSE	no	no	211	221	11	D	R	0	1405.735	2	1.52E-02	90.05	NaN	NaN	0
2613	PLLLTPVLSHPIFDNR	sp|Q04207-2|TF65_MOUSE	yes	no	172	187	16	R	A	0	1831.036	3	5.25E-03	78.69	NaN	NaN	0
2614	PLNPKANR	sp|P63260|ACTG_MOUSE	no	no	109	116	8	A	E	0	908.519	2	2.14E-02	79.47	1.29	1.14	4
2615	PLPAATAEGPAAVTLAAPAFSR	sp|P14602|HSPB1_MOUSE	yes	yes	58	79	22	R	A	0	2078.116	2;3	4.30E-08	153.65	NaN	NaN	0
2616	PLPTFSSLNLR	sp|P20152|VIME_MOUSE	yes	yes	414	424	11	L	E	0	1243.693	2	1.77E-02	84.51	NaN	NaN	0
2617	PLQDVYKIGGIGTVPVGR	sp|P10126|EF1A1_MOUSE	yes	no	249	266	18	L	V	0	1868.052	2;3	4.64E-03	60.06	1.29	1.03	12
2618	PLTGGEPVSLGSLR	sp|P11352|GPX1_MOUSE	yes	yes	21	34	14	R	G	0	1381.757	2	2.31E-04	154.65	NaN	NaN	0
2619	PLVALLDGR	sp|P56546|CTBP2_MOUSE	yes	no	34	42	9	R	D	0	952.571	2	7.86E-03	148.52	NaN	NaN	0
2620	PLVCPAYQAYFR	sp|Q61897|KT33B_MOUSE	no	no	97	108	12	D	T	0	1483.728	2	5.97E-03	99.28	NaN	NaN	0
2621	PLYDIPYMFEAR	sp|Q78PY7|SND1_MOUSE	yes	yes	392	403	12	R	E	0	1513.728	2	1.01E-03	96.75	0.11	0.07	1
2622	PLYGLGELPQGFAR	sp|Q61598-2|GDIB_MOUSE	yes	no	191	204	14	Y	L	0	1516.804	2	5.87E-03	84.30	NaN	NaN	0
2623	PLYSNPPLNGAR	sp|P05202|AATM_MOUSE	yes	yes	314	325	12	R	I	0	1297.678	2	1.09E-03	145.91	NaN	NaN	0
2624	PMTVDFIR	sp|P00493|HPRT_MOUSE	yes	yes	94	101	8	I	L	0	977.500	2	2.84E-02	107.29	NaN	NaN	0
2625	PNYQALLR	sp|Q04857|CO6A1_MOUSE	yes	yes	1004	1011	8	V	G	0	973.535	2	1.74E-02	86.79	NaN	NaN	0
2626	PQAPATVGLAFR	sp|P62869|ELOB_MOUSE	yes	yes	69	80	12	R	A	0	1226.677	2	2.64E-03	125.97	NaN	NaN	0
2627	PQPAASKPADR	sp|A2A5X5|KR161_MOUSE	yes	yes	492	502	11	A	-	0	1136.594	2	1.40E-02	67.39	2.03	1.21	1
2628	PQTGLSFLGPEPEDLEDLYSR	sp|P54775|PRS6B_MOUSE	yes	yes	23	43	21	R	Y	0	2362.133	2	6.34E-03	69.77	NaN	NaN	0
2629	PQYKYAAGVR	sp|P29341|PABP1_MOUSE	yes	yes	509	518	10	V	N	0	1151.609	2	5.53E-03	140.16	1.25	1.18	1
2630	PSAYNFDNSPVLQEWVTATDIR	sp|P02468|LAMC1_MOUSE	yes	yes	227	248	22	R	V	0	2522.208	2	1.10E-02	55.13	NaN	NaN	0
2631	PSCCGGYGFSSFY	sp|Q925H6|KR193_MOUSE	no	no	75	87	13	R	-	0	1487.549	2	3.44E-03	97.16	NaN	NaN	0
2632	PSDFIKPGKMCR	sp|P21812|MCPT4_MOUSE	yes	yes	133	144	12	R	A	0	1434.711	4	4.17E-02	46.84	1.49	0.79	1
2633	PSENLGQVLFGER	sp|P58021|TM9S2_MOUSE	yes	yes	91	103	13	R	I	0	1444.731	2	6.14E-04	148.66	NaN	NaN	0
2634	PSESIVVPGNTR	sp|Q60847|COCA1_MOUSE	yes	no	1978	1989	12	R	T	0	1254.657	2	2.50E-03	127.56	NaN	NaN	0
2635	PSGASTGIYEALELR	sp|P17182|ENOA_MOUSE	yes	no	36	50	15	V	D	0	1562.794	2	7.54E-04	106.14	NaN	NaN	0
2636	PSIAYFPQIVSVAAR	sp|P85094|ISC2A_MOUSE	yes	yes	29	43	15	R	M	0	1617.888	2	4.97E-02	68.97	NaN	NaN	0
2637	PSIVGRPR	sp|P63260|ACTG_MOUSE	no	no	32	39	8	F	H	1	880.524	2	2.22E-03	182.39	NaN	NaN	0
2638	PSLVGR	sp|Q8CDW1|F228A_MOUSE	yes	no	268	273	6	R	R	0	627.370	2	5.39E-03	186.74	NaN	NaN	0
2639	PSSISWDGLDPGKLYTLVLTDPDA	sp|P70296|PEBP1_MOUSE	yes	yes	50	76	27	R	K	0	2899.460	3	6.11E-07	125.83	1.31	1.03	2
2640	PSVKQNSLDEDLIR	sp|Q02053|UBA1_MOUSE	yes	yes	371	384	14	P	K	0	1612.842	2	1.65E-04	102.65	1.42	1.21	4
2641	PSYVAFTDTER	sp|P63017|HSP7C_MOUSE	no	no	39	49	11	T	L	0	1284.599	2	2.22E-03	140.78	NaN	NaN	0
2642	PSYVAFTPEGER	sp|P20029|GRP78_MOUSE	yes	yes	64	75	12	T	L	0	1351.641	2	7.50E-03	95.42	NaN	NaN	0
2643	PTLLLFR	sp|Q91W90|TXND5_MOUSE	yes	yes	382	388	7	Y	G	0	858.533	2	2.50E-02	167.25	NaN	NaN	0
2644	PTLVEAAR	sp|P07724|ALBU_MOUSE	yes	yes	445	452	8	T	N	0	855.481	2	5.72E-02	91.85	NaN	NaN	0
2645	PTNEAFEKLPR	sp|Q62009-5|POSTN_MOUSE	yes	no	276	286	11	A	G	0	1300.678	2	1.15E-02	69.72	1.46	1.08	3
2646	PTSTNPIASIFAWTR	sp|P54071|IDHP_MOUSE	yes	yes	363	377	15	R	G	0	1660.857	2	4.32E-05	168.41	NaN	NaN	0
2647	PTYNPTLPYKR	sp|O54891|LEG6_MOUSE	yes	no	11	21	11	Q	P	0	1348.714	2	4.49E-02	48.28	1.37	1.08	2
2648	PVAEEFR	sp|Q00623|APOA1_MOUSE	yes	yes	166	172	7	S	D	0	846.424	2	8.18E-02	94.66	NaN	NaN	0
2649	PVAVALDTKGPEIR	sp|P52480|KPYM_MOUSE	no	no	107	120	14	R	T	0	1464.830	3	1.43E-04	105.03	1.07	0.96	7
2650	PVCVPCPGGR	sp|Q497I4|KRT35_MOUSE	yes	no	445	454	10	R	F	0	1097.511	2	2.57E-02	86.67	NaN	NaN	0
2651	PVEEAYKR	sp|E9Q557|DESP_MOUSE	yes	yes	2323	2330	8	L	G	0	990.513	2	5.65E-03	121.09	1.64	1.10	3
2652	PVLLTEAPLNPKANR	sp|P63260|ACTG_MOUSE	no	no	102	116	15	H	E	0	1631.936	2	5.73E-06	127.02	0.95	0.89	2
2653	PVNPLCIYR	sp|P32261|ANT3_MOUSE	yes	yes	49	57	9	I	S	0	1130.591	2	3.41E-02	91.32	NaN	NaN	0
2654	PWEIILVCNR	sp|Q08189|TGM3_MOUSE	yes	yes	37	46	10	Q	S	0	1298.681	2	7.09E-02	67.33	NaN	NaN	0
2655	PWEVPKKLKY	sp|Q3THS6|METK2_MOUSE	yes	no	386	395	10	F	-	0	1286.739	2	5.94E-03	80.69	1.36	1.11	3
2656	PYLPNVDEEVQIGHVPR	sp|P11276|FINC_MOUSE	yes	yes	2165	2181	17	R	G	0	1961.001	3	4.01E-04	119.46	NaN	NaN	0
2657	QAALQVADGFISR	sp|P24452|CAPG_MOUSE	yes	yes	311	323	13	R	M	0	1374.726	2	1.01E-03	138.55	NaN	NaN	0
2658	QAAPCVLFFDELDSIAKAR	sp|Q01853|TERA_MOUSE	yes	yes	568	586	19	R	G	0	2150.083	3	3.53E-05	90.72	1.15	0.96	4
2659	QAEEEKVPLPELVR	sp|P56399|UBP5_MOUSE	yes	yes	511	524	14	R	A	0	1635.883	2;3	3.35E-05	125.73	1.07	1.01	5
2660	QAEIIELR	sp|Q61897|KT33B_MOUSE	no	no	269	276	8	C	R	0	970.545	2	1.92E-02	157.91	NaN	NaN	0
2661	QAEMLDDLMEKR	sp|Q9WTP6-2|KAD2_MOUSE	yes	no	107	118	12	R	K	0	1477.691	2	2.71E-02	69.03	NaN	NaN	0
2662	QAHLTNQYMQR	sp|P29341|PABP1_MOUSE	yes	yes	375	385	11	R	M	0	1388.662	3	2.01E-02	79.31	NaN	NaN	0
2663	QALQDLLSEYMGNAGR	sp|P26231|CTNA1_MOUSE	yes	yes	342	357	16	R	K	0	1764.847	2	7.94E-07	119.65	0.30	0.20	1
2664	QATKDAGQISGLNVLR	sp|P38647|GRP75_MOUSE	yes	yes	203	218	16	R	V	0	1669.911	3	2.18E-09	154.69	1.08	0.94	5
2665	QATKDAGTIAGLNVLR	sp|P63017|HSP7C_MOUSE	yes	yes	156	171	16	R	I	0	1626.905	2;3	3.26E-16	195.92	1.29	0.97	16
2666	QATKDAGTIAGLNVMR	sp|P20029|GRP78_MOUSE	yes	yes	183	198	16	R	I	0	1644.862	2;3	2.76E-08	145.70	1.21	0.92	7
2667	QATKDAGVIAGLNVLR	sp|Q61696|HS71A_MOUSE	yes	no	156	171	16	R	I	0	1624.926	2;3	6.91E-08	131.03	1.09	1.00	7
2668	QAVDVSPLR	sp|P97461|RS5_MOUSE	yes	yes	137	145	9	R	R	0	983.540	2	1.09E-02	142.56	NaN	NaN	0
2669	QAVDVSPLRR	sp|P97461|RS5_MOUSE	yes	yes	137	146	10	R	V	1	1139.641	2	5.59E-02	70.94	NaN	NaN	0
2670	QAVLYVDSR	sp|O54983|CRYM_MOUSE	yes	yes	242	250	9	R	E	0	1049.551	2	1.99E-02	116.52	NaN	NaN	0
2671	QAVTNPNNTFYATKR	sp|P38647|GRP75_MOUSE	yes	yes	108	122	15	R	L	0	1723.864	3	4.29E-03	83.69	0.84	0.82	1
2672	QAWDQMMSTLKELEAR	sp|Q7TPV4|MBB1A_MOUSE	yes	yes	569	584	16	R	S	0	1935.918	3	1.76E-03	72.90	1.33	0.91	1
2673	QDEHGYISR	sp|P14602|HSPB1_MOUSE	yes	no	132	140	9	R	C	0	1103.500	2	1.50E-02	134.30	NaN	NaN	0

2674	QDFKTDLR	sp|P84244|H33_MOUSE	no	no	77	84	8	A	F	0	1021.519	2	3.03E-03	138.08	1.27	0.82	3
2675	QDGALVQHQQWDGKESTITR	sp|Q05816|FABP5_MOUSE	yes	yes	90	109	20	F	K	0	2296.120	3	8.23E-02	23.29	1.14	1.06	3
2676	QDIAFAYQR	sp|P07356|ANXA2_MOUSE	yes	yes	69	77	9	R	R	0	1110.546	2	4.94E-05	196.88	NaN	NaN	0
2677	QDLATLDVTKLTPLSHEVISR	sp|Q9Z0N1|IF2G_MOUSE	yes	yes	18	38	21	R	Q	0	2335.275	3;4	6.90E-06	97.69	1.21	0.93	2
2678	QDPSVLHTEEMR	sp|Q99L47|F10A1_MOUSE	yes	yes	18	29	12	R	F	0	1440.667	3	7.97E-02	54.34	NaN	NaN	0
2679	QDSLESMKFGDSNTVMR	sp|E9Q557|DESP_MOUSE	yes	yes	921	937	17	R	F	0	1943.872	3	3.51E-08	133.86	1.60	0.97	2
2680	QDVDNASLAR	sp|P20152|VIME_MOUSE	yes	yes	208	217	10	R	L	0	1087.526	2	1.14E-02	117.52	NaN	NaN	0
2681	QEAEEAKEALLQASR	sp|P26041|MOES_MOUSE	yes	yes	394	408	15	R	D	0	1671.843	3	5.83E-03	64.45	1.18	0.92	2
2682	QEALEWLIR	sp|Q6P1B1|XPP1_MOUSE	yes	yes	606	614	9	R	E	0	1156.624	2	5.07E-03	119.62	13.28	10.99	1
2683	QEDIPEVSCIHNGLR	sp|P11087|CO1A1_MOUSE	yes	no	23	37	15	G	V	0	1765.842	2	5.91E-04	126.77	NaN	NaN	0
2684	QEGDLGPVYGFQWR	sp|P07607|TYSY_MOUSE	yes	yes	121	134	14	R	H	0	1650.779	2	3.69E-03	92.86	NaN	NaN	0
2685	QEIAQEFKTLFGR	sp|P48036|ANXA5_MOUSE	yes	yes	49	61	13	R	D	0	1565.820	2;3	4.23E-08	157.35	1.23	0.98	10
2686	QEIIKLFDER	sp|Q8BLX7|COGA1_MOUSE	yes	yes	1421	1430	10	R	M	0	1289.698	2	3.76E-03	93.35	NaN	NaN	0
2687	QEIYSSHNQPSCGGR	sp|Q8K4L4|POF1B_MOUSE	yes	yes	527	541	15	R	T	0	1718.743	3	2.08E-04	148.57	NaN	NaN	0
2688	QEKALSAIAELLTSEHER	sp|P30999-2|CTND1_MOUSE	yes	no	702	719	18	R	V	0	2024.054	3	1.77E-03	70.84	1.27	0.77	1
2689	QELEAELAKVR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1654	1664	11	R	A	0	1284.704	2	3.25E-02	73.44	NaN	NaN	0
2690	QELLCLKQNHEEEVNTLR	sp|Q61897|KT33B_MOUSE	yes	no	185	202	18	R	C	0	2252.122	3;4	3.48E-07	106.75	1.82	1.18	6
2691	QELVTKIDHILDAL	sp|Q91YQ5|RPN1_MOUSE	yes	no	595	608	14	R	-	0	1606.893	2;3	2.75E-06	150.49	1.43	0.90	1
2692	QEPSDSPMFIINR	sp|Q61495|DSG1A_MOUSE	no	no	201	213	13	R	K	0	1532.729	2	1.45E-03	120.84	NaN	NaN	0
2693	QEQDTYALSSYTR	sp|Q8QZT1|THIL_MOUSE	yes	yes	206	218	13	R	S	0	1560.706	2	3.00E-04	159.52	NaN	NaN	0
2694	QFILVMNALDNR	sp|Q9Z1F9|SAE2_MOUSE	yes	yes	108	119	12	R	A	0	1432.750	2	8.21E-03	93.62	NaN	NaN	0
2695	QFTCKPGVANR	sp|Q6NXH9|K2C73_MOUSE	yes	no	4	14	11	R	G	0	1276.635	2;3	3.17E-03	80.01	1.67	0.99	1
2696	QFTSSSSIKGSSGLGGGSSR	sp|Q9QWL7|K1C17_MOUSE	yes	no	7	26	20	R	T	0	1885.913	2;3	1.67E-12	151.42	1.58	0.95	5
2697	QFTSSSSMKGSCGIGGGSSR	sp|Q61781|K1C14_MOUSE	no	no	7	26	20	R	M	0	1976.868	2;3	4.25E-13	154.42	1.52	0.98	8
2698	QFVTATDVVR	sp|Q61233|PLSL_MOUSE	yes	yes	348	357	10	R	G	0	1134.603	2	2.94E-02	81.02	NaN	NaN	0
2699	QFYINVER	sp|P60843|IF4A1_MOUSE	yes	no	248	255	8	R	E	0	1067.540	2	4.11E-02	112.41	NaN	NaN	0
2700	QGAFLVNAAR	sp|P56546|CTBP2_MOUSE	yes	no	263	272	10	R	G	0	1045.567	2	6.24E-03	78.94	1.02	0.83	1
2701	QGANINEIR	sp|P60335|PCBP1_MOUSE	yes	yes	298	306	9	R	Q	0	1013.525	2	1.74E-02	129.63	NaN	NaN	0
2702	QGFGELLQAVPLADSFR	sp|P28352|APEX1_MOUSE	yes	yes	237	253	17	R	H	0	1846.958	2	2.87E-08	192.24	NaN	NaN	0
2703	QGIFPASYVQINR	sp|Q9R1Z8|VINEX_MOUSE	yes	yes	566	578	13	R	E	0	1491.783	2	1.00E-02	77.19	NaN	NaN	0
2704	QGITKPAIR	sp|P62806|H4_MOUSE	yes	yes	28	36	9	I	R	0	982.592	2	3.13E-06	175.88	0.90	0.61	5
2705	QGVEADINGLR	sp|Q61414|K1C15_MOUSE	yes	no	196	206	11	R	R	0	1170.599	2	2.26E-03	140.48	NaN	NaN	0
2706	QGVEADINGLRR	sp|Q61414|K1C15_MOUSE	yes	no	196	207	12	R	V	1	1326.700	2	5.31E-03	100.93	NaN	NaN	0
2707	QIASGPSVTGGSITVMAPDSCSPC	sp|Q6IMF0|KRT83_MOUSE	yes	yes	454	480	27	R	A	0	2759.268	2;3	1.99E-21	187.51	NaN	NaN	0
2708	QIDNAKLAADDFR	sp|Q61897|KT33B_MOUSE	no	no	130	142	13	V	T	0	1475.737	2	8.38E-04	124.42	0.67	0.46	2
2709	QIDNAKLASDDFR	sp|Q9D646|KRT34_MOUSE	no	no	130	142	13	V	T	0	1491.732	2	1.02E-02	62.16	0.89	0.61	2
2710	QIDQFLVVAR	sp|Q924K8-2|MTA3_MOUSE	yes	no	191	200	10	R	A	0	1187.666	2	2.66E-02	85.36	NaN	NaN	0
2711	QIEYEYKLAQALHEMR	sp|P14733|LMNB1_MOUSE	yes	yes	236	251	16	R	E	0	2021.004	3	9.32E-05	91.52	NaN	NaN	0
2712	QIEYYFGDFNLPR	sp|P32067|LA_MOUSE	yes	yes	20	32	13	H	D	0	1660.789	2	1.54E-03	107.53	NaN	NaN	0
2713	QIIQQNPSLLPALLQQIGR	sp|P54728|RD23B_MOUSE	yes	yes	290	308	19	R	E	0	2129.232	2;3	6.16E-11	189.59	NaN	NaN	0
2714	QINDIQLSR	sp|Q9QZD9|EIF3I_MOUSE	yes	yes	190	198	9	R	D	0	1085.583	2	2.64E-02	98.73	NaN	NaN	0
2715	QINLSNIR	sp|Q78PY7|SND1_MOUSE	yes	yes	48	55	8	R	A	0	956.540	2	1.15E-01	69.81	NaN	NaN	0
2716	QINWTVLYR	sp|Q8BP67|RL24_MOUSE	yes	yes	48	56	9	R	R	0	1191.640	2	5.22E-04	138.40	0.30	0.24	1
2717	QIQCLQKTGIR	sp|Q9DBC7|KAP0_MOUSE	yes	yes	64	74	11	R	T	0	1343.734	3	3.89E-02	71.03	1.14	0.99	2
2718	QIQQNINDAEQR	sp|P04104|K2C1_MOUSE	yes	yes	429	440	12	S	G	0	1455.707	2	3.09E-02	71.18	NaN	NaN	0
2719	QISLEDALR	sp|Q9CY64|BIEA_MOUSE	yes	yes	55	63	9	R	S	0	1043.561	2	6.04E-02	74.42	NaN	NaN	0
2720	QITLNDLPVGR	sp|O08807|PRDX4_MOUSE	yes	yes	216	226	11	R	S	0	1224.683	2	3.09E-03	134.20	NaN	NaN	0
2721	QITVNDLPVGR	sp|Q61171|PRDX2_MOUSE	yes	yes	140	150	11	R	S	0	1210.667	2	3.19E-03	133.42	NaN	NaN	0
2722	QIVSGPSVTGGSITVMAPDSCSPC	sp|Q9Z2T6|KRT85_MOUSE	yes	yes	466	492	27	R	A	0	2787.299	2;3	1.08E-16	156.20	14.56	9.91	1
2723	QIWQNLGLDEAR	sp|Q8BGQ7|SYAC_MOUSE	yes	yes	154	165	12	R	I	0	1441.731	2	8.19E-04	149.41	NaN	NaN	0
2724	QIYPPINVLPSLSR	sp|P62814|VATB2_MOUSE	yes	yes	387	400	14	R	L	0	1595.904	2	1.24E-03	102.50	NaN	NaN	0
2725	QKAQVEQELTTLR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	2083	2095	13	R	L	0	1542.837	2	8.70E-04	85.84	NaN	NaN	0
2726	QKGLVEDTLR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1812	1821	10	R	Q	0	1157.640	2	4.27E-02	51.29	NaN	NaN	0
2727	QKSTELLIR	sp|P84244|H33_MOUSE	no	no	56	64	9	Y	K	0	1086.640	2	1.31E-05	157.66	1.30	0.79	5
2728	QKTGTAEMSSILEER	sp|Q03265|ATPA_MOUSE	yes	yes	44	58	15	L	I	0	1678.820	2	1.88E-13	182.31	NaN	NaN	0
2729	QKVAPLGAELQESAR	sp|Q00623|APOA1_MOUSE	yes	yes	140	154	15	R	Q	0	1595.863	2;3	2.55E-05	110.06	1.72	1.26	6
2730	QKVTSLTACLVNQNLR	sp|P01831|THY1_MOUSE	yes	yes	20	35	16	G	L	0	1843.994	2;3	1.15E-16	203.53	NaN	NaN	0
2731	QLCDNAGFDATNILNKLR	sp|P80313|TCPH_MOUSE	yes	yes	448	465	18	R	A	0	2062.027	2;3	2.53E-05	97.10	1.31	0.95	5
2732	QLDGITAER	sp|Q8BGZ7|K2C75_MOUSE	yes	no	211	219	9	R	G	0	1001.514	2	4.10E-02	77.14	NaN	NaN	0
2733	QLDGVLGER	sp|Q922U2|K2C5_MOUSE	yes	no	223	231	9	R	G	0	985.519	2	2.04E-02	99.53	NaN	NaN	0
2734	QLDLDSILAEVR	sp|Q6IME9|K2C72_MOUSE	yes	no	298	309	12	R	A	0	1370.741	2	2.63E-04	163.51	NaN	NaN	0
2735	QLEEAEEEAQR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	1878	1888	11	R	A	0	1330.600	2	1.36E-06	191.53	NaN	NaN	0
2736	QLEKSLLQALNEVKGR	sp|Q9JHU4|DYHC1_MOUSE	yes	yes	3742	3757	16	R	I	0	1825.042	3	4.26E-02	41.54	NaN	NaN	0
2737	QLELSKVR	sp|P48678|LMNA_MOUSE	yes	no	103	110	8	L	E	0	971.576	2	7.02E-03	113.26	1.27	0.94	3
2738	QLEQENASLESR	sp|Q497I4|KRT35_MOUSE	yes	no	117	128	12	R	I	0	1402.669	2	3.49E-10	208.27	NaN	NaN	0
2739	QLEQQVEEFR	sp|P06728|APOA4_MOUSE	yes	yes	295	304	10	R	R	0	1304.636	2	2.27E-08	219.03	NaN	NaN	0
2740	QLEQQVEEFRR	sp|P06728|APOA4_MOUSE	yes	yes	295	305	11	R	T	1	1460.737	2	1.37E-02	93.35	NaN	NaN	0
2741	QLFHPEQLITGKEDAANNYAR	sp|P68373|TBA1C_MOUSE	no	no	85	105	21	R	G	0	2414.198	2;3;4	4.15E-17	180.05	1.21	1.06	16
2742	QLHDDYFYHDEL	sp|Q8BP92|RCN2_MOUSE	yes	no	309	320	12	R	-	0	1593.674	2	4.30E-02	66.99	NaN	NaN	0
2743	QLIMANPQMQQLIQR	sp|Q8R317-2|UBQL1_MOUSE	no	no	198	212	15	R	N	0	1810.955	2;3	4.35E-05	168.31	NaN	NaN	0
2744	QLLAGLDKVASDLDR	sp|Q9R269|PEPL_MOUSE	yes	yes	504	518	15	R	Q	0	1612.878	2	1.74E-05	117.00	NaN	NaN	0
2745	QLLEEELAR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1633	1641	9	R	L	0	1099.587	2	4.67E-02	79.15	NaN	NaN	0
2746	QLLLTADDR	sp|P05064|ALDOA_MOUSE	yes	yes	61	69	9	R	V	0	1043.561	2	1.78E-02	128.60	NaN	NaN	0
2747	QLLQANPILEAFGNAKTVKNDNS	sp|Q8VDD5|MYH9_MOUSE	no	no	210	234	25	R	F	0	2727.430	3;4	1.09E-03	63.38	1.12	0.89	3
2748	QLLTLSNELSQAR	sp|P26040|EZRI_MOUSE	yes	yes	530	542	13	R	D	0	1471.800	2	2.61E-04	162.31	NaN	NaN	0
2749	QLPIPAELSCVR	sp|Q9D7P7|CLIC3_MOUSE	yes	yes	193	204	12	R	R	0	1381.739	2	9.92E-03	89.30	NaN	NaN	0
2750	QLQLAQEAAQKR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1938	1949	12	R	L	0	1382.763	2	3.40E-02	48.57	NaN	NaN	0
2751	QLQNIIQATSR	sp|E9Q557|DESP_MOUSE	yes	yes	283	293	11	R	E	0	1270.699	2	2.22E-03	140.78	NaN	NaN	0
2752	QLSSGVSEIR	sp|P14602|HSPB1_MOUSE	yes	no	84	93	10	R	Q	0	1074.567	2	5.45E-02	75.82	NaN	NaN	0
2753	QLTLYPGAER	sp|Q6IME9|K2C72_MOUSE	yes	no	4	13	10	R	L	0	1146.603	2	1.42E-02	106.40	NaN	NaN	0
2754	QLVEADINGLR	sp|Q497I4|KRT35_MOUSE	no	no	194	204	11	R	R	0	1226.662	2	1.39E-02	92.87	NaN	NaN	0
2755	QLVEADINSLR	sp|Q9D646|KRT34_MOUSE	no	no	153	163	11	R	R	0	1256.673	2	1.98E-06	184.44	NaN	NaN	0
2756	QLVEADINSLRR	sp|Q9D646|KRT34_MOUSE	no	no	153	164	12	R	I	1	1412.774	2	1.71E-06	188.26	NaN	NaN	0
2757	QLVEADTNGLR	sp|Q62168|K1H2_MOUSE	yes	no	152	162	11	R	R	0	1214.626	2	1.69E-03	97.45	3.30	2.05	2
2758	QLVESDLNGLR	sp|Q61897|KT33B_MOUSE	yes	no	153	163	11	R	R	0	1242.657	2	3.03E-04	158.05	NaN	NaN	0
2759	QLVESDLNGLRR	sp|Q61897|KT33B_MOUSE	yes	no	153	164	12	R	I	1	1398.758	2;3	2.48E-04	145.28	NaN	NaN	0
2760	QMNPYIQVTSHQNR	sp|Q02053|UBA1_MOUSE	yes	yes	538	551	14	R	V	0	1714.821	3	1.06E-03	117.20	NaN	NaN	0
2761	QMSGAQIKIANPVEGSSGR	sp|P60335|PCBP1_MOUSE	yes	yes	307	325	19	R	Q	0	1928.974	3	6.52E-05	80.14	1.36	1.10	5
2762	QMSLLLR	sp|Q03265|ATPA_MOUSE	yes	yes	323	329	7	R	R	0	859.495	2	1.25E-01	73.64	NaN	NaN	0
2763	QNGDDPLMTYR	sp|P48678|LMNA_MOUSE	yes	no	472	482	11	R	F	0	1308.577	2	9.54E-03	102.40	NaN	NaN	0
2764	QNLEPFFDTYVNDLR	sp|Q8BGZ7|K2C75_MOUSE	yes	no	195	209	15	R	R	0	1869.890	2	7.16E-04	110.97	NaN	NaN	0
2765	QNLEPFFDTYVNDLRR	sp|Q8BGZ7|K2C75_MOUSE	yes	no	195	210	16	R	Q	1	2025.991	2;3	3.77E-03	86.55	NaN	NaN	0
2766	QNLIKCIENLEELQSLR	sp|Q3UM45|PP1R7_MOUSE	yes	yes	108	124	17	R	E	0	2099.105	3	3.84E-08	131.82	1.18	0.93	1
2767	QNQEYQVLLDIR	sp|Q8K0Y2|KT33A_MOUSE	yes	yes	335	346	12	R	S	0	1517.784	2	3.52E-10	208.08	NaN	NaN	0
2768	QNQEYQVLLDVKAR	sp|Q61897|KT33B_MOUSE	no	no	335	348	14	R	L	0	1702.900	2;3	7.66E-09	173.44	2.00	1.25	10
2769	QNQEYQVLLDVR	sp|Q9D646|KRT34_MOUSE	no	no	335	346	12	R	A	0	1503.768	2	6.93E-16	240.60	0.01	0.01	1
2770	QNYLFEQYR	sp|Q9ER72-2|SYCC_MOUSE	yes	no	108	116	9	R	E	0	1259.594	2	2.06E-02	112.11	NaN	NaN	0
2771	QPFFQKR	sp|Q9EQU5-2|SET_MOUSE	yes	no	65	71	7	R	S	0	949.513	2	2.02E-02	97.47	NaN	NaN	0
2772	QPLTITVR	sp|P01027|CO3_MOUSE	yes	yes	418	425	8	R	T	0	926.555	2	6.40E-02	86.33	NaN	NaN	0
2773	QPYAVSELAGHQTSAESWGTGR	sp|Q9D8E6|RL4_MOUSE	yes	yes	50	71	22	R	A	0	2331.088	3	7.64E-04	86.56	NaN	NaN	0
2774	QQEGFKGTFPDAR	sp|Q99K48|NONO_MOUSE	yes	yes	368	380	13	R	E	0	1479.711	2	5.03E-02	43.03	NaN	NaN	0
2775	QQIKAAYLQENGKPLDEVLR	sp|P10107|ANXA1_MOUSE	yes	yes	78	97	20	R	K	0	2312.249	3;4	4.12E-08	105.79	1.08	0.99	11
2776	QQLGPNSGEVESHLSFLEKSLR	sp|P06728|APOA4_MOUSE	yes	yes	327	348	22	R	E	0	2454.250	4	2.08E-03	56.72	0.91	0.76	3

2777	QQQEKLLAEENQR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	2484	2496	13	R	L	0	1612.817	3	2.51E-04	106.32	1.19	0.72	1
2778	QQQLTAMKVLQR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	803	814	12	R	N	0	1442.803	3	1.73E-02	58.27	1.08	0.77	2
2779	QQSNVDELGCSHLGQSYESR	sp|P08121|CO3A1_MOUSE	yes	yes	24	43	20	A	D	0	2293.003	2	9.56E-17	230.71	NaN	NaN	0
2780	QQWDGKESTITR	sp|Q05816|FABP5_MOUSE	yes	yes	98	109	12	H	K	0	1447.706	3	1.16E-02	65.30	1.83	1.45	3
2781	QSEELSKLR	sp|Q8K4L4|POF1B_MOUSE	yes	yes	518	526	9	R	Q	0	1088.583	2	3.13E-02	66.06	NaN	NaN	0
2782	QSGQCLDIDECR	sp|Q9WVH9|FBLN5_MOUSE	yes	yes	36	47	12	R	T	0	1479.608	2	3.46E-10	208.51	NaN	NaN	0
2783	QSSGPGASSGPGGDHSELIVR	sp|P57776-2|EF1D_MOUSE	yes	yes	39	59	21	R	I	0	1993.945	3	1.72E-03	88.18	NaN	NaN	0
2784	QSTFSGSLGFGSR	sp|O08640|KRA14_MOUSE	yes	yes	92	104	13	C	G	0	1329.631	2	1.56E-03	105.03	NaN	NaN	0
2785	QSTITFHSGSR	sp|Q8BGZ7|K2C75_MOUSE	yes	no	4	14	11	R	R	0	1219.595	2	2.98E-02	74.21	NaN	NaN	0
2786	QSVEADINGLR	sp|P02535-3|K1C10_MOUSE	no	no	235	245	11	R	R	0	1200.610	2	1.78E-06	186.74	NaN	NaN	0
2787	QSVEADINGLRR	sp|P02535-3|K1C10_MOUSE	no	no	235	246	12	R	V	1	1356.711	2;3	7.87E-11	227.72	NaN	NaN	0
2788	QSVEGDINGLR	sp|Q9Z2K1|K1C16_MOUSE	yes	no	210	220	11	R	K	0	1186.594	2	6.28E-03	117.25	NaN	NaN	0
2789	QSVNHQMAQEDAQR	sp|Q07076|ANXA7_MOUSE	yes	yes	310	323	14	R	L	0	1640.733	3	1.02E-01	46.80	NaN	NaN	0
2790	QTFSPFGQIMEIR	sp|P52912|TIA1_MOUSE	yes	no	232	244	13	R	V	0	1552.771	2	4.93E-03	92.65	NaN	NaN	0
2791	QTGKTSIAIDTIINQKR	sp|Q03265|ATPA_MOUSE	yes	yes	215	231	17	R	F	0	1886.059	4	2.78E-02	45.00	1.84	1.15	2
2792	QTLMWSATWPKEVR	sp|Q61656|DDX5_MOUSE	no	no	274	287	14	R	Q	0	1731.877	2;3	1.05E-02	58.08	1.35	1.11	5
2793	QTNLENLDQAFSVAER	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	119	134	16	R	D	0	1833.886	2	1.37E-04	147.09	NaN	NaN	0
2794	QTNPSAMEVEEDDPVPEIR	sp|Q01853|TERA_MOUSE	yes	yes	714	732	19	R	R	0	2154.974	2	1.08E-05	99.41	27.80	22.77	2
2795	QTPVLYAMLDHSR	sp|P27573|MYP0_MOUSE	yes	yes	215	227	13	R	S	0	1529.766	2;3	1.56E-03	104.09	NaN	NaN	0
2796	QTQVSVLPEGGETPLFKQFFKNW	sp|P13020-2|GELS_MOUSE	yes	no	323	346	24	R	D	0	2835.471	4	6.03E-02	28.68	1.37	1.24	2
2797	QVAEEWVNQGR	sp|Q9DCJ9|NPL_MOUSE	yes	yes	65	75	11	R	N	0	1314.632	2	1.45E-06	190.57	NaN	NaN	0
2798	QVCEQLISGQMSR	sp|Q60847|COCA1_MOUSE	yes	no	2912	2924	13	R	F	0	1534.723	2	1.06E-04	173.59	NaN	NaN	0
2799	QVDQLTNDKAR	sp|P20152|VIME_MOUSE	yes	yes	160	170	11	R	V	0	1286.658	2	9.04E-07	156.14	NaN	NaN	0
2800	QVEAELLPCLR	sp|Q8CG76|ARK72_MOUSE	yes	yes	214	224	11	R	H	0	1326.697	2	7.43E-02	61.34	NaN	NaN	0
2801	QVEPLDPPAGSAPGER	sp|Q91WQ3|SYYC_MOUSE	yes	yes	451	466	16	R	V	0	1618.795	2	6.35E-04	108.14	NaN	NaN	0
2802	QVIDCQLADVNNLGKYR	sp|Q9CPY7-2|AMPL_MOUSE	yes	no	410	426	17	R	S	0	2005.005	2;3	3.51E-08	133.86	1.09	0.99	5
2803	QVLLGDQIPKFTIATLPPP	sp|Q60692|PSB6_MOUSE	yes	no	220	238	19	R	-	0	2047.172	2	3.61E-12	144.97	1.33	1.02	5
2804	QVLLSEPQEAAALYR	sp|Q8R146-2|APEH_MOUSE	yes	no	4	18	15	R	G	0	1686.894	2	2.85E-02	62.36	NaN	NaN	0
2805	QVQSLTCEVDALKGTNESLER	sp|P20152|VIME_MOUSE	yes	yes	322	342	21	R	Q	0	2376.159	2;3	3.45E-21	182.76	1.08	0.94	10
2806	QVSASELCTSGILDR	sp|Q8R0W0|EPIPL_MOUSE	yes	no	2703	2717	15	R	D	0	1634.793	2	4.75E-04	134.25	NaN	NaN	0
2807	QVVDRPLPVR	sp|P19096|FAS_MOUSE	yes	yes	375	384	10	L	G	1	1177.693	2	1.37E-01	51.28	NaN	NaN	0
2808	QVVTLLNELKR	sp|Q921H8|THIKA_MOUSE	yes	no	386	396	11	R	R	0	1311.787	2	2.70E-03	85.52	NaN	NaN	0
2809	QWYESHYALPLGR	sp|P62242|RS8_MOUSE	yes	yes	111	123	13	R	K	0	1618.789	2;3	1.51E-04	122.97	NaN	NaN	0
2810	QYAKDIGFIKLD	sp|P62274|RS29_MOUSE	yes	no	45	56	12	R	-	0	1409.756	2;3	1.71E-03	84.30	0.90	0.88	1
2811	QYDIDDAITKNLIDR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	4104	4118	15	R	S	0	1791.900	2;3	2.15E-05	113.47	1.24	0.87	3
2812	QYDISNPQKPR	sp|P17563|SBP1_MOUSE	yes	no	334	344	11	R	L	0	1344.679	2;3	1.48E-02	66.66	1.13	0.96	4
2813	QYEQLAEKNR	sp|P02535-3|K1C10_MOUSE	yes	no	313	322	10	N	K	0	1277.636	2	2.81E-04	138.63	NaN	NaN	0
2814	QYKIPDWFLNR	sp|P62270|RS18_MOUSE	yes	yes	76	86	11	R	Q	0	1478.767	2;3	1.47E-07	177.44	1.26	0.98	8
2815	QYYTLLNQAPDMLHR	sp|P97855|G3BP1_MOUSE	yes	yes	18	32	15	R	F	0	1861.915	2;3	3.54E-04	141.85	NaN	NaN	0
2816	RAEDGSVIDYELIDQDAR	sp|P07356|ANXA2_MOUSE	yes	yes	179	196	18	R	E	1	2063.976	2;3	6.53E-04	107.15	NaN	NaN	0
2817	RAPAAQPPAAAAPSAVGSPAAAP	sp|Q9D1L0|CHCH2_MOUSE	yes	yes	28	51	24	R	Q	1	2152.150	3	4.55E-06	120.63	NaN	NaN	0
2818	RAPFDLFENR	sp|P07901|HS90A_MOUSE	yes	yes	347	356	10	R	K	1	1263.636	2	1.33E-02	110.08	NaN	NaN	0
2819	RDDPSGQMLLLLSDAR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	3768	3783	16	R	K	1	1785.904	3	5.37E-03	78.08	NaN	NaN	0
2820	RGDLPFVVTR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	1923	1932	10	R	R	1	1158.651	2;3	4.98E-03	93.20	2.57	2.29	2
2821	RGEEGHDPKEPEQLR	sp|Q8BG05|ROA3_MOUSE	yes	yes	21	35	15	R	K	1	1775.855	4	9.92E-03	55.01	0.98	0.64	4
2822	RGNDVAFHFNPR	sp|P16110|LEG3_MOUSE	yes	yes	165	176	12	R	F	1	1428.701	3	1.14E-02	85.52	NaN	NaN	0
2823	RHPDYSVSLLLR	sp|P07724|ALBU_MOUSE	yes	yes	361	372	12	R	L	1	1454.799	2;3	5.02E-04	128.54	1.25	1.15	2
2824	RKCCESNMEPLFEGYIEALR	sp|P97861|KRT86_MOUSE	no	no	144	163	20	N	R	1	2501.150	3;4	4.94E-05	78.71	2.29	1.40	2
2825	RKPDTIEVQQMKAQAR	sp|P26041|MOES_MOUSE	no	no	295	310	16	R	E	1	1898.016	4	6.42E-05	92.77	1.03	0.88	6
2826	RLDLPIER	sp|P70698|PYRG1_MOUSE	yes	yes	269	276	8	R	Q	1	1010.587	2	1.54E-02	90.70	1.04	0.84	3
2827	RLTYEIEDEKR	sp|E9Q557|DESP_MOUSE	yes	yes	1125	1135	11	T	R	1	1450.742	3	4.77E-02	47.71	1.50	0.93	4
2828	RPDGEGCVDENECR	sp|Q61555|FBN2_MOUSE	yes	yes	2323	2336	14	R	T	1	1691.663	3	2.57E-03	97.27	NaN	NaN	0
2829	RPDQQLQGDGKLIDR	sp|Q9CY58-3|PAIRB_MOUSE	yes	no	112	126	15	R	R	1	1737.912	3	6.78E-04	95.24	1.06	0.96	5
2830	RPELEDSTLR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	417	426	10	R	Y	1	1214.626	2	1.18E-02	115.92	NaN	NaN	0
2831	RPLSYGGYGFSTFY	sp|Q925H7|KR194_MOUSE	yes	yes	71	84	14	R	-	1	1613.751	2	3.82E-02	61.41	NaN	NaN	0
2832	RPLYYGGYGFSR	sp|O08632|KR195_MOUSE	yes	yes	49	60	12	P	F	1	1434.704	3	1.35E-02	80.31	NaN	NaN	0
2833	RPPGFSPFR	sp|O08677-2|KNG1_MOUSE	yes	no	380	388	9	R	S	1	1059.561	2	4.51E-01	47.85	NaN	NaN	0
2834	RPQYSNPPVQGEVMEGADNQG	sp|P62960|YBOX1_MOUSE	yes	yes	203	232	30	R	Q	2	3222.523	4	1.80E-04	76.00	NaN	NaN	0
2835	RPSCCGGYGFSSFY	sp|Q925H6|KR193_MOUSE	yes	yes	74	87	14	R	-	1	1643.650	2	1.85E-03	100.11	NaN	NaN	0
2836	RQAVDVSPLR	sp|P97461|RS5_MOUSE	yes	yes	136	145	10	R	R	1	1139.641	2	2.19E-01	55.26	NaN	NaN	0
2837	RQLVEADINSLR	sp|Q9D646|KRT34_MOUSE	no	no	152	163	12	M	R	1	1412.774	2;3	3.11E-04	160.22	NaN	NaN	0
2838	RQLVESDLNGLR	sp|Q61897|KT33B_MOUSE	yes	no	152	163	12	L	R	1	1398.758	2;3	2.08E-04	124.21	40.78	21.67	1
2839	RQSVEADINGLR	sp|P02535-3|K1C10_MOUSE	no	no	234	245	12	L	R	1	1356.711	2;3	1.92E-04	168.31	NaN	NaN	0
2840	RVEENAQQQKATGSEMSQR	sp|E9Q557|DESP_MOUSE	yes	yes	1437	1455	19	R	K	1	2176.029	4	2.27E-12	148.85	0.14	0.08	1
2841	RVPFSLLR	sp|P14602|HSPB1_MOUSE	yes	no	5	12	8	R	S	1	986.603	2	1.66E-01	60.83	NaN	NaN	0
2842	SAAEEVDGLGVVRPHYGSVLDNE	sp|Q9JKF1|IQGA1_MOUSE	yes	yes	2	25	24	M	L	1	2568.257	3	3.71E-06	122.18	NaN	NaN	0
2843	SAAESISESVPVGPKVR	sp|P56399|UBP5_MOUSE	yes	yes	779	795	17	R	D	0	1711.911	3	9.29E-07	109.07	1.48	1.36	4
2844	SAEVSLPEKR	sp|Q7TSN7|IGSF5_MOUSE	yes	yes	323	332	10	K	S	0	1114.598	2	3.16E-02	77.66	0.03	0.03	2
2845	SAFNLLHLVTKSQPVAPR	sp|Q8BU85|MSRB3_MOUSE	yes	yes	69	86	18	M	A	0	1977.116	3	6.40E-03	53.45	0.82	0.78	2
2846	SAFPPITLQEPR	sp|Q9R1Z8|VINEX_MOUSE	yes	yes	628	640	13	R	S	0	1501.793	2	9.85E-03	77.78	NaN	NaN	0
2847	SAFSNLFGGEPLSYTR	sp|Q62351|TFR1_MOUSE	yes	yes	7	22	16	R	F	0	1744.842	2	3.61E-04	128.64	NaN	NaN	0
2848	SAGACTAAAFLR	sp|Q9CPY7-2|AMPL_MOUSE	yes	no	427	438	12	R	E	0	1194.582	2	2.39E-03	128.88	NaN	NaN	0
2849	SAGVDDQENWHEGKENIR	sp|Q9CPY7-2|AMPL_MOUSE	yes	no	74	91	18	R	A	0	2082.936	3;4	3.14E-07	109.04	1.04	0.98	7
2850	SAHLQWMVVR	sp|P41105|RL28_MOUSE	yes	yes	2	11	10	M	N	0	1225.639	2	5.45E-03	140.49	NaN	NaN	0
2851	SAINEVVTR	sp|P62900|RL31_MOUSE	yes	yes	15	23	9	R	E	0	987.535	2	1.78E-02	128.91	NaN	NaN	0
2852	SAKAGVIFPVGR	sp|Q9QZQ8-2|H2AY_MOUSE	yes	no	16	27	12	R	M	0	1200.698	3	4.84E-02	45.36	1.46	0.91	1
2853	SALKAVFQYIDENQDR	sp|Q9D1A2|CNDP2_MOUSE	yes	yes	2	17	16	M	Y	0	1895.938	2	2.05E-09	154.74	1.23	1.05	2
2854	SALQIQNVNWQVPMNR	sp|Q08189|TGM3_MOUSE	yes	yes	2	17	16	M	R	0	1896.963	2	7.94E-12	177.88	0.03	0.03	1
2855	SANLVAATLGAILNR	sp|P17710-3|HXK1_MOUSE	yes	no	382	396	15	R	L	0	1482.852	2	2.05E-02	67.33	NaN	NaN	0
2856	SASIEENCLSSELIR	sp|Q7TMD7|DSG4_MOUSE	yes	yes	275	289	15	Y	L	0	1706.815	2	1.11E-03	75.32	0.12	0.09	1
2857	SASVVSVISR	sp|P61804|DAD1_MOUSE	yes	yes	2	11	10	M	F	0	1003.566	2	3.15E-02	77.74	NaN	NaN	0
2858	SAVEKGEELSCEER	sp|O70456|1433S_MOUSE	yes	yes	28	41	14	K	N	0	1621.725	3	6.09E-05	120.54	1.32	1.15	2
2859	SAVLSGGSSSSYR	sp|Q9R0H5|K2C71_MOUSE	no	no	20	32	13	C	A	0	1256.600	2	1.54E-03	107.93	NaN	NaN	0
2860	SAVPPGADKKAEAGAGSATEFQF	sp|P63325|RS10_MOUSE	yes	yes	130	153	24	R	G	0	2391.182	4	7.29E-04	69.09	1.14	1.11	1
2861	SAYKGDSGGPLLCAGVAHGIVSYC	sp|P21812|MCPT4_MOUSE	yes	yes	196	220	25	R	G	0	2491.228	3;4	1.40E-05	101.86	1.56	0.91	5
2862	SAYQEAMDISKKEMPPTNPIR	sp|O70456|1433S_MOUSE	yes	yes	149	169	21	R	L	0	2405.172	3;4	2.98E-05	79.29	1.08	0.94	21
2863	SCESCLPALSCR	sp|Q9D646|KRT34_MOUSE	yes	no	2	13	12	M	T	0	1438.600	2	5.70E-04	138.24	0.01	0.01	1
2864	SCQSNMEPLFEGYICALR	sp|Q99M74|KRT82_MOUSE	yes	yes	158	175	18	R	R	0	2173.960	2	6.31E-04	107.98	NaN	NaN	0
2865	SCWDEPLSIAVR	sp|Q32Q92-2|ACOT6_MOUSE	yes	no	13	24	12	R	G	0	1431.682	2	3.32E-03	117.79	NaN	NaN	0
2866	SCYDLSCHAR	sp|Q9CZD3|SYG_MOUSE	yes	yes	455	464	10	R	A	0	1267.507	3	1.95E-02	96.17	NaN	NaN	0
2867	SCYSILR	sp|A2A5X5|KR161_MOUSE	yes	yes	413	419	7	R	R	0	897.438	2	2.98E-02	85.27	0.03	0.02	1
2868	SDAAPTPVPQSAPR	sp|Q8BJW6-2|EIF2A_MOUSE	yes	no	409	422	14	R	N	0	1392.700	2	1.24E-03	102.50	NaN	NaN	0
2869	SDAAVDTSSEITTKDLKEKKEVVEE	sp|P26350|PTMA_MOUSE	yes	yes	2	31	30	M	D	0	3277.616	5	1.18E-01	32.61	1.07	1.01	2
2870	SDEDNKPDAGPDAAGKESAAR	sp|Q9WTQ5-2|AKA12_MOUSE	yes	no	1364	1384	21	R	E	0	2099.936	4	1.67E-05	89.86	1.48	1.35	3
2871	SDFDPGQDTYQHPPKDSSGQR	sp|Q99KI0|ACON_MOUSE	yes	yes	535	555	21	R	V	0	2361.026	4	1.76E-03	64.71	0.95	0.85	4
2872	SDGKISEQSDAKLKEIVTNFLAGFE	sp|Q03265|ATPA_MOUSE	yes	no	528	553	26	R	-	0	2822.434	3	1.36E-03	57.24	1.66	1.07	1
2873	SDGVIKVFNDMKVR	sp|P18760|COF1_MOUSE	yes	yes	8	21	14	V	K	0	1606.850	2	2.39E-02	48.53	0.83	0.75	2
2874	SDILPLDVIGR	sp|Q8CIV8|TBCE_MOUSE	yes	yes	2	12	11	M	R	0	1196.677	2	1.70E-02	86.01	NaN	NaN	0
2875	SDKLPYKVADIGLAAWGR	sp|P50247|SAHH_MOUSE	yes	yes	2	19	18	M	K	0	1959.058	3	4.64E-03	60.06	1.08	1.02	3
2876	SDLLMPR	sp|P00329|ADH1_MOUSE	yes	yes	115	121	7	R	G	0	830.432	2	6.83E-02	107.43	NaN	NaN	0
2877	SDQLTGLSLLPLSEKAVR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	3103	3120	18	R	A	0	1926.079	3	1.66E-06	102.89	1.23	1.00	6
2878	SDSEKLNLDSIIGR	sp|P62137|PP1A_MOUSE	yes	yes	2	15	14	M	L	0	1545.800	2	8.95E-04	131.56	0.19	0.39	3
2879	SDTFINLR	sp|O08529|CAN2_MOUSE	yes	yes	462	469	8	R	E	0	964.498	2	3.85E-02	121.74	NaN	NaN	0

2880	SEADSDKNSTISELR	sp|E9Q557|DESP_MOUSE	yes	yes	1751	1765	15	R	S	0	1650.770	3	1.31E-05	120.70	1.65	1.01	4
2881	SEAGEFQLPFDPR	sp|Q9JLF6|TGM1_MOUSE	yes	yes	227	239	13	R	N	0	1491.699	2	1.93E-02	72.89	NaN	NaN	0
2882	SEAHLTELLEEVCDR	sp|Q9QXT0|CNPY2_MOUSE	yes	yes	74	88	15	R	M	0	1799.836	3	1.74E-02	69.26	NaN	NaN	0
2883	SEDCFILDHGR	sp|P13020-2|GELS_MOUSE	yes	no	277	287	11	R	D	0	1347.588	2;3	4.74E-03	124.46	NaN	NaN	0
2884	SEGFDTYR	sp|P17918|PCNA_MOUSE	yes	yes	54	61	8	R	C	0	973.414	2	4.06E-02	114.20	NaN	NaN	0
2885	SEIDGCKKQISQIQQNINDAEQR	sp|P04104|K2C1_MOUSE	yes	yes	418	440	23	R	G	0	2701.309	3;4	1.19E-10	136.96	1.68	0.88	11
2886	SEIDLFNIR	sp|P48036|ANXA5_MOUSE	yes	yes	275	283	9	R	K	0	1105.577	2	2.55E-05	157.91	0.00	0.00	1
2887	SEIDLLNIR	sp|P14824|ANXA6_MOUSE	yes	yes	630	638	9	R	R	0	1071.592	2	2.88E-03	164.96	NaN	NaN	0
2888	SEIDNVKKQCANLQNAIAEAEQR	sp|Q922U2|K2C5_MOUSE	yes	no	392	414	23	R	G	0	2628.293	4	4.24E-05	86.56	0.98	0.53	2
2889	SEIENAKKQASNLETAIADAEQR	sp|Q9R0H5|K2C71_MOUSE	yes	no	361	383	23	R	G	0	2515.251	3;4	5.18E-04	71.65	1.57	0.97	6
2890	SEILSAILVPLTVR	sp|Q8BGW1-2|FTO_MOUSE	yes	no	429	442	14	R	Q	0	1509.913	2	5.27E-02	61.41	NaN	NaN	0
2891	SELDMLDIR	sp|P14824|ANXA6_MOUSE	yes	yes	282	290	9	R	E	0	1090.533	2	1.51E-02	134.25	NaN	NaN	0
2892	SELKKAGGANYDAQSE	sp|Q9CQI6|COTL1_MOUSE	yes	no	127	142	16	R	-	0	1666.780	3	6.97E-05	94.53	1.22	1.19	5
2893	SEPDLYCDPR	sp|P97350|PKP1_MOUSE	yes	yes	156	165	10	R	G	0	1250.524	2	3.95E-02	53.57	4.56	2.56	1
2894	SEPELKLVAR	sp|P08030|APT_MOUSE	yes	yes	2	11	10	M	R	0	1140.650	2	1.82E-03	133.91	0.33	0.26	5
2895	SEPTQALELTEDDIKEDGIVPLR	sp|Q8CDN6|TXNL1_MOUSE	yes	yes	212	234	23	R	Y	0	2567.297	3	4.24E-05	86.56	1.29	1.08	5
2896	SEQKIWSPLVTEEGKR	sp|O70400|PDLI1_MOUSE	yes	yes	84	99	16	R	H	0	1885.990	4	8.67E-03	54.28	1.50	1.33	4
2897	SEVDMLKIR	sp|P07356|ANXA2_MOUSE	yes	yes	296	304	9	R	S	0	1089.585	2;3	6.99E-06	168.83	1.23	0.96	11
2898	SFDKDAMVAR	sp|Q93092|TALDO_MOUSE	yes	yes	112	121	10	L	A	0	1138.544	2	2.90E-02	81.63	2.90	2.75	1
2899	SFELFADKVPKTAENFR	sp|P17742|PPIA_MOUSE	yes	yes	21	37	17	V	A	0	1998.021	3	8.84E-05	88.39	0.98	0.84	6
2900	SFGGGLGSGFGGR	sp|Q61781|K1C14_MOUSE	no	no	72	84	13	S	F	0	1154.547	2	8.43E-03	82.07	NaN	NaN	0
2901	SFGGGTGSGFTSLLMER	sp|P68373|TBA1C_MOUSE	no	no	140	156	17	H	L	0	1702.799	2	1.77E-03	98.06	NaN	NaN	0
2902	SFITTDVNPYYDSFVR	sp|Q8BMJ2|SYLC_MOUSE	yes	yes	206	221	16	R	W	0	1922.905	2	5.17E-04	117.00	NaN	NaN	0
2903	SFLEFAEDVIQVPR	sp|P35922-9|FMR1_MOUSE	yes	no	277	290	14	R	N	0	1648.846	2	3.08E-03	95.26	NaN	NaN	0
2904	SFNLPYQDAR	sp|Q6P542|ABCF1_MOUSE	yes	yes	706	715	10	R	K	0	1209.578	2	3.37E-02	76.33	NaN	NaN	0
2905	SFPDFPIPGVLFR	sp|P08030|APT_MOUSE	yes	yes	15	27	13	R	D	0	1490.792	2	6.07E-03	89.19	NaN	NaN	0
2906	SFPVQDFLLSQLR	sp|Q8CG70|P3H3_MOUSE	yes	yes	304	316	13	R	R	0	1548.830	2	1.68E-02	73.93	NaN	NaN	0
2907	SFSAASAITPSVSR	sp|Q922U2|K2C5_MOUSE	yes	no	16	29	14	R	T	0	1379.705	2	3.01E-13	199.31	116.57	92.70	1
2908	SFSSCSAIMPR	sp|Q99M74|KRT82_MOUSE	yes	yes	16	26	11	R	M	0	1241.553	2	1.76E-02	84.69	NaN	NaN	0
2909	SFSVCSAGLGR	sp|Q4974|KRT35_MOUSE	yes	no	48	58	11	R	G	0	1139.539	2	4.94E-03	123.51	NaN	NaN	0
2910	SFVNDIFER	sp|Q9D2U9|H2B3A_MOUSE	yes	no	65	73	9	N	I	0	1125.546	2	2.22E-02	103.19	NaN	NaN	0
2911	SFYGTALFLCR	sp|P19096|FAS_MOUSE	yes	yes	1388	1398	11	R	R	0	1333.649	2	3.04E-02	52.39	0.33	0.31	1
2912	SGAQASSTPLSPTR	sp|P48678|LMNA_MOUSE	yes	no	12	25	14	R	I	0	1358.679	2	5.26E-05	175.01	NaN	NaN	0
2913	SGASLLSNMSR	sp|P97350|PKP1_MOUSE	yes	yes	594	604	11	R	H	0	1121.550	2	9.36E-05	144.10	0.07	0.04	1
2914	SGCCGYGPSCYR	sp|O08884|KRA62_MOUSE	yes	yes	142	153	12	R	R	0	1422.512	2	3.43E-04	158.06	NaN	NaN	0
2915	SGDLGDMEPLKGAPLMQKI	sp|P30999-2|CTND1_MOUSE	yes	no	893	911	19	R	-	0	1999.012	3	5.25E-05	84.65	1.48	0.98	2
2916	SGDPVNYYVDTAVR	sp|P62908|RS3_MOUSE	yes	yes	160	173	14	H	H	0	1554.731	2	7.86E-05	117.20	0.42	0.35	1
2917	SGEGEVSGLLR	sp|Q62318|TIF1B_MOUSE	yes	no	473	483	11	R	K	0	1102.562	2	9.00E-07	196.88	NaN	NaN	0
2918	SGETEDTFIADLVVGLCTGQIKTG/	sp|P17182|ENOA_MOUSE	yes	no	373	400	28	R	S	0	2994.443	3	7.33E-04	83.99	1.15	0.99	2
2919	SGEYSCIFLPEPVGR	sp|P18572-2|BASI_MOUSE	yes	no	82	96	15	R	S	0	1709.808	2	7.42E-04	107.69	NaN	NaN	0
2920	SGFSSVSVCR	sp|P50446|K2C6A_MOUSE	yes	no	29	38	10	R	S	0	1084.497	2	8.55E-03	128.81	NaN	NaN	0
2921	SGGIERPFVLSR	sp|Q8BHN3|GANAB_MOUSE	yes	no	591	602	12	R	A	1	1316.720	3	4.02E-03	109.44	NaN	NaN	0
2922	SGGKYVDSEGHLYTVPIR	sp|P49817|CAV1_MOUSE	yes	yes	2	19	18	M	E	0	1976.996	3	6.63E-08	125.73	1.30	0.94	9
2923	SGGLGYGYGGFGGLGCGCNSIR	sp|Q8C1I6|KR163_MOUSE	yes	yes	8	29	22	Y	R	0	2164.942	2	9.88E-10	179.19	NaN	NaN	0
2924	SGGLGYGYGSSFGGLGCGCNSIR	sp|Q925I0|KR192_MOUSE	yes	yes	8	30	23	Y	R	0	2281.984	2	2.43E-04	92.79	NaN	NaN	0
2925	SGGMSNELNNIISR	sp|Q91V92|ACLY_MOUSE	yes	yes	653	666	14	R	T	0	1490.715	2	1.86E-04	159.12	NaN	NaN	0
2926	SGIDILVGTPGR	sp|Q9JIK5|DDX21_MOUSE	yes	yes	379	390	12	R	I	0	1183.656	2	1.29E-02	81.71	NaN	NaN	0
2927	SGKKLEDGPKFLKSGDAAIVDMVI	sp|P10126|EF1A1_MOUSE	yes	yes	383	423	41	R	F	0	4422.206	6	6.84E-04	54.28	1.07	1.04	1
2928	SGKSPILVATAVAAR	sp|P16381|DDX3L_MOUSE	yes	no	488	502	15	R	G	0	1439.846	3	3.08E-04	80.39	1.66	0.96	2
2929	SGKYDLDFKSPDDPSR	sp|P17182|ENOA_MOUSE	yes	yes	254	269	16	R	Y	0	1825.848	3;4	8.74E-09	152.37	1.16	0.97	9
2930	SGLFVVGPESAGAHPGPACYR	sp|Q8K010|OPLA_MOUSE	yes	yes	364	384	21	R	K	0	2128.016	3	7.41E-02	43.70	NaN	NaN	0
2931	SGNYSSQSFGGFLR	sp|Q9QZU5|KR151_MOUSE	yes	yes	7	20	14	N	Q	0	1505.690	2	1.13E-03	107.46	NaN	NaN	0
2932	SGPFGQLFR	sp|Q922F4|TBB6_MOUSE	yes	yes	78	86	9	R	P	0	1007.519	2	4.33E-02	82.43	NaN	NaN	0
2933	SGQGAFGNMCR	sp|Q9D8E6|RL4_MOUSE	yes	yes	87	97	11	R	G	0	1183.486	2	1.64E-04	135.55	0.09	0.07	1
2934	SGQPGPVGPAGVR	sp|Q01149|CO1A2_MOUSE	yes	yes	1074	1086	13	R	G	0	1177.620	2	2.86E-03	98.90	NaN	NaN	0
2935	SGQQIVGPPR	sp|Q9CZ44|NSF1C_MOUSE	yes	no	102	111	10	R	K	0	1037.562	2	4.85E-02	75.42	12.60	11.76	1
2936	SGTDVDAANLR	sp|P70677|CASP3_MOUSE	yes	yes	65	75	11	R	E	0	1117.536	2	1.00E-03	150.04	NaN	NaN	0
2937	SGTVDPQELQKALTTMGFR	sp|Q6P069-2|SORCN_MOUSE	yes	no	102	120	19	R	L	0	2078.047	3	1.35E-02	48.29	0.98	0.84	4
2938	SGVEVLFNELEIPVEEHSFGR	sp|P46735-2|MYO1B_MOUSE	yes	no	662	682	21	R	S	0	2386.181	3	7.61E-03	67.23	NaN	NaN	0
2939	SGVVSTGLKVR	sp|P58252|EF2_MOUSE	yes	yes	418	428	11	F	I	0	1101.651	2	2.49E-03	88.02	1.08	1.02	3
2940	SGYLLPDTKAYGDR	sp|P08113|ENPL_MOUSE	yes	yes	725	738	14	R	I	0	1554.768	3	6.60E-04	80.75	1.32	0.98	8
2941	SHYSSYYGGLGYGYGSFGGPGCG(	sp|Q925H6|KR193_MOUSE	yes	yes	2	29	28	M	R	0	2979.234	3	1.73E-05	98.30	NaN	NaN	0
2942	SIESTLDDLFR	sp|A2ASQ1-3|AGRIN_MOUSE	yes	no	991	1001	11	R	N	0	1294.641	2	2.43E-02	75.82	NaN	NaN	0
2943	SIGTENTEENRR	sp|P05064|ALDOA_MOUSE	yes	yes	46	57	12	Q	F	1	1404.659	2	2.32E-03	129.89	NaN	NaN	0
2944	SIIATDHTYR	sp|Q04857|CO6A1_MOUSE	yes	yes	200	209	10	L	R	0	1175.594	2	1.23E-02	113.93	NaN	NaN	0
2945	SILCCLR	sp|Q9R0Q7|TEBP_MOUSE	yes	yes	72	78	7	R	K	0	920.457	2	6.50E-02	114.02	NaN	NaN	0
2946	SILKIDDVVNTR	sp|P80315|TCPD_MOUSE	yes	yes	528	539	12	R	-	0	1371.772	2	8.16E-02	51.73	1.04	0.90	2
2947	SILPITEFSDITR	sp|Q61029-2|LAP2B_MOUSE	yes	no	234	246	13	S	R	0	1490.798	2	7.55E-04	89.23	25.02	15.29	1
2948	SILPTAPR	sp|Q8BGD9|IF4B_MOUSE	yes	yes	71	78	8	R	A	0	853.502	2	3.82E-02	122.74	NaN	NaN	0
2949	SILYVSPHPDAFPSLR	sp|Q9Z1Q9|SYVC_MOUSE	yes	yes	2	17	16	M	A	0	1797.941	2	2.94E-05	162.29	NaN	NaN	0
2950	SIPMTVDFIR	sp|P00493|HPRT_MOUSE	yes	yes	92	101	10	R	L	0	1177.617	2	1.14E-02	117.70	NaN	NaN	0
2951	SIQEELQHLR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1320	1329	10	R	Q	0	1251.657	3	1.27E-02	112.36	NaN	NaN	0
2952	SIQFVDWCPTGFKVGINYQPPTV\	sp|P05213|TBA1B_MOUSE	no	no	340	373	34	R	A	0	3772.940	4	1.58E-06	76.97	0.98	0.71	2
2953	SIQLDGLVWGASKLVPVGYGIR	sp|P57776-2|EF1D_MOUSE	yes	no	196	217	22	R	K	0	2327.300	2	4.49E-06	127.58	1.39	1.08	1
2954	SISFNVASSSGR	sp|Q6NXH9|K2C73_MOUSE	yes	no	55	66	12	R	T	0	1210.594	2	1.83E-03	136.27	NaN	NaN	0
2955	SITGQGADKPPVGVFIER	sp|P09803|CADH1_MOUSE	yes	yes	193	211	19	Y	E	0	1983.079	3	5.36E-05	84.25	0.99	0.82	5
2956	SITLNMASGSGKNGGFGFGR	sp|Q9R0H5|K2C71_MOUSE	yes	no	55	74	20	R	N	0	1956.948	3	1.04E-11	130.27	1.53	1.01	10
2957	SIVGRPR	sp|P63260|ACTG_MOUSE	no	no	33	39	7	P	H	1	783.472	2	7.07E-02	102.71	NaN	NaN	0
2958	SIVVIDPDTGR	sp|Q9R269|PEPL_MOUSE	yes	yes	1656	1666	11	R	E	0	1170.625	2	3.25E-02	73.44	NaN	NaN	0
2959	SKAEAETFYQSKYEELQITAGKHGI	sp|P04104|K2C1_MOUSE	yes	yes	373	400	28	R	N	0	3171.547	5	3.47E-06	115.45	1.78	1.07	5
2960	SKAEELGLPILGVLR	sp|Q921H8|THIKA_MOUSE	yes	no	291	305	15	R	S	0	1593.945	3	8.24E-03	58.89	1.39	1.10	3
2961	SKEQAELEAAR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1864	1874	11	R	Q	0	1230.620	3	2.08E-03	92.87	1.48	1.25	2
2962	SKLILFPR	sp|P47963|RL13_MOUSE	yes	yes	122	129	8	R	K	0	972.612	2;3	8.36E-03	105.52	0.96	0.85	6
2963	SKQQPTQFINPETPGYVGFANLPI	sp|P42208|SEPT2_MOUSE	yes	yes	2	29	28	M	K	0	3166.595	3	1.38E-02	46.86	1.05	0.83	7
2964	SKSESPKEPEQLR	sp|P49312|ROA1_MOUSE	yes	no	2	14	13	M	K	0	1513.774	3	9.64E-04	83.09	1.13	1.05	9
2965	SKSFQQSSLGR	sp|Q8K310|MATR3_MOUSE	yes	yes	2	12	11	M	D	0	1223.626	2	3.96E-04	124.51	1.42	1.02	9
2966	SLAAEEEAAR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1896	1905	10	R	Q	0	1045.504	2	1.27E-02	112.36	NaN	NaN	0
2967	SLADFEKALTDYR	sp|Q8BG32|PSD11_MOUSE	yes	yes	298	310	13	R	A	0	1527.757	3	3.07E-03	73.93	1.14	1.05	1
2968	SLAPQIKVIAPWR	sp|P16460|ASSY_MOUSE	yes	yes	134	146	13	Y	M	0	1477.877	3	7.70E-03	66.27	1.33	1.03	2
2969	SLCNPSPCGPR	sp|Q9Z2T6|KRT85_MOUSE	yes	yes	55	65	11	R	M	0	1243.544	2	5.52E-03	122.70	NaN	NaN	0
2970	SLCNVGFGR	sp|Q99M74|KRT82_MOUSE	yes	no	56	64	9	R	P	0	1008.481	2	1.97E-02	117.76	NaN	NaN	0
2971	SLDIQCEQLSDAR	sp|Q91VI7|RINI_MOUSE	yes	yes	2	14	13	M	W	0	1533.709	2	7.23E-02	50.90	NaN	NaN	0
2972	SLDLDGIISEVKAQYDSICQR	sp|P04104|K2C1_MOUSE	yes	yes	352	372	21	R	S	0	2409.185	2;3	9.62E-22	200.74	1.97	1.15	9
2973	SLDLDSIIAEVKAQYEDIANR	sp|Q8BGZ7|K2C75_MOUSE	no	no	314	334	21	R	S	0	2362.202	2;3	4.67E-22	204.31	2.07	1.29	5
2974	SLEELLLDANQLR	sp|Q80U72|SCRIB_MOUSE	yes	no	37	49	13	R	E	0	1512.815	2	1.46E-03	119.39	NaN	NaN	0
2975	SLEPFFENYLSTLR	sp|Q8VED5|K2C79_MOUSE	yes	no	186	199	14	R	R	0	1714.857	2;3	4.07E-04	148.52	NaN	NaN	0
2976	SLEQNVQLPAALLSR	sp|Q61881|MCM7_MOUSE	yes	yes	500	514	15	R	F	0	1637.910	2	2.62E-03	92.77	NaN	NaN	0
2977	SLESCLLDLR	sp|Q148V8|FA83H_MOUSE	yes	yes	778	787	10	R	D	0	1204.612	2	1.37E-02	108.70	NaN	NaN	0
2978	SLETENAGLR	sp|P48678|LMNA_MOUSE	yes	no	51	60	10	R	L	0	1088.546	2	2.13E-03	152.97	NaN	NaN	0
2979	SLETVYLER	sp|Q3UM45|PP1R7_MOUSE	yes	yes	323	331	9	R	N	0	1108.576	2	7.25E-03	149.72	NaN	NaN	0
2980	SLFSSAENEPPVPLVGNWRPPQP	sp|P16015|CAH3_MOUSE	yes	yes	227	253	27	R	V	1	2957.551	3;4	3.98E-16	178.35	0.55	0.48	8
2981	SLFSSIGEVESAKLIR	sp|P70372|ELAV1_MOUSE	yes	yes	38	53	16	R	D	0	1734.952	3	4.55E-03	65.37	1.38	0.98	3
2982	SLGGGTGSGMGTLLISKIR	sp|P99024|TBB5_MOUSE	no	no	138	156	19	H	E	0	1803.988	2;3	4.97E-16	173.87	1.22	1.11	21

2983	SLGGVSEASR	sp|P35175|CYT1_MOUSE	yes	yes	2	11	10	M	A	0	961.483	2	1.37E-02	108.40	NaN	NaN	0
2984	SLGKFGIICMEDLIHEIYTVGKR	sp|P14148|RL7_MOUSE	yes	yes	200	222	23	R	F	0	2678.392	4	1.15E-03	63.98	2.13	1.24	1
2985	SLGKGSAPPGPVPEGQIR	sp|O09131|GSTO1_MOUSE	yes	yes	8	25	18	R	V	0	1745.942	3	2.68E-07	112.16	1.15	1.02	4
2986	SLGLQLPDGQR	sp|Q5SUR0|PUR4_MOUSE	yes	yes	407	417	11	R	R	0	1182.636	2	5.11E-03	122.70	NaN	NaN	0
2987	SLGNAGNEIGR	sp|Q6P253-4|DMKN_MOUSE	yes	no	97	107	11	R	Q	0	1086.542	2	1.71E-03	144.70	NaN	NaN	0
2988	SLGSALRPSTSR	sp|P20152|VIME_MOUSE	yes	yes	39	50	12	Y	S	1	1230.668	2	8.32E-03	93.35	NaN	NaN	0
2989	SLGVAAEGLPDQYADGEAAR	sp|Q9QXF8|GNMT_MOUSE	yes	yes	10	29	20	R	V	0	1988.944	2	1.49E-06	146.78	NaN	NaN	0
2990	SLGYAYVNFQQPADAER	sp|P29341|PABP1_MOUSE	yes	yes	51	67	17	R	A	0	1927.906	2	1.65E-05	162.81	NaN	NaN	0
2991	SLHDALCVIR	sp|P80316|TCPE_MOUSE	yes	yes	401	410	10	R	N	0	1182.618	3	1.59E-02	101.66	NaN	NaN	0
2992	SLHDALCVLAQTVKDPR	sp|P80314|TCPB_MOUSE	yes	yes	389	405	17	R	T	0	1922.004	3	7.56E-05	90.56	1.25	0.95	2
2993	SLIGSKTQIPTQR	sp|Q9R1P4|PSA1_MOUSE	yes	yes	110	122	13	V	Y	0	1427.810	2	5.03E-04	96.67	1.11	0.95	4
2994	SLILLDLSYNHLR	sp|P50608|FMOD_MOUSE	yes	yes	224	236	13	R	R	0	1555.872	3	5.16E-03	91.96	NaN	NaN	0
2995	SLIQKAKLAEQAER	sp|O70456|1433S_MOUSE	yes	yes	5	18	14	A	Y	0	1583.900	3	3.94E-03	70.89	1.18	1.04	4
2996	SLKDLEGKWR	sp|Q05816|FABP5_MOUSE	yes	yes	3	12	10	A	L	0	1230.672	2	5.29E-03	84.48	0.95	0.85	4
2997	SLKFYSL	sp|Q99KP6-3|PRP19_MOUSE	yes	no	413	419	7	R	-	0	856.469	2	4.61E-02	71.50	1.39	0.89	1
2998	SLLDLENGR	sp|Q9R269|PEPL_MOUSE	yes	yes	808	816	9	R	N	0	1015.530	2	3.43E-02	91.09	NaN	NaN	0
2999	SLLDSDHHPSEIAESHR	sp|P35492|HUTH_MOUSE	yes	yes	370	386	17	R	F	0	1928.898	4	1.81E-02	65.11	NaN	NaN	0
3000	SLLEDIR	sp|Q9JJ59-2|ABCB9_MOUSE	yes	no	33	39	7	R	H	0	844.465	2	6.17E-02	120.62	NaN	NaN	0
3001	SLLEGEGSSSGGGGGR	sp|P02535-3|K1C10_MOUSE	yes	no	440	455	16	R	P	0	1405.643	2	2.62E-04	136.81	NaN	NaN	0
3002	SLLESEDCNLPCNPCATTNASGSC	sp|Q9D646|KRT34_MOUSE	yes	no	358	390	33	R	C	0	3645.468	3	6.25E-24	201.80	1.88	1.17	4
3003	SLLESLDGR	sp|Q6IFX4|K1C39_MOUSE	yes	no	393	401	9	R	L	0	988.519	2	4.42E-02	81.53	NaN	NaN	0
3004	SLLFEGVIGDR	sp|Q9Z184|PADI3_MOUSE	yes	yes	511	521	11	R	R	0	1204.645	2	5.73E-02	66.27	NaN	NaN	0
3005	SLMNLGGGR	sp|P04104|K2C1_MOUSE	yes	yes	67	75	9	K	S	0	903.460	2	4.00E-02	106.68	NaN	NaN	0
3006	SLMPYFLLTQAVR	sp|P14685|PSMD3_MOUSE	yes	yes	352	364	13	R	T	0	1537.833	2	4.05E-02	64.10	NaN	NaN	0
3007	SLNESKIEIER	sp|E9Q557|DESP_MOUSE	yes	yes	1707	1717	11	R	L	0	1316.694	3	1.64E-02	65.23	1.72	1.02	5
3008	SLQQLAEER	sp|P16546-2|SPTN1_MOUSE	yes	no	1197	1205	9	R	S	0	1072.551	2	2.89E-02	96.34	NaN	NaN	0
3009	SLQSVAEER	sp|Q9CZM2|RL15_MOUSE	yes	yes	97	105	9	R	A	0	1017.509	2	1.62E-02	132.01	NaN	NaN	0
3010	SLSGAQIDDNIPR	sp|O08553|DPYL2_MOUSE	yes	yes	540	552	13	F	R	0	1384.695	2	9.66E-04	139.78	NaN	NaN	0
3011	SLSLSLADSGHLPDVR	sp|Q9QY23|PKP3_MOUSE	yes	no	283	298	16	R	G	0	1665.869	3	1.95E-03	96.21	NaN	NaN	0
3012	SLTMVEDNEDDDEDGEELLHHHF	sp|P48678|LMNA_MOUSE	yes	no	546	568	23	R	G	0	2734.141	4	9.15E-10	154.07	NaN	NaN	0
3013	SLYNLGGKNISVSMACGASSGR	sp|Q8VED5|K2C79_MOUSE	yes	no	61	82	22	R	A	0	2228.068	3	1.97E-16	162.11	1.59	1.03	2
3014	SLYNLGGTR	sp|Q8BGZ7|K2C75_MOUSE	yes	no	61	69	9	R	R	0	979.509	2	1.78E-02	128.58	NaN	NaN	0
3015	SLYSLGGGR	sp|Q9R0H5|K2C71_MOUSE	yes	no	46	54	9	R	S	0	908.472	2	4.12E-03	157.68	NaN	NaN	0
3016	SLYSSSPGGAYVTR	sp|P20152|VIME_MOUSE	yes	yes	51	64	14	R	S	0	1443.699	2	6.56E-06	143.56	0.00	0.00	1
3017	SLYYTGEKGQR	sp|P09405|NUCL_MOUSE	yes	yes	462	472	11	V	Q	0	1300.641	2	1.68E-04	134.98	0.97	0.93	1
3018	SMLEVNYPMENGIVR	sp|P61161|ARP2_MOUSE	yes	yes	66	80	15	R	N	0	1750.838	2	5.50E-05	164.88	NaN	NaN	0
3019	SMSFQGIR	sp|E9Q557|DESP_MOUSE	yes	yes	2219	2226	8	R	Q	0	924.449	2	3.38E-02	133.60	NaN	NaN	0
3020	SMVEDITGLR	sp|E9Q557|DESP_MOUSE	yes	yes	2804	2813	10	R	L	0	1119.559	2	8.55E-03	128.81	NaN	NaN	0
3021	SNASDALDKIR	sp|P11499|HS90B_MOUSE	no	no	45	55	11	I	Y	0	1188.610	2	2.98E-07	173.19	1.19	1.11	3
3022	SNFKTCDESSFCKR	sp|Q8BHN3|GANAB_MOUSE	yes	no	36	49	14	R	Q	0	1764.756	4	1.18E-02	55.72	1.48	1.21	1
3023	SNLEPLFDNYITNLR	sp|Q99M73|KRT84_MOUSE	yes	yes	216	230	15	R	R	0	1807.911	2	7.61E-04	105.28	NaN	NaN	0
3024	SNLPDNLKKLFR	sp|Q9JHU4|DYHC1_MOUSE	yes	yes	2024	2035	12	R	S	0	1443.820	3	1.90E-02	56.21	1.40	0.85	2
3025	SNLVDNTNQVEVLQR	sp|Q61655|DD19A_MOUSE	yes	yes	67	81	15	R	D	0	1727.880	2	3.49E-04	141.00	NaN	NaN	0
3026	SNQDQILNNLSKR	sp|Q61398|PCOC1_MOUSE	yes	yes	446	458	13	R	K	0	1528.796	3	1.10E-03	79.09	1.79	1.37	6
3027	SNSMLNNVFNLCR	sp|P97350|PKP1_MOUSE	yes	yes	661	673	13	F	N	0	1567.724	2	1.54E-10	217.09	NaN	NaN	0
3028	SNSSDALDKIR	sp|P07901|HS90A_MOUSE	yes	yes	50	60	11	I	Y	0	1204.605	2	8.21E-04	113.24	0.83	0.78	2
3029	SNTGGQAFPQCVFDHWQILPGDI	sp|P58252|EF2_MOUSE	yes	yes	802	839	38	R	K	1	4243.977	4	8.83E-02	34.68	NaN	NaN	0
3030	SNTSFSCISR	sp|Q3TTY5|K22E_MOUSE	yes	no	38	47	10	R	H	0	1157.514	2	6.14E-03	137.89	NaN	NaN	0
3031	SNWPTYPQLYVR	sp|Q9CQM9|GLRX3_MOUSE	yes	yes	299	310	12	F	G	0	1522.757	2	3.11E-02	71.09	NaN	NaN	0
3032	SPAQILLR	sp|Q9JII6|AK1A1_MOUSE	yes	yes	244	251	8	R	W	0	896.544	2	6.70E-03	175.12	NaN	NaN	0
3033	SPDDELLYLPVR	sp|O88898-6|P63_MOUSE	yes	no	297	308	12	R	G	0	1415.730	2	1.38E-03	142.08	NaN	NaN	0
3034	SPDFTNENPLETR	sp|Q8VDN2|AT1A1_MOUSE	yes	yes	228	240	13	R	N	0	1518.695	2	9.82E-11	223.03	NaN	NaN	0
3035	SPFLQKQLTQPETSYGR	sp|Q62418-3|DBNL_MOUSE	yes	no	287	303	17	R	E	0	1979.011	3	2.93E-08	137.45	1.11	0.95	4
3036	SPIAEAVFR	sp|Q9D358-2|PPAC_MOUSE	yes	no	20	28	9	R	K	0	988.534	2	7.80E-08	218.55	NaN	NaN	0
3037	SPKLFYADHPFIFLVR	sp|P19324|SERPH_MOUSE	yes	yes	377	392	16	R	D	0	1949.056	3;4	7.13E-08	130.27	1.69	1.03	3
3038	SPNDLLALFR	sp|Q3UQ28|PXDN_MOUSE	yes	yes	650	659	10	R	Y	0	1144.624	2	1.24E-02	113.69	NaN	NaN	0
3039	SPNQNVQQAAAGALR	sp|P97350|PKP1_MOUSE	yes	yes	299	313	15	R	N	0	1523.781	2	4.17E-12	229.97	NaN	NaN	0
3040	SPPPGMGLNQNR	sp|Q8VIJ6|SFPQ_MOUSE	yes	yes	33	44	12	R	G	0	1266.614	2	8.32E-03	93.35	NaN	NaN	0
3041	SPPSVKQNSLDEDLIR	sp|Q02053|UBA1_MOUSE	yes	yes	369	384	16	R	K	0	1796.927	3	2.99E-11	167.69	1.16	1.09	6
3042	SPQENLVPCDVLLLR	sp|Q9EPE9|AT131_MOUSE	yes	yes	325	339	15	R	G	0	1751.924	2	1.74E-02	69.26	NaN	NaN	0
3043	SPSGGAAGPLLTPSQSLDGSR	sp|Q6WVG3|KCD12_MOUSE	yes	yes	187	207	21	R	R	0	1953.976	2	1.29E-03	92.47	NaN	NaN	0
3044	SPSQEPSAPGKAEAVGEQAR	sp|Q8JZQ9|EIF3B_MOUSE	yes	yes	88	107	20	R	G	0	1994.966	3	4.12E-08	105.79	1.19	0.99	7
3045	SPSWEPFR	sp|P14602|HSPB1_MOUSE	yes	no	13	20	8	R	D	0	1004.472	2	1.46E-03	190.93	NaN	NaN	0
3046	SPVHPESSEGEEHSVVPQR	sp|Q2VIS4|FILA2_MOUSE	yes	no	1198	1216	19	R	H	0	2085.972	3;4	1.24E-15	209.70	0.17	0.17	1
3047	SPWSNKYDPPLEDGAMPSAR	sp|P47757-2|CAPZB_MOUSE	yes	no	73	92	20	R	L	0	2217.016	3	1.48E-16	178.32	1.16	1.00	5
3048	SPYTVTVGQACNPAACR	sp|Q8BTM8|FLNA_MOUSE	yes	yes	468	484	17	R	A	0	1850.840	2	5.92E-06	174.62	NaN	NaN	0
3049	SQENLKIKGGLSEAR	sp|P35173|CYT3_MOUSE	yes	yes	2	16	15	M	P	0	1628.885	3	1.10E-02	52.53	1.12	0.97	5
3050	SQERPTFYR	sp|P47811-2|MK14_MOUSE	yes	no	2	10	9	M	Q	1	1182.578	2	2.17E-02	105.98	NaN	NaN	0
3051	SQETKIPISLVLR	sp|Q6P9R2|OXSR1_MOUSE	yes	yes	427	439	13	R	L	0	1482.877	3	2.00E-05	135.81	1.23	1.17	1
3052	SQFIGYPITLFVEKER	sp|P07901|HS90A_MOUSE	yes	yes	211	226	16	H	D	0	1926.025	3	4.42E-02	41.09	1.35	1.21	3
3053	SQFIGYPITLYLEKER	sp|P11499|HS90B_MOUSE	yes	yes	206	221	16	H	E	0	1956.036	2;3	3.14E-03	69.19	1.27	1.12	3
3054	SQGCGSNFYRPGYFSSKSIQSSYYC	sp|Q9QZU5|KR151_MOUSE	yes	yes	114	150	37	R	-	1	4157.759	3	3.49E-06	112.05	1.46	0.98	3
3055	SQGVFQCGPASVNAIKAGDVDR	sp|Q08189|TGM3_MOUSE	yes	yes	361	382	22	R	N	0	2275.102	3	1.84E-08	112.58	1.08	0.86	7
3056	SQHVQVEEGSEPDAFWEALGGK	sp|P13020-2|GELS_MOUSE	yes	no	576	601	26	R	T	0	2890.352	4	7.52E-03	48.77	1.22	1.10	5
3057	SQIQSQISALEEQLQQIR	sp|P02535-3|K1C10_MOUSE	yes	no	394	411	18	L	A	0	2098.102	2	3.48E-06	168.64	NaN	NaN	0
3058	SQLEAVFLR	sp|O35405|PLD3_MOUSE	yes	yes	456	464	9	R	D	0	1061.587	2	3.35E-02	91.87	NaN	NaN	0
3059	SQLLTLMDGLKQR	sp|Q01853|TERA_MOUSE	yes	yes	326	338	13	V	A	0	1501.829	2	4.91E-03	119.25	1.07	0.91	2
3060	SQLNQYQKDVSKR	sp|Q8K4L4|POF1B_MOUSE	yes	yes	478	490	13	R	E	0	1592.827	4	7.43E-03	66.71	0.98	0.89	5
3061	SQNIITDSSSLNAEAIR	sp|Q62261|SPTB2_MOUSE	yes	no	1548	1564	17	R	Q	0	1817.912	2	1.77E-03	98.06	NaN	NaN	0
3062	SQVEEELFSVR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	2127	2137	11	R	V	0	1321.651	2	2.76E-03	136.70	NaN	NaN	0
3063	SQVISPPLAQAIR	sp|Q61033|LAP2A_MOUSE	yes	yes	364	376	13	R	D	0	1378.793	2	7.28E-03	85.54	NaN	NaN	0
3064	SRLECEINTYR	sp|Q8K0Y2|KT33A_MOUSE	yes	yes	347	357	11	R	G	1	1439.683	2;3	3.19E-04	156.81	0.02	0.01	1
3065	SRPQGPFQDSSR	sp|Q2VIS4|FILA2_MOUSE	yes	yes	1246	1257	12	R	Q	1	1360.648	3	1.71E-02	75.91	NaN	NaN	0
3066	SSDFAKIIGNTENLVR	sp|Q99K85|SERC_MOUSE	yes	yes	46	61	16	R	E	0	1762.921	3	1.20E-22	218.63	0.96	0.90	3
3067	SSDSQVHSGVQVEGR	sp|P11088|FILA_MOUSE	yes	yes	22	36	15	Q	R	0	1570.734	3	1.48E-07	195.60	NaN	NaN	0
3068	SSENPNEVFR	sp|P56399|UBP5_MOUSE	yes	yes	453	462	10	R	F	0	1177.536	2	2.07E-02	94.36	NaN	NaN	0
3069	SSFFVNGLTLGGQKCSVIR	sp|P62962|PROF1_MOUSE	yes	no	57	75	19	R	D	0	2069.073	2;3	2.46E-21	200.99	1.01	0.92	9
3070	SSGALLPKPQMR	sp|Q9CPQ1|COX6C_MOUSE	yes	yes	2	13	12	M	G	0	1283.702	2	2.76E-04	121.02	2.12	1.31	3
3071	SSGGFSGGSFSR	sp|P02535-3|K1C10_MOUSE	no	no	40	51	12	Y	G	0	1131.495	2	2.78E-04	162.49	NaN	NaN	0
3072	SSGLGQYGSPSGQTSSSTR	sp|Q8VHD8|HORN_MOUSE	yes	no	545	563	19	R	Q	0	1842.834	2	1.17E-15	211.16	NaN	NaN	0
3073	SSGLTAVWVAR	sp|Q8CIE6|COPA_MOUSE	yes	yes	413	423	11	R	N	0	1145.619	2	4.36E-01	47.30	NaN	NaN	0
3074	SSGPYGGGGQYFAKPR	sp|P49312|ROA1_MOUSE	yes	yes	285	300	16	R	N	0	1627.774	3	2.71E-05	99.99	1.36	0.91	8
3075	SSGSGYGGFGYGYR	sp|Q925H7|KR194_MOUSE	yes	yes	57	70	14	F	R	0	1413.595	2	9.37E-04	130.10	NaN	NaN	0
3076	SSGSPYGGGYGSGGGSGGYGSR	sp|Q8BG05-2|ROA3_MOUSE	no	no	334	355	22	R	R	0	1909.783	2	3.18E-12	196.40	NaN	NaN	0
3077	SSIEQKTER	sp|Q9CQV8-2|1433B_MOUSE	yes	no	63	71	9	I	N	0	1076.546	2	2.27E-04	148.32	1.11	0.95	4
3078	SSILPFTPPVVKR	sp|Q62432-2|SMAD2_MOUSE	yes	no	2	14	13	M	L	0	1439.850	2	4.44E-02	44.43	1.25	0.95	5
3079	SSITPGTVLIILTGR	sp|P47911|RL6_MOUSE	yes	yes	150	164	15	R	H	0	1526.903	2;3	5.05E-04	132.65	NaN	NaN	0
3080	SSKELLLQPVTISR	sp|P59999|ARPC4_MOUSE	yes	yes	42	55	14	R	N	0	1569.909	3	6.40E-02	38.38	1.26	1.16	3
3081	SSLEKSSPTPR	sp|P57776-2|EF1D_MOUSE	yes	no	89	99	11	L	A	0	1187.615	2	1.97E-02	80.25	1.31	1.05	1
3082	SSLQTAISDAEQR	sp|Q8BGZ7|K2C75_MOUSE	yes	no	390	402	13	C	G	0	1404.685	2	1.01E-05	145.52	0.23	0.14	1
3083	SSLSSAQADFNQLAELDR	sp|P16546-2|SPTN1_MOUSE	yes	no	2118	2135	18	R	Q	0	1950.928	2	3.95E-09	200.48	NaN	NaN	0
3084	SSNECFKCGR	sp|P53996-2|CNBP_MOUSE	yes	no	2	11	10	M	S	0	1243.507	2	2.17E-13	218.60	0.99	0.84	6
3085	SSPVIIDASTAIDAPSNLR	sp|P11276|FINC_MOUSE	yes	yes	1982	2000	19	R	F	0	1926.006	2	5.91E-06	131.67	NaN	NaN	0

3086	SSPYPTDVAR	sp|Q60597-2|ODO1_MOUSE	yes	no	447	456	10	R	V	0	1091.525	2	1.18E-01	56.04	NaN	NaN	0
3087	SSQPLKLLDASWYLPKLGR	sp|Q99J99|THTM_MOUSE	yes	yes	25	43	19	R	D	0	2171.210	4	6.19E-03	78.08	1.23	1.18	1
3088	SSSASAANGNDSKKFKGDNR	sp|P17225|PTBP1_MOUSE	yes	yes	32	51	20	M	S	0	2039.962	4	3.34E-03	58.69	1.60	1.10	1
3089	SSSSFGGGLGSGFGGR	sp|Q61781|K1C14_MOUSE	no	no	69	84	16	F	F	0	1415.643	2	2.75E-04	135.72	NaN	NaN	0
3090	SSTLEVQTLSVAPTALENLHKER	sp|Q9EST1|GSDMA_MOUSE	yes	yes	110	132	23	R	K	0	2522.334	4	1.08E-05	114.46	1.64	1.55	1
3091	SSTPLPTVSSSAENTR	sp|Q61029-2|LAP2B_MOUSE	no	no	157	172	16	R	Q	0	1632.796	2	1.03E-03	101.05	NaN	NaN	0
3092	SSVAVLTQESFAEHR	sp|Q8VDJ3|VIGLN_MOUSE	yes	yes	2	16	15	M	S	0	1659.822	2	7.63E-04	104.95	NaN	NaN	0
3093	STGEKGFGYKGSSFHR	sp|P17742|PPIA_MOUSE	yes	yes	40	55	16	L	I	0	1743.833	3;4	1.61E-02	49.19	0.94	0.90	7
3094	STGKGIVEFASKPAAR	sp|Q8VIJ6|SFPQ_MOUSE	yes	yes	402	417	16	R	K	0	1617.884	4	1.63E-04	82.59	1.60	1.13	2
3095	STGTFVVSQPLNYR	sp|Q9JLJ2|AL9A1_MOUSE	yes	yes	2	15	14	M	G	0	1567.800	2	1.82E-03	100.22	NaN	NaN	0
3096	STKTGTAYTFFTPNNIKQVSDLISV	sp|Q61656|DDX5_MOUSE	yes	yes	435	461	27	R	E	0	3000.592	4	9.91E-04	74.29	NaN	NaN	0
3097	STLDLMADVVYCPR	sp|Q9JI90|RNF14_MOUSE	yes	yes	299	312	14	Q	P	0	1638.775	2	6.15E-02	39.01	0.94	0.89	1
3098	STLNEIYFGKTKDIVNGLR	sp|P47757-2|CAPZB_MOUSE	yes	no	226	244	19	R	S	0	2167.164	4	2.30E-04	76.38	0.87	0.85	1
3099	STPAITLENPDIKYPLR	sp|Q9DCN2-2|NB5R3_MOUSE	yes	no	7	23	17	R	L	0	1927.042	3	1.63E-03	72.43	2.06	1.28	1
3100	STPEYFAER	sp|P14824|ANXA6_MOUSE	yes	yes	251	259	9	R	L	0	1098.498	2	2.34E-02	101.65	NaN	NaN	0
3101	STSCISGVCSVR	sp|Q9R0H5|K2C71_MOUSE	yes	no	481	492	12	N	G	0	1311.591	2	3.71E-02	69.03	NaN	NaN	0
3102	STVAQLVKR	sp|Q03265|ATPA_MOUSE	yes	yes	254	262	9	R	L	0	1000.603	2	8.57E-05	153.05	1.62	1.11	3
3103	STVDPPAPSAGR	sp|P80313|TCPH_MOUSE	yes	yes	525	536	12	R	G	0	1153.573	2	4.39E-03	105.03	NaN	NaN	0
3104	SVAAFTADPLSLLR	sp|Q4LDD4-3|ARAP1_MOUSE	yes	no	1178	1191	14	R	H	0	1459.804	2	5.70E-04	132.97	0.40	0.32	1
3105	SVAYKNVVGAR	sp|Q9CQV8-2|1433B_MOUSE	no	no	45	55	11	L	R	0	1162.646	2	8.82E-04	111.63	1.29	1.02	4
3106	SVAYKNVVGGQR	sp|O70456|1433S_MOUSE	yes	yes	45	56	12	L	A	0	1276.689	2	4.41E-04	113.24	0.89	0.85	2
3107	SVCHLQKVFER	sp|P07356|ANXA2_MOUSE	yes	yes	221	231	11	R	Y	0	1401.719	3;4	2.68E-03	85.81	1.15	0.97	9
3108	SVCTEAGMFAIR	sp|P46471|PRS7_MOUSE	yes	yes	387	398	12	R	A	0	1340.622	2	4.48E-03	103.91	NaN	NaN	0
3109	SVDEIIR	sp|P35700|PRDX1_MOUSE	yes	yes	152	158	7	R	L	0	830.450	2	5.04E-02	140.98	NaN	NaN	0
3110	SVEADINGLRR	sp|P02535-3|K1C10_MOUSE	no	no	236	246	11	Q	V	1	1228.652	2	4.88E-03	123.79	NaN	NaN	0
3111	SVGGSGGGSFGDNLVTR	sp|P48678|LMNA_MOUSE	yes	yes	629	645	17	R	S	0	1565.743	2	1.32E-05	166.48	NaN	NaN	0
3112	SVLADFQQR	sp|Q9CYD3|CRTAP_MOUSE	yes	yes	136	144	9	R	E	0	1062.546	2	2.16E-02	106.42	NaN	NaN	0
3113	SVLDAAQIVGLNCLR	sp|Q61699-2|HS105_MOUSE	yes	no	155	169	15	R	L	0	1627.872	2	7.09E-04	111.83	NaN	NaN	0
3114	SVLGEADQKGSLVAPDR	sp|Q8BGQ7|SYAC_MOUSE	yes	yes	617	633	17	R	L	0	1740.901	3	7.02E-03	55.44	1.28	1.10	4
3115	SVLISLKQAPLVH	sp|O08585|CLCA_MOUSE	yes	no	223	235	13	R	-	0	1403.850	3	7.95E-03	65.84	0.97	0.92	3
3116	SVLLEIQKQLLDYR	sp|Q99K85|SERC_MOUSE	yes	yes	20	33	14	H	G	0	1716.977	2;3	4.77E-07	177.88	0.97	0.92	2
3117	SVMDATQIAGLNCLR	sp|Q61316|HSP74_MOUSE	yes	yes	155	169	15	R	L	0	1647.807	2	6.98E-05	160.48	NaN	NaN	0
3118	SVPADIFQMQATTR	sp|Q9WVH9|FBLN5_MOUSE	yes	yes	360	373	14	R	Y	0	1563.772	2	2.31E-02	68.97	NaN	NaN	0
3119	SVPMSTVFYPSDGVATEKAVELAA	sp|P40142|TKT_MOUSE	yes	yes	439	471	33	R	T	0	3557.790	4	2.45E-02	43.90	1.14	1.00	2
3120	SVSLYYTGEKGQR	sp|P09405|NUCL_MOUSE	yes	yes	460	472	13	R	Q	0	1486.742	2;3	1.65E-08	172.09	1.06	0.84	13
3121	SVSSPLLSTDAVSFLR	sp|Q99K30|ES8L2_MOUSE	yes	yes	369	384	16	R	G	0	1677.894	2	4.34E-03	83.54	NaN	NaN	0
3122	SWDSEEILEGYKR	sp|Q8BP47|SYNC_MOUSE	yes	yes	490	502	13	R	E	0	1610.758	3	1.08E-02	61.11	1.02	0.84	3
3123	SWSLVTFR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	811	818	8	R	T	0	994.524	2	3.76E-02	124.98	NaN	NaN	0
3124	SYARPSTGSLR	sp|Q8VCW2|K1C25_MOUSE	yes	yes	12	22	11	R	G	1	1193.615	3	5.16E-03	122.46	NaN	NaN	0
3125	SYDVPPPPMEPDHPFYSNISKDR	sp|Q9DBJ1|PGAM1_MOUSE	yes	yes	118	140	23	R	R	0	2687.233	4	1.54E-02	45.89	1.17	1.08	3
3126	SYELQESNVR	sp|Q8C1B7-3|SEP11_MOUSE	yes	no	84	93	10	R	L	0	1223.578	2	1.46E-03	112.83	2.54	1.58	1
3127	SYLDKVR	sp|Q9QWL7|K1C17_MOUSE	no	no	97	103	7	A	A	0	879.481	2	8.82E-03	129.47	1.57	1.00	5
3128	SYMDKVR	sp|P02535-3|K1C10_MOUSE	yes	no	148	154	7	A	A	0	897.438	2	7.44E-03	134.81	1.84	1.13	4
3129	SYMEKVR	sp|Q61897|KT33B_MOUSE	no	no	69	75	7	A	Q	0	911.453	2	7.19E-03	135.77	1.98	1.22	2
3130	SYQDPSNAQFLESIR	sp|Q9CZ44|NSF1C_MOUSE	yes	no	200	214	15	R	R	0	1753.827	2	2.35E-04	147.12	NaN	NaN	0
3131	SYQGKKNIPR	sp|O08553|DPYL2_MOUSE	yes	no	2	11	10	M	I	0	1189.657	3	4.09E-02	52.58	1.18	1.04	4
3132	SYTCNSGNYSSQSFGGFLR	sp|Q9QZU5|KR151_MOUSE	yes	yes	2	20	19	M	Q	0	2130.907	3	6.38E-04	103.88	NaN	NaN	0
3133	SYTVGVTMMHR	sp|P19324|SERPH_MOUSE	yes	yes	228	238	11	R	T	0	1280.601	2	3.15E-04	157.14	NaN	NaN	0
3134	TADGSLQSASSEGSR	sp|P35922-9|FMR1_MOUSE	yes	no	526	540	15	R	L	0	1451.649	2	2.16E-02	87.52	NaN	NaN	0
3135	TAEIENAKCQR	sp|Q9Z2T6|KRT85_MOUSE	no	no	350	360	11	L	A	0	1318.630	2	9.28E-07	155.48	1.69	1.13	1
3136	TAEVSVPKELVALMSAIR	sp|P24527|LKHA4_MOUSE	yes	yes	158	175	18	Y	D	0	1913.066	3	2.87E-02	43.79	1.29	0.99	2
3137	TAGWNIPMGMLYNR	sp|Q921I1|TRFE_MOUSE	yes	yes	479	492	14	R	I	0	1622.770	2	1.01E-03	124.12	NaN	NaN	0
3138	TAICIENSCMVR	sp|Q62009-5|POSTN_MOUSE	yes	no	466	477	12	R	G	0	1452.652	2	1.67E-02	76.07	NaN	NaN	0
3139	TAIIKEIVSR	sp|O08586|PTEN_MOUSE	yes	yes	2	11	10	M	N	0	1128.687	2	2.84E-04	138.45	1.13	1.07	3
3140	TAIKGVGR	sp|P62270|RS18_MOUSE	yes	yes	31	38	8	I	R	0	800.487	2	7.98E-04	154.49	1.02	0.81	3
3141	TALENEFVLLKKDVDAAYMGR	sp|Q8VED5|K2C79_MOUSE	yes	no	238	258	21	R	M	0	2382.225	3;4	2.79E-08	109.65	1.69	0.99	4
3142	TALINSTGEEVAMR	sp|P48678|LMNA_MOUSE	yes	no	528	541	14	R	K	0	1490.740	2	2.73E-04	153.18	NaN	NaN	0
3143	TALLELWELR	sp|P16546-2|SPTN1_MOUSE	yes	no	450	459	10	R	R	0	1242.697	2	1.46E-02	104.82	NaN	NaN	0
3144	TANLGAGAAQPLR	sp|P08226|APOE_MOUSE	yes	yes	202	214	13	R	D	0	1238.673	2	7.05E-04	146.36	NaN	NaN	0
3145	TATLRPYLSAVR	sp|P59999|ARPC4_MOUSE	yes	yes	2	13	12	M	A	1	1346.767	2	5.00E-03	101.72	NaN	NaN	0
3146	TAVLETMTAFR	sp|P10518|HEM2_MOUSE	yes	yes	298	308	11	R	R	0	1238.633	2	7.20E-03	112.94	NaN	NaN	0
3147	TAVVQKR	sp|P62908|RS3_MOUSE	yes	yes	70	76	7	L	F	0	800.487	2	1.51E-02	105.39	0.99	0.81	2
3148	TCLLNETGDEPFQYKN	sp|P15105|GLNA_MOUSE	yes	no	358	373	16	R	-	0	1927.862	2	3.19E-16	196.18	0.83	0.71	4
3149	TCVAPDVFAENMKLR	sp|Q8JZK9|HMCS1_MOUSE	yes	yes	416	430	15	R	E	0	1749.854	3	1.87E-05	115.91	1.08	0.92	6
3150	TDAVTHAAEGLGR	sp|Q8CF02|FM25C_MOUSE	yes	yes	74	86	13	I	L	0	1296.642	2	3.28E-03	97.63	NaN	NaN	0
3151	TDDPLLQLLQKAQQER	sp|Q9DAR7|DCPS_MOUSE	yes	yes	322	337	16	R	N	0	1895.011	3	1.80E-04	80.39	0.93	0.79	4
3152	TDDYLDQPCCETINR	sp|Q61598-2|GDIB_MOUSE	yes	no	158	172	15	R	I	0	1898.778	2	5.50E-05	164.88	NaN	NaN	0
3153	TDESQPWVLPVVR	sp|P05201|AATC_MOUSE	yes	yes	43	55	13	R	K	0	1524.794	2	1.49E-03	115.33	NaN	NaN	0
3154	TDGLEIVVSPR	sp|Q9CQJ4|RING2_MOUSE	yes	yes	33	43	11	I	S	0	1184.640	2	3.11E-02	73.84	NaN	NaN	0
3155	TDGLVSLLTTSKDADEPQR	sp|Q9R0N0|GALK1_MOUSE	yes	yes	69	87	19	R	L	0	2045.028	3	2.16E-03	67.65	1.86	1.45	4
3156	TDIGDTMVYLVH	sp|Q8BMJ2|SYLC_MOUSE	yes	no	1167	1178	12	R	-	0	1362.649	2	1.21E-02	83.86	NaN	NaN	0
3157	TDITYPAGFMDVISIDKTGENFR	sp|P62702|RS4X_MOUSE	yes	yes	78	100	23	R	L	0	2589.242	2;3	4.64E-05	84.95	1.21	0.98	13
3158	TDKSSASAPDVDDPEAFPALA	sp|Q9CY58-3|PAIRB_MOUSE	yes	no	366	386	21	R	-	0	2102.964	2	3.50E-03	52.19	0.98	0.90	7
3159	TDLEFTFVQLKKDLDAECLR	sp|Q0VBK2|K2C80_MOUSE	yes	no	179	198	20	R	R	0	2440.231	3	2.19E-02	44.79	2.37	1.62	1
3160	TDLGPTYNGWQVLDATPQER	sp|Q08189|TGM3_MOUSE	yes	yes	341	360	20	R	S	0	2260.076	2;3	2.53E-03	89.86	NaN	NaN	0
3161	TDLTDYLNR	sp|Q9CZ13|QCR1_MOUSE	yes	yes	214	222	9	R	H	0	1109.535	2	1.64E-03	172.23	NaN	NaN	0
3162	TDYLMKILTER	sp|P63260|ACTG_MOUSE	no	no	186	196	11	L	G	0	1381.728	2	4.73E-04	122.46	1.49	1.21	4
3163	TDYNASVSVPDSSGPER	sp|P61979-3|HNRPK_MOUSE	yes	no	70	86	17	R	I	0	1779.791	2	4.93E-05	151.39	NaN	NaN	0
3164	TEAESWYQTKYEELQQTAGR	sp|Q922U2|K2C5_MOUSE	yes	no	349	368	20	R	H	0	2417.114	2;3	2.11E-28	223.36	1.33	0.94	11
3165	TEAPLNPKANR	sp|P63260|ACTG_MOUSE	no	no	106	116	11	L	E	0	1209.647	2	4.23E-04	123.79	1.22	0.97	6
3166	TECQNAEYQQLLDIKTR	sp|P02535-3|K1C10_MOUSE	yes	no	414	430	17	E	L	0	2109.016	2;3	4.59E-07	119.80	1.84	1.17	4
3167	TEEGPTLSYGR	sp|Q8K310|MATR3_MOUSE	yes	yes	150	160	11	R	D	0	1208.567	2	6.50E-04	152.70	NaN	NaN	0
3168	TEFNLNQYYR	sp|Q60847|COCA1_MOUSE	yes	no	190	199	10	R	R	0	1346.626	2	2.12E-05	192.91	NaN	NaN	0
3169	TEIIILATR	sp|P62908|RS3_MOUSE	yes	yes	46	54	9	R	T	0	1028.623	2	2.05E-02	113.10	NaN	NaN	0
3170	TELPQFVSYFQHR	sp|Q3UDE2|TTL12_MOUSE	yes	yes	390	402	13	R	E	0	1650.815	3	7.67E-03	84.37	NaN	NaN	0
3171	TELQSALLLR	sp|P62254|UB2G1_MOUSE	yes	yes	2	11	10	M	R	0	1142.666	2	9.33E-03	125.75	NaN	NaN	0
3172	TELTELKR	sp|A6BLY7|K1C28_MOUSE	yes	yes	302	309	8	R	S	0	988.555	3	2.04E-02	81.30	1.25	0.81	2
3173	TENPGDASDLQGR	sp|Q9R269|PEPL_MOUSE	yes	yes	491	503	13	R	Q	0	1358.606	2	4.06E-03	95.26	NaN	NaN	0
3174	TEQMTLR	sp|P68040|GBLP_MOUSE	yes	yes	2	8	7	M	G	0	877.433	2	4.72E-02	146.54	NaN	NaN	0
3175	TETDGFYKSR	sp|O08738|CASP6_MOUSE	yes	yes	2	11	10	M	E	0	1202.557	2	1.01E-03	120.06	0.94	0.89	2
3176	TETEGQKLEYEQLLNVKAHLEKEIE	sp|Q9Z320|K1C27_MOUSE	yes	yes	352	380	29	R	L	0	3550.761	5	4.59E-03	54.66	1.40	0.90	1
3177	TETTGATGQASSLLSGR	sp|P39061-2|COIA1_MOUSE	yes	no	1271	1287	17	R	L	0	1635.806	2	2.15E-03	92.26	3.83	2.28	1
3178	TEWQLNAHR	sp|Q60847|COCA1_MOUSE	yes	no	1249	1257	9	R	D	0	1153.563	3	1.43E-02	135.71	NaN	NaN	0
3179	TEYCTGTTGVLR	sp|Q99M74|KRT82_MOUSE	yes	yes	461	472	12	R	N	0	1356.634	2	3.53E-03	115.33	NaN	NaN	0
3180	TFEGVDPKKTSMR	sp|Q61598-2|GDIB_MOUSE	yes	no	121	133	13	R	D	0	1494.750	3;4	3.41E-02	46.88	1.27	1.17	7
3181	TFIAIKPDGVQR	sp|Q01768|NDKB_MOUSE	yes	no	7	18	12	R	G	0	1343.756	2;3	3.34E-07	158.58	1.04	0.94	15
3182	TFKTVFAEHISDECKR	sp|P27659|RL3_MOUSE	yes	yes	101	116	16	R	R	0	1966.957	4	9.69E-02	41.42	2.02	1.24	1
3183	TFLVGER	sp|Q9D8N0|EF1G_MOUSE	yes	yes	150	156	7	R	V	0	820.444	2	6.80E-02	108.09	NaN	NaN	0
3184	TFTNPEHASDAMR	sp|O89086|RBM3_MOUSE	yes	yes	53	65	13	I	A	0	1475.646	2	9.28E-03	79.49	NaN	NaN	0
3185	TFVAELKGLDPAR	sp|P08249|MDHM_MOUSE	yes	yes	179	191	13	N	V	0	1415.777	2	2.06E-02	50.09	1.19	1.04	2
3186	TFVQENVYDEFVER	sp|P47738|ALDH2_MOUSE	yes	yes	327	340	14	R	S	0	1773.821	2	2.99E-06	150.05	0.24	0.20	3
3187	TFYGLHQDFPSVVVVGLGKR	sp|Q9CPY7-2|AMPL_MOUSE	yes	no	54	73	20	R	S	0	2218.190	3;4	6.46E-06	100.02	0.98	0.91	5
3188	TFYNELR	sp|P63260|ACTG_MOUSE	no	no	89	95	7	H	V	0	941.461	2	8.94E-02	89.12	NaN	NaN	0

3189	TGAFWR	sp|P09470|ACE_MOUSE	yes	yes	228	233	6	D	S	0	736.366	2	3.20E-02	89.78	0.08	0.06	1
3190	TGAIVDVPVGEELLGR	sp|Q03265|ATPA_MOUSE	yes	yes	134	149	16	R	V	0	1623.883	2	6.73E-04	105.28	NaN	NaN	0
3191	TGALCWFLDEAAAR	sp|Q9CQ60|6PGL_MOUSE	yes	yes	232	245	14	R	L	0	1579.745	2	1.10E-03	111.12	NaN	NaN	0
3192	TGASLADIMAKR	sp|Q8BP67|RL24_MOUSE	yes	yes	83	94	12	I	N	0	1232.655	2	3.77E-04	116.24	0.94	0.79	4
3193	TGCTFPEKPDFH	sp|P55264-2|ADK_MOUSE	yes	no	334	345	12	R	-	0	1434.624	3	7.98E-03	69.82	1.07	1.01	3
3194	TGEAIVDAALSALR	sp|Q922R8|PDIA6_MOUSE	yes	yes	119	132	14	R	Q	0	1385.751	2;3	4.55E-03	89.51	NaN	NaN	0
3195	TGFGAFGFGSSGIR	sp|Q9QZU5|KR151_MOUSE	yes	yes	100	113	14	N	S	0	1359.657	2	1.16E-03	103.14	NaN	NaN	0
3196	TGIDLGTTGR	sp|Q8VH51-3|RBM39_MOUSE	yes	no	190	199	10	R	L	0	989.514	2	1.46E-02	104.82	NaN	NaN	0
3197	TGIGSGLSLSGIVHPELSR	sp|P50544|ACADV_MOUSE	yes	yes	514	532	19	R	S	0	1879.016	3	6.46E-06	129.46	NaN	NaN	0
3198	TGKEDAANNYAR	sp|P68373|TBA1C_MOUSE	no	no	94	105	12	I	G	0	1308.606	2	7.45E-02	39.56	1.23	1.18	3
3199	TGLLLLSVQKR	sp|E9Q557|DESP_MOUSE	yes	yes	2208	2218	11	H	S	0	1226.771	2	1.47E-03	99.99	2.18	1.37	1
3200	TGNKYNVYPTYDFACPIVDSIEGV	sp|Q8CGC7|SYEP_MOUSE	yes	yes	367	395	29	R	T	0	3299.592	4	3.25E-03	64.58	1.37	1.19	2
3201	TGQCECQPGITGQHCER	sp|P02468|LAMC1_MOUSE	yes	yes	949	965	17	R	C	0	2016.820	3	6.03E-04	109.50	NaN	NaN	0
3202	TGSEAPQDLLEKLIKSR	sp|Q8C1A5|THOP1_MOUSE	yes	yes	527	543	17	R	Q	0	1884.032	4	8.46E-07	110.97	1.11	1.02	4
3203	TGTNLAPSLWLHR	sp|Q09PK2|APRV1_MOUSE	yes	yes	106	118	13	F	F	0	1464.784	2;3	1.83E-06	184.11	NaN	NaN	0
3204	TGWVKPIIIGR	sp|O88844|IDHC_MOUSE	yes	yes	122	132	11	V	H	0	1238.750	2	2.04E-03	93.35	1.06	0.91	4
3205	TGYTLDVTTGQR	sp|Q7TMK9-2|HNRPQ_MOUSE	yes	no	131	142	12	R	K	0	1310.647	2	1.69E-04	169.89	0.25	0.24	1
3206	THPNLPVSVILR	sp|P02772|FETA_MOUSE	yes	yes	357	368	12	R	I	0	1344.788	2;3	4.06E-03	109.00	NaN	NaN	0
3207	TIAACNLPIVQGPCR	sp|Q07456|AMBP_MOUSE	yes	yes	282	296	15	R	A	0	1668.844	2	4.95E-04	133.16	NaN	NaN	0
3208	TIAMDGTEGLVR	sp|P56480|ATPB_MOUSE	yes	yes	110	121	12	R	G	0	1261.634	2	3.97E-03	110.08	NaN	NaN	0
3209	TIAQDYGVLKADEGISFR	sp|P35700|PRDX1_MOUSE	yes	yes	111	128	18	R	G	0	1982.011	3	6.00E-05	88.57	1.29	1.18	7
3210	TICALGDGAAWPVQGLIR	sp|Q91YT0|NDUV1_MOUSE	yes	yes	423	440	18	H	H	0	1896.988	2	4.32E-03	88.43	NaN	NaN	0
3211	TICSHVQNMIKGVTLGFR	sp|P51410|RL9_MOUSE	yes	yes	72	89	18	R	Y	0	2060.066	4	9.44E-03	50.18	1.40	1.06	2
3212	TIDIEPDIETLLSQQSGNS	sp|P11352|GPX1_MOUSE	yes	no	183	201	19	R	-	0	2058.996	2	1.08E-02	69.61	NaN	NaN	0
3213	TIEELQQKILCAKSENAR	sp|Q9D646|KRT34_MOUSE	yes	no	109	126	18	R	L	0	2130.110	3	5.12E-03	58.25	1.87	1.08	2
3214	TIEELQQKILCGKSENAR	sp|Q8K0Y2|KT33A_MOUSE	yes	yes	109	126	18	R	L	0	2116.095	3;4	2.31E-07	114.63	1.82	1.10	11
3215	TIEELQQKILCGKSENGR	sp|Q61897|KT33B_MOUSE	yes	no	109	126	18	R	L	0	2102.079	3;4	5.23E-05	90.45	1.82	1.18	12
3216	TIEELQQKILCSKSENAR	sp|Q61765|K1H1_MOUSE	no	no	109	126	18	R	L	0	2146.105	3;4	4.26E-03	61.48	2.02	1.20	8
3217	TIGISVDPR	sp|P47963|RL13_MOUSE	yes	yes	93	101	9	R	R	0	956.529	2	3.98E-02	85.81	NaN	NaN	0
3218	TILAETEGMLKDLQKSVEEEER	sp|Q99PL5|RRBP1_MOUSE	yes	yes	1332	1353	22	R	V	0	2547.274	3	2.30E-02	43.16	1.61	1.13	1
3219	TIMPKDIQLAR	sp|P84244|H33_MOUSE	no	no	119	129	11	V	R	0	1284.722	2	8.98E-05	144.57	1.29	0.90	10
3220	TINEVENQILTR	sp|P57780|ACTN4_MOUSE	no	no	747	758	12	R	D	0	1428.757	2	1.39E-06	191.79	NaN	NaN	0
3221	TIPWLEDR	sp|P57780|ACTN4_MOUSE	yes	yes	313	320	8	R	V	0	1028.529	2	7.24E-02	79.47	NaN	NaN	0
3222	TIQFVDWCPTGFKVGINYQPPTV	sp|P68373|TBA1C_MOUSE	no	no	340	373	34	R	A	0	3786.956	4	1.05E-06	85.62	1.29	1.25	3
3223	TIQVSDFVR	sp|Q9Z247|FKBP9_MOUSE	yes	yes	162	170	9	R	Y	0	1063.566	2	2.02E-02	114.97	NaN	NaN	0
3224	TITDAVTHAAEGLGR	sp|Q8CF02|FM25C_MOUSE	yes	yes	72	86	15	H	L	0	1510.774	2;3	5.69E-06	179.56	NaN	NaN	0
3225	TITPGSEQIR	sp|Q99KI0|ACON_MOUSE	yes	yes	415	424	10	F	A	0	1100.583	2	1.14E-02	117.70	NaN	NaN	0
3226	TITVALADGGRPDNTGR	sp|Q8BGQ7|SYAC_MOUSE	yes	yes	304	320	17	R	G	1	1712.881	3	5.36E-03	81.66	NaN	NaN	0
3227	TIVEEVQDGKVISSR	sp|Q9QWL7|K1C17_MOUSE	yes	no	411	425	15	R	E	0	1658.884	2;3	1.09E-19	209.60	1.62	0.98	18
3228	TIVYFPVR	sp|P19157|GSTP1_MOUSE	yes	yes	5	12	8	Y	G	0	993.565	2	4.15E-02	111.01	NaN	NaN	0
3229	TKCEEIKATVIR	sp|P97861|KRT86_MOUSE	no	no	299	310	12	R	H	0	1446.786	2;3;4	2.48E-07	164.53	1.78	1.18	12
3230	TKEEINELNR	sp|Q9Z2T6|KRT85_MOUSE	no	no	335	344	10	R	M	0	1244.636	2;3	7.67E-04	149.23	0.87	0.54	4
3231	TKFETEQALR	sp|Q9QWL7|K1C17_MOUSE	yes	no	171	180	10	R	M	0	1221.635	2;3	3.51E-03	94.80	1.66	1.22	9
3232	TKFETEQSLR	sp|Q61781|K1C14_MOUSE	yes	yes	208	217	10	R	M	0	1237.630	2;3	4.13E-04	130.56	1.76	1.13	7
3233	TKLEAAVTQSEQQGEAALTDAR	sp|Q6IMF0|KRT83_MOUSE	yes	yes	349	370	22	N	C	0	2316.156	3	1.61E-03	61.35	1.44	1.01	3
3234	TKTLVKNCIVLIDSTPYR	sp|P62242|RS8_MOUSE	yes	yes	93	110	18	R	Q	0	2120.166	3	3.88E-02	40.43	1.07	0.97	4
3235	TKTPGPGAQSALR	sp|P62264|RS14_MOUSE	yes	yes	105	117	13	R	A	0	1282.699	2;3	6.41E-05	125.47	1.16	0.86	7
3236	TKVMDVHDGKVVSTHEQVLR	sp|Q61781|K1C14_MOUSE	no	no	462	481	20	R	T	0	2277.190	4;5	2.03E-02	45.36	1.86	1.14	5
3237	TKWELLQQLDVGSR	sp|Q3TTY5|K22E_MOUSE	yes	no	229	242	14	R	T	0	1671.894	2;3	1.77E-08	162.81	2.73	1.71	13
3238	TKYEDEINKR	sp|P04104|K2C1_MOUSE	yes	yes	276	285	10	R	T	0	1294.652	3;4	2.28E-04	141.88	1.24	0.86	7
3239	TKYESELSLR	sp|Q61897|KT33B_MOUSE	yes	no	143	152	10	R	Q	0	1224.635	2;3	5.16E-09	185.25	2.22	1.22	11
3240	TKYETELALR	sp|Q62168|K1H2_MOUSE	yes	no	142	151	10	R	Q	0	1222.656	2	1.15E-03	117.79	1.58	1.02	4
3241	TKYETELGLR	sp|Q61765|K1H1_MOUSE	yes	no	143	152	10	R	Q	0	1208.640	2;3	3.49E-04	134.49	1.68	1.13	13
3242	TKYETELSLR	sp|Q8K0Y2|KT33A_MOUSE	no	no	143	152	10	R	Q	0	1238.651	2;3	1.84E-04	144.57	2.09	1.15	6
3243	TKYETEVSLR	sp|Q497I4|KRT35_MOUSE	no	no	184	193	10	R	Q	0	1224.635	3	5.53E-03	83.08	1.70	0.98	3
3244	TKYQTELSMR	sp|Q9D646|KRT34_MOUSE	yes	no	143	152	10	R	Q	0	1255.623	2;3	2.30E-06	169.89	2.09	1.22	9
3245	TLAEIAKVELDNMPLR	sp|Q99K48|NONO_MOUSE	yes	no	122	137	16	R	G	0	1811.982	2;3	3.04E-08	144.73	1.08	0.68	3
3246	TLAFEELR	sp|Q6NZJ6|IF4G1_MOUSE	yes	no	1437	1444	8	R	R	0	977.518	2	7.93E-02	76.06	NaN	NaN	0
3247	TLDLPIYVTR	sp|Q8CIE6|COPA_MOUSE	yes	yes	563	572	10	R	V	0	1189.671	2	1.37E-02	108.47	NaN	NaN	0
3248	TLDPALLRPGR	sp|P62334|PRS10_MOUSE	no	no	284	294	11	D	L	1	1207.704	2	8.55E-02	70.94	NaN	NaN	0
3249	TLEAVQDLLEQGR	sp|P19096|FAS_MOUSE	yes	yes	430	442	13	R	Q	0	1470.768	2	2.61E-04	162.31	NaN	NaN	0
3250	TLEDILFR	sp|Q8VCM7|FIBG_MOUSE	yes	yes	67	74	8	R	A	0	1005.550	2	3.75E-02	125.31	NaN	NaN	0
3251	TLEGELHDLR	sp|P48678|LMNA_MOUSE	yes	no	157	166	10	R	G	0	1181.604	2;3	5.29E-03	141.10	NaN	NaN	0
3252	TLELQGLINDLQR	sp|E9Q557|DESP_MOUSE	yes	yes	1775	1787	13	R	E	0	1511.831	2;3	7.73E-11	225.23	NaN	NaN	0
3253	TLETLIR	sp|P25206|MCM3_MOUSE	yes	no	617	623	7	R	L	0	844.502	2	7.66E-02	98.42	NaN	NaN	0
3254	TLETPAAQMEGFLNR	sp|Q62261|SPTB2_MOUSE	yes	yes	2191	2205	15	R	K	0	1676.819	2	4.31E-04	136.60	NaN	NaN	0
3255	TLFGLR	sp|Q9CWJ9|PUR9_MOUSE	yes	no	380	385	6	R	L	0	705.417	2	7.72E-02	100.36	NaN	NaN	0
3256	TLFSNIVLSGGSTLFKGFGDR	sp|Q8R5C5|ACTY_MOUSE	yes	no	293	313	21	R	L	0	2215.164	3	1.81E-03	87.35	1.36	0.98	2
3257	TLGDQLSLLLGAR	sp|Q64449-2|MRC2_MOUSE	yes	no	124	136	13	R	A	0	1355.777	2	5.00E-02	60.16	NaN	NaN	0
3258	TLIEFLLR	sp|Q9CPY7-2|AMPL_MOUSE	yes	no	475	482	8	R	F	0	1003.607	2	3.71E-02	127.02	NaN	NaN	0
3259	TLINELVKGILPR	sp|Q9JHU4|DYHC1_MOUSE	yes	yes	4448	4460	13	R	S	0	1464.903	3	8.99E-03	64.12	1.36	0.91	1
3260	TLIQNCGASTIR	sp|P80318|TCPG_MOUSE	yes	yes	450	461	12	R	L	0	1332.682	2	3.51E-03	115.57	NaN	NaN	0
3261	TLKLTTPTYGDLNHLVSATMSGVT	sp|P99024|TBB5_MOUSE	no	no	214	241	28	R	F	0	3049.558	3	2.57E-03	59.89	0.81	0.63	3
3262	TLLIKTVETR	sp|P20152|VIME_MOUSE	yes	yes	441	450	10	R	D	0	1172.713	2;3	1.41E-06	174.42	1.20	0.90	20
3263	TLLLAGVFR	sp|Q9QZE5|COPG1_MOUSE	yes	yes	827	835	9	H	G	0	988.607	2	4.44E-02	109.71	NaN	NaN	0
3264	TLLVADPR	sp|P14131|RS16_MOUSE	yes	yes	118	125	8	R	R	0	883.513	2	4.82E-02	99.14	NaN	NaN	0
3265	TLMELLNQMDGFDTLHR	sp|P62334|PRS10_MOUSE	yes	yes	256	272	17	R	V	0	2032.971	3	4.70E-04	116.06	NaN	NaN	0
3266	TLMNLGGLAVAR	sp|Q9WVA4|TAGL2_MOUSE	yes	yes	128	139	12	R	D	0	1214.681	2	1.46E-03	141.08	NaN	NaN	0
3267	TLQEEHVTVAQLR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1498	1510	13	R	E	0	1522.810	3	6.82E-03	86.94	NaN	NaN	0
3268	TLQEQLENGPNTQLAR	sp|Q99PL5|RRBP1_MOUSE	yes	yes	985	1000	16	R	L	0	1810.917	2	6.73E-04	105.28	NaN	NaN	0
3269	TLSDYNIQKESTLHLVLR	sp|P62983|RS27A_MOUSE	yes	no	55	72	18	R	L	0	2129.148	3;4	2.50E-07	113.33	0.90	0.71	6
3270	TLTAVHDAILEDLVFPSEIVGKR	sp|P62082|RS7_MOUSE	yes	yes	121	143	23	R	I	0	2522.374	3;4	4.56E-11	148.38	1.15	0.91	9
3271	TLTGMALNFIR	sp|Q60847|COCA1_MOUSE	yes	no	1276	1286	11	N	Q	0	1235.670	2	1.45E-02	91.55	NaN	NaN	0
3272	TLVLLDNLNVR	sp|O54734|OST48_MOUSE	yes	yes	32	42	11	R	D	0	1268.745	2	1.86E-03	143.50	NaN	NaN	0
3273	TLYDAELSQLQQDVTDTNVILSMI	sp|Q3TTY5|K22E_MOUSE	yes	no	336	362	27	R	N	0	3095.472	2;3	3.46E-12	141.21	NaN	NaN	0
3274	TMLELINQLDGFDPR	sp|P46471|PRS7_MOUSE	yes	yes	298	312	15	R	G	0	1760.877	2	5.66E-04	129.38	NaN	NaN	0
3275	TMLELLNQLDGFDSR	sp|P62192|PRS4_MOUSE	yes	yes	308	322	15	R	G	0	1750.856	2	2.74E-07	185.67	NaN	NaN	0
3276	TMQNTSDLDTAR	sp|Q02257|PLAK_MOUSE	yes	yes	192	203	12	R	C	0	1351.604	2	9.87E-03	89.44	NaN	NaN	0
3277	TMVQSPSGVILQEAADIHAR	sp|E9Q557|DESP_MOUSE	yes	yes	995	1014	20	R	Y	0	2122.084	3	2.12E-06	143.04	NaN	NaN	0
3278	TNEKVELQELNDR	sp|P20152|VIME_MOUSE	yes	no	101	113	13	R	F	0	1586.790	2;3	8.32E-13	195.20	1.09	0.85	16
3279	TNFNSAHDTDR	sp|Q08189|TGM3_MOUSE	yes	yes	295	305	11	I	N	0	1276.543	2	2.27E-03	140.45	NaN	NaN	0
3280	TNGKEPELLEPIPYEFMA	sp|O09167|RL21_MOUSE	yes	no	143	160	18	R	-	0	2077.008	2	2.66E-05	96.77	0.89	0.77	4
3281	TNIIPVLEDAR	sp|Q80WS3|FBLL1_MOUSE	yes	yes	202	212	11	R	H	0	1239.682	2	8.18E-03	98.18	34.21	23.26	1
3282	TNLIVNYLPQNMTQEELR	sp|P70372|ELAV1_MOUSE	yes	yes	20	37	18	R	S	0	2175.099	2	4.73E-02	48.29	NaN	NaN	0
3283	TNLLQVCER	sp|Q64727|VINC_MOUSE	yes	yes	979	987	9	R	I	0	1131.571	2	5.11E-03	153.97	NaN	NaN	0
3284	TNQELQEINR	sp|P07356|ANXA2_MOUSE	yes	yes	136	145	10	R	V	0	1243.616	2	9.20E-14	257.09	NaN	NaN	0
3285	TNRPPLSLSR	sp|P35980|RL18_MOUSE	yes	yes	56	65	10	R	M	1	1139.641	3	1.41E-03	158.02	NaN	NaN	0
3286	TNSTFNQVVLKR	sp|P35980|RL18_MOUSE	yes	yes	39	50	12	R	L	0	1405.768	3	1.30E-04	127.87	1.50	1.03	8
3287	TNVIQSLLAR	sp|Q9EP69|SAC1_MOUSE	yes	yes	396	405	10	R	R	0	1113.651	2	3.03E-02	79.66	NaN	NaN	0
3288	TNVNEPASDTLQEVKMR	sp|P21844|CMA1_MOUSE	yes	yes	152	168	17	R	L	0	1930.942	3	4.30E-05	96.10	1.57	0.93	7
3289	TNYNDRYDEIR	sp|P12970|RL7A_MOUSE	yes	yes	224	234	11	R	R	1	1457.654	3	1.55E-02	89.30	NaN	NaN	0
3290	TPAASAVNLAGAR	sp|Q8BTI8-3|SRRM2_MOUSE	yes	no	2241	2253	13	R	T	0	1197.647	2	1.25E-02	58.32	4.14	2.40	3
3291	TPCTVSCNIPVVSGKECEEIIR	sp|Q8K0E8|FIBB_MOUSE	yes	yes	215	236	22	R	K	0	2547.213	3	7.70E-06	88.18	0.73	0.68	5

3292	TPDLKALLNVVDSAR	sp|O35405|PLD3_MOUSE	yes	yes	303	317	15	R	S	0	1610.899	3	2.15E-05	113.52	1.19	1.00	4
3293	TPEFLR	sp|Q9D8N0|EF1G_MOUSE	yes	no	46	51	6	R	K	0	761.407	2	3.54E-02	154.29	NaN	NaN	0
3294	TPEQCPSVVSLLSESYNPHVR	sp|Q3TXS7|PSMD1_MOUSE	yes	yes	629	649	21	R	Y	0	2398.159	3	2.38E-06	130.05	NaN	NaN	0
3295	TPEQVTEIANR	sp|Q9D880|TIM50_MOUSE	yes	yes	33	43	11	R	G	0	1256.636	2	7.47E-03	111.63	NaN	NaN	0
3296	TPFGAYGGLLKDFSATDLTEFAAR	sp|Q8BWT1|THIM_MOUSE	yes	yes	15	38	24	R	A	0	2547.265	3	1.17E-15	158.94	0.98	0.93	2
3297	TPKGTQGVVTNFEIFR	sp|Q8JZQ9|EIF3B_MOUSE	yes	yes	522	537	16	R	M	0	1792.947	3	7.60E-03	57.15	0.99	0.95	1
3298	TPLYDLR	sp|Q91VH6|MEMO1_MOUSE	yes	yes	98	104	7	R	I	0	876.471	2	5.93E-02	125.50	NaN	NaN	0
3299	TPPSEEDSAEAER	sp|Q8BJU0-2|SGTA_MOUSE	yes	no	81	93	13	R	L	0	1416.601	2	1.49E-03	115.12	0.05	0.04	1
3300	TPQAPTPANLVVGPR	sp|Q8BTI8-3|SRRM2_MOUSE	yes	no	2281	2295	15	R	S	0	1516.836	2	5.45E-04	130.47	NaN	NaN	0
3301	TPSALAILENANVLAR	sp|P05063|ALDOC_MOUSE	yes	yes	158	173	16	R	Y	0	1651.926	2	7.34E-04	102.65	NaN	NaN	0
3302	TPSQEQLLAEALAAAR	sp|Q640N1-2|AEBP1_MOUSE	yes	no	389	404	16	R	G	0	1667.884	2	1.72E-02	67.65	NaN	NaN	0
3303	TPTPAGPTIMPLIR	sp|Q9QYS9-8|QKI_MOUSE	yes	no	243	256	14	R	Q	0	1463.817	2	2.77E-03	96.46	NaN	NaN	0
3304	TPVSEDMLGR	sp|P62814|VATB2_MOUSE	yes	yes	121	130	10	R	V	0	1103.528	2	7.24E-03	133.76	NaN	NaN	0
3305	TQDECILHFLR	sp|P97496-2|SMRC1_MOUSE	yes	no	652	662	11	R	L	0	1430.698	3	8.46E-03	107.03	NaN	NaN	0
3306	TQEEIVAKVR	sp|P08003|PDIA4_MOUSE	yes	yes	149	158	10	R	E	0	1171.656	3	3.40E-02	57.53	1.28	0.98	6
3307	TQGPEALFEDHR	sp|Q9Z184|PADI3_MOUSE	yes	yes	187	198	12	R	L	0	1398.653	3	2.34E-03	129.54	NaN	NaN	0
3308	TQGTKIASDGLKGR	sp|P97351|RS3A_MOUSE	yes	yes	52	65	14	R	V	0	1430.784	4	2.37E-03	73.93	0.98	0.72	4
3309	TQIISATAHNANIILQNDNAR	sp|Q9Z320|K1C27_MOUSE	yes	yes	137	157	21	R	L	0	2277.183	2;3	1.99E-23	253.93	0.10	0.06	2
3310	TQLGLLMDGFNSLLR	sp|Q9EP69|SAC1_MOUSE	yes	yes	466	480	15	R	Y	0	1676.892	2	2.00E-02	67.65	NaN	NaN	0
3311	TQNLDPFFENYISILR	sp|P04104|K2C1_MOUSE	yes	yes	232	247	16	R	R	0	1968.995	2;3	6.73E-08	187.00	NaN	NaN	0
3312	TQNLDPFFENYISILRR	sp|P04104|K2C1_MOUSE	yes	yes	232	248	17	R	K	1	2125.096	3	1.48E-02	68.41	NaN	NaN	0
3313	TQVCGILR	sp|Q00612|G6PD1_MOUSE	yes	no	10	17	8	R	E	0	945.507	2	3.07E-02	138.83	NaN	NaN	0
3314	TRPLEQAVAAIVCTFQEYAGR	sp|P62818|S10A3_MOUSE	yes	yes	2	22	21	M	C	1	2379.201	3	1.56E-02	51.31	NaN	NaN	0
3315	TSACGLFSVCYPR	sp|Q76MZ3|2AAA_MOUSE	yes	no	145	157	13	R	V	0	1516.680	2	1.53E-03	109.00	NaN	NaN	0
3316	TSFLDDAFR	sp|Q9JHU4|DYHC1_MOUSE	yes	yes	3610	3618	9	R	K	0	1070.503	2	2.04E-02	113.62	NaN	NaN	0
3317	TSIDAYDNFDNISLAQR	sp|Q68FD5|CLH1_MOUSE	yes	yes	1482	1498	17	R	L	0	1941.907	2	3.31E-08	135.09	1.97	1.26	1
3318	TSQESELNNMQDLVEDFKKKYED	sp|Q3TTY5|K22E_MOUSE	yes	no	269	296	28	R	T	0	3429.636	4;5;6	3.49E-08	110.01	2.13	1.18	3
3319	TSYQPSSPSR	sp|Q8R2Q0|TRI29_MOUSE	yes	yes	483	492	10	R	L	0	1108.515	2	1.73E-02	99.57	NaN	NaN	0
3320	TSYSSVTMSR	sp|Q8VED5|K2C79_MOUSE	yes	no	31	40	10	R	G	0	1117.507	2	1.63E-03	154.84	NaN	NaN	0
3321	TTGIVMDSGDGVTHTVPIYEGYAI	sp|P63260|ACTG_MOUSE	no	no	148	177	30	R	L	0	3182.607	3;4	2.25E-08	106.62	NaN	NaN	0
3322	TTIFSPEGR	sp|Q9R1P0|PSA4_MOUSE	yes	yes	9	17	9	R	L	0	1006.508	2	1.97E-02	117.89	NaN	NaN	0
3323	TTNLDPIFQAYIGMLKKQVDR	sp|Q3TTY5|K22E_MOUSE	yes	no	243	263	21	R	L	0	2450.299	3;4	7.15E-16	155.49	3.28	1.88	7
3324	TTPSVVAFTADGER	sp|P38647|GRP75_MOUSE	yes	yes	86	99	14	R	L	0	1449.710	2	1.12E-03	108.58	1.87	1.32	1
3325	TTPSYVAFTDTER	sp|P63017|HSP7C_MOUSE	no	no	37	49	13	R	L	0	1486.694	2	5.73E-04	149.69	NaN	NaN	0
3326	TTQQIVLQGPGPWGFR	sp|O70400|PDLI1_MOUSE	yes	yes	2	17	16	M	L	0	1783.937	2	4.18E-02	50.31	NaN	NaN	0
3327	TTVINMPR	sp|Q9CQW9|IFM3_MOUSE	yes	no	43	50	8	R	E	0	930.496	2	3.37E-02	116.90	NaN	NaN	0
3328	TTYLVLDEADR	sp|Q61656|DDX5_MOUSE	yes	yes	242	252	11	R	M	0	1294.641	2	6.69E-03	115.33	NaN	NaN	0
3329	TVCVPCSPCLQTR	sp|Q62168|K1H2_MOUSE	yes	no	394	406	13	H	Y	0	1576.716	2	1.98E-02	72.68	NaN	NaN	0
3330	TVCVPHTVCVPCSPCLQTR	sp|Q62168|K1H2_MOUSE	yes	no	388	406	19	R	Y	0	2270.043	3	3.67E-02	48.91	NaN	NaN	0
3331	TVEEGAETPVYLALLPPDATEPHG	sp|Q8K354|CBR3_MOUSE	yes	yes	243	270	28	R	D	0	3001.540	3	4.84E-12	131.04	NaN	NaN	0
3332	TVENIKDPLFR	sp|Q9JHU4|DYHC1_MOUSE	yes	yes	4399	4409	11	R	F	0	1330.725	3	4.27E-02	62.47	1.29	0.77	2
3333	TVEVPEDEVVR	sp|Q80WJ7|LYRIC_MOUSE	yes	yes	131	141	11	R	N	0	1270.641	2	9.93E-04	108.70	4.97	3.46	1
3334	TVGQEKKGYFEDR	sp|P15105|GLNA_MOUSE	yes	yes	328	340	13	R	R	0	1555.763	3	4.41E-02	44.51	0.64	0.52	4
3335	TVIDYNGER	sp|P09103|PDIA1_MOUSE	yes	yes	455	463	9	R	T	0	1065.509	2	3.32E-04	144.77	50.01	39.18	2
3336	TVIPANKLQELQVNLVR	sp|P35492|HUTH_MOUSE	yes	yes	176	192	17	R	S	0	1934.131	3	6.97E-04	75.38	1.11	1.07	2
3337	TVKSVGMIAGGTGITPMLQVIR	sp|Q9DCN2-2|NB5R3_MOUSE	yes	no	148	169	22	R	A	0	2228.239	3	2.67E-08	105.06	2.11	1.30	1
3338	TVLFTNAR	sp|Q9CZU3|SK2L2_MOUSE	yes	yes	493	500	8	R	K	0	920.508	2	2.90E-02	130.27	NaN	NaN	0
3339	TVLSGGTTMYPGIADR	sp|P63260|ACTG_MOUSE	no	no	297	312	16	N	M	0	1637.808	2	1.88E-04	142.91	NaN	NaN	0
3340	TVLVTWTPPR	sp|P11276|FINC_MOUSE	yes	yes	1011	1020	10	R	A	0	1168.660	2	2.47E-02	88.13	NaN	NaN	0
3341	TVNALEIELQAQHCMR	sp|Q9D646|KRT34_MOUSE	no	no	278	293	16	R	N	0	1911.930	2;3	1.45E-26	262.42	0.03	0.02	2
3342	TVNALEIELQAQHELR	sp|Q8K0Y2|KT33A_MOUSE	yes	yes	278	293	16	R	N	0	1862.985	2;3	1.24E-18	242.48	NaN	NaN	0
3343	TVNALEIELQAQHSMR	sp|Q61897|KT33B_MOUSE	no	no	278	293	16	R	N	0	1838.931	3	3.27E-04	131.45	NaN	NaN	0
3344	TVPFCSTFAAFFTR	sp|P40142|TKT_MOUSE	yes	yes	382	395	14	R	A	0	1650.786	2	6.04E-03	83.63	0.02	0.02	1
3345	TVPQYKYAAGVR	sp|P29341|PABP1_MOUSE	yes	yes	507	518	12	R	N	0	1351.725	3	2.22E-02	52.25	1.26	0.98	5
3346	TVVSGLVNHVPLEQMQNR	sp|P31230|AIMP1_MOUSE	yes	yes	186	203	18	R	M	0	2020.052	3	3.16E-03	93.12	NaN	NaN	0
3347	TVVSGLVQFVPKEELQDR	sp|Q91WQ3|SYYC_MOUSE	yes	yes	401	418	18	R	L	0	2043.100	3	7.59E-05	84.65	1.06	0.84	5
3348	TWEKLLLAAR	sp|P14206|RSSA_MOUSE	yes	yes	54	63	10	R	A	0	1199.703	2;3	2.94E-06	166.66	1.10	0.98	12
3349	TWKPTLVILR	sp|Q9WV32|ARC1B_MOUSE	yes	yes	85	94	10	R	I	0	1225.755	3	9.13E-07	176.95	1.22	0.93	2
3350	TYLDKVR	sp|Q61781|K1C14_MOUSE	no	no	134	140	7	A	A	0	893.497	2	1.07E-02	122.18	1.66	0.96	5
3351	TYLDVEPITGFTLQFAKR	sp|Q08857|CD36_MOUSE	yes	yes	369	386	18	R	L	0	2098.110	3	1.35E-03	72.43	1.23	0.81	1
3352	TYLPSQVSR	sp|O55029|COPB2_MOUSE	yes	yes	760	768	9	R	V	0	1049.551	2	3.98E-02	85.81	NaN	NaN	0
3353	TYSLGSALR	sp|P20152|VIME_MOUSE	yes	yes	37	45	9	R	P	0	966.513	2	2.34E-02	101.65	NaN	NaN	0
3354	TYSLGSALRPSTSR	sp|P20152|VIME_MOUSE	yes	yes	37	50	14	R	S	1	1494.779	2;3	1.10E-03	110.92	0.35	0.33	1
3355	VAAAESMPLLLECAR	sp|Q8BKC5-2|IPO5_MOUSE	yes	no	661	675	15	R	V	0	1629.822	2	3.00E-03	90.71	NaN	NaN	0
3356	VAAALPGMESTQDR	sp|P35279-2|RAB6A_MOUSE	yes	no	170	183	14	R	S	0	1444.698	2	5.48E-03	85.84	NaN	NaN	0
3357	VAAGVLCELAQDKEAADAIDAEG	sp|Q02257|PLAK_MOUSE	yes	yes	603	637	35	R	N	0	3620.781	4	1.47E-10	147.35	1.12	0.65	1
3358	VAAPKHWMLDKLTGVFAPR	sp|P62702|RS4X_MOUSE	yes	yes	12	30	19	R	P	0	2136.167	3;4;5	3.90E-03	59.73	1.05	1.02	6
3359	VAEDDEDDDVDTKKQKTEEDD	sp|P26350|PTMA_MOUSE	yes	no	91	111	21	R	-	0	2438.009	3;4	1.69E-08	117.37	0.82	0.79	9
3360	VAELSSDDFHLDR	sp|Q61543|GSLG1_MOUSE	yes	yes	294	306	13	R	H	0	1502.700	3	1.49E-03	115.12	NaN	NaN	0
3361	VAFGEDIDLPETFDAR	sp|P10605|CATB_MOUSE	yes	yes	72	87	16	R	E	0	1793.847	2	1.63E-03	97.90	NaN	NaN	0
3362	VAFSVAR	sp|P27659|RL3_MOUSE	yes	yes	262	268	7	R	A	0	748.423	2	2.10E-02	170.17	NaN	NaN	0
3363	VAILKANLR	sp|Q01853|TERA_MOUSE	yes	yes	654	662	9	R	K	0	996.644	2;3	6.76E-04	133.23	1.22	1.03	11
3364	VALLSHAPLDFLPNTQR	sp|Q8C6K9|CO6A6_MOUSE	yes	yes	2009	2025	17	R	S	0	1891.032	3	3.28E-04	123.02	NaN	NaN	0
3365	VALSEPQPER	sp|Q99MR6-3|SRRT_MOUSE	yes	no	449	458	10	R	R	0	1124.583	2	1.40E-02	107.45	NaN	NaN	0
3366	VALTGLTVAEYFR	sp|P56480|ATPB_MOUSE	yes	yes	282	294	13	R	D	0	1438.782	2	1.81E-06	184.34	NaN	NaN	0
3367	VAMKFLR	sp|Q01768|NDKB_MOUSE	yes	yes	36	42	7	L	A	0	863.505	2	1.06E-02	122.79	1.15	0.97	4
3368	VAPAPAGVFTDIPISNIR	sp|Q8BMF4|ODP2_MOUSE	yes	yes	407	424	18	R	R	0	1837.010	2	6.87E-04	105.90	NaN	NaN	0
3369	VAPEEHPTLLTEAPLNPKANR	sp|P68134|ACTS_MOUSE	yes	no	98	118	21	R	E	0	2296.218	4	3.13E-03	54.83	1.20	1.10	8
3370	VAPEEHPVLLTEAPLNPKANR	sp|P63260|ACTG_MOUSE	no	no	96	116	21	R	E	0	2294.238	2;3;4	2.93E-21	186.56	1.22	0.95	28
3371	VAQLEQVYIR	sp|P62320|SMD3_MOUSE	yes	yes	55	64	10	R	G	0	1217.677	2	1.07E-03	163.66	NaN	NaN	0
3372	VAQLVKR	sp|Q03265|ATPA_MOUSE	yes	no	256	262	7	T	L	0	812.523	2	2.53E-02	90.99	1.02	0.84	2
3373	VASILHDDCAFLSAFGDLSKPER	sp|Q9D1Q6|ERP44_MOUSE	yes	yes	181	203	23	R	Y	0	2547.243	4	1.32E-03	61.96	1.48	1.27	2
3374	VAVEEVDEEGKFVR	sp|P48678|LMNA_MOUSE	yes	no	440	453	14	R	L	0	1604.805	2;3	1.39E-08	166.86	1.49	0.88	9
3375	VAVQGDVVR	sp|Q8CGC7|SYEP_MOUSE	yes	yes	757	765	9	R	E	0	941.529	2	2.12E-02	93.65	NaN	NaN	0
3376	VAVSADPNVPNVIVTR	sp|Q99PT1|GDIR1_MOUSE	yes	yes	59	74	16	R	L	0	1649.910	2	8.24E-05	151.59	NaN	NaN	0
3377	VAVVNQIAR	sp|Q62261|SPTB2_MOUSE	yes	no	905	913	9	R	Q	0	968.577	2	1.56E-02	133.12	NaN	NaN	0
3378	VAVVQYSGQGQQQPGR	sp|Q04857|CO6A1_MOUSE	yes	yes	870	885	16	R	A	0	1700.859	2	1.38E-08	203.11	NaN	NaN	0
3379	VCDCTTPTECR	sp|P55849-2|DSC1_MOUSE	yes	no	664	674	11	R	M	0	1397.537	2	1.70E-02	86.11	NaN	NaN	0
3380	VCEEIAIIPSKKLR	sp|P63276|RS17_MOUSE	yes	yes	34	47	14	R	N	0	1654.944	3;4	8.23E-05	116.51	1.15	1.07	8
3381	VCENIPIVLCGNKVDIKDR	sp|P62827|RAN_MOUSE	yes	yes	111	129	19	R	K	0	2241.161	3;4	7.81E-12	132.79	1.03	0.88	11
3382	VCLLHEKTPVSEHVTKCCSGSLVEI	sp|P07724|ALBU_MOUSE	yes	yes	484	508	25	R	R	0	2924.431	5;6	1.78E-03	52.36	1.16	1.03	8
3383	VCLNLPYFLR	sp|A2AN08-4|UBR4_MOUSE	yes	no	259	268	10	R	Y	0	1293.690	2	1.19E-02	115.71	NaN	NaN	0
3384	VCMVYDLYPTLTPLAVAYAR	sp|Q9CWJ9|PUR9_MOUSE	yes	yes	286	305	20	R	A	0	2315.169	2	4.89E-02	47.08	NaN	NaN	0
3385	VCPLSLSAAFGMVR	sp|Q9D7P9|SPB12_MOUSE	yes	yes	30	43	14	F	L	0	1506.769	2	6.94E-02	69.92	NaN	NaN	0
3386	VCSAPCSGNVVVGTPNACAPCAC	sp|P97861|KRT86_MOUSE	yes	no	453	486	34	R	-	0	3440.428	3	5.41E-16	156.40	1.93	1.23	4
3387	VCTLAIIDPGDSDIIR	sp|P62889|RL30_MOUSE	yes	yes	91	106	16	R	S	0	1756.903	2	3.66E-05	157.68	NaN	NaN	0
3388	VDAKPEVQSQPPR	sp|P97379-2|G3BP2_MOUSE	yes	no	245	257	13	R	V	0	1449.758	3	3.42E-02	66.71	1.20	1.12	1
3389	VDFNVPMKNNQITNNQR	sp|P09411|PGK1_MOUSE	yes	no	23	39	17	R	I	0	2030.996	3	3.14E-05	98.06	1.29	0.99	6
3390	VDILDPALLR	sp|O88685|PRS6A_MOUSE	yes	yes	338	347	10	R	S	0	1123.660	2	1.40E-02	107.45	NaN	NaN	0
3391	VDILENQAMDTR	sp|P15626|GSTM2_MOUSE	yes	yes	97	108	12	R	I	0	1403.672	2	3.94E-03	110.38	NaN	NaN	0
3392	VDKGGDPALIR	sp|P26638|SYSC_MOUSE	yes	yes	10	20	11	R	E	0	1139.630	3	2.16E-03	91.96	1.25	0.97	5
3393	VDLFYLHAPDHSTPVEETLR	sp|Q8CG76|ARK72_MOUSE	yes	yes	143	162	20	R	A	0	2338.159	4	3.95E-03	81.02	NaN	NaN	0
3394	VDMLKIR	sp|P07356|ANXA2_MOUSE	yes	yes	298	304	7	E	S	0	873.511	2	2.66E-02	89.30	1.24	1.07	4

3395	VDNIIKAAPR	sp|P80314|TCPB_MOUSE	yes	yes	517	526	10	R	K	0	1095.640	3	6.54E-03	77.19	1.24	1.19	1
3396	VDQLTAQLADLAAR	sp|Q64727|VINC_MOUSE	yes	yes	548	561	14	R	G	0	1483.800	2	3.85E-04	149.30	NaN	NaN	0
3397	VDSLIPWIR	sp|Q9QXZ0-3|MACF1_MOUSE	yes	no	266	274	9	R	Q	0	1097.623	2	2.18E-02	105.52	NaN	NaN	0
3398	VDTNKAQKEDIVLNSQNR	sp|Q3V188|ENDOU_MOUSE	yes	no	152	169	18	R	I	0	2071.066	4	7.96E-05	83.76	1.26	1.00	5
3399	VDTWFNQPAR	sp|P47963|RL13_MOUSE	yes	yes	22	31	10	R	K	0	1232.594	2	1.41E-03	157.96	NaN	NaN	0
3400	VDVADQAQDKDR	sp|Q8BGD9|IF4B_MOUSE	yes	yes	168	179	12	R	D	0	1358.643	3	4.16E-02	46.88	0.90	0.83	3
3401	VDYAGVTVDELGKVLTPTQVMNI	sp|P70296|PEBP1_MOUSE	yes	yes	27	49	23	R	P	0	2504.295	3	6.12E-07	108.08	0.93	0.89	3
3402	VEDIIKAINTFPYR	sp|Q60847|COCA1_MOUSE	yes	no	500	513	14	R	G	0	1677.909	3	4.02E-04	148.70	2.15	1.52	3
3403	VEDLIVSELR	sp|Q91UZ5|IMPA2_MOUSE	yes	yes	63	72	10	R	K	0	1171.645	2	2.25E-02	91.55	NaN	NaN	0
3404	VEDVEALDQKGYNAR	sp|Q8CI94|PYGB_MOUSE	yes	yes	716	730	15	R	E	0	1705.827	3	6.27E-02	51.03	1.30	1.01	6
3405	VEDYLSAILNR	sp|P07724|ALBU_MOUSE	yes	yes	473	483	11	C	V	0	1291.677	2	1.77E-02	84.48	NaN	NaN	0
3406	VEELLAEAR	sp|Q9R0N0|GALK1_MOUSE	yes	yes	9	17	9	R	R	0	1028.550	2	3.53E-02	90.15	NaN	NaN	0
3407	VEENAQQQKATGSEMSQR	sp|E9Q557|DESP_MOUSE	yes	yes	1438	1455	18	R	K	0	2019.928	3	8.40E-14	181.34	1.55	1.09	6
3408	VEEVDEEGKFVR	sp|P48678|LMNA_MOUSE	yes	no	442	453	12	A	L	0	1434.699	2	1.50E-03	88.02	1.74	1.03	3
3409	VEEVQDGKVISSR	sp|Q9QWL7|K1C17_MOUSE	yes	no	413	425	13	I	E	0	1444.752	2	1.95E-05	136.33	1.50	0.94	3
3410	VEEVVPSVIEPSFGLGR	sp|Q9CZD3|SYG_MOUSE	yes	yes	557	573	17	H	I	0	1812.962	2	1.87E-02	64.57	NaN	NaN	0
3411	VEFDTFGELKVPTDKYYGAQTVR	sp|P97807-2|FUMH_MOUSE	yes	no	9	31	23	R	S	0	2662.328	4	2.88E-02	40.72	1.08	1.03	5
3412	VEFLRPSFIDGTIR	sp|Q9JKF6|PVRL1_MOUSE	yes	yes	97	110	14	R	L	1	1648.894	3	1.72E-02	71.98	NaN	NaN	0
3413	VEIIANDQGNR	sp|P63017|HSP7C_MOUSE	no	no	26	36	11	K	T	0	1227.621	2	2.75E-04	160.18	NaN	NaN	0
3414	VEKDGLILTSR	sp|Q99LX0|PARK7_MOUSE	yes	yes	146	156	11	R	G	0	1229.698	2	3.36E-04	126.10	0.85	0.81	3
3415	VEKLKPVPIAR	sp|P24452|CAPG_MOUSE	yes	yes	26	36	11	R	E	0	1248.792	3	5.40E-02	67.21	1.02	1.00	3
3416	VELSTGMPR	sp|Q8BL97-3|SRSF7_MOUSE	yes	no	79	87	9	R	R	0	988.501	2	2.08E-02	111.46	NaN	NaN	0
3417	VEPVDASGTEKAFEPATGR	sp|Q9JLJ2|AL9A1_MOUSE	yes	yes	20	38	19	R	V	0	1959.954	3	1.33E-02	48.38	0.99	0.85	4
3418	VEQIAAIAQELNELDYYDSHNVNT	sp|P57780|ACTN4_MOUSE	yes	yes	471	495	25	R	C	0	2904.389	3	1.10E-06	125.83	NaN	NaN	0
3419	VESDLNGLRR	sp|Q61897|KT33B_MOUSE	yes	no	155	164	10	L	I	1	1157.615	2	1.70E-02	100.02	NaN	NaN	0
3420	VESPVLPPVLVPR	sp|P97454|SMAD5_MOUSE	yes	no	131	143	13	R	H	0	1400.839	2	6.83E-03	86.91	NaN	NaN	0
3421	VESTEQLIEIASR	sp|P02468|LAMC1_MOUSE	yes	yes	1136	1148	13	R	E	0	1473.768	2	7.18E-03	85.84	NaN	NaN	0
3422	VETPVLPPVLVPR	sp|Q62432-2|SMAD2_MOUSE	yes	no	140	152	13	R	H	0	1414.855	2	1.01E-02	77.12	NaN	NaN	0
3423	VEVGPVCFK	sp|Q01149|CO1A2_MOUSE	yes	no	1364	1372	9	R	-	0	1033.527	2	2.90E-03	107.57	1.38	1.12	8
3424	VEVKKAVPKEDIHAGGGGAR	sp|Q9CX86|ROA0_MOUSE	yes	yes	168	187	20	R	A	0	2017.107	5	1.15E-02	64.25	1.17	0.81	1
3425	VEVTEFEDIKSGYR	sp|Q9EQU5-2|SET_MOUSE	yes	no	110	123	14	R	I	0	1670.815	3	5.45E-04	85.84	0.92	0.88	3
3426	VFANAPDSACVIGLR	sp|P12382|K6PL_MOUSE	yes	yes	699	713	15	R	K	0	1588.803	2	6.67E-04	117.20	NaN	NaN	0
3427	VFAVVITDGR	sp|Q02788|CO6A2_MOUSE	yes	yes	740	749	10	R	H	0	1075.603	2	2.85E-02	82.42	NaN	NaN	0
3428	VFDMLNR	sp|P60843|IF4A1_MOUSE	yes	no	162	168	7	R	R	0	893.443	2	3.99E-03	188.61	NaN	NaN	0
3429	VFDRPLPVSR	sp|Q9R1P4|PSA1_MOUSE	yes	yes	98	107	10	F	L	1	1184.667	2	1.25E-01	54.26	NaN	NaN	0
3430	VFGETTNSLSVAWDHADGPVQQ	sp|Q60847|COCA1_MOUSE	yes	no	2035	2058	24	R	I	0	2676.257	3	3.42E-04	84.17	NaN	NaN	0
3431	VFIMDSCDELIPEYLNFIR	sp|P11499|HS90B_MOUSE	yes	yes	360	378	19	R	G	0	2373.139	2	6.26E-06	130.27	NaN	NaN	0
3432	VFLDPNTLSDDGTVALR	sp|Q9QUR6|PPCE_MOUSE	yes	yes	112	128	17	R	G	0	1831.932	2	3.84E-05	152.94	NaN	NaN	0
3433	VFLWGSFR	sp|Q8VE37|RCC1_MOUSE	yes	yes	140	147	8	R	D	0	1010.534	2	8.87E-03	172.14	NaN	NaN	0
3434	VFNETPINPR	sp|Q9QZE5|COPG1_MOUSE	yes	yes	33	42	10	R	K	0	1185.614	2	2.67E-02	85.15	NaN	NaN	0
3435	VFNIMR	sp|Q99L45|IF2B_MOUSE	yes	yes	181	186	6	R	E	0	778.416	2	6.15E-02	118.18	NaN	NaN	0
3436	VFPSIVGRPR	sp|P63260|ACTG_MOUSE	no	no	30	39	10	A	H	1	1126.661	2	6.68E-03	135.86	NaN	NaN	0
3437	VFQHLGNLQVLR	sp|Q80X72|LRC15_MOUSE	yes	yes	192	203	12	R	L	0	1422.810	3	2.81E-04	162.26	NaN	NaN	0
3438	VFSGVVSTGLKVR	sp|P58252|EF2_MOUSE	yes	yes	416	428	13	R	I	0	1347.787	3	5.24E-04	96.06	1.28	1.05	9
3439	VFSWGFGGYGR	sp|Q8BK67|RCC2_MOUSE	yes	yes	349	359	11	R	L	0	1231.577	2	7.74E-03	110.38	NaN	NaN	0
3440	VFTTQELVQAFTHAPAALEADR	sp|Q8BK64|AHSA1_MOUSE	yes	yes	225	246	22	R	G	0	2414.223	3	5.37E-07	130.89	NaN	NaN	0
3441	VFYLKMKGDYYR	sp|O70456|1433S_MOUSE	no	no	118	129	12	R	Y	0	1581.801	3	1.97E-02	55.26	1.10	1.00	3
3442	VGASFLQR	sp|P05202|AATM_MOUSE	yes	yes	140	147	8	R	F	0	876.482	2	7.59E-04	198.87	NaN	NaN	0
3443	VGDNDFLEVR	sp|O08582|GTPB1_MOUSE	yes	yes	153	162	10	R	V	0	1162.562	2	1.94E-02	96.23	NaN	NaN	0
3444	VGDVYIPR	sp|Q62093|SRSF2_MOUSE	yes	yes	40	47	8	R	D	0	917.497	2	2.54E-02	116.73	NaN	NaN	0
3445	VGDYGSLSGR	sp|Q9WUU7|CATZ_MOUSE	yes	yes	192	201	10	R	E	0	1009.483	2	1.46E-02	104.82	NaN	NaN	0
3446	VGEFVATDLDTGR	sp|Q61495|DSG1A_MOUSE	no	no	404	416	13	R	A	0	1378.673	2	2.02E-03	101.43	NaN	NaN	0
3447	VGEIIKR	sp|Q01768|NDKB_MOUSE	yes	no	21	27	7	L	F	0	813.507	2	5.10E-03	143.85	1.12	0.97	4
3448	VGEIVVFR	sp|Q9R0P6|SC11A_MOUSE	yes	yes	79	86	8	R	I	0	917.533	2	3.71E-02	127.02	NaN	NaN	0
3449	VGFGQCAGKVLPALSPA	sp|P35505|FAAA_MOUSE	yes	no	403	419	17	R	-	0	1670.881	2	5.40E-03	60.55	0.95	0.90	5
3450	VGGGIDVPVPR	sp|Q3U0V1|FUBP2_MOUSE	yes	yes	322	332	11	R	H	0	1064.598	2	3.64E-03	130.01	NaN	NaN	0
3451	VGGIKEDTEEHHLR	sp|O88569|ROA2_MOUSE	no	no	109	122	14	F	D	0	1618.806	4	2.91E-03	72.89	1.20	1.02	7
3452	VGGIKEDTEEYNLR	sp|Q8BG05-2|ROA3_MOUSE	no	no	108	121	14	F	D	0	1621.795	3	1.19E-06	153.32	1.18	0.75	9
3453	VGGLSPDTPEEKIR	sp|Q60668-4|HNRPD_MOUSE	yes	no	167	180	14	F	E	0	1496.784	3	9.19E-05	114.70	0.93	0.79	6
3454	VGGNIEVLGFNAR	sp|Q6PDQ2|CHD4_MOUSE	yes	yes	1400	1412	13	R	Q	0	1344.715	2	2.04E-04	166.45	NaN	NaN	0
3455	VGGVQSLGGTGALR	sp|P05201|AATC_MOUSE	yes	yes	101	114	14	R	I	0	1270.699	2	4.96E-04	145.43	NaN	NaN	0
3456	VGHSELVGEIIR	sp|P50516-2|VATA_MOUSE	yes	no	45	56	12	R	L	0	1307.720	3	8.32E-03	93.35	NaN	NaN	0
3457	VGIGAFPTEQDNEIGELLQTR	sp|P46664|PURA2_MOUSE	yes	yes	304	324	21	R	G	0	2286.149	2	4.93E-03	72.57	NaN	NaN	0
3458	VGINSFGFGGSNVHVILQPNTR	sp|P19096|FAS_MOUSE	yes	yes	388	409	22	N	Q	0	2312.203	3	6.17E-05	108.08	NaN	NaN	0
3459	VGLENFLLR	sp|Q91YJ2|SNX4_MOUSE	yes	yes	156	164	9	R	V	0	1059.608	2	4.34E-02	82.29	NaN	NaN	0
3460	VGLIGSCTNSSYEDMGR	sp|Q99KI0|ACON_MOUSE	yes	yes	379	395	17	R	S	0	1844.803	2	4.99E-04	114.63	NaN	NaN	0
3461	VGLKAPGIIPR	sp|Q03265|ATPA_MOUSE	yes	yes	172	182	11	R	I	0	1119.713	2;3	3.49E-04	125.75	1.58	0.87	11
3462	VGLLEALLPGQPEAVAR	sp|P51855|GSHB_MOUSE	yes	yes	314	330	17	R	L	0	1731.988	2	5.88E-03	79.32	NaN	NaN	0
3463	VGLPLPVPFSEPGYR	sp|Q99K30|ES8L2_MOUSE	yes	no	224	238	15	R	R	0	1626.877	2	1.79E-02	68.97	NaN	NaN	0
3464	VGMGQKDSYVGDEAQSKR	sp|P63260|ACTG_MOUSE	no	no	45	62	18	M	G	0	1953.921	4	1.07E-01	36.13	1.21	1.17	1
3465	VGNLGLATSFFNER	sp|P16381|DDX3L_MOUSE	yes	no	534	547	14	R	N	0	1523.773	2	1.91E-04	158.52	NaN	NaN	0
3466	VGQMVISGVDR	sp|Q9DBG5|PLIN3_MOUSE	yes	yes	185	195	11	R	V	0	1159.602	2	1.83E-02	83.23	NaN	NaN	0
3467	VGTGIVHAINNVVR	sp|Q02788|CO6A2_MOUSE	yes	yes	932	945	14	H	G	0	1447.826	3	1.13E-03	107.65	NaN	NaN	0
3468	VGTKCCTLPEDQR	sp|P07724|ALBU_MOUSE	yes	yes	457	469	13	R	L	0	1562.718	2;3	3.03E-08	164.20	1.35	1.16	13
3469	VGVPTETGALTLNR	sp|Q8BWT1|THIM_MOUSE	yes	yes	77	90	14	R	L	0	1426.778	2	8.92E-04	131.66	NaN	NaN	0
3470	VGVVQYSHEGTFEAIR	sp|Q02788|CO6A2_MOUSE	yes	yes	675	690	16	R	L	0	1790.895	3	6.27E-05	153.22	NaN	NaN	0
3471	VGVVQYSSDTR	sp|Q60847|COCA1_MOUSE	yes	no	179	189	11	R	T	0	1209.599	2	3.46E-04	155.00	NaN	NaN	0
3472	VGWEQLLTTIAR	sp|P57780|ACTN4_MOUSE	no	no	735	746	12	R	T	0	1385.767	2	5.85E-04	152.47	NaN	NaN	0
3473	VHHGTPLSEAPHDDAHGNFQYDI	sp|Q8BH97|RCN3_MOUSE	yes	yes	34	62	29	R	D	0	3253.471	5	7.67E-05	76.90	NaN	NaN	0
3474	VHIEIGPDGR	sp|Q9Z2X1|HNRPF_MOUSE	no	no	317	326	10	R	V	0	1091.572	2;3	2.88E-04	138.22	0.07	0.05	1
3475	VHIGQVIMSIR	sp|Q6ZWV3|RL10_MOUSE	yes	no	129	139	11	R	T	0	1251.712	3	8.34E-03	107.55	NaN	NaN	0
3476	VIAPGSSLPTSLTIPNPQETSNVVV	sp|Q61495|DSG1A_MOUSE	yes	yes	917	944	28	R	V	0	2905.540	2;3	4.92E-05	89.98	NaN	NaN	0
3477	VIAPGSSLPTSLTIPNPR	sp|Q7TSF1|DSG1B_MOUSE	yes	yes	920	937	18	R	E	0	1819.020	2	2.24E-04	123.14	NaN	NaN	0
3478	VICPLPSASSSIVAPTELR	sp|O35902|DSG3_MOUSE	yes	yes	960	978	19	R	G	0	1996.066	2	1.07E-03	100.97	NaN	NaN	0
3479	VIDKDGIHNLENIAFPKR	sp|Q9R1P3|PSB2_MOUSE	yes	yes	182	199	18	R	D	0	2078.127	5	1.38E-07	120.90	1.45	1.39	3
3480	VIEPFSR	sp|Q8BG32|PSD11_MOUSE	yes	yes	338	344	7	R	V	0	846.460	2	8.94E-02	89.14	NaN	NaN	0
3481	VIGLLDVFTPAR	sp|P47811-2|MK14_MOUSE	yes	no	83	94	12	N	S	0	1299.755	2	1.38E-02	79.49	NaN	NaN	0
3482	VIGLSSDLQQVGGASAR	sp|Q9DCH4|EIF3F_MOUSE	yes	yes	266	282	17	R	I	0	1656.880	2	4.31E-03	86.49	NaN	NaN	0
3483	VIGSGCNLDSAR	sp|P06151|LDHA_MOUSE	no	no	158	169	12	R	F	0	1247.593	2	1.53E-03	140.14	NaN	NaN	0
3484	VIHGNQIATNGVVHVIDR	sp|Q62009-5|POSTN_MOUSE	yes	no	213	230	18	R	V	0	1941.054	3;4	4.15E-05	140.46	NaN	NaN	0
3485	VIIEKYYTR	sp|P63276|RS17_MOUSE	yes	yes	15	23	9	R	L	0	1183.660	2;3	1.05E-03	126.71	1.02	0.96	4
3486	VIIPFSGWCDGNSNMSR	sp|P97350|PKP1_MOUSE	yes	yes	380	396	17	R	E	0	1938.872	2	1.24E-02	70.78	NaN	NaN	0
3487	VIKDFMIQGGDFTAR	sp|P30412|PPIC_MOUSE	yes	yes	90	104	15	R	D	0	1696.861	3	1.93E-04	89.91	1.18	1.06	5
3488	VILQDFTGVPAVVDFAAMR	sp|P28271|ACOC_MOUSE	yes	yes	83	101	19	R	D	0	2048.077	2;3	5.36E-03	81.81	NaN	NaN	0
3489	VILQPDVHPGNCWAFQGPQGFA	sp|Q8BJS4-3|SUN2_MOUSE	yes	no	572	596	25	R	L	0	2791.402	3	5.72E-06	112.85	NaN	NaN	0
3490	VINETSQHHDDLE	sp|P20152|VIME_MOUSE	yes	no	454	466	13	Q	-	0	1535.685	2	6.69E-04	147.26	NaN	NaN	0
3491	VIQPTSGMIGNLSMTPELSSAHN\	sp|Q61495|DSG1A_MOUSE	yes	yes	945	973	29	R	V	0	3080.564	3	1.13E-08	120.93	NaN	NaN	0
3492	VISGVLQLGNIAFKKER	sp|Q8VDD5|MYH9_MOUSE	yes	yes	342	358	17	R	N	0	1871.099	3;4	2.08E-04	129.05	1.41	1.37	3
3493	VISSIEQKTER	sp|Q9CQV8-2|1433B_MOUSE	yes	no	61	71	11	R	N	0	1288.699	3	2.79E-03	84.48	1.10	1.01	5
3494	VITIMQNPR	sp|P62270|RS18_MOUSE	yes	yes	67	75	9	R	Q	0	1070.591	2	1.29E-05	160.26	99.18	80.35	1
3495	VITNFNSAHDTDR	sp|Q08189|TGM3_MOUSE	yes	yes	293	305	13	R	N	0	1488.696	3	1.46E-03	119.39	NaN	NaN	0
3496	VIVCNTKQDNNWGKEER	sp|P16110|LEG3_MOUSE	yes	yes	184	200	17	R	Q	0	2089.001	4	4.67E-03	62.86	1.18	1.02	6
3497	VKADFKELVLSNNDLHEPGVR	sp|Q91VI7|RINI_MOUSE	yes	yes	163	183	21	R	I	0	2379.255	4	6.98E-02	26.36	1.14	1.12	1

3498	VKKQCKGVQDSIADAEQR	sp|Q3TTY5|K22E_MOUSE	yes	no	434	451	18	H	G	0	2059.048	4	2.53E-05	97.10	3.11	2.01	3
3499	VKNFGIWLR	sp|P62717|RL18A_MOUSE	yes	yes	75	83	9	R	Y	0	1131.655	3	5.28E-03	97.43	1.21	0.91	2
3500	VLAALQAGNR	sp|P26039|TLN1_MOUSE	yes	yes	1964	1973	10	H	G	0	1011.583	2	2.61E-02	86.14	NaN	NaN	0
3501	VLANPGNSQVAR	sp|P70168|IMB1_MOUSE	yes	yes	43	54	12	R	V	0	1224.658	2	1.93E-03	134.98	NaN	NaN	0
3502	VLCVINPGNPTGQVQTR	sp|Q8QZR5|ALAT1_MOUSE	yes	yes	236	252	17	R	E	0	1851.963	2	5.43E-03	81.35	NaN	NaN	0
3503	VLDASWYSPGTR	sp|P52196|THTR_MOUSE	yes	yes	31	42	12	R	Q	0	1350.657	2	6.01E-02	61.11	NaN	NaN	0
3504	VLDEADEMLSR	sp|P60843|IF4A1_MOUSE	yes	no	180	190	11	F	G	0	1276.597	2	4.42E-03	125.97	NaN	NaN	0
3505	VLDELTLAR	sp|Q61781|K1C14_MOUSE	no	no	230	238	9	R	A	0	1028.587	2	1.51E-02	134.26	NaN	NaN	0
3506	VLDELTLCR	sp|Q9Z320|K1C27_MOUSE	no	no	187	195	9	R	T	0	1117.580	2	8.44E-06	172.23	0.36	0.29	2
3507	VLDELTLSKSDLEMQIESLNEELAY	sp|P02535-3|K1C10_MOUSE	yes	no	247	281	35	R	D	0	4176.061	5;6	1.32E-16	173.95	2.34	1.51	5
3508	VLDILEDYCMWR	sp|Q91ZW3|SMCA5_MOUSE	yes	yes	510	521	12	R	N	0	1611.743	2	2.43E-02	73.44	NaN	NaN	0
3509	VLDPFTIKPLDR	sp|P40142|TKT_MOUSE	yes	yes	531	542	12	R	K	0	1412.803	2;3	7.47E-04	101.53	1.14	0.96	10
3510	VLDTASGLPAQGLCLR	sp|Q9CRB3|HIUH_MOUSE	yes	yes	12	27	16	H	L	0	1669.882	2	9.76E-07	121.99	3.42	2.91	1
3511	VLEAKELALQPKDDIVDR	sp|Q9CZD3|SYG_MOUSE	yes	yes	94	111	18	R	A	0	2051.126	3;4	2.10E-07	116.06	1.12	1.08	5
3512	VLELLLPIR	sp|A3KMP2-2|TTC38_MOUSE	yes	no	204	212	9	R	Y	0	1064.696	2	1.97E-02	117.89	NaN	NaN	0
3513	VLFDTGLVNPR	sp|P10493|NID1_MOUSE	yes	yes	1055	1065	11	R	G	0	1229.677	2	1.84E-02	82.95	NaN	NaN	0
3514	VLFFDELDSIAKAR	sp|Q01853|TERA_MOUSE	yes	yes	573	586	14	C	G	0	1622.867	3	6.46E-03	66.00	1.17	1.02	4
3515	VLGELWPLFGGR	sp|P55096|ABCD3_MOUSE	yes	yes	485	496	12	R	L	0	1342.740	2	7.76E-03	94.77	NaN	NaN	0
3516	VLGLGLGGLR	sp|Q8VHN8-3|SDO5_MOUSE	yes	no	81	90	10	R	L	0	953.602	2	2.17E-02	92.84	NaN	NaN	0
3517	VLGLVLLR	sp|P27048|RSMB_MOUSE	yes	no	66	73	8	R	G	0	881.606	2	3.78E-02	124.34	NaN	NaN	0
3518	VLIAAHGNSLR	sp|Q9DBJ1|PGAM1_MOUSE	yes	no	181	191	11	R	G	0	1149.662	2;3	6.43E-03	116.55	NaN	NaN	0
3519	VLITGATGLLGR	sp|Q99LB6-2|MAT2B_MOUSE	yes	no	20	31	12	R	A	0	1169.713	2	4.52E-03	103.44	NaN	NaN	0
3520	VLITTDLLAR	sp|P60843|IF4A1_MOUSE	yes	no	325	334	10	R	G	0	1113.676	2	6.79E-03	135.43	NaN	NaN	0
3521	VLKEGIEYR	sp|Q61599|GDIR2_MOUSE	yes	yes	99	107	9	F	V	0	1105.613	3	1.84E-02	108.43	1.38	1.10	3
3522	VLKEGVEYR	sp|Q99PT1|GDIR1_MOUSE	yes	yes	103	111	9	F	I	0	1091.598	3	1.36E-03	123.42	1.22	0.99	3
3523	VLLATLSIPITPER	sp|P23116|EIF3A_MOUSE	yes	yes	322	335	14	R	T	0	1521.913	2	1.39E-04	164.64	NaN	NaN	0
3524	VLLEAAVR	sp|P28271|ACOC_MOUSE	yes	no	41	48	8	R	N	0	869.533	2	3.75E-02	125.50	NaN	NaN	0
3525	VLLFSDGNSQGATAEAIEKAVQEA	sp|Q04857|CO6A1_MOUSE	yes	yes	936	961	26	R	A	0	2731.378	3	3.91E-10	142.32	1.12	0.80	5
3526	VLLGETGKEKLPR	sp|P62281|RS11_MOUSE	yes	yes	23	35	13	R	Y	0	1438.851	3;4	1.49E-02	54.34	1.22	0.97	10
3527	VLLQEEGAR	sp|E9Q557|DESP_MOUSE	yes	yes	1188	1196	9	R	K	0	1013.551	2	3.19E-03	163.15	NaN	NaN	0
3528	VLMIKALELDSNLYR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	741	755	15	C	I	0	1776.981	3	1.03E-04	97.45	1.26	0.85	3
3529	VLNLGKDSNNLCLHFNPR	sp|P16045|LEG1_MOUSE	yes	yes	32	49	18	F	F	0	2110.074	4	1.93E-02	46.89	0.76	0.72	2
3530	VLNTNIDGR	sp|P62270|RS18_MOUSE	yes	yes	15	23	9	R	R	0	1000.530	2	3.62E-03	160.59	NaN	NaN	0
3531	VLQALEGLKMVEKDQDGGR	sp|Q9CZX8|RS19_MOUSE	yes	yes	103	121	19	R	K	0	2085.089	3;4	4.13E-04	75.55	1.21	1.02	7
3532	VLQDLVMDILR	sp|Q9JIF7|COPB_MOUSE	yes	yes	317	327	11	R	V	0	1313.738	2	7.81E-03	110.08	NaN	NaN	0
3533	VLQPGTALFSR	sp|Q91X96|MSS4_MOUSE	yes	yes	30	40	11	R	R	0	1187.666	2	1.99E-02	79.66	NaN	NaN	0
3534	VLQQKLEAIEDDSGR	sp|Q9JMA1|UBP14_MOUSE	yes	yes	210	224	15	R	E	0	1699.874	3	5.32E-02	53.30	1.00	0.87	2
3535	VLSAPPHFHFGQTNR	sp|Q9D8N0|EF1G_MOUSE	yes	yes	31	45	15	R	T	0	1706.864	4	1.10E-02	73.30	NaN	NaN	0
3536	VLSIGDGIAR	sp|Q03265|ATPA_MOUSE	yes	yes	74	83	10	R	V	0	999.571	2	1.43E-02	106.16	NaN	NaN	0
3537	VLSRPEEVEAEAVNR	sp|O08553|DPYL2_MOUSE	yes	yes	224	238	15	H	S	1	1696.874	3	7.16E-04	110.97	NaN	NaN	0
3538	VLSRPNAQELPSMYQR	sp|O35129|PHB2_MOUSE	yes	yes	108	123	16	R	L	1	1887.963	3	3.86E-04	126.77	NaN	NaN	0
3539	VLSSIEQKSNEEGSEEKGPEVKEYR	sp|O70456|1433S_MOUSE	yes	yes	61	85	25	R	E	0	2850.388	4;5	1.10E-04	90.48	1.27	1.00	11
3540	VLTVTAVQENLMSALAEAR	sp|Q64737|PUR2_MOUSE	yes	no	386	404	19	R	K	0	2015.072	2;3	1.88E-03	97.38	NaN	NaN	0
3541	VLVALEQQSPDIAQGVHLDR	sp|Q3THS6|METK2_MOUSE	yes	yes	106	125	20	N	N	0	2187.165	3	2.05E-08	176.10	NaN	NaN	0
3542	VLVDQTTGLSR	sp|P70372|ELAV1_MOUSE	yes	yes	137	147	11	R	G	0	1187.651	2	1.22E-04	171.92	NaN	NaN	0
3543	VLVLYDEIKKYT	sp|P51881|ADT2_MOUSE	yes	no	287	298	12	F	-	0	1482.833	2;3	2.10E-03	77.19	1.41	0.88	3
3544	VLVNDAQKVTEGQQER	sp|Q62318|TIF1B_MOUSE	yes	no	313	328	16	R	L	0	1812.933	3	3.09E-02	44.93	1.38	1.06	7
3545	VLVSLSAAGR	sp|P97429|ANXA4_MOUSE	yes	yes	151	160	10	R	D	0	971.576	2	7.04E-03	134.51	NaN	NaN	0
3546	VLVTGKTAEYDVAFGER	sp|Q04857|CO6A1_MOUSE	yes	yes	982	998	17	R	H	0	1853.952	3	5.23E-02	51.80	1.44	0.87	5
3547	VLYPNDNFFEGKELR	sp|Q8CI94|PYGB_MOUSE	yes	no	279	293	15	R	L	0	1839.916	3	3.39E-04	77.78	1.17	0.89	5
3548	VMGNQVFPEVTR	sp|P97350|PKP1_MOUSE	yes	yes	611	622	12	R	L	0	1375.692	2	2.26E-04	166.04	NaN	NaN	0
3549	VMKFSVSPVVR	sp|P58252|EF2_MOUSE	yes	yes	496	506	11	R	V	0	1247.706	2;3	1.90E-04	132.32	1.18	1.07	12
3550	VMLGETNPADSKPGTIR	sp|Q01768|NDKB_MOUSE	yes	no	89	105	17	R	G	0	1784.909	2;3	2.70E-11	159.81	1.26	1.00	21
3551	VMLYPSR	sp|O55142|RL35A_MOUSE	yes	yes	103	109	7	R	I	0	864.453	2	4.27E-02	154.11	NaN	NaN	0
3552	VNAAKNKTGVAPIIDVVR	sp|P14115|RL27A_MOUSE	yes	yes	88	105	18	R	S	0	1864.089	3;4	2.26E-02	56.12	1.07	0.88	7
3553	VNEILSALER	sp|Q99K41|EMIL1_MOUSE	yes	yes	494	503	10	R	R	0	1142.630	2	1.29E-02	111.86	NaN	NaN	0
3554	VNIAFNYDMPEDSDTYLHR	sp|Q9Z1N5|DX39B_MOUSE	yes	yes	356	374	19	R	V	0	2299.022	3	4.70E-04	110.56	NaN	NaN	0
3555	VNLAMDVGKAR	sp|P52480|KPYM_MOUSE	no	no	490	500	11	R	G	0	1172.634	2;3	2.96E-03	118.90	1.25	1.00	9
3556	VNLCDCTHPSQCPLR	sp|P55850-2|DSC3_MOUSE	yes	no	667	681	15	R	S	0	1855.813	3	3.58E-03	87.52	NaN	NaN	0
3557	VNMSGVSSSNGVVDPR	sp|Q9CZY3|UB2V1_MOUSE	yes	yes	88	103	16	R	A	0	1603.762	2	4.99E-04	118.31	NaN	NaN	0
3558	VNPTVFFDITADDEPLGR	sp|P17742|PPIA_MOUSE	yes	yes	2	19	18	M	V	0	2004.979	2	6.11E-04	108.71	NaN	NaN	0
3559	VNQAIWLLCTGAR	sp|P97461|RS5_MOUSE	yes	yes	147	159	13	R	E	0	1500.787	2;3	5.69E-05	177.16	NaN	NaN	0
3560	VNVTGIYR	sp|P49717|MCM4_MOUSE	yes	yes	387	394	8	R	A	0	920.508	2	2.07E-02	155.88	NaN	NaN	0
3561	VNYDTTESKLR	sp|Q62376|RU17_MOUSE	yes	no	110	120	11	R	R	0	1324.662	3	2.68E-03	85.81	1.08	0.72	6
3562	VPAPSIEDICSVLSTVCR	sp|Q8R323|RFC3_MOUSE	yes	yes	184	201	18	R	K	0	2001.986	2	5.26E-03	84.65	NaN	NaN	0
3563	VPAPTNLQFTEVTPESFR	sp|Q60847|COCA1_MOUSE	yes	no	1655	1672	18	R	G	0	2032.027	2;3	5.72E-06	160.55	NaN	NaN	0
3564	VPDGMVGLIIGR	sp|Q3U0V1|FUBP2_MOUSE	yes	yes	152	163	12	R	G	0	1225.685	2	4.52E-03	103.43	NaN	NaN	0
3565	VPDVLVADPPTAR	sp|Q8BHN3|GANAB_MOUSE	yes	no	115	127	13	R	L	0	1348.735	2	6.06E-03	89.23	NaN	NaN	0
3566	VPELFANR	sp|Q8VE37|RCC1_MOUSE	yes	yes	207	214	8	R	G	0	944.508	2	3.08E-02	138.83	NaN	NaN	0
3567	VPFSLLR	sp|P14602|HSPB1_MOUSE	yes	no	6	12	7	R	S	0	830.501	2	4.28E-02	153.88	NaN	NaN	0
3568	VPGDQTSTTIR	sp|Q80YX1-5|TENA_MOUSE	yes	no	670	680	11	R	E	0	1173.599	2	5.11E-03	122.70	NaN	NaN	0
3569	VPKDEQGSAADSEDSPTIEAVR	sp|P10518|HEM2_MOUSE	yes	yes	85	106	22	R	L	0	2300.077	3	1.90E-16	162.83	1.11	0.96	4
3570	VPLDVAYAR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	3054	3062	9	R	G	0	1002.550	2	1.68E-02	130.75	NaN	NaN	0
3571	VPLVAPEDLR	sp|Q8CIG8|ANM5_MOUSE	yes	yes	155	164	10	R	D	0	1107.629	2	3.98E-02	74.84	NaN	NaN	0
3572	VPNYQALLR	sp|Q04857|CO6A1_MOUSE	yes	yes	1003	1011	9	R	G	0	1072.603	2	1.84E-02	124.98	NaN	NaN	0
3573	VPPPPLAPR	sp|A2BDX3|MOCS3_MOUSE	yes	yes	44	52	9	R	A	0	942.565	2	3.12E-02	94.11	NaN	NaN	0
3574	VPPPPPALR	sp|Q9JMH9-4|MY18A_MOUSE	yes	no	211	219	9	L	E	0	942.565	2	1.07E-02	81.30	14.03	9.66	1
3575	VPPPPPIAR	sp|Q9Z204-4|HNRPC_MOUSE	yes	no	130	138	9	R	A	0	942.565	2	6.97E-02	71.50	NaN	NaN	0
3576	VPQLLIAPFKEEDEWDSPHIVR	sp|Q60716-2|P4HA2_MOUSE	yes	no	321	342	22	R	Y	0	2617.354	4	2.21E-03	55.45	1.34	1.27	3
3577	VPTPNVSVVDLTCR	sp|P16858|G3P_MOUSE	yes	no	233	246	14	R	L	0	1555.803	2;3	2.04E-04	156.96	19.73	11.53	2
3578	VPVDVAYKR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	2726	2734	9	R	G	0	1045.592	3	1.67E-02	74.46	1.39	0.96	5
3579	VPVDVAYQR	sp|Q8R0W0|EPIPL_MOUSE	yes	no	746	754	9	R	G	0	1045.556	2	1.14E-02	141.48	NaN	NaN	0
3580	VPVLGSLLNLPGIR	sp|Q9CR60|GOT1B_MOUSE	yes	yes	112	125	14	R	S	0	1446.892	2	4.30E-04	147.73	NaN	NaN	0
3581	VQAVVAVAR	sp|Q62261|SPTB2_MOUSE	yes	no	478	486	9	R	E	0	911.555	2	2.05E-02	113.26	NaN	NaN	0
3582	VQCHQDQSACFQGNGR	sp|Q9D7Z7|LYPD5_MOUSE	yes	yes	152	167	16	R	M	0	1890.785	3	6.41E-04	107.69	NaN	NaN	0
3583	VQDAYTLR	sp|P35492|HUTH_MOUSE	yes	yes	391	398	8	R	C	0	964.498	2	2.92E-02	141.52	NaN	NaN	0
3584	VQDDEVGDGTTSVTVLAAELLR	sp|P80314|TCPB_MOUSE	yes	yes	90	111	22	R	E	0	2287.154	3	1.24E-02	51.88	NaN	NaN	0
3585	VQEIVGALR	sp|Q3UFY7-3|5NT3B_MOUSE	yes	no	21	29	9	R	R	0	983.576	2	4.18E-02	113.74	NaN	NaN	0
3586	VQEQVMMTVKR	sp|P97350|PKP1_MOUSE	yes	yes	41	51	11	R	Q	0	1347.700	3	3.03E-03	81.63	1.77	1.13	2
3587	VQGGGSGQFSAVPLNLIGLKAGR	sp|Q99K85|SERC_MOUSE	yes	yes	75	97	23	F	S	0	2225.228	3	3.66E-05	88.87	1.10	0.92	3
3588	VQIALAQYSGDPR	sp|Q60847|COCA1_MOUSE	yes	no	1236	1248	13	R	T	0	1416.736	2	8.01E-04	143.94	NaN	NaN	0
3589	VQIDNAKLAADDFR	sp|Q61897|KT33B_MOUSE	no	no	129	142	14	V	T	0	1574.805	2	1.31E-08	167.69	1.77	1.12	3
3590	VQIDNAKLASDDFR	sp|Q9D646|KRT34_MOUSE	no	no	129	142	14	V	T	0	1590.800	2	4.88E-04	145.69	1.46	1.00	2
3591	VQIHIPR	sp|P22599|A1AT2_MOUSE	yes	yes	302	308	7	L	L	0	861.518	2	4.35E-02	94.26	NaN	NaN	0
3592	VQISAVHSEEDIDR	sp|O88986|KBL_MOUSE	yes	yes	387	400	14	R	C	0	1596.774	3	2.43E-03	97.80	NaN	NaN	0
3593	VQSTPVTIQVIDVR	sp|O35902|DSG3_MOUSE	yes	no	365	378	14	R	E	0	1553.878	2	7.27E-03	78.81	NaN	NaN	0
3594	VRPLPAATAEGPAAVTLAAPAFSR	sp|P14602|HSPB1_MOUSE	yes	yes	56	79	24	Y	A	1	2333.286	3	5.03E-06	119.76	NaN	NaN	0
3595	VSDTSVVLSMDNNR	sp|Q8BGZ7|K2C75_MOUSE	no	no	300	313	14	Q	S	0	1535.725	2	1.87E-04	159.00	NaN	NaN	0
3596	VSEEWYNR	sp|Q80X19-2|COEA1_MOUSE	yes	no	838	845	8	R	V	0	1081.483	2	2.82E-02	143.12	NaN	NaN	0
3597	VSEIFQVLPETEQEIR	sp|Q9D952|EVPL_MOUSE	yes	yes	1197	1212	16	R	R	0	1915.989	2	8.01E-04	102.29	NaN	NaN	0
3598	VSFCPLSLWR	sp|Q8VBZ3|CLPT1_MOUSE	yes	yes	305	314	10	R	W	0	1263.643	2	1.95E-02	96.17	NaN	NaN	0
3599	VSFELFADKVPKTAENFR	sp|P17742|PPIA_MOUSE	yes	yes	20	37	18	R	A	0	2097.090	2;3;4	8.77E-08	124.29	1.16	0.95	19
3600	VSFSKSTI	sp|P17225|PTBP1_MOUSE	no	no	520	527	8	R	-	0	867.470	2	9.62E-03	101.60	1.31	1.04	6

3601	VSGSGHSSSTGKYTSTSGQNYNST	sp|Q8VHD8|HORN_MOUSE	yes	yes	362	386	25	H	Q	0	2549.138	4	2.90E-10	142.45	1.74	1.14	4
3602	VSIGGCAGSGFR	sp|Q8BGZ7|K2C75_MOUSE	yes	no	71	82	12	R	G	0	1166.550	2	6.43E-03	98.11	NaN	NaN	0
3603	VSISEGDDKIEYR	sp|P35550|FBRL_MOUSE	yes	yes	129	141	13	R	A	0	1509.731	3	2.57E-04	105.65	1.20	0.81	9
3604	VSLDEALQR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	4308	4316	9	R	G	0	1029.546	2	5.32E-04	152.34	39.95	31.77	1
3605	VSLDVNHFAPEELTVKTKEGVVEI	sp|P14602|HSPB1_MOUSE	yes	no	101	131	31	R	Q	0	3489.810	7	2.49E-03	57.85	1.07	0.97	1
3606	VSNMYSSSSCKLPSPSR	sp|Q497I4|KRT35_MOUSE	yes	no	28	44	17	R	G	0	1885.866	3	1.98E-05	100.04	1.97	1.23	7
3607	VSTALSCLLGLPLR	sp|Q9D7H3|RTCA_MOUSE	yes	yes	22	35	14	R	V	0	1498.854	2	7.27E-03	78.81	NaN	NaN	0
3608	VSTLANTLSR	sp|Q8CGN5-2|PLIN1_MOUSE	yes	no	221	230	10	R	H	0	1060.588	2	6.94E-01	38.88	NaN	NaN	0
3609	VSTPTLVEAAR	sp|P07724|ALBU_MOUSE	yes	yes	442	452	11	Q	N	0	1142.630	2	1.77E-02	84.48	0.16	0.15	1
3610	VSVSVSTSHTSMSGSSSR	sp|P04104|K2C1_MOUSE	yes	yes	509	526	18	N	G	0	1781.821	3	6.29E-06	158.45	NaN	NaN	0
3611	VSVVDLTCR	sp|P16858|G3P_MOUSE	yes	no	238	246	9	N	L	0	1047.538	2	4.03E-04	179.51	NaN	NaN	0
3612	VSWQDLKDFMR	sp|O35326|SRSF5_MOUSE	yes	yes	119	129	11	R	Q	0	1423.692	3	4.80E-03	75.82	1.17	1.00	5
3613	VSWTPPSDSVDR	sp|Q60847|COCA1_MOUSE	yes	no	1403	1414	12	R	Y	0	1344.631	2	2.40E-03	128.85	NaN	NaN	0
3614	VTAEDKGTGNKNKITITNDQNR	sp|P20029|GRP78_MOUSE	yes	yes	512	533	22	R	L	0	2416.231	5	1.02E-02	48.05	1.09	0.96	5
3615	VTAIYIDPATHR	sp|P19096|FAS_MOUSE	yes	yes	1053	1064	12	R	Q	0	1355.720	3	2.18E-03	131.69	NaN	NaN	0
3616	VTAVIPCFPYAR	sp|Q9D7G0|PRPS1_MOUSE	yes	no	85	96	12	R	Q	0	1392.722	2	8.61E-03	94.47	NaN	NaN	0
3617	VTDKLTPIHDHIFCCR	sp|Q60692|PSB6_MOUSE	yes	yes	63	78	16	R	S	0	2010.977	3	1.80E-02	48.62	0.71	0.67	1
3618	VTGLHQQPLCTSVNTIYDNAVQG	sp|Q922Q8|LRC59_MOUSE	yes	yes	268	292	25	R	H	0	2783.403	3	2.93E-12	164.06	NaN	NaN	0
3619	VTGNKILR	sp|P62301|RS13_MOUSE	yes	yes	66	73	8	F	I	0	899.555	2	1.09E-02	99.14	0.99	0.92	4
3620	VTGTNKGISPVPINLR	sp|P39054-2|DYN2_MOUSE	yes	no	108	123	16	R	V	0	1664.957	3	4.52E-03	65.47	1.20	0.90	2
3621	VTHLLGYPTQNVSR	sp|Q6P3A4|VSIG8_MOUSE	yes	no	340	353	14	R	S	0	1583.842	3	7.20E-04	137.62	NaN	NaN	0
3622	VTIMPKDIQLAR	sp|P84244|H33_MOUSE	no	no	118	129	12	R	R	0	1383.791	2;3	2.75E-08	179.67	1.55	0.89	31
3623	VTLMQLPTR	sp|Q8JZQ9|EIF3B_MOUSE	yes	yes	482	490	9	R	Q	0	1057.595	2	3.76E-03	159.79	NaN	NaN	0
3624	VTLSKHQTVQLPR	sp|Q91Z31|PTBP2_MOUSE	yes	no	407	419	13	R	E	0	1505.868	4	6.72E-02	39.01	1.62	0.95	3
3625	VTPPEGYDVVTVFR	sp|O70400|PDLI1_MOUSE	yes	yes	313	326	14	R	E	0	1577.809	2	2.12E-02	69.92	NaN	NaN	0
3626	VTTVTEIGKDVIGLR	sp|Q8CIE6|COPA_MOUSE	yes	yes	1203	1217	15	R	I	0	1599.920	3	1.40E-01	32.70	1.43	1.03	3
3627	VTWAPPPSIELTNLLVR	sp|P11276|FINC_MOUSE	yes	yes	1375	1391	17	R	Y	0	1905.072	2	4.31E-03	86.49	NaN	NaN	0
3628	VTYYLDWIHR	sp|P21845|TRYB2_MOUSE	yes	yes	261	270	10	R	Y	0	1364.688	3	9.33E-03	125.75	NaN	NaN	0
3629	VVAEPVELAQEFR	sp|Q9DCT2|NDUS3_MOUSE	yes	yes	218	230	13	R	K	0	1485.783	2	9.16E-03	79.88	NaN	NaN	0
3630	VVANSKESYELR	sp|P67984|RL22_MOUSE	yes	yes	102	113	12	R	Y	0	1393.720	3	1.75E-02	58.04	1.36	0.93	7
3631	VVDALGNAIDGKGPIGSKTR	sp|Q03265|ATPA_MOUSE	yes	yes	150	169	20	R	R	0	1967.080	3;4	6.70E-07	102.89	1.37	0.89	19
3632	VVDLMAYMASKE	sp|P16858|G3P_MOUSE	yes	no	322	333	12	R	-	0	1355.647	2	1.50E-02	61.11	1.20	1.12	5
3633	VVDRPLPVR	sp|P19096|FAS_MOUSE	yes	yes	376	384	9	Q	G	1	1049.635	2	4.68E-02	79.06	NaN	NaN	0
3634	VVFDDTYDR	sp|P16015|CAH3_MOUSE	yes	yes	68	76	9	R	S	0	1128.509	2	5.93E-03	152.34	NaN	NaN	0
3635	VVFQEFR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	712	718	7	R	Q	0	923.487	2	5.61E-02	131.30	NaN	NaN	0
3636	VVGAMQLYSVDR	sp|Q68FD5|CLH1_MOUSE	yes	yes	177	188	12	R	K	0	1336.681	2	1.66E-04	170.04	NaN	NaN	0
3637	VVGNPFDSR	sp|P47738|ALDH2_MOUSE	yes	yes	349	357	9	R	T	0	989.493	2	1.86E-02	123.86	NaN	NaN	0
3638	VVGPISGADLHGMLEIPDLR	sp|Q61495|DSG1A_MOUSE	yes	yes	887	906	20	R	G	0	2088.104	3	2.55E-04	114.55	NaN	NaN	0
3639	VVGPVPGADLHGMLEIPDLR	sp|Q7TSF1|DSG1B_MOUSE	yes	yes	890	909	20	R	D	0	2084.109	3	1.49E-03	96.38	NaN	NaN	0
3640	VVGSEFVQKYLGEGPR	sp|P54775|PRS6B_MOUSE	yes	yes	230	245	16	R	M	0	1763.921	3	4.38E-03	77.75	1.13	0.99	7
3641	VVHIMDFQR	sp|Q8K310|MATR3_MOUSE	yes	yes	399	407	9	R	G	0	1143.586	3	1.71E-02	130.31	NaN	NaN	0
3642	VVIEDGVGDAVLTR	sp|P01027|CO3_MOUSE	yes	yes	292	305	14	R	K	0	1441.778	2	6.55E-03	81.63	NaN	NaN	0
3643	VVLAPQDVVVAR	sp|Q8BKG3|PTK7_MOUSE	yes	yes	219	230	12	R	N	0	1264.750	2	9.40E-03	90.61	NaN	NaN	0
3644	VVLEIDNAR	sp|Q61414|K1C15_MOUSE	yes	no	170	178	9	R	L	0	1027.566	2	1.83E-02	125.82	NaN	NaN	0
3645	VVLIGGKPDR	sp|P61979-3|HNRPK_MOUSE	yes	no	168	177	10	R	V	0	1052.634	2;3	4.87E-03	86.90	1.21	0.82	10
3646	VVLIPYVLPR	sp|Q9D2R0|AACS_MOUSE	yes	yes	236	245	10	R	E	0	1167.738	2	7.53E-02	66.27	NaN	NaN	0
3647	VVLPMELPIR	sp|P00405|COX2_MOUSE	yes	yes	142	151	10	R	M	0	1165.689	2	1.17E-02	116.52	NaN	NaN	0
3648	VVQCSDLGLKTVPKEISPDTTLLDL	sp|P28653|PGS1_MOUSE	yes	yes	74	107	34	R	K	0	3809.972	4	9.97E-07	86.54	NaN	NaN	0
3649	VVSSIEQKTEGAEKKQQMAR	sp|P63101|1433Z_MOUSE	yes	yes	61	80	20	R	E	0	2246.169	4;5	4.51E-03	52.19	1.09	0.98	10
3650	VVVDALSGLKGDLAGR	sp|P30275|KCRU_MOUSE	yes	yes	191	206	16	R	Y	0	1568.889	3	4.18E-03	66.39	1.39	1.03	2
3651	VVVLGLLPR	sp|Q61205|PA1B3_MOUSE	yes	yes	134	142	9	R	G	0	964.643	2	2.21E-02	103.74	NaN	NaN	0
3652	VWAQEMLLR	sp|Q8R5F8|ES8L1_MOUSE	yes	yes	71	79	9	R	V	0	1144.606	2	3.99E-02	85.68	NaN	NaN	0
3653	VWIRPDTPSR	sp|Q91WT9-2|CBS_MOUSE	yes	no	39	48	10	R	C	1	1225.657	3	2.13E-02	82.26	NaN	NaN	0
3654	VWQVTIGTR	sp|P68040|GBLP_MOUSE	yes	yes	309	317	9	R	-	0	1058.587	2	1.95E-02	118.71	NaN	NaN	0
3655	VYDPSTSSLSVR	sp|Q60847|COCA1_MOUSE	yes	no	1854	1865	12	R	W	0	1309.651	2	4.22E-03	107.09	NaN	NaN	0
3656	VYEEDAVPGLTPCR	sp|Q9CZ13|QCR1_MOUSE	yes	yes	256	269	14	R	F	0	1604.751	2	2.86E-03	96.14	NaN	NaN	0
3657	VYEELLAIPVVR	sp|Q8CGC7|SYEP_MOUSE	yes	yes	1196	1207	12	R	G	0	1399.808	2	7.76E-03	94.77	NaN	NaN	0
3658	VYGALMWALGKVVGTPEVLR	sp|Q8BH64|EHD2_MOUSE	yes	yes	232	251	20	R	V	0	2158.197	3	2.76E-02	42.72	1.16	0.73	1
3659	VYHDPSTQEPVTYSQLQQR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	3082	3100	19	R	C	0	2275.087	3	6.44E-04	103.66	NaN	NaN	0
3660	VYIGSFWSQPLLVPDNR	sp|Q8BH64|EHD2_MOUSE	yes	yes	252	268	17	R	R	0	1990.031	2	2.62E-03	94.20	NaN	NaN	0
3661	VYSLDDIR	sp|P97311|MCM6_MOUSE	yes	yes	566	573	8	R	R	0	979.497	2	6.88E-02	82.43	NaN	NaN	0
3662	VYSPSVLFLHPDMGIGGAER	sp|Q9DBE8|ALG2_MOUSE	yes	yes	12	31	20	R	L	0	2144.073	3	1.82E-02	52.19	NaN	NaN	0
3663	WALSQSNPSALR	sp|Q01853|TERA_MOUSE	yes	yes	454	465	12	R	E	0	1328.684	2	1.05E-04	174.23	NaN	NaN	0
3664	WDPAPGPVQQYR	sp|Q60847|COCA1_MOUSE	yes	no	1956	1967	12	R	I	0	1412.684	2	8.32E-03	93.35	NaN	NaN	0
3665	WEYENELSKVR	sp|E9Q557|DESP_MOUSE	yes	yes	1354	1364	11	R	N	0	1451.705	3	3.16E-02	51.29	1.54	0.92	3
3666	WFGFLEAQQAFR	sp|Q8CGC7|SYEP_MOUSE	yes	yes	150	161	12	R	S	0	1498.736	2	1.28E-02	81.92	NaN	NaN	0
3667	WFLTCINQPQFR	sp|Q9D8N0|EF1G_MOUSE	yes	yes	190	201	12	R	A	0	1608.787	2	2.46E-04	164.65	NaN	NaN	0
3668	WFQQKYDGIILPGK	sp|Q9CXW4|RL11_MOUSE	yes	no	165	178	14	R	-	0	1691.904	2;3	6.94E-13	188.40	1.05	0.86	11
3669	WGTDEVKFLSILCSR	sp|P97429|ANXA4_MOUSE	yes	yes	186	200	15	R	N	0	1809.908	3	9.60E-03	55.76	1.31	1.05	6
3670	WIDNPTVDDR	sp|Q64727|VINC_MOUSE	yes	yes	503	512	10	R	G	0	1229.568	2	1.19E-02	115.57	NaN	NaN	0
3671	WILENDPTELDLR	sp|P46935|NEDD4_MOUSE	yes	yes	674	686	13	R	F	0	1612.810	2	5.23E-02	59.23	NaN	NaN	0
3672	WIVNLIR	sp|P60229|EIF3E_MOUSE	yes	yes	370	376	7	R	N	0	912.555	2	7.99E-02	96.05	NaN	NaN	0
3673	WLPSTSPVTGYR	sp|P11276|FINC_MOUSE	yes	yes	1652	1663	12	R	V	0	1362.693	2	3.40E-02	70.09	NaN	NaN	0
3674	WLSTSIPEAQWQSSLAR	sp|P19096|FAS_MOUSE	yes	yes	712	728	17	R	T	0	1958.985	2	8.95E-04	102.08	NaN	NaN	0
3675	WQAVLAQTDVR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1091	1101	11	R	Q	0	1285.678	2	7.47E-03	111.63	NaN	NaN	0
3676	WQFLTLR	sp|Q8BMJ2|SYLC_MOUSE	yes	yes	222	228	7	R	E	0	962.534	2	6.82E-02	107.59	NaN	NaN	0
3677	WQKIDKQIDFR	sp|E9Q557|DESP_MOUSE	yes	yes	879	889	11	R	L	0	1475.789	3	2.64E-02	56.09	1.50	0.83	1
3678	WQLDKIKADLR	sp|E9Q557|DESP_MOUSE	yes	yes	245	255	11	R	E	0	1384.783	3	4.80E-03	75.82	1.55	0.90	2
3679	WSLQSEAHR	sp|Q61553|FSCN1_MOUSE	yes	yes	101	109	9	R	R	0	1112.536	3	1.97E-02	117.53	NaN	NaN	0
3680	WSPVASTLPELVQR	sp|Q99KJ8|DCTN2_MOUSE	yes	yes	320	333	14	R	L	0	1581.852	2	1.15E-03	104.55	NaN	NaN	0
3681	WTELLPLIQQYEVVR	sp|Q91VI7|RINI_MOUSE	yes	yes	15	29	15	R	L	0	1886.030	2;3	1.97E-04	125.73	0.02	0.01	1
3682	WTGMIIGPPR	sp|Q9CZY3|UB2V1_MOUSE	no	no	48	57	10	R	T	0	1126.596	2	1.33E-03	114.97	0.12	0.10	2
3683	WTLGFCDER	sp|Q9CQ60|6PGL_MOUSE	yes	yes	73	81	9	R	L	0	1182.513	2	9.56E-02	67.33	NaN	NaN	0
3684	WTQLLANSATR	sp|P16546-2|SPTN1_MOUSE	yes	no	2045	2055	11	R	K	0	1259.662	2	2.51E-03	138.63	NaN	NaN	0
3685	WVEQNLGPEFVER	sp|Q9JM14|NT5C_MOUSE	yes	yes	117	129	13	R	I	0	1601.784	2	9.85E-04	139.30	NaN	NaN	0
3686	WVGGPEIELIAIATGGR	sp|P80316|TCPE_MOUSE	yes	yes	324	340	17	R	I	0	1737.941	2	6.76E-04	105.89	NaN	NaN	0
3687	WVVIGDENYGEGSSR	sp|Q99KI0|ACON_MOUSE	yes	yes	657	671	15	R	E	0	1666.759	2	6.26E-04	122.33	NaN	NaN	0
3688	YADHPFIFLVR	sp|P19324|SERPH_MOUSE	yes	yes	382	392	11	F	D	0	1376.724	3	3.66E-03	129.89	NaN	NaN	0
3689	YADLTEDQLPSCESLKDTIAR	sp|Q9DBJ1|PGAM1_MOUSE	yes	yes	142	162	21	R	A	0	2424.148	3	6.50E-16	157.85	0.97	0.91	5
3690	YAEIVHLTLPDGTKR	sp|P62814|VATB2_MOUSE	yes	yes	68	82	15	R	S	0	1711.926	4	1.24E-03	75.02	1.09	1.04	3
3691	YAICSALAASALPALVMSKGHR	sp|Q9D8E6|RL4_MOUSE	yes	yes	122	143	22	R	I	0	2286.198	3;4	3.25E-12	149.47	1.05	0.95	9
3692	YALPLGR	sp|P62242|RS8_MOUSE	yes	yes	117	123	7	H	K	0	788.454	2	7.05E-02	102.98	NaN	NaN	0
3693	YALYDASFETKESR	sp|Q9R0P5|DEST_MOUSE	yes	yes	82	95	14	R	K	0	1678.784	2;3	6.38E-04	81.70	0.99	0.89	11
3694	YAYGFEKPSAIQQR	sp|P60843|IF4A1_MOUSE	no	no	48	61	14	I	A	0	1656.826	2	2.49E-04	98.94	1.42	1.12	5
3695	YAYTDWQTFTQPR	sp|P55849-2|DSC1_MOUSE	yes	no	806	818	13	R	L	0	1675.763	2	5.42E-04	150.49	NaN	NaN	0
3696	YCMQLAQIQEMIGSVEEQLAQLR	sp|Q61781|K1C14_MOUSE	no	no	372	394	23	R	C	0	2737.324	3	7.95E-06	118.32	NaN	NaN	0
3697	YCVQLSQIQSQISALEEQLQQIR	sp|P02535-3|K1C10_MOUSE	yes	no	389	411	23	R	A	0	2761.407	2;3	8.56E-28	237.50	NaN	NaN	0
3698	YDAGVKR	sp|P07356|ANXA2_MOUSE	yes	yes	199	205	7	L	K	0	807.424	2	1.54E-02	104.21	1.03	0.99	5
3699	YDALEVFAGSGTSGQR	sp|Q61398|PCOC1_MOUSE	yes	yes	91	106	16	R	L	0	1656.774	2	3.53E-02	53.57	NaN	NaN	0
3700	YDDMAAAMKAVTEQGHELSNEE	sp|Q9CQV8-2|1433B_MOUSE	yes	no	19	41	23	R	N	0	2594.138	4	4.57E-02	34.22	1.26	1.17	3
3701	YDDMAACMKSVTEQGAELSNEE	sp|P63101|1433Z_MOUSE	yes	yes	19	41	23	R	N	0	2633.104	3	7.96E-17	178.35	1.16	0.97	4
3702	YDERPGPSPLPHR	sp|Q62376|RU17_MOUSE	yes	yes	219	231	13	R	D	1	1519.753	4	7.96E-03	83.47	NaN	NaN	0
3703	YDGATIVPGDQGADYQHFIQQCT	sp|Q9CQI6|COTL1_MOUSE	yes	yes	31	57	27	R	L	0	3068.357	3	9.15E-03	51.83	NaN	NaN	0

3704	YDLLCLEGLAR	sp|Q9WUA2|SYFB_MOUSE	yes	yes	72	82	11	R	G	0	1321.670	2	2.85E-02	74.61	NaN	NaN	0
3705	YDLLEKNINIVR	sp|Q99KI0|ACON_MOUSE	yes	yes	45	56	12	R	K	0	1488.830	3	5.08E-04	110.08	1.28	0.99	8
3706	YDLTVPFAR	sp|Q61035|SYHC_MOUSE	yes	no	129	137	9	R	Y	0	1080.560	2	2.21E-02	103.55	NaN	NaN	0
3707	YDSRPGGYGYGYGR	sp|O89086|RBM3_MOUSE	yes	yes	115	128	14	R	S	1	1566.685	2;3	7.11E-04	137.93	NaN	NaN	0
3708	YEALAEQNRR	sp|Q9Z320|K1C27_MOUSE	no	no	254	263	10	E	D	1	1248.621	2	4.53E-03	143.96	NaN	NaN	0
3709	YEALVETNRR	sp|Q61897|KT33B_MOUSE	no	no	232	241	10	Q	E	1	1249.642	2	2.45E-02	88.50	NaN	NaN	0
3710	YEDANPWLLVDPVAPR	sp|Q9Z2L6|MINP1_MOUSE	yes	yes	53	68	16	R	R	0	1853.931	2	6.00E-04	110.78	NaN	NaN	0
3711	YEDMAAFMKSAVEKGEELSCEER	sp|O70456|1433S_MOUSE	yes	yes	19	41	23	R	N	0	2708.177	4	2.07E-02	43.84	1.18	1.01	4
3712	YEDSNNLGTSHLLR	sp|Q9DB77|QCR2_MOUSE	yes	yes	71	84	14	R	L	0	1617.775	3	6.72E-04	139.30	NaN	NaN	0
3713	YEEEVLSR	sp|P08551|NFL_MOUSE	yes	yes	178	185	8	R	E	0	1023.487	2	3.76E-02	124.98	NaN	NaN	0
3714	YEEEVSLR	sp|P97861|KRT86_MOUSE	no	no	194	201	8	R	A	0	1023.487	2	3.01E-02	135.83	NaN	NaN	0
3715	YEFQGNHFQVTR	sp|Q99KK7|DPP3_MOUSE	yes	yes	237	248	12	R	G	0	1524.711	3	3.70E-03	113.24	NaN	NaN	0
3716	YEMGNNPENLLVVDSR	sp|Q61495|DSG1A_MOUSE	no	no	423	438	16	R	T	0	1848.868	2	3.11E-05	161.24	NaN	NaN	0
3717	YEQLAEKNR	sp|P02535-3|K1C10_MOUSE	yes	no	314	322	9	Q	K	0	1149.578	2	1.33E-05	157.38	1.43	1.00	11
3718	YFCCGNYFPGYPCYGTNFHGTYR	sp|Q9D3I6|KRA71_MOUSE	yes	yes	4	26	23	R	A	0	2900.157	3	7.00E-07	128.01	NaN	NaN	0
3719	YFPGYPCYGTNFHGTYR	sp|Q9D3I6|KRA71_MOUSE	yes	yes	10	26	17	N	A	0	2098.900	3	6.27E-03	77.51	NaN	NaN	0
3720	YFPIIDDLR	sp|Q9Z320|K1C27_MOUSE	yes	yes	128	136	9	R	T	0	1150.602	2	2.05E-02	113.18	NaN	NaN	0
3721	YFTWDPTR	sp|Q8BHN3|GANAB_MOUSE	yes	no	438	445	8	R	F	0	1084.498	2	3.79E-02	123.98	NaN	NaN	0
3722	YFYFYNTGLQNQR	sp|Q9QUR6|PPCE_MOUSE	yes	yes	86	98	13	R	V	0	1712.795	2;3	6.71E-05	176.42	NaN	NaN	0
3723	YGASSGQTSGCGSGQSTR	sp|Q8VHD8|HORN_MOUSE	yes	no	577	594	18	R	Y	0	1746.723	2	3.06E-19	235.40	NaN	NaN	0
3724	YGCGYGSGCCSYR	sp|Q925H4|KR211_MOUSE	yes	yes	109	121	13	R	K	0	1545.544	2	1.27E-04	172.09	NaN	NaN	0
3725	YGDFFIR	sp|Q8QZY1|EIF3L_MOUSE	yes	yes	539	545	7	R	Q	0	916.444	2	5.22E-02	138.07	NaN	NaN	0
3726	YGEAGDGPGWGGPHPR	sp|Q9Z1Q9|SYVC_MOUSE	yes	yes	24	39	16	R	I	0	1608.707	3	1.95E-02	79.88	NaN	NaN	0
3727	YGELADCCTKQEPER	sp|P07724|ALBU_MOUSE	yes	yes	108	122	15	N	N	0	1854.788	2	2.15E-05	113.47	1.22	1.09	4
3728	YGEPTLR	sp|Q8VDM4|PSMD2_MOUSE	yes	yes	681	687	7	R	R	0	834.424	2	6.06E-02	116.54	NaN	NaN	0
3729	YGFIEGNVVIPR	sp|P15379-2|CD44_MOUSE	yes	no	81	92	12	R	I	0	1362.730	2	5.31E-03	100.93	NaN	NaN	0
3730	YGGLHFSDQVEVFSPPGSDR	sp|Q02788|CO6A2_MOUSE	yes	yes	111	130	20	R	A	0	2193.013	3	2.39E-03	90.72	NaN	NaN	0
3731	YGGQPLFSEKFPTLWSGAR	sp|Q00PI9|HNRL2_MOUSE	yes	yes	262	280	19	R	S	0	2140.074	3	3.67E-06	101.92	1.22	0.94	8
3732	YGINTTDIFQTVDLWEGKNMACV	sp|Q9WVA4|TAGL2_MOUSE	yes	yes	103	127	25	R	T	0	2958.400	3	2.27E-10	145.25	1.10	0.85	3
3733	YGKAQCEDDLAEKQR	sp|Q8BSY0|ASPH_MOUSE	yes	yes	362	376	15	R	S	0	1809.832	4	5.05E-03	66.25	1.41	0.83	1
3734	YGKSPYLYPLYGLGELPQGFAR	sp|Q61598-2|GDIB_MOUSE	yes	no	183	204	22	R	L	0	2488.279	3	7.64E-04	86.56	1.19	1.02	2
3735	YGLFPANYVELR	sp|Q60598|SRC8_MOUSE	yes	yes	534	545	12	R	Q	0	1440.740	2	1.09E-02	86.77	0.33	0.27	2
3736	YGPPGTGKTLLAR	sp|P62334|PRS10_MOUSE	yes	yes	173	185	13	L	A	0	1329.741	2	6.03E-03	69.03	1.14	0.98	4
3737	YGSGSGESSGFSQGGSGQGR	sp|Q8VHD8|HORN_MOUSE	yes	no	624	643	20	R	S	0	1847.767	2;3	7.18E-31	277.98	NaN	NaN	0
3738	YGVNPGPIVGTTR	sp|Q61029-2|LAP2B_MOUSE	no	no	126	138	13	R	K	0	1329.704	2	7.83E-03	83.88	NaN	NaN	0
3739	YGVNQLEEMLRPLVEAGLR	sp|P10518|HEM2_MOUSE	yes	yes	56	74	19	R	C	1	2186.152	3	3.82E-04	114.03	NaN	NaN	0
3740	YHTSQSGDEMTSLSEYVSR	sp|P11499|HS90B_MOUSE	yes	yes	457	475	19	R	M	0	2175.938	3	6.19E-06	130.56	1.93	1.97	1
3741	YHVPVVVVPEGSTSDTQEQAILR	sp|Q9DBG6|RPN2_MOUSE	yes	yes	267	289	23	R	L	0	2523.297	3	8.66E-06	117.37	NaN	NaN	0
3742	YIANTVELR	sp|Q9DBG6|RPN2_MOUSE	yes	yes	358	366	9	R	V	0	1077.582	2	3.35E-02	91.87	NaN	NaN	0
3743	YIEIFKSSR	sp|O35737|HNRH1_MOUSE	no	no	180	188	9	R	A	0	1141.613	2;3	9.31E-03	85.53	1.22	0.84	6
3744	YIETDPANR	sp|P13020-2|GELS_MOUSE	yes	no	679	687	9	R	D	0	1077.509	2	1.79E-02	128.36	NaN	NaN	0
3745	YIEVFKSSQEEVR	sp|Q9Z2X1|HNRPF_MOUSE	yes	no	180	192	13	R	S	0	1612.810	3	5.49E-03	76.73	0.98	0.95	5
3746	YIFTMLSSLAR	sp|Q64511|TOP2B_MOUSE	yes	yes	814	824	11	R	L	0	1300.685	2	1.30E-02	94.82	NaN	NaN	0
3747	YIGIVKQAGLDR	sp|Q9Z2X1|HNRPF_MOUSE	yes	no	219	230	12	R	M	0	1331.756	2;3	2.04E-03	78.32	1.21	0.92	13
3748	YIHLENLLAR	sp|Q3UKJ7-2|SMU1_MOUSE	yes	no	114	123	10	R	S	0	1240.693	3	3.47E-04	175.93	NaN	NaN	0
3749	YIIGQKGSGIR	sp|Q8VDJ3|VIGLN_MOUSE	yes	yes	986	996	11	R	K	0	1190.677	3	3.16E-02	51.29	1.82	1.44	1
3750	YIPLPDEKSR	sp|Q01853|TERA_MOUSE	yes	yes	644	653	10	I	V	0	1216.645	2	4.76E-02	50.11	1.33	1.08	3
3751	YIQPWESEFIDSQR	sp|Q99PV0|PRP8_MOUSE	yes	yes	1371	1384	14	R	V	0	1796.837	2	3.64E-02	62.29	NaN	NaN	0
3752	YITGESKEQVANSAFVER	sp|P11499|HS90B_MOUSE	yes	yes	485	502	18	Y	V	0	2026.996	3	4.45E-03	60.76	1.17	0.90	6
3753	YIVPMITVDGKR	sp|Q9JII6|AK1A1_MOUSE	yes	yes	298	309	12	R	V	0	1390.764	3	1.43E-03	89.30	1.19	1.07	5
3754	YIVQNPEQEPLSPFLR	sp|Q8K4L4|POF1B_MOUSE	yes	yes	140	155	16	R	G	0	1929.000	2	7.31E-08	185.27	NaN	NaN	0
3755	YKLLGGLAVR	sp|P62908|RS3_MOUSE	yes	yes	107	116	10	R	R	0	1088.671	2;3	3.57E-04	133.99	1.27	1.06	15
3756	YKTDLEKDIISDTSGDFR	sp|P07356|ANXA2_MOUSE	yes	yes	151	168	18	M	K	0	2102.017	3	4.04E-02	39.91	1.11	0.93	9
3757	YKTPDEEFKEVEVDR	sp|Q60847|COCA1_MOUSE	yes	no	1600	1614	15	R	S	0	1882.895	3;4	1.46E-05	119.46	1.58	1.03	8
3758	YKVDENGKISR	sp|P62983|RS27A_MOUSE	yes	yes	106	116	11	Y	L	0	1307.683	3	4.32E-02	62.34	1.02	0.91	2
3759	YLAADKDGNVTCER	sp|Q61553|FSCN1_MOUSE	yes	yes	69	82	14	R	E	0	1610.736	3	3.05E-03	72.62	0.94	0.91	3
3760	YLAEFATGNDR	sp|P62259|1433E_MOUSE	yes	yes	131	141	11	R	K	0	1255.583	2	6.51E-04	152.69	NaN	NaN	0
3761	YLAEKYEWDVAEAR	sp|P58252|EF2_MOUSE	yes	yes	634	647	14	R	K	0	1741.831	3	7.33E-05	118.21	1.18	0.91	9
3762	YLAEVACGDDR	sp|P68254-2|1433T_MOUSE	yes	no	128	138	11	R	K	0	1267.550	2	4.01E-03	127.87	NaN	NaN	0
3763	YLAEVATGDDKKR	sp|O70456|1433S_MOUSE	yes	yes	130	142	13	R	I	0	1464.757	2;3;4	4.44E-08	156.14	0.99	0.97	11
3764	YLAEVATGEKR	sp|P61982|1433G_MOUSE	yes	yes	133	143	11	R	A	0	1235.651	2;3	1.21E-03	103.08	1.12	0.91	6
3765	YLDLILNDFVR	sp|Q99MN1|SYK_MOUSE	yes	yes	229	239	11	R	Q	0	1379.745	2	9.54E-03	102.40	NaN	NaN	0
3766	YLGGSSCIAGVLVPVQGEPGR	sp|Q8R0W0|EPIPL_MOUSE	yes	no	2742	2762	21	R	Q	0	2115.078	2	3.93E-08	163.53	NaN	NaN	0
3767	YLGHNYVTAIR	sp|Q921I1|TRFE_MOUSE	yes	yes	333	343	11	L	N	0	1305.683	2	2.89E-04	159.12	NaN	NaN	0
3768	YLGTQPEPDIVGLDSGHIR	sp|P52196|THTR_MOUSE	yes	yes	188	206	19	R	G	0	2066.043	3	3.05E-05	127.97	NaN	NaN	0
3769	YLHDESGLNR	sp|P42208|SEPT2_MOUSE	yes	yes	129	138	10	R	R	0	1202.568	3	1.37E-02	108.47	NaN	NaN	0
3770	YLLGTSLAR	sp|P16460|ASSY_MOUSE	yes	yes	87	95	9	R	P	0	992.565	2	2.53E-03	111.39	9.76	8.07	1
3771	YLLPAILNPR	sp|Q99KC8|VMA5A_MOUSE	yes	yes	143	152	10	R	Y	0	1168.697	2	5.60E-03	105.52	6.08	3.92	1
3772	YLNFVKGVVDSDDLPLNVSR	sp|P08113|ENPL_MOUSE	yes	yes	429	448	20	K	E	0	2249.169	3	1.07E-03	71.38	1.17	0.95	3
3773	YLPEFR	sp|P70697|DCUP_MOUSE	yes	yes	42	47	6	R	E	0	823.423	2	7.08E-02	105.42	NaN	NaN	0
3774	YLQDLLAWVEENQR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	427	440	14	R	R	0	1775.884	3	3.03E-02	65.37	NaN	NaN	0
3775	YLRPPNTSLFVR	sp|Q9R0U0-3|SRS10_MOUSE	yes	no	4	15	12	R	N	1	1461.809	3	4.34E-03	105.65	NaN	NaN	0
3776	YLSPKYIKMFVLDEADEMLSR	sp|P60843|IF4A1_MOUSE	yes	yes	170	190	21	R	G	0	2547.275	4	3.01E-02	41.12	1.11	0.78	1
3777	YLSYTLNPDYIR	sp|P97449|AMPN_MOUSE	yes	yes	843	854	12	R	K	0	1516.756	2	4.34E-03	105.65	0.20	0.14	2
3778	YLTTAVITNKDVR	sp|P60229|EIF3E_MOUSE	yes	yes	256	268	13	R	K	0	1492.825	3	1.63E-02	52.07	1.14	0.97	4
3779	YLTVAAIFR	sp|Q7TMM9|TBB2A_MOUSE	yes	no	310	318	9	R	G	0	1052.602	2	1.43E-02	135.83	NaN	NaN	0
3780	YLTVAAVFR	sp|P99024|TBB5_MOUSE	no	no	310	318	9	R	G	0	1038.586	2	8.53E-03	147.19	NaN	NaN	0
3781	YLTVATVFR	sp|Q922F4|TBB6_MOUSE	no	no	310	318	9	R	G	0	1068.597	2	1.22E-03	124.92	0.01	0.01	1
3782	YLVVLNFR	sp|P10852|4F2_MOUSE	yes	yes	456	463	8	R	D	0	1022.591	2	2.64E-02	146.21	NaN	NaN	0
3783	YLYGTGAVAGVYLPGSR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	3587	3603	17	R	Q	0	1742.899	2	4.31E-03	86.49	NaN	NaN	0
3784	YNPENLATLER	sp|Q9DBZ5|EIF3K_MOUSE	yes	yes	21	31	11	R	Y	0	1318.652	2	1.79E-02	84.19	NaN	NaN	0
3785	YNSLSILPAALGKPVR	sp|Q9DB60|PGFS_MOUSE	yes	yes	108	123	16	R	D	0	1697.983	3	3.90E-03	67.14	1.22	0.95	3
3786	YPAHSR	sp|P14602|HSPB1_MOUSE	yes	no	23	28	6	W	L	0	729.356	2	9.34E-02	91.58	NaN	NaN	0
3787	YPEDKITPENLPQILLQLKR	sp|Q8K310|MATR3_MOUSE	yes	yes	128	147	20	R	R	0	2407.348	4	1.46E-02	58.69	1.61	1.09	1
3788	YPENFFLLR	sp|P62137|PP1A_MOUSE	no	no	114	122	9	K	G	0	1197.618	2	2.09E-02	110.41	NaN	NaN	0
3789	YPGAYYIFQJKSGNEGR	sp|Q9WVH9|FBLN5_MOUSE	yes	yes	374	390	17	R	E	0	1961.964	3	3.72E-02	55.76	1.35	1.12	4
3790	YPLFEGQETGKKETVEE	sp|Q9CZD3|SYG_MOUSE	yes	no	713	729	17	R	-	0	1982.947	3	3.15E-03	67.65	1.02	1.00	5
3791	YPLIIDPSGQATEFIMNEYKDR	sp|Q9JHU4|DYHC1_MOUSE	yes	yes	3584	3605	22	R	K	0	2599.263	3	2.30E-02	43.16	1.42	0.93	1
3792	YPLSGLVLPTLR	sp|Q8C0I1|ADAS_MOUSE	yes	yes	105	116	12	R	D	0	1327.786	2	1.14E-02	85.55	NaN	NaN	0
3793	YPSLSLHGIEGAFSGSGAKTVIPR	sp|Q9D1A2|CNDP2_MOUSE	yes	yes	311	334	24	R	K	0	2443.286	4	1.57E-03	57.48	1.53	1.17	3
3794	YQAGGLTVHDVTTTLTSLLAR	sp|Q8R0W0|EPIPL_MOUSE	yes	no	2483	2503	21	C	A	0	2216.180	2;3	2.31E-06	130.83	NaN	NaN	0
3795	YQDILVFR	sp|Q64674|SPEE_MOUSE	yes	yes	48	55	8	R	S	0	1052.566	2	2.40E-02	150.40	NaN	NaN	0
3796	YQEALHLGSQLLR	sp|Q8BG32|PSD11_MOUSE	yes	yes	143	155	13	R	E	0	1526.821	3	1.59E-03	102.73	NaN	NaN	0
3797	YQELINDIAKDIR	sp|Q9JKF1|IQGA1_MOUSE	yes	yes	1478	1490	13	R	N	0	1589.841	3	2.38E-04	107.65	1.35	1.00	2
3798	YQGGFLISR	sp|Q11011|PSA_MOUSE	yes	yes	843	851	9	R	L	0	1039.545	2	2.17E-02	106.20	NaN	NaN	0
3799	YQILPLHSQIPR	sp|O70133|DHX9_MOUSE	yes	no	683	694	12	R	E	0	1463.825	3	2.78E-03	124.21	NaN	NaN	0
3800	YQKQAPGPAR	sp|Q9QWL7|K1C17_MOUSE	yes	no	120	129	10	W	D	0	1114.588	2	6.76E-03	76.94	1.40	0.99	3
3801	YQKSTELLIR	sp|P84244|H33_MOUSE	no	no	55	64	10	R	K	0	1249.703	2;3	5.14E-06	155.48	1.33	0.91	18
3802	YQQFKDFQR	sp|Q9Z1N5|DX39B_MOUSE	yes	no	330	338	9	R	R	0	1258.610	3	8.65E-03	87.48	1.35	0.96	8
3803	YRPGTVALR	sp|P84244|H33_MOUSE	no	no	42	50	9	R	E	1	1031.588	2;3	7.16E-03	145.25	2.18	1.95	2
3804	YRVPDVLVADPPTAR	sp|Q8BHN3|GANAB_MOUSE	yes	no	113	127	15	R	L	1	1667.900	3	4.14E-02	54.28	NaN	NaN	0
3805	YSDFEWLR	sp|O70492|SNX3_MOUSE	yes	yes	71	78	8	R	S	0	1114.508	2	5.81E-02	91.07	NaN	NaN	0
3806	YSMYLTPKGGGR	sp|Q8R2Q0|TRI29_MOUSE	yes	yes	471	482	12	R	T	0	1328.655	3	5.98E-03	72.29	1.00	0.95	3

3807	YSPNTQVEILPQGR	sp|P24452|CAPG_MOUSE	yes	yes	326	339	14	R	E	0	1600.821	2	2.51E-07	201.65	NaN	NaN	0
3808	YSPSEAGLHEMDIR	sp|Q8BTM8|FLNA_MOUSE	yes	yes	1832	1845	14	R	Y	0	1603.730	3	6.72E-03	80.96	NaN	NaN	0
3809	YSSQLSQVQCLITNVESQLGEIR	sp|Q61897|KT33B_MOUSE	no	no	307	329	23	R	A	0	2651.323	2;3	1.40E-09	153.56	NaN	NaN	0
3810	YSVDIPLDKTVVNKDVFR	sp|P61358|RL27_MOUSE	yes	yes	85	102	18	R	D	0	2107.131	3;4	1.55E-03	71.69	0.95	0.84	8
3811	YSVVSEQLEPAAASTYR	sp|Q9QY23|PKP3_MOUSE	yes	no	195	211	17	R	A	0	1869.911	2	3.77E-08	187.56	NaN	NaN	0
3812	YTAILNQIPSQSSSIR	sp|Q80X19-2|COEA1_MOUSE	yes	no	1636	1651	16	R	T	0	1776.937	2	2.92E-05	162.46	NaN	NaN	0
3813	YTEGAELVDSVLDVVR	sp|P99024|TBB5_MOUSE	no	no	106	121	16	H	K	0	1763.894	2;3	4.58E-08	193.47	NaN	NaN	0
3814	YTMGDAPDFDR	sp|P10649|GSTM1_MOUSE	yes	yes	33	43	11	R	S	0	1286.524	2	7.84E-02	60.16	NaN	NaN	0
3815	YTNLTLR	sp|O88342|WDR1_MOUSE	yes	yes	390	396	7	R	D	0	879.481	2	5.10E-03	143.85	3.68	3.57	4
3816	YTQKAPQVSTPTLVEAAR	sp|P07724|ALBU_MOUSE	yes	yes	435	452	18	R	N	0	1959.043	2;3	8.86E-12	157.98	1.25	1.01	20
3817	YTTPAGEVR	sp|Q11011|PSA_MOUSE	yes	yes	165	173	9	R	Y	0	992.493	2	3.64E-02	89.05	NaN	NaN	0
3818	YTYSEWHSFTQPR	sp|P55850-2|DSC3_MOUSE	yes	no	815	827	13	R	L	0	1700.758	3	2.85E-03	98.94	NaN	NaN	0
3819	YVGSMVADIHR	sp|Q9QXD6|F16P1_MOUSE	yes	yes	245	255	11	R	T	0	1246.613	3	1.43E-02	91.96	NaN	NaN	0
3820	YVLCTAPR	sp|P25206|MCM3_MOUSE	yes	yes	357	364	8	R	A	0	978.496	2	4.33E-02	104.37	NaN	NaN	0
3821	YVMTTTTLER	sp|Q6ZWX6|IF2A_MOUSE	yes	yes	235	244	10	R	T	0	1213.601	2	5.73E-03	139.43	NaN	NaN	0
3822	YVNKDMSIQELAVLVSGQK	sp|Q9R269|PEPL_MOUSE	yes	no	1737	1755	19	R	-	0	2121.114	3	4.16E-04	75.53	1.29	1.07	2
3823	YVQELPLETDGALR	sp|Q99KC8|VMA5A_MOUSE	yes	yes	129	142	14	R	Y	0	1602.825	2	1.08E-03	113.76	NaN	NaN	0
3824	YVWLVYEQEQPLSCDEPILSNKSG	sp|P70296|PEBP1_MOUSE	yes	yes	120	146	27	R	G	0	3238.524	3	6.77E-02	26.16	1.08	1.02	3
3825	YWEIFPNTFR	sp|P28654|PGS2_MOUSE	yes	yes	331	340	10	R	C	0	1371.661	2	1.73E-02	99.57	NaN	NaN	0
3826	YWLEEAECR	sp|Q8JZQ9|EIF3B_MOUSE	yes	yes	284	292	9	R	D	0	1254.534	2	4.51E-02	80.69	NaN	NaN	0
3827	YWPQEAGEYAVHVLCNSEDIR	sp|Q8BTM8|FLNA_MOUSE	yes	yes	635	655	21	R	L	0	2535.149	3	1.47E-02	53.03	NaN	NaN	0
3828	YYCFQGNKFLR	sp|Q91X72|HEMO_MOUSE	yes	yes	197	207	11	R	F	0	1494.708	3	3.24E-03	79.15	1.01	0.87	4
3829	YYIQQDTKGDYQKALLYLCGGDD	sp|P07356|ANXA2_MOUSE	yes	no	317	339	23	Y	-	0	2726.253	3	4.89E-07	112.36	1.03	1.00	4
3830	YYNEATGGKYVPR	sp|P99024|TBB5_MOUSE	no	no	50	62	13	V	A	0	1516.731	2	4.23E-05	127.71	1.15	1.00	6
3831	YYPTEDVPR	sp|P47911|RL6_MOUSE	yes	yes	123	131	9	R	K	0	1138.530	2	2.00E-02	116.05	NaN	NaN	0

ST1C Supplementary Table 1C: Peptides identified by shotgun proteomics prior to TAILS (preTAILS) with a labeled N-terminus (i.e. dimethylated with heavy (+/+) or light (Adamts9-Und4/+) formaldehyde).

Abbreviations: aa - amino acids; PEP - Posterior Error Probability; Score - Andromeda score for the best associated MS/MS spectrum; Ratio H/L - ratio between heavy and light label partners; NaN - non-quantifiable ratio.

Index	Sequence	Leading razor protein	Unique (Groups)	Unique (Proteins)	Start position	End position	Length (# aa)	Amino acid before	Amino acid after	Missed cleavages	Mass (Da)	Charges	PEP	Score	Ratio H/L	Ratio H/L normalized	Ratio H/L count
1	AAEKQIPGGGSGGGGSGSGGGGG	sp|Q8BMA6|SRP68_MOUSE	yes	yes	2	30	29	M	S	0	2229.012	3	1.72E-07	53.20	1.47	1.32	2
2	AEGQVLVLDGR	sp|P19253|RL13A_MOUSE	yes	yes	2	12	11	M	G	0	1155.625	2	2.72E-03	111.79	1.05	0.96	7
3	AGKCTYNPEPDQR	sp|O89023|TPP1_MOUSE	yes	yes	16	28	13	I	W	0	1534.683	2	1.21E-03	98.94	1.30	1.17	4
4	ALDLENIMR	sp|Q9CQE0-2|RN138_MOUSE	yes	no	72	80	9	R	R	0	1073.554	2	6.70E-02	87.48	0.00	0.00	1
5	APNVLASEPEIPKGIR	sp|Q9WTP6-2|KAD2_MOUSE	yes	no	2	17	16	M	A	0	1689.941	3	8.28E-05	85.47	1.12	1.06	7
6	APQGTGLGFR	sp|P29699|FETUA_MOUSE	yes	yes	19	28	10	S	E	0	1002.525	2	1.03E-03	119.68	1.11	0.94	8
7	CGYYGNYYGGR	sp|Q925H3|KRA65_MOUSE	yes	no	2	12	11	M	G	0	1328.524	2	4.00E-35	166.66	3.93	2.18	5
8	DGIQKAYDELR	sp|Q9DA73|CCD89_MOUSE	yes	yes	331	341	11	V	L	0	1306.652	2	8.94E-03	100.69	1.21	0.81	3
9	DIDLPETFDAR	sp|P10605|CATB_MOUSE	yes	yes	77	87	11	E	E	0	1290.609	2	2.02E-02	85.81	0.95	0.92	3
10	DPAIYFKEQFLDGDAWTNR	sp|P14211|CALR_MOUSE	yes	yes	18	36	19	A	W	0	2285.075	2;3	4.54E-35	136.49	0.97	0.78	6
11	EELQITAGKHGDSVR	sp|P04104|K2C1_MOUSE	yes	yes	386	400	15	Y	N	0	1638.833	4	2.03E-02	79.65	5.01	3.53	3
12	FAKLVRPPVQVYGIEGR	sp|Q9DB20|ATPO_MOUSE	yes	yes	24	40	17	P	Y	1	1928.100	4	8.86E-03	66.83	0.34	0.21	4
13	FDITADDEPLGR	sp|P17742|PPIA_MOUSE	yes	yes	8	19	12	F	V	0	1347.631	2	1.75E-03	96.23	4.15	2.67	1
14	FSSGGACGIGGGYGGSFSSSSFGG	sp|Q61781|K1C14_MOUSE	yes	yes	52	84	33	R	F	0	2934.263	3	5.30E-03	27.54	NaN	NaN	0
15	FTPSLDSDFTFTLPAGR	sp|Q9CXE7|TMED5_MOUSE	yes	yes	28	44	17	G	K	0	1870.910	2	8.62E-03	70.78	1.30	0.87	1
16	GAYKYIQELWR	sp|Q9CZM2|RL15_MOUSE	yes	yes	2	12	11	M	K	0	1425.741	2;3	2.81E-12	142.08	1.02	0.93	13
17	GGIGTVPVGR	sp|P10126|EF1A1_MOUSE	yes	no	257	266	10	I	V	0	911.519	2	2.45E-19	157.96	0.80	0.68	4
18	GLKMAATFIGNSTAIQELFKR	sp|Q9D6F9|TBB4A_MOUSE	yes	yes	360	380	21	R	I	0	2295.241	4	1.30E-04	67.65	0.07	0.06	1
19	GLLSQGSPLSWEETQR	sp|P97494|GSH1_MOUSE	yes	yes	2	17	16	M	H	0	1786.885	2	5.81E-21	132.84	1.21	1.06	4
20	GSVKPYTNFDAER	sp|P07356|ANXA2_MOUSE	yes	yes	25	37	13	Y	D	0	1482.710	3	7.76E-04	107.74	1.67	1.59	5
21	GVQVETISPGDGR	sp|P26883|FKB1A_MOUSE	yes	yes	2	14	13	M	T	0	1313.658	2	6.57E-58	180.48	1.34	0.99	5
22	IDLPETFDAR	sp|P10605|CATB_MOUSE	yes	yes	78	87	10	D	E	0	1175.582	2	3.10E-02	91.55	1.13	0.93	8
23	ILNLPESWDWR	sp|P97821|CATC_MOUSE	yes	yes	227	237	11	Q	N	0	1427.720	2	1.25E-03	116.55	1.38	1.32	3
24	KGYKVR	sp|O89019-6|INVS_MOUSE	yes	no	567	572	6	Y	K	0	749.455	2	3.29E-02	4.42	NaN	NaN	0
25	LEQQNQVLR	sp|Q3TTY5|K22E_MOUSE	yes	no	220	228	9	F	T	0	1126.610	2	1.14E-18	157.96	8.58	5.37	4
26	LKLLTH	sp|Q8BMA3-2|CNKR3_MOUSE	yes	no	309	314	6	R	-	0	723.464	2	3.29E-02	0.00	NaN	NaN	0
27	LPETFDAR	sp|P10605|CATB_MOUSE	yes	yes	80	87	8	D	E	0	947.471	2	5.07E-02	62.46	1.02	0.83	6
28	LQAQLQMFR	sp|Q8BK06-3|FBX9_MOUSE	yes	no	28	36	9	D	A	0	1133.602	2	9.12E-02	80.44	1.18	1.03	4
29	LYSSSDDVIELTPSNFNR	sp|Q922R8|PDIA6_MOUSE	yes	yes	20	37	18	G	E	0	2055.975	2;3	1.08E-82	182.31	1.32	1.16	9
30	MCGYYGNYYGGR	sp|Q925H3|KRA65_MOUSE	yes	no	1	12	12	-	G	0	1459.565	2	2.48E-25	155.11	2.25	1.39	4
31	MKLNISFPATGCQKLIEVDDER	sp|P62754|RS6_MOUSE	yes	yes	1	22	22	-	K	0	2563.277	4	1.99E-06	69.77	0.95	0.94	3
32	MKPLVVFVLGGPGAGKGTQCAR	sp|Q9DBP5|KCY_MOUSE	yes	yes	1	22	22	-	I	0	2242.208	4	1.50E-02	40.62	0.77	0.69	1
33	MKTILSNQTVDIPENVEITLKGR	sp|P51410|RL9_MOUSE	yes	yes	1	23	23	-	T	0	2598.405	4	6.59E-07	73.67	1.02	0.78	2
34	NSLVTASSDGTVKMLDLIEGR	sp|Q8BHD1|POC1B_MOUSE	yes	yes	241	261	21	G	L	0	2205.131	2;3	1.90E-02	42.64	NaN	NaN	0
35	QAQLSEARERYQQGNGGVTER	sp|Q8BXG3-2|IFT57_MOUSE	yes	no	237	257	21	A	T	2	2376.153	2;3	3.36E-04	67.65	1.23	0.95	20
36	QIASGPSVTGGSITVMAPDSCSPC	sp|Q6IMF0|KRT83_MOUSE	yes	yes	454	480	27	R	A	0	2759.268	2;3	4.92E-25	141.23	0.03	0.02	2
37	QKTGTAEMSSILEER	sp|Q03265|ATPA_MOUSE	yes	yes	44	58	15	L	I	0	1678.820	3	3.56E-08	111.78	0.77	0.71	5
38	QSTLVIAEHANDSLAPITLNTITAA	sp|Q99LC5|ETFA_MOUSE	yes	yes	20	46	27	F	L	0	2776.472	3	9.92E-09	62.03	0.97	0.93	1
39	RSLLEGEGSSSGGGGGR	sp|P02535-3|K1C10_MOUSE	yes	no	439	455	17	Y	P	1	1561.745	3	7.87E-04	79.51	3.90	2.65	3
40	SAAATSAVPAPNHQPEVFCNQIFI	sp|P47738|ALDH2_MOUSE	yes	yes	20	53	34	L	K	0	3776.775	4	1.98E-03	29.33	1.12	1.05	5
41	SDVLELTDENFESR	sp|P27773|PDIA3_MOUSE	yes	yes	25	38	14	A	V	0	1652.753	2	6.08E-169	225.32	1.12	0.90	9
42	SHYSSYYGGLGYGYGSFGGPGCGI	sp|Q925H6|KR193_MOUSE	yes	yes	2	29	28	M	R	0	2979.234	3	1.53E-303	243.35	2.45	1.52	5
43	SLYSSSPGGAYVTR	sp|P20152|VIME_MOUSE	yes	yes	51	64	14	R	S	0	1443.699	2	3.63E-34	152.88	0.89	0.75	6
44	SNIPFITVPLSR	sp|Q9Z110-2|P5CS_MOUSE	yes	no	44	55	12	W	A	0	1342.761	2	1.37E-02	83.20	1.78	1.26	7
45	SNSGPYRGGYGGGYGGGSF	sp|Q9CX86|ROA0_MOUSE	yes	yes	287	305	19	R	-	1	1795.755	2	3.94E-24	164.53	0.10	0.06	3
46	SSEAPPLVNEDVKR	sp|Q91YQ5|RPN1_MOUSE	yes	yes	26	39	14	A	T	0	1539.789	3	1.39E-05	98.59	1.59	0.99	8
47	SSGGACGIGGGYGGSFSSSSFGGG	sp|Q61781|K1C14_MOUSE	yes	yes	53	84	32	F	F	0	2787.194	3	4.55E-17	66.47	4.13	2.78	3
48	SSSPGGAYVTR	sp|P20152|VIME_MOUSE	yes	yes	54	64	11	Y	S	0	1080.520	2	3.94E-02	81.02	2.02	1.18	1
49	SVLLAPGAVGPPETLR	sp|Q9JKN5|OLIG1_MOUSE	yes	yes	189	204	16	G	P	0	1575.898	2	1.96E-02	64.24	1.39	1.28	3
50	SYGGRGGGGGGGSTYGSGGR	sp|Q3TTY5|K22E_MOUSE	yes	no	551	570	20	G	S	1	1702.741	3	2.01E-04	80.42	0.01	0.00	1
51	SYYGSYYGGLGSGIR	sp|O08632|KR195_MOUSE	yes	yes	2	16	15	M	G	0	1598.737	2	2.11E-46	165.86	3.57	2.14	8
52	SYYSGYSGGLGYGYGGFGGLGCGI	sp|Q8C1I6|KR163_MOUSE	yes	yes	2	29	28	M	R	0	2885.217	2;3	9.62E-16	81.97	1.62	1.15	7
53	TATFAQALQSVPETQVSILDNGLR	sp|Q9CZ13|QCR1_MOUSE	yes	yes	35	58	24	G	V	0	2558.334	2;3	1.31E-24	105.51	1.58	1.08	3
54	TFYNELR	sp|P63260|ACTG_MOUSE	yes	no	89	95	7	H	V	0	941.461	2	5.34E-05	117.39	1.16	0.89	6
55	TQAIFYRRTTDIPIIIQVWNSR	sp|O35646|CAN6_MOUSE	yes	yes	565	586	22	D	K	2	2690.466	4	3.14E-02	31.49	NaN	NaN	0
56	TVAEVVETMEDLVTYTKNLGPGN	sp|Q64727|VINC_MOUSE	yes	yes	146	178	33	L	Q	0	3699.823	4	2.75E-02	14.38	0.05	0.04	1
57	VGVKPVGSDPDFQPELSGAGSR	sp|Q8CDN6|TXNL1_MOUSE	yes	yes	2	23	22	M	L	0	2198.097	3	6.09E-29	116.35	1.17	1.05	7
58	VHLTDAEKAAVSCLWGKVNSDEV	sp|P02088|HBB1_MOUSE	yes	yes	2	31	30	M	L	0	3167.567	5	2.14E-22	82.13	1.48	1.12	2
59	VHLTDAEKSAVSCLWAKVNPDEV	sp|P02089|HBB2_MOUSE	yes	yes	2	31	30	M	L	0	3207.598	5	1.26E-02	29.34	1.70	1.52	1
60	VKVGVNGFGR	sp|P16858|G3P_MOUSE	yes	yes	2	11	10	M	I	0	1031.588	2;3	9.81E-06	136.99	1.14	0.99	14
61	VLDLDLFR	sp|P26638|SYSC_MOUSE	yes	yes	2	9	8	M	V	0	989.555	2	1.54E-05	136.75	1.15	1.06	9
62	VLLTMIAR	sp|O08547|SC22B_MOUSE	yes	yes	2	9	8	M	V	0	915.558	2	7.70E-03	106.36	1.65	1.02	1
63	VLSGEDKSNIKAAWGKIGGHGAE	sp|P01942|HBA_MOUSE	yes	yes	2	32	31	M	M	0	3212.621	6	3.22E-03	37.46	1.28	1.28	1
64	VNFTVDQIR	sp|P58252|EF2_MOUSE	yes	yes	2	10	9	M	A	0	1090.577	2	1.11E-02	112.71	1.15	0.89	7
65	VNPTVFFDITADDEPLGR	sp|P17742|PPIA_MOUSE	yes	yes	2	19	18	M	V	0	2004.979	2;3	5.74E-27	133.93	1.25	0.97	20
66	VSSSLPDICYR	sp|P53996-2|CNBP_MOUSE	yes	no	39	49	11	F	C	0	1295.618	2	8.08E-03	96.23	1.16	0.99	4
67	VTIIDAPGHR	sp|P10126|EF1A1_MOUSE	yes	yes	87	96	10	Y	D	0	1077.593	3	1.24E-02	104.22	2.51	1.68	4
68	YRRQEYEKALQEYSSISEQLPSTNF	sp|Q9D2X8|CH076_MOUSE	yes	yes	65	93	29	A	D	2	3551.747	5	3.17E-02	26.77	NaN	NaN	0
69	YVTIIDAPGHR	sp|P10126|EF1A1_MOUSE	yes	yes	86	96	11	Y	D	0	1240.656	3	2.88E-09	136.50	2.24	1.26	3

ST1D Supplementary Table 1D: Peptides identified by TAILS with an unlabeled N-terminus (i.e. free, acetylated, or after pyro-Glu formation).

Abbreviations: aa - amino acids; PEP - Posterior Error Probability; Score - Andromeda score for the best associated MS/MS spectrum; Ratio H/L - ratio between heavy and light label partners; NaN - non-quantifiable ratio.

Index	Sequence	Leading razor protein	Unique (Groups)	Unique (Proteins)	Start position	End position	Length (# aa)	Amino acid before	Amino acid after	Missed cleavages	Mass (Da)	Charges	PEP	Score	Ratio H/L	Ratio H/L normalized	Ratio H/L count
1	AAAAAAAAAAGAAGGR	sp|Q8CCS6-2|PABP2_MOUSE	yes	no	2	17	16	M	G	0	1197.621	2	3.69E-11	151.16	0.02	0.01	2
2	AAAAAAAAAGAAGGR	sp|Q8CCS6-2|PABP2_MOUSE	yes	no	3	17	15	A	G	0	1126.584	2	2.59E-06	113.24	NaN	NaN	0
3	AAAAAAGPEMVR	sp|P63085|MK01_MOUSE	yes	yes	2	13	12	M	G	0	1113.560	2	4.15E-06	152.64	NaN	NaN	0
4	AAAAAAPGGGGGEPR	sp|Q63844|MK03_MOUSE	yes	yes	2	16	15	M	G	0	1208.590	2	3.36E-06	103.76	NaN	NaN	0
5	AAAAAASHLNLDALR	sp|Q8CH72|TRI32_MOUSE	yes	yes	2	16	15	M	E	0	1463.785	2	1.28E-10	163.80	NaN	NaN	0
6	AAAAAEQQQFYLLLGNLLSPDNV	sp|Q8BKC5|IPO5_MOUSE	yes	yes	2	26	25	M	K	0	2700.424	3	3.54E-16	101.41	NaN	NaN	0
7	AAAAAGPASSQR	sp|Q9CX34|SUGT1_MOUSE	yes	yes	2	13	12	M	L	0	1056.531	2	1.38E-04	148.28	NaN	NaN	0
8	AAAAAMAEQEGAR	sp|Q9D1H7|GET4_MOUSE	yes	yes	2	14	13	M	N	0	1245.577	2	8.70E-04	114.72	NaN	NaN	0
9	AAAAATAAAAAAPSGGGGGGEEI	sp|Q9Z2D6-2|MECP2_MOUSE	yes	yes	2	25	24	M	L	0	1969.909	2	2.37E-05	63.23	NaN	NaN	0
10	AAAAATAATKGNGGGSGR	sp|Q9D3B1|HACD2_MOUSE	yes	yes	2	19	18	M	V	0	1487.744	2	1.39E-14	135.09	1.49	1.01	4
11	AAAAATAVGPGAGSAGVAGPGG	sp|Q9WVG6-2|CARM1_MOUSI	yes	no	2	37	36	M	L	0	3007.493	3	1.03E-02	38.55	NaN	NaN	0
12	AAAAGAAAAAAAEGEAPAEMGA	sp|Q9Z148-2|EHMT2_MOUSE	yes	no	2	31	30	M	G	0	2777.402	3	7.52E-09	82.18	0.78	0.54	2
13	AAAAGAVVASAASGPAEGKKITEL	sp|Q8CH25-2|SLTM_MOUSE	yes	no	2	26	25	M	V	0	2295.255	3	2.24E-11	106.35	1.17	0.87	6
14	AAAAPGPVELGFAEEAPAWR	sp|P46718|PDCD2_MOUSE	yes	yes	2	21	20	M	L	0	2009.001	2	3.63E-02	40.97	NaN	NaN	0
15	AAAAQLSLTQLSSGNPVYEKYYR	sp|P42567|EPS15_MOUSE	yes	yes	2	24	23	M	Q	0	2529.286	2;3	1.19E-16	124.20	1.13	0.89	13
16	AAAATMAAAAR	sp|Q8C754-2|VPS52_MOUSE	yes	no	2	12	11	M	E	0	974.497	2	1.46E-02	73.50	0.65	0.38	3
17	AAAAVVEFQR	sp|Q8BG32|PSD11_MOUSE	yes	yes	2	11	10	M	A	0	1060.567	2	6.10E-13	200.60	257.04	254.82	1
18	AAAAVVVPAEWIKNWEKSGR	sp|B1AZI6|THOC2_MOUSE	yes	yes	2	21	20	M	G	0	2181.170	3	3.21E-03	60.76	1.41	1.23	4
19	AAADGDDSLYPIAVLIDELR	sp|Q76MZ3|2AAA_MOUSE	yes	yes	2	21	20	M	N	0	2116.069	3	8.53E-02	33.25	NaN	NaN	0
20	AAAEPDADPKAAIPVDLR	sp|Q8R2T8-2|TF3C5_MOUSE	yes	no	2	19	18	M	R	0	1818.948	2	2.80E-02	45.00	1.37	0.88	2
21	AAAGGGAAAAAGR	sp|P35282|RAB21_MOUSE	yes	yes	2	14	13	M	A	0	970.494	2	4.73E-07	153.33	NaN	NaN	0
22	AAAMDVDTPSGTNSGAGKKR	sp|P62878|RBX1_MOUSE	yes	yes	2	21	20	M	F	0	1932.932	3	1.23E-07	99.04	1.14	1.14	9
23	AAAQAVEEMR	sp|P52432|RPAC1_MOUSE	yes	yes	2	11	10	M	T	0	1074.513	2	1.73E-03	82.42	NaN	NaN	0
24	AAATASSALKR	sp|Q9Z160|COG1_MOUSE	yes	yes	2	12	11	M	L	0	1045.588	2	1.46E-15	170.89	1.33	0.96	7
25	AAATLSFGPER	sp|Q80TM9-7|NISCH_MOUSE	yes	no	2	12	11	M	E	0	1118.572	2	3.72E-02	60.26	NaN	NaN	0
26	AAATPTETPAPEGSGLGMDAR	sp|Q7TSV4|PGM2_MOUSE	yes	yes	2	22	21	M	L	0	1998.932	2	3.09E-05	64.71	NaN	NaN	0
27	AAAVASLATLAAEPR	sp|P0CB42|ALKB1_MOUSE	yes	yes	5	19	15	M	E	0	1410.783	2	1.21E-06	125.97	NaN	NaN	0
28	AAAVAVAAASR	sp|E9Q1P8|I2BP2_MOUSE	yes	yes	2	12	11	M	R	0	956.540	2	1.21E-02	78.34	8.94	8.47	1
29	AAAVSGVVR	sp|Q8BR90|CE051_MOUSE	yes	yes	2	10	9	M	R	0	828.482	2	1.48E-02	95.36	NaN	NaN	0
30	AAAVVDPQQSVVMR	sp|P43883|PLIN2_MOUSE	yes	yes	2	15	14	M	V	0	1469.766	2	2.97E-03	66.99	NaN	NaN	0
31	AAAVVEEAAAGDVQR	sp|Q8VEJ4|NLE1_MOUSE	yes	yes	2	16	15	M	L	0	1455.732	2	2.37E-06	115.91	NaN	NaN	0
32	AAAVVEFQR	sp|Q8BG32|PSD11_MOUSE	yes	yes	3	11	9	A	A	0	989.529	2	1.05E-02	117.89	NaN	NaN	0
33	AADIEQVFR	sp|Q9QX47-2|SON_MOUSE	yes	no	2	10	9	M	S	0	1047.535	2	1.17E-02	109.29	NaN	NaN	0
34	AADISQWAGPLCLQEVDEPPQHA	sp|P70296|PEBP1_MOUSE	yes	yes	2	26	25	M	V	0	2800.360	2;3;4	3.31E-27	171.29	NaN	NaN	0
35	AAEAAGGKYR	sp|O35382|EXOC4_MOUSE	yes	yes	2	11	10	M	S	0	992.504	2	9.68E-04	118.03	2.34	1.48	4
36	AAESALQVVEKLQAR	sp|Q8CB77|ELOA1_MOUSE	yes	yes	2	16	15	M	L	0	1611.894	2	2.71E-22	186.77	1.25	1.02	8
37	AAETQTLNFGPEWLR	sp|Q6Y7W8|PERQ2_MOUSE	yes	yes	2	16	15	M	A	0	1731.858	2	9.18E-06	88.56	NaN	NaN	0
38	AAFGILSYEHR	sp|A2AGH6-2|MED12_MOUSE	yes	no	2	12	11	M	P	0	1262.641	2	9.37E-03	82.42	NaN	NaN	0
39	AAGAAAALAFLNQESR	sp|Q9CPP0|NPM3_MOUSE	yes	yes	2	17	16	M	A	0	1559.806	2	6.78E-29	206.49	NaN	NaN	0
40	AAGAAEAGEAAVAVVEVGSAQQ	sp|Q9CQM9|GLRX3_MOUSE	yes	yes	2	29	28	M	L	0	2742.382	2;3	4.95E-18	114.90	NaN	NaN	0
41	AAGESMAQR	sp|Q9D8S4|ORN_MOUSE	yes	yes	34	42	9	M	M	0	919.418	2	1.60E-03	138.40	NaN	NaN	0
42	AAGFKTVEPLEYYR	sp|Q9D753|EXOS8_MOUSE	yes	yes	2	15	14	M	R	0	1642.836	2	2.53E-18	181.26	1.27	0.93	10
43	AAGGAVAVAPECR	sp|O89050|MKLN1_MOUSE	yes	yes	2	14	13	M	L	0	1227.603	2	3.87E-03	72.29	NaN	NaN	0
44	AAGPISER	sp|Q8QZY9|SF3B4_MOUSE	yes	yes	2	9	8	M	N	0	799.419	2	1.58E-02	114.50	NaN	NaN	0
45	AAGTLYTYPENWR	sp|Q9D8N0|EF1G_MOUSE	yes	yes	2	14	13	M	A	0	1540.731	2	8.63E-04	98.11	0.00	0.00	2
46	AAGTSNYWEDLR	sp|O88630|GOSR1_MOUSE	yes	yes	2	13	12	M	K	0	1381.626	2	3.26E-03	97.46	NaN	NaN	0
47	AAHLSYGR	sp|Q9D2N9|VP33A_MOUSE	yes	yes	2	9	8	M	V	0	873.446	2	2.05E-03	145.34	NaN	NaN	0
48	AAKPKLYYFNGR	sp|P24472|GSTA4_MOUSE	yes	yes	2	13	12	M	G	0	1426.772	3	2.80E-03	88.60	1.26	1.19	6
49	AALAGDEAWR	sp|O54785|LIMK2_MOUSE	yes	yes	2	11	10	M	C	0	1058.515	2	5.50E-02	59.91	NaN	NaN	0
50	AALTCITCR	sp|Q91VY9|ZN622_MOUSE	yes	yes	2	10	9	M	V	0	1064.511	2	2.80E-02	79.15	NaN	NaN	0
51	AALTDVQR	sp|Q9Z0Y1|DCTN3_MOUSE	yes	yes	2	9	8	M	L	0	872.472	2	2.31E-03	143.12	NaN	NaN	0
52	AALVIDNGSGMCKAGFAGDDAPI	sp|P63260|ACTG_MOUSE	yes	yes	6	28	23	I	A	0	2292.063	2	6.43E-11	107.21	1.27	1.00	8
53	AALVVDNGSGMCKAGFAGDDAP	sp|P60710|ACTB_MOUSE	yes	no	6	28	23	I	A	0	2278.047	2	1.42E-17	133.84	1.08	1.00	7
54	AALVVSETAEPGSR	sp|Q5NCQ5|DPH1_MOUSE	yes	yes	2	15	14	M	V	0	1385.715	2	3.97E-03	63.19	NaN	NaN	0
55	AALYGGVEGGGTR	sp|Q9QZ08|NAGK_MOUSE	yes	yes	2	14	13	M	S	0	1206.599	2	9.47E-04	90.61	NaN	NaN	0
56	AAMAVGGAGGSR	sp|Q8CIG8|ANM5_MOUSE	yes	yes	2	13	12	M	V	0	1003.487	2	2.63E-02	59.16	NaN	NaN	0
57	AANATMATSGSAR	sp|Q91VC3|IF4A3_MOUSE	yes	yes	2	14	13	M	K	0	1207.562	2	9.21E-04	92.86	NaN	NaN	0
58	AANATTNPSQLLPLELVDKCIGSR	sp|P62322|LSM5_MOUSE	yes	yes	2	25	24	M	I	0	2567.338	2;3	4.41E-43	195.97	1.17	1.01	11
59	AANNKFCFDFFR	sp|Q9D7P9|SPB12_MOUSE	yes	yes	6	17	12	T	E	0	1535.698	2	3.71E-03	81.92	1.13	1.04	1
60	AANSQGNFDGKFEALDLAELTKK	sp|Q9D6K8|FUND2_MOUSE	yes	yes	2	29	28	M	K	0	3219.610	4	1.93E-02	35.93	1.90	1.22	3
61	AANVGSMFQYWKR	sp|P53564-3|CUX1_MOUSE	yes	yes	2	14	13	M	F	0	1556.756	2	1.62E-02	62.09	1.50	0.93	1
62	AAPAAPAAGETGPDAR	sp|Q9D6Y9|GLGB_MOUSE	yes	yes	2	17	16	M	L	0	1421.690	2	2.40E-06	98.94	NaN	NaN	0
63	AAPAAVLGPSALGQSGPGSMAPV	sp|Q8VE80|THOC3_MOUSE	yes	yes	2	33	32	M	Y	0	3009.444	3	5.36E-05	58.09	NaN	NaN	0
64	AAPAGGGGSAVSVLAPNGR	sp|Q8VBT9|ASPC1_MOUSE	yes	yes	2	20	19	M	R	0	1607.838	2	3.08E-02	42.63	NaN	NaN	0
65	AAPAKGENLSLVVHGPGDIR	sp|Q64442|DHSO_MOUSE	yes	yes	2	21	20	M	L	0	2000.080	3	2.26E-10	112.55	1.03	0.96	6
66	AAPAPSLISVFSSPQELGASLAQLV	sp|Q9CQ60|6PGL_MOUSE	yes	yes	2	29	28	M	A	0	2807.518	3	3.29E-18	115.55	NaN	NaN	0
67	AAPEDVAALQAEITR	sp|A2BDX3|MOCS3_MOUSE	yes	yes	2	16	15	M	R	0	1553.805	2	2.77E-02	49.60	NaN	NaN	0
68	AAPESLRPR	sp|Q9JHL1|NHRF2_MOUSE	yes	yes	2	10	9	M	L	1	995.551	2	1.82E-02	89.89	NaN	NaN	0
69	AAPQDVHVR	sp|Q6QD59|SEC20_MOUSE	yes	yes	2	10	9	M	I	0	991.520	2	1.51E-02	94.85	NaN	NaN	0
70	AAQALAAQAVASR	sp|Q8BLY2|SYTC2_MOUSE	yes	yes	2	14	13	M	L	0	1226.673	2	8.21E-02	43.03	NaN	NaN	0
71	AAQAVSLLR	sp|Q8BJY1|PSMD5_MOUSE	yes	yes	2	10	9	M	E	0	927.550	2	2.71E-05	156.35	583.32	458.51	1
72	AASAIKGLSALR	sp|Q9D8T7-2|SLIRP_MOUSE	yes	no	2	13	12	M	S	0	1156.693	2	1.20E-06	135.81	1.13	0.99	8
73	AASALYACTKCTQR	sp|Q80XP8|FA76B_MOUSE	yes	yes	2	15	14	M	Y	0	1599.750	2	4.64E-04	84.37	1.51	1.19	1
74	AASEDELLLPR	sp|Q61249|IGBP1_MOUSE	yes	yes	2	12	11	M	L	0	1212.635	2	1.23E-03	139.86	NaN	NaN	0
75	AASELYTKFAR	sp|Q99104|MYO5A_MOUSE	yes	yes	2	12	11	M	V	0	1255.656	2	1.64E-06	145.91	1.17	1.02	6
76	AASGDPGSAESYR	sp|P54822|PUR8_MOUSE	yes	yes	2	14	13	M	S	0	1266.548	2	8.17E-04	119.25	NaN	NaN	0
77	AASKVKQDMPPPGGYGPIDYKR	sp|Q9ERS2|NDUAD_MOUSE	yes	yes	2	23	22	M	N	0	2374.210	4	3.88E-02	40.62	1.49	1.21	1
78	AASPSKTEIQTIFKR	sp|Q99K28|ARFG2_MOUSE	yes	no	2	16	15	M	L	0	1675.926	3	1.68E-05	96.67	1.34	1.30	7
79	AATAAVPGAAAGR	sp|Q8CHW4|EI2BE_MOUSE	yes	yes	2	14	13	M	A	0	1082.583	2	9.61E-04	89.30	10.99	7.07	4
80	AATFFGEVVKAPCR	sp|Q9JK23|PSMG1_MOUSE	yes	yes	2	15	14	M	A	0	1551.787	2;3	8.62E-19	186.13	1.11	1.02	14
81	AATMSEPR	sp|Q9DCC4|P5CR3_MOUSE	yes	yes	2	9	8	M	R	0	861.401	2	1.41E-02	115.49	NaN	NaN	0
82	AATTGSGVKVPR	sp|Q9CZY3-2|UB2V1_MOUSE	yes	no	2	13	12	M	N	0	1142.641	2	1.41E-56	253.76	1.24	1.15	9
83	AAVAVAVR	sp|Q61749|EI2BD_MOUSE	yes	yes	2	9	8	M	E	0	755.465	2	4.93E-02	86.47	NaN	NaN	0
84	AAVGSPGSLESAPR	sp|Q9JMA2|TGT_MOUSE	yes	yes	2	15	14	M	I	0	1297.663	2	4.12E-04	94.09	NaN	NaN	0
85	AAVKTLNPKAEVAR	sp|P80317|TCPZ_MOUSE	yes	yes	2	15	14	M	A	0	1466.857	2;3	4.83E-04	92.94	1.14	0.96	19
86	AAVPELLEQQEEDR	sp|Q9D8U8|SNX5_MOUSE	yes	yes	2	15	14	M	S	0	1625.790	2	3.92E-04	102.52	NaN	NaN	0
87	AAVPSAVHLPR	sp|Q3UFF7|LYPL1_MOUSE	yes	yes	2	12	11	M	C	0	1116.640	2	3.04E-03	113.93	8.85	8.37	1
88	AAVTVNSAKR	sp|Q9D110|MTHFS_MOUSE	yes	yes	2	11	10	M	G	0	1015.577	2	2.42E-04	130.98	1.53	1.32	5
89	AAWRPPR	sp|Q9R0N0|GALK1_MOUSE	yes	yes	2	8	7	M	V	1	852.472	2	2.61E-03	132.96	0.00	0.00	1
90	AAYKLVLIR	sp|Q9DBJ1|PGAM1_MOUSE	yes	yes	2	10	9	M	H	0	1045.665	2	3.34E-14	172.21	1.19	0.93	13
91	ACGLVASNLNLKPGECLKVR	sp|P16045|LEG1_MOUSE	yes	yes	2	21	20	M	G	0	2198.166	2;3;4	3.54E-27	171.35	1.09	0.95	35
92	ACLLETPIR	sp|Q9DBR3-2|ARMC8_MOUSE	yes	no	2	10	9	M	M	0	1071.575	2	1.25E-02	99.44	NaN	NaN	0
93	ADAAASPVGKR	sp|Q6ZPY7-2|KDM3B_MOUSE	yes	no	2	12	11	M	L	0	1041.557	2	9.90E-06	158.05	1.12	0.84	9
94	ADAWEEIRR	sp|Q8CCJ3|UFL1_MOUSE	yes	yes	2	10	9	M	L	1	1144.563	2	1.81E-02	90.15	NaN	NaN	0
95	ADEDGEGIHPSAPHR	sp|Q3UHD6-2|SNX27_MOUSE	yes	no	2	16	15	M	N	0	1586.707	3	1.28E-02	57.29	NaN	NaN	0
96	ADEEKLPPGWEKR	sp|Q9QUR7|PIN1_MOUSE	yes	yes	2	14	13	M	M	0	1553.784	3	1.39E-05	127.36	0.98	0.95	8
97	ADEELEALR	sp|P56812|PDCD5_MOUSE	yes	yes	2	10	9	M	K	0	1044.509	2	2.10E-02	85.53	NaN	NaN	0
98	ADEGKSYNEHDDR	sp|Q99JX7|NXF1_MOUSE	yes	yes	2	14	13	M	V	0	1534.628	3	2.95E-05	118.52	1.17	0.91	7

99	ADEIAKAQVAQPGGDTIFGKIIR	sp|P70349|HINT1_MOUSE	yes	yes	2	24	23	M	K	0	2397.302	2;3;4	3.90E-17	131.56	0.98	0.97	13
100	ADFDTYDDR	sp|Q9WUK2-2|IF4H_MOUSE	yes	no	2	10	9	M	A	0	1116.436	2	2.01E-02	86.90	NaN	NaN	0
101	ADGELNVDSLITR	sp|P62141|PP1B_MOUSE	yes	yes	2	14	13	M	L	0	1401.710	2	8.94E-04	95.26	NaN	NaN	0
102	ADGGGSPFLGR	sp|Q9R1Z8|VINEX_MOUSE	yes	yes	407	417	11	M	R	0	1032.499	2	2.14E-02	68.54	NaN	NaN	0
103	ADGQLPFPCSYPSR	sp|Q9JK92|HSPB8_MOUSE	yes	yes	2	15	14	M	L	0	1593.725	2	3.31E-03	65.04	NaN	NaN	0
104	ADIDKLNIDSIIQR	sp|P63087|PP1G_MOUSE	yes	no	2	15	14	M	L	0	1612.878	2;3	2.08E-18	182.57	1.15	1.04	11
105	ADIDNKEQSELDQDLEDVEEVEEE	sp|P28656|NP1L1_MOUSE	yes	yes	2	36	35	M	Q	0	4061.856	4	1.15E-16	106.37	1.14	0.91	5
106	ADIQTER	sp|P62281|RS11_MOUSE	yes	yes	2	8	7	M	A	0	831.409	2	2.04E-02	125.25	NaN	NaN	0
107	ADISQWAGPLCLQEVDEPPQHAL	sp|P70296|PEBP1_MOUSE	yes	yes	3	26	24	A	V	0	2729.323	3	5.93E-02	31.75	NaN	NaN	0
108	ADKEAAFDDAVEER	sp|Q60972|RBBP4_MOUSE	yes	yes	2	15	14	M	V	0	1564.701	2	1.94E-08	147.09	1.32	0.94	10
109	ADKMDMSLDDIIKLNR	sp|Q9JJW6-2|ALRF2_MOUSE	yes	no	2	17	16	M	N	0	1876.939	3	2.87E-03	71.08	1.18	1.15	7
110	ADLEEQLSDEEKVR	sp|P47754|CAZA2_MOUSE	yes	yes	2	15	14	M	I	0	1659.795	2	4.39E-35	214.18	1.14	0.96	11
111	ADLSLDELIR	sp|Q8BG81|PDIP3_MOUSE	yes	yes	2	11	10	M	K	0	1143.614	2	1.40E-02	100.88	NaN	NaN	0
112	ADLSLVDALTEPPPEIEGEIKR	sp|P27546-3|MAP4_MOUSE	yes	no	2	23	22	M	D	0	2391.253	2	4.12E-11	112.55	1.00	0.95	3
113	ADMQNLVER	sp|P40124|CAP1_MOUSE	yes	yes	2	10	9	M	L	0	1074.513	2	1.42E-03	140.05	0.00	0.00	1
114	ADNAFSFR	sp|Q8VBV7|CSN8_MOUSE	yes	yes	7	14	8	M	K	0	926.425	2	4.45E-02	94.31	NaN	NaN	0
115	ADNEKLDNQR	sp|O35343|IMA3_MOUSE	yes	yes	2	11	10	M	L	0	1201.569	2	7.78E-06	136.70	1.26	0.96	6
116	ADNPVLELLLR	sp|Q8C0C7|SYFA_MOUSE	yes	yes	2	12	11	M	R	0	1251.719	2	7.05E-04	145.31	NaN	NaN	0
117	ADPAECNIKVMCR	sp|Q61768|KINH_MOUSE	yes	yes	2	14	13	M	F	0	1562.700	2	1.79E-08	150.49	1.29	1.06	10
118	ADPDVLTEVPAALKR	sp|Q9D0D5|T2EA_MOUSE	yes	yes	2	16	15	M	L	0	1593.873	2	4.64E-08	120.21	1.21	0.91	8
119	ADPESPWSQIGR	sp|Q99JV5|STAR4_MOUSE	yes	yes	2	13	12	M	K	0	1341.631	2	9.58E-03	70.09	NaN	NaN	0
120	ADPKYADLPGIAR	sp|Q99KJ8|DCTN2_MOUSE	yes	yes	2	14	13	M	N	0	1385.730	2	2.66E-03	79.88	1.32	0.98	8
121	ADSGPAGGAALAAPAPGPGSGST	sp|Q62084|PP14B_MOUSE	yes	yes	2	27	26	M	V	0	2146.040	3	3.48E-06	68.57	NaN	NaN	0
122	ADSVKTFLQDLGR	sp|Q61070|EI24_MOUSE	yes	yes	2	14	13	M	G	0	1448.762	2	2.63E-12	165.86	1.26	0.99	4
123	ADTAPQLKR	sp|Q9DAR7|DCPS_MOUSE	yes	yes	2	10	9	M	K	0	998.551	2	9.27E-04	126.07	0.99	0.94	6
124	ADTFLEHMCR	sp|P52480-2|KPYM_MOUSE	yes	no	23	32	10	M	L	0	1278.549	2	1.43E-02	105.98	NaN	NaN	0
125	ADTQYILPNDIGVSSLDCR	sp|Q99KK7|DPP3_MOUSE	yes	yes	2	20	19	M	E	0	2136.016	3	1.95E-05	78.67	NaN	NaN	0
126	ADVLSVLR	sp|Q8JZM7|CDC73_MOUSE	yes	yes	2	9	8	M	Q	0	871.513	2	3.71E-02	101.72	NaN	NaN	0
127	AEAEAGGDEAR	sp|Q8CHP8|PGP_MOUSE	yes	yes	2	12	11	M	C	0	1074.458	2	9.29E-03	95.48	NaN	NaN	0
128	AEAEEDCHSDADR	sp|Q8BK06-3|FBX9_MOUSE	yes	no	2	14	13	M	V	0	1503.553	2	8.82E-04	106.32	NaN	NaN	0
129	AECCVPVCPR	sp|Q60930|VDAC2_MOUSE	yes	yes	2	11	10	M	P	0	1246.526	2	4.10E-02	63.73	NaN	NaN	0
130	AEDCRDDIGR	sp|P70372|ELAV1_MOUSE	yes	yes	10	19	10	M	T	1	1205.510	2	9.37E-03	126.19	NaN	NaN	0
131	AEEGIAAGGVMDVNTALQEVLKT	sp|P63323|RS12_MOUSE	yes	yes	2	33	32	M	G	0	3261.703	3;4	7.69E-12	89.02	1.23	1.00	10
132	AEELLLER	sp|P21981|TGM2_MOUSE	yes	no	2	9	8	M	C	0	971.529	2	4.38E-02	95.50	NaN	NaN	0
133	AEEQPQVELFVKAGSDGAKIGNCI	sp|Q9Z1Q5|CLIC1_MOUSE	yes	yes	2	29	28	M	L	0	3061.493	3;4	2.37E-04	55.66	1.00	0.99	5
134	AEEVSSLMKATVLMR	sp|Q3UFY7-3|5NT3B_MOUSE	yes	no	2	16	15	M	Q	0	1663.864	2	2.48E-21	171.46	1.07	0.94	5
135	AEGEDVGWWR	sp|Q80Y55|BSDC1_MOUSE	yes	yes	2	11	10	M	S	0	1203.531	2	6.08E-02	40.50	NaN	NaN	0
136	AEGGAADLDTQR	sp|Q8R5H1-4|UBP15_MOUSE	yes	no	2	13	12	M	S	0	1202.553	2	1.59E-04	140.63	26.68	21.18	1
137	AEGQVLVLDGR	sp|P19253|RL13A_MOUSE	yes	yes	2	12	11	M	G	0	1155.625	2	6.76E-15	193.73	NaN	NaN	0
138	AEGSAVSDPQHAAR	sp|Q8CA72|GAN_MOUSE	yes	yes	2	15	14	M	L	0	1394.654	2	3.30E-17	192.18	NaN	NaN	0
139	AEGTAVLR	sp|Q6PEB6|PHOCN_MOUSE	yes	yes	4	11	8	M	R	0	815.450	2	5.68E-02	79.47	NaN	NaN	0
140	AEHLLKPLPADR	sp|Q9JL62|GLTP_MOUSE	yes	yes	5	16	12	L	Q	0	1358.767	2	1.19E-03	101.53	1.25	1.15	4
141	AELEEVTLDGKPLQALR	sp|Q9JIX8-4|ACINU_MOUSE	yes	no	60	76	17	M	V	0	1881.021	2	5.69E-09	129.05	0.95	0.88	8
142	AELGLNEHHQNEVINYMR	sp|Q9JHQ5|LZTL1_MOUSE	yes	yes	2	19	18	M	F	0	2166.028	3	1.76E-15	159.95	NaN	NaN	0
143	AELQMLLEEEIPSGKR	sp|Q8CBW3-5|ABI1_MOUSE	yes	no	2	17	16	M	A	0	1841.956	2	1.37E-15	156.49	1.10	1.01	3
144	AELSEEALLSVLPTIR	sp|P56399|UBP5_MOUSE	yes	yes	2	17	16	M	V	0	1739.967	2	2.12E-08	149.00	NaN	NaN	0
145	AELTALESLIEMGFPR	sp|Q922Y1|UBXN1_MOUSE	yes	yes	2	17	16	M	G	0	1775.913	2	1.34E-68	210.37	NaN	NaN	0
146	AELTNYKDAASNR	sp|Q8R4U7|LUZP1_MOUSE	yes	yes	2	14	13	M	H	0	1451.701	2	8.18E-11	111.12	1.29	0.83	4
147	AEMKSPTKAEPATPAEAAQSDR	sp|Q7TPV4|MBB1A_MOUSE	yes	yes	2	23	22	M	H	0	2285.096	3	1.89E-02	42.35	1.32	0.98	9
148	AENGESSGPPRPSR	sp|Q9QZM0|UBQL2_MOUSE	yes	yes	2	15	14	M	G	1	1439.675	2	7.99E-05	133.47	NaN	NaN	0
149	AENLLDGPPNPKR	sp|P45481|CBP_MOUSE	yes	yes	2	14	13	M	A	0	1419.747	2	9.65E-03	64.83	1.17	0.73	3
150	AENPGLENHR	sp|O35344|IMA4_MOUSE	yes	yes	2	11	10	M	I	0	1135.537	2	1.95E-09	147.30	NaN	NaN	0
151	AEPSGAETRPQIR	sp|Q99NB8|UBQL4_MOUSE	yes	yes	2	14	13	M	V	1	1410.722	2	9.01E-04	94.69	NaN	NaN	0
152	AEPWGNELASAAAR	sp|Q60772|CDN2C_MOUSE	yes	yes	2	15	14	M	G	0	1441.695	2	4.24E-04	91.81	NaN	NaN	0
153	AEQVALSR	sp|Q00612|G6PD1_MOUSE	yes	yes	2	9	8	M	T	0	872.472	2	2.57E-02	108.57	NaN	NaN	0
154	AERPEDLNLPNAVITR	sp|Q9JKP7|DPOE3_MOUSE	yes	yes	2	17	16	M	I	1	1806.959	2	9.82E-07	123.14	0.03	0.03	1
155	AESEVLHR	sp|Q3TZX8-3|NOL9_MOUSE	yes	no	2	9	8	M	R	0	939.477	2	3.04E-03	136.80	NaN	NaN	0
156	AESIIIR	sp|P60670-2|NPL4_MOUSE	yes	no	2	8	7	M	V	0	800.476	2	2.11E-02	120.65	NaN	NaN	0
157	AESPAFLSAKDEGSFAYLTIKDR	sp|A6H630-4|CF211_MOUSE	yes	no	2	24	23	M	T	0	2515.260	3	9.03E-04	57.48	0.96	0.95	1
158	AESSESLSASSPAR	sp|P97310|MCM2_MOUSE	yes	yes	2	15	14	M	Q	0	1377.637	2	1.19E-07	160.84	NaN	NaN	0
159	AETECQNAEYQQLLDIKTR	sp|P02535-3|K1C10_MOUSE	yes	no	412	430	19	R	L	0	2309.096	3	1.25E-09	100.04	0.99	0.83	2
160	AETLEFNDIFQEVKGSMNDGR	sp|Q08943|SSRP1_MOUSE	yes	no	2	22	21	M	L	0	2399.106	2;3	6.10E-03	52.19	0.84	0.66	7
161	AETVADTR	sp|O70492|SNX3_MOUSE	yes	yes	2	9	8	M	R	0	861.419	2	2.38E-02	109.71	NaN	NaN	0
162	AEVEETLKR	sp|P62627|DLRB1_MOUSE	yes	yes	2	10	9	M	L	0	1073.572	2	5.95E-10	168.83	1.12	0.99	8
163	AEVQQLR	sp|Q9CR98|F136A_MOUSE	yes	yes	2	8	7	M	V	0	842.461	2	3.41E-02	110.61	NaN	NaN	0
164	AEYDLTTR	sp|P60229|EIF3E_MOUSE	yes	yes	2	9	8	M	I	0	967.461	2	4.00E-02	100.02	NaN	NaN	0
165	AFKDTGKTPVEPEVAIHR	sp|P60867|RS20_MOUSE	yes	yes	2	19	18	M	I	0	1994.059	3;4	4.49E-10	112.82	1.27	1.04	22
166	AFLCQR	sp|Q3THG9|AASD1_MOUSE	yes	yes	2	7	6	M	D	0	793.390	2	7.10E-02	112.58	NaN	NaN	0
167	AFPKKKLR	sp|Q9DCJ9|NPL_MOUSE	yes	yes	2	9	8	M	G	0	986.639	3	8.34E-02	54.16	NaN	NaN	0
168	AGAEAPQPQKR	sp|Q9Z120|TRMB_MOUSE	yes	yes	3	13	11	M	Y	0	1151.605	2	3.33E-04	123.79	1.07	0.94	4
169	AGAGPTMLLR	sp|Q9D2U5|LSMD1_MOUSE	yes	yes	2	11	10	M	E	0	985.538	2	1.40E-02	96.34	NaN	NaN	0
170	AGGEAGVTLGQPHLSR	sp|Q9Z0N2|IF2H_MOUSE	yes	yes	2	17	16	M	Q	0	1548.801	2	3.01E-11	139.34	0.08	0.06	1
171	AGGEGGVTLGQPHLSR	sp|Q9Z0N1|IF2G_MOUSE	yes	yes	2	17	16	M	Q	0	1534.785	2;3	2.85E-22	205.33	NaN	NaN	0
172	AGGVDGPIGIPFPDHSSDILSGLNE	sp|O88939-2|ZBT7A_MOUSE	yes	no	2	28	27	M	T	0	2747.352	2;3	1.53E-30	159.66	NaN	NaN	0
173	AGIAIKLAKDR	sp|O08529|CAN2_MOUSE	yes	yes	2	12	11	M	E	0	1154.714	2;3	4.14E-04	121.02	1.55	1.38	20
174	AGKHGDSVR	sp|P04104|K2C1_MOUSE	yes	yes	392	400	9	T	N	0	925.473	2	1.98E-02	89.17	4.90	3.18	4
175	AGKPVLHYFNAR	sp|P10648|GSTA2_MOUSE	yes	no	2	13	12	M	G	0	1371.741	3	7.52E-04	108.35	1.09	1.01	6
176	AGLELLSDQGYR	sp|Q921I9|EXOS4_MOUSE	yes	yes	2	13	12	M	I	0	1320.667	2	4.72E-03	78.90	NaN	NaN	0
177	AGLGHPSAFGR	sp|Q9CWS0|DDAH1_MOUSE	yes	yes	2	12	11	M	A	0	1068.547	2	1.35E-09	178.46	NaN	NaN	0
178	AGLNSLEAVKR	sp|Q6IRU2|TPM4_MOUSE	yes	yes	2	12	11	M	K	0	1156.656	2	4.26E-32	207.88	0.90	0.80	16
179	AGLPVRDPAVDR	sp|Q8BIQ5-2|CSTF2_MOUSE	yes	no	2	13	12	M	S	1	1264.689	2	3.26E-03	99.50	NaN	NaN	0
180	AGLSDLELR	sp|Q6DVA0|LEMD2_MOUSE	yes	yes	2	10	9	M	R	0	972.524	2	1.24E-02	100.02	NaN	NaN	0
181	AGNFDSEER	sp|Q64010-2|CRK_MOUSE	yes	no	2	10	9	M	S	0	1023.426	2	1.24E-02	99.86	0.01	0.01	1
182	AGNKVPPALASHQPDR	sp|Q9WU56-4|TRUA_MOUSE	yes	no	2	17	16	M	K	0	1656.870	3	1.85E-06	104.20	1.17	0.98	5
183	AGPLCLQEVDEPPQHALR	sp|P70296|PEBP1_MOUSE	yes	yes	9	26	18	W	V	0	2029.005	2	4.01E-20	177.67	NaN	NaN	0
184	AGSAVDSANHLTYFFGNITR	sp|P48025|KSYK_MOUSE	yes	yes	2	21	20	M	E	0	2140.034	2	4.19E-12	133.24	NaN	NaN	0
185	AGSAWVSKVSR	sp|Q9D6R2|IDH3A_MOUSE	yes	yes	2	12	11	M	L	0	1146.615	2	3.95E-04	121.68	1.09	0.89	5
186	AGSSAEQAADYR	sp|Q9ER72|SYCC_MOUSE	yes	yes	2	13	12	M	S	0	1224.537	2	6.14E-03	76.33	NaN	NaN	0
187	AGSSSGSGVQGASAGGLAADASR	sp|P11088|FILA_MOUSE	yes	yes	47	69	23	R	R	0	1919.893	2;3	2.09E-16	114.15	NaN	NaN	0
188	AGTLYTYPENWR	sp|Q9D8N0|EF1G_MOUSE	yes	yes	3	14	12	A	A	0	1469.694	2	2.94E-02	58.17	NaN	NaN	0
189	AGTTTIEAVKR	sp|P21107-2|TPM3_MOUSE	yes	yes	2	12	11	M	K	0	1145.640	2	1.33E-55	244.01	0.94	0.82	10
190	AGTVVLDDVELR	sp|P25206|MCM3_MOUSE	yes	yes	2	13	12	M	E	0	1285.688	2	3.30E-03	100.38	NaN	NaN	0
191	AGVDQHEGTIQVQGQNLFFR	sp|Q8VCR7|ABHEB_MOUSE	yes	yes	2	21	20	M	E	0	2243.108	2;3	5.10E-11	112.55	23.92	23.03	2
192	AGVSFSGHR	sp|Q9QXS6-2|DREB_MOUSE	yes	no	2	10	9	M	L	0	916.452	2	1.53E-05	162.49	0.18	0.12	2
193	AGWIQAQQLQGDALR	sp|P42230|STA5A_MOUSE	yes	yes	2	16	15	M	Q	0	1653.859	2	1.12E-02	58.08	NaN	NaN	0
194	AHATPPSALEQGGPIR	sp|Q9DBW3|GTL3B_MOUSE	yes	yes	2	17	16	M	V	0	1600.832	2	6.27E-03	59.71	NaN	NaN	0
195	AIVHTLPVPLEPAR	sp|Q91YU6|LZTS2_MOUSE	yes	yes	2	15	14	M	E	0	1511.882	2	4.64E-04	84.37	NaN	NaN	0
196	AKCLLTSSLSVR	sp|Q9D9V3-2|ECHD1_MOUSE	yes	no	2	13	12	M	T	0	1333.739	2	1.13E-03	102.52	1.27	1.16	3
197	AKFMTPVIQDNPSGWGPCAVPE	sp|O70194|EIF3D_MOUSE	yes	yes	2	26	25	M	D	0	2831.352	2;3	4.91E-08	97.84	1.37	1.28	14
198	AKIAQGAMYR	sp|P14824|ANXA6_MOUSE	yes	yes	2	11	10	M	G	0	1107.586	2	2.71E-15	183.67	1.36	0.98	27
199	AKLLSCVLGPR	sp|Q9Z1Q2|ABHGA_MOUSE	yes	yes	2	12	11	M	L	0	1212.701	2	2.96E-06	140.24	1.25	0.93	6
200	AKPLTDQEKR	sp|Q9ET01|PYGL_MOUSE	yes	yes	2	11	10	M	R	0	1184.651	3	1.09E-02	87.18	0.89	0.85	5
201	AKPLTDSER	sp|Q8CI94|PYGB_MOUSE	yes	yes	2	10	9	M	Q	0	1015.530	2	3.27E-14	172.56	0.90	0.84	4

202	AKVEQVLSLEPQHELKFR	sp|Q9QY76|VAPB_MOUSE	yes	yes	2	19	18	M	G	0	2150.185	4	3.96E-06	91.32	1.35	0.87	4
203	AKWGEGDPR	sp|Q8BK64|AHSA1_MOUSE	yes	yes	2	10	9	M	W	0	1014.488	2	1.92E-02	90.15	1.34	1.00	8
204	ALASVLQR	sp|O55234|PSB5_MOUSE	yes	yes	2	9	8	M	P	0	856.513	2	4.38E-02	95.53	NaN	NaN	0
205	ALDGPEQMELEEGKAGSGLR	sp|P62196|PRS8_MOUSE	yes	yes	2	21	20	M	Q	0	2086.000	2;3	2.80E-16	141.07	1.18	1.04	23
206	ALETVPKDLR	sp|Q9Z199|SPT4B_MOUSE	yes	no	2	11	10	M	H	0	1140.650	2	2.56E-06	147.62	1.08	0.94	9
207	ALGSLNITLQQHR	sp|Q8VI93|OAS3_MOUSE	yes	yes	32	44	13	G	A	0	1449.805	2	5.17E-02	52.07	0.79	0.73	5
208	ALKQISSNR	sp|Q9R0P3|ESTD_MOUSE	yes	yes	2	10	9	M	C	0	1015.577	2	8.63E-10	167.93	1.32	0.98	10
209	ALLAEHLLKPLPADR	sp|Q9JL62|GLTP_MOUSE	yes	yes	2	16	15	M	Q	0	1655.972	2;3	2.02E-11	147.12	1.29	1.17	13
210	ALNVAPVR	sp|Q8C181-3|MBNL2_MOUSE	yes	no	2	9	8	M	D	0	838.502	2	1.53E-02	114.78	NaN	NaN	0
211	ALQALHSSGVGLR	sp|Q3TUH1-2|TAM41_MOUSE	yes	no	2	14	13	M	R	0	1307.731	2	8.11E-04	119.39	NaN	NaN	0
212	ALVIDNGSGMCKAGFAGDDAPR	sp|P63260|ACTG_MOUSE	yes	yes	7	28	22	A	A	0	2221.026	2	1.62E-06	86.54	1.08	0.91	8
213	ALVVDNGSGMCKAGFAGDDAPR	sp|P60710|ACTB_MOUSE	yes	no	7	28	22	A	A	0	2207.010	2	4.12E-11	112.55	1.08	0.98	7
214	AMFEQMR	sp|Q9DBZ5-2|EIF3K_MOUSE	yes	no	2	8	7	M	A	0	911.399	2	3.31E-02	114.19	NaN	NaN	0
215	AMQKIFAR	sp|P21550|ENOB_MOUSE	yes	yes	2	9	8	M	E	0	963.532	2	5.52E-03	122.74	0.67	0.62	5
216	AMVSEFLKQAR	sp|P10107|ANXA1_MOUSE	yes	yes	2	12	11	M	F	0	1278.675	2	7.14E-56	251.43	1.14	1.01	50
217	ANHAPFETDISTLTR	sp|Q9QXD6|F16P1_MOUSE	yes	yes	2	16	15	M	F	0	1671.822	2;3	1.85E-06	120.63	NaN	NaN	0
218	ANIAVQR	sp|P61087|UBE2K_MOUSE	yes	yes	2	8	7	M	I	0	770.440	2	2.13E-02	118.69	NaN	NaN	0
219	ANKAPSQMER	sp|P31725|S10A9_MOUSE	yes	yes	2	11	10	M	S	0	1130.550	2	1.25E-02	83.05	1.84	1.57	4
220	ANKGPSYGMSR	sp|P37804|TAGL_MOUSE	yes	yes	2	12	11	M	E	0	1166.550	2	5.70E-05	133.32	1.19	1.10	15
221	ANLEESFPR	sp|Q6NS46|RRP5_MOUSE	yes	yes	2	10	9	M	G	0	1061.514	2	1.81E-02	90.15	NaN	NaN	0
222	ANNKFCFDFFR	sp|Q9D7P9|SPB12_MOUSE	yes	yes	7	17	11	A	E	0	1464.661	2	1.94E-03	107.09	1.17	1.00	2
223	ANRGPSYGLSR	sp|Q9WVA4|TAGL2_MOUSE	yes	no	2	12	11	M	E	1	1176.600	2	4.83E-03	129.37	NaN	NaN	0
224	ANSANTNTVPKLYR	sp|Q99PM3|TF2AA_MOUSE	yes	yes	2	15	14	M	S	0	1547.806	2	1.27E-25	191.06	0.96	0.91	7
225	ANVADTKLYDILGVPPGASENELK	sp|Q9QYJ0|DNJA2_MOUSE	yes	yes	2	29	28	M	K	0	3031.598	4	1.76E-06	70.72	1.27	0.88	2
226	APMLTDPR	sp|A2AGH6-2|MED12_MOUSE	yes	no	579	586	8	Q	S	0	899.453	2	1.17E-01	58.92	0.99	0.93	5
227	APVNIFKAGADEER	sp|P80314|TCPB_MOUSE	yes	yes	7	20	14	L	A	0	1515.768	2	1.26E-02	62.29	1.36	0.84	1
228	AQAAVAVAEVTQLLCAAGGALEL	sp|Q8BZ20|PAR12_MOUSE	yes	yes	2	28	27	M	R	0	2694.437	3	1.79E-06	73.07	NaN	NaN	0
229	AQAEGAYHRPLATSR	sp|Q9CQ56|USE1_MOUSE	yes	yes	2	16	15	M	L	1	1626.823	3	3.65E-06	100.11	NaN	NaN	0
230	AQALSEEEFQR	sp|Q8VD04|GRAP1_MOUSE	yes	yes	2	12	11	M	M	0	1306.615	2	7.72E-03	124.42	NaN	NaN	0
231	AQASAAPKAGTATGR	sp|P56480|ATPB_MOUSE	yes	yes	48	62	15	A	I	0	1356.711	2	6.35E-07	114.63	0.78	0.64	7
232	AQDGVELEKSVR	sp|Q8CAK3-2|CS066_MOUSE	yes	no	2	13	12	M	R	0	1329.689	2	3.14E-04	115.12	1.06	1.01	5
233	AQDQGEKENPMR	sp|Q9CXW4|RL11_MOUSE	yes	yes	2	13	12	M	E	0	1401.631	2	1.38E-10	156.81	1.15	0.95	27
234	AQELQHPEFAR	sp|Q60604-2|ADSV_MOUSE	yes	no	2	12	11	M	A	0	1324.652	2	2.14E-09	172.76	NaN	NaN	0
235	AQGLIEVER	sp|Q8JZL3|THTPA_MOUSE	yes	yes	2	10	9	M	K	0	1013.551	2	8.63E-05	96.34	NaN	NaN	0
236	AQKPDGGAGLR	sp|Q9QYH6|MAGD1_MOUSE	yes	yes	2	12	11	M	G	0	1068.568	2	1.57E-02	72.29	1.01	0.97	3
237	AQNLKDLAGR	sp|O35129|PHB2_MOUSE	yes	yes	2	11	10	M	L	0	1084.599	2	3.14E-11	170.52	0.86	0.67	10
238	AQPGKILKEQKYDR	sp|Q8VBW6|ULA1_MOUSE	yes	yes	2	15	14	M	Q	0	1672.926	4	2.15E-02	59.23	0.82	0.80	3
239	AQPKNLEGYVGFANLPNQVYR	sp|O55131|SEPT7_MOUSE	yes	yes	21	41	21	M	K	0	2377.218	2;3	4.71E-13	122.19	1.33	0.89	12
240	AQWNQLQQLDTR	sp|P42227-2|STAT3_MOUSE	yes	no	2	13	12	M	Y	0	1499.748	2	2.49E-10	181.66	NaN	NaN	0
241	ASALEQFVNSVR	sp|O88543|CSN3_MOUSE	yes	yes	2	13	12	M	Q	0	1319.683	2	1.04E-30	226.73	NaN	NaN	0
242	ASASYHISNLLEKMTSSDKDFR	sp|Q6ZQ38|CAND1_MOUSE	yes	yes	2	23	22	M	F	0	2499.206	3;4	4.69E-04	67.23	1.54	1.53	5
243	ASAVLSSVLTTASR	sp|Q9JMB0|GKAP1_MOUSE	yes	yes	2	15	14	M	F	0	1361.751	2	2.28E-03	70.89	NaN	NaN	0
244	ASAVSPANLPAVLLQPR	sp|Q61191|HCFC1_MOUSE	yes	yes	2	18	17	M	W	0	1702.973	2;3	7.61E-07	112.96	NaN	NaN	0
245	ASCASIDIEDATQHLR	sp|Q3UJB9-2|EDC4_MOUSE	yes	no	2	17	16	M	D	0	1785.832	2	5.75E-08	142.91	NaN	NaN	0
246	ASCDEIKEHPR	sp|Q8C650-2|SEP10_MOUSE	yes	no	2	12	11	M	S	0	1340.614	3	2.21E-02	65.18	1.48	1.02	2
247	ASDTPGFYMDKLNKYR	sp|Q03963|E2AK2_MOUSE	yes	yes	2	17	16	M	Q	0	1904.909	3	5.49E-05	82.65	1.01	0.96	3
248	ASEKPQDLMVTCTAPVNIAVIKYV	sp|Q99JF5|MVD1_MOUSE	yes	yes	2	28	27	M	D	0	3074.605	4	3.88E-02	31.77	1.10	1.02	1
249	ASEMEPEVQAIDR	sp|Q6WKZ8-2|UBR2_MOUSE	yes	no	2	14	13	M	S	0	1473.677	2	2.88E-02	55.20	NaN	NaN	0
250	ASESGKLWGGR	sp|Q91YI0|ARLY_MOUSE	yes	yes	2	12	11	M	F	0	1146.578	2	1.80E-16	186.46	1.28	0.95	8
251	ASFGWKR	sp|Q9D6K7-2|TTC33_MOUSE	yes	no	2	8	7	M	R	0	850.445	2	1.66E-04	148.33	0.93	0.88	4
252	ASFVTEVLAHSGSLEKEDLGTR	sp|O54692|ZW10_MOUSE	yes	yes	2	23	22	M	I	0	2345.186	3	3.93E-03	52.72	1.22	0.97	2
253	ASGADSKGDDLSTAILKQKNRPNF	sp|Q01853|TERA_MOUSE	yes	yes	2	25	24	M	L	1	2541.326	5	2.68E-02	39.66	1.08	0.93	2
254	ASGCKIGPSILNSDLANLGAECLR	sp|Q8VEE0|RPE_MOUSE	yes	yes	2	25	24	M	M	0	2515.252	2;3	1.65E-34	172.80	1.03	0.97	7
255	ASGNAQIGKSAPDFTATAVVDGA	sp|Q61171|PRDX2_MOUSE	yes	yes	2	34	33	M	G	0	3426.742	4	1.01E-12	92.87	0.93	0.87	5
256	ASGRPEELWEAVVGAAER	sp|Q9D1F4|AKTS1_MOUSE	yes	yes	2	19	18	M	F	1	1925.960	2;3	1.73E-04	65.42	NaN	NaN	0
257	ASGSMATSEEER	sp|Q9DBC7|KAP0_MOUSE	yes	yes	2	13	12	M	S	0	1253.519	2	1.84E-06	162.49	NaN	NaN	0
258	ASGVAVSDGVIKVFNDMKVR	sp|P18760|COF1_MOUSE	yes	yes	2	21	20	M	K	0	2091.115	2;3	1.33E-27	182.15	0.99	0.90	67
259	ASGVQVADEVCR	sp|Q9R0P5|DEST_MOUSE	yes	yes	2	13	12	M	I	0	1289.603	2	1.16E-04	148.96	NaN	NaN	0
260	ASGVTVNDEVIKVFNDMKVR	sp|P45591|COF2_MOUSE	yes	yes	2	21	20	M	K	0	2220.157	3	2.17E-27	178.06	0.93	0.90	14
261	ASIWVGPR	sp|O35639|ANXA3_MOUSE	yes	yes	2	9	8	M	G	0	884.487	2	9.71E-03	121.31	NaN	NaN	0
262	ASKEMFEDTVEER	sp|Q60973|RBBP7_MOUSE	yes	yes	2	14	13	M	V	0	1569.698	2	7.67E-13	169.37	1.25	0.96	17
263	ASKLLR	sp|Q9WUR9|KAD4_MOUSE	yes	no	2	7	6	M	A	0	686.444	2	4.54E-02	83.61	1.34	1.21	4
264	ASLFSFTSPAVKR	sp|P97454|SMAD5_MOUSE	yes	yes	5	17	13	M	L	0	1409.767	2	9.24E-04	94.12	0.92	0.85	5
265	ASLKDLEGKWR	sp|Q05816|FABP5_MOUSE	yes	yes	2	12	11	M	L	0	1301.709	2;3	3.50E-23	196.15	1.03	0.95	37
266	ASLLQSER	sp|Q8CBY8-2|DCTN4_MOUSE	yes	no	2	9	8	M	V	0	902.482	2	5.02E-03	131.06	NaN	NaN	0
267	ASLPPHAGPATPLSPTR	sp|P21619|LMNB2_MOUSE	yes	yes	2	18	17	M	L	0	1668.895	2	3.45E-06	83.76	NaN	NaN	0
268	ASLSLAPVNIFKAGADEER	sp|P80314|TCPB_MOUSE	yes	yes	2	20	19	M	A	0	1987.038	2;3	2.48E-27	181.40	1.14	0.99	17
269	ASNLNLKPGECLKVR	sp|P16045|LEG1_MOUSE	yes	yes	7	21	15	V	G	0	1697.925	2;3	3.00E-11	144.29	0.90	0.86	21
270	ASNVTNKTDPR	sp|Q9Z204-4|HNRPC_MOUSE	yes	no	2	12	11	M	S	0	1201.605	2	1.33E-06	147.26	1.19	0.91	9
271	ASPAAGGVVIVGSGLIGR	sp|Q99KP3|CRYL1_MOUSE	yes	yes	2	19	18	M	S	0	1579.905	2	8.40E-09	97.10	NaN	NaN	0
272	ASSDIQVKELEKR	sp|P54227|STMN1_MOUSE	yes	yes	2	14	13	M	A	0	1501.810	3	5.45E-03	73.88	0.90	0.89	5
273	ASSGYNPYVEIIEQPR	sp|P15307|REL_MOUSE	yes	yes	2	17	16	M	Q	0	1821.890	2	2.69E-03	62.06	10.01	8.24	1
274	ASSSSFTYYCPPSSSPVWSEPLYSLI	sp|Q8K2I1|FNTB_MOUSE	yes	yes	2	32	31	M	E	1	3572.667	3	3.62E-26	120.13	NaN	NaN	0
275	ASSSTETQLQR	sp|Q8VDC1|FYCO1_MOUSE	yes	yes	2	12	11	M	I	0	1206.584	2	1.13E-02	118.28	NaN	NaN	0
276	ASSVGNVADSTEPTKR	sp|Q8CGY8|OGT1_MOUSE	yes	yes	2	17	16	M	M	0	1617.796	2	2.03E-09	134.14	1.42	1.22	9
277	ASSVGNVADSTGLAELAHR	sp|Q8CGY8-2|OGT1_MOUSE	yes	yes	2	20	19	M	E	0	1853.923	2	5.86E-13	148.06	NaN	NaN	0
278	ASTADGDMGETLEQMR	sp|Q91V01|MBOA5_MOUSE	yes	yes	2	17	16	M	G	0	1710.719	2	3.89E-03	61.27	NaN	NaN	0
279	ASTVVAVGLTIAAAGFAGR	sp|Q9CQV7|TIM14_MOUSE	yes	no	2	20	19	M	Y	0	1730.968	2	5.09E-08	82.01	NaN	NaN	0
280	ASVALSEAEKVYIVHGVQEDLR	sp|Q9D0M0|EXOS7_MOUSE	yes	yes	2	23	22	M	V	0	2412.265	3	8.49E-17	129.43	1.62	1.00	3
281	ASVDFKTYVDQACR	sp|Q9QZV9|NXT1_MOUSE	yes	yes	2	15	14	M	A	0	1658.772	2	1.55E-04	106.42	1.21	0.74	3
282	ASVGTLAFDEYGR	sp|P80316|TCPE_MOUSE	yes	yes	2	14	13	M	P	0	1384.662	2	8.53E-04	98.94	NaN	NaN	0
283	ASVGTLAFDEYGRPFLIIKDQDR	sp|P80316|TCPE_MOUSE	yes	yes	2	24	23	M	K	1	2610.344	3	3.24E-23	151.42	1.15	0.97	8
284	ASWAEPSEPAALR	sp|O35465|FKBP8_MOUSE	yes	no	2	14	13	M	L	0	1383.678	2	1.78E-03	78.88	NaN	NaN	0
285	ASYFDEHDCEPLNPER	sp|Q9CY62|RN181_MOUSE	yes	yes	2	17	16	M	E	0	1977.816	2;3	1.70E-10	156.67	NaN	NaN	0
286	ASYYEILDVPR	sp|Q9QYI5-2|DNJB2_MOUSE	yes	no	2	12	11	M	S	0	1324.666	2	1.45E-02	75.82	0.30	0.29	1
287	ATAATEEPPFHGLLPKKETGASSF	sp|Q64514-2|TPP2_MOUSE	yes	no	2	29	28	M	Y	0	3061.533	4	3.88E-13	109.41	1.11	1.04	5
288	ATALSEEELDNEDYYSLLNVR	sp|Q5U458|DJC11_MOUSE	yes	yes	2	22	21	M	R	0	2443.139	3	4.26E-02	38.88	NaN	NaN	0
289	ATATPVQQQR	sp|P14733|LMNB1_MOUSE	yes	yes	2	11	10	M	A	0	1098.578	2	9.02E-06	163.88	NaN	NaN	0
290	ATDELASKLSR	sp|Q9D8Y0|EFHD2_MOUSE	yes	yes	2	12	11	M	R	0	1189.630	2	1.86E-23	201.00	1.00	0.84	16
291	ATEEKKPETEAAR	sp|P61965|WDR5_MOUSE	yes	yes	2	14	13	M	A	0	1458.731	3	3.37E-04	106.32	1.41	1.13	5
292	ATEGMILTNHDHQIR	sp|Q8BUV3|GEPH_MOUSE	yes	yes	2	16	15	M	V	0	1734.847	3	8.95E-03	59.25	NaN	NaN	0
293	ATESSPLTTHVLDTASGLPAQGLC	sp|Q9CRB3|HIUH_MOUSE	yes	yes	2	27	26	M	L	0	2694.365	2;3	1.32E-61	235.25	NaN	NaN	0
294	ATEVHNLQELR	sp|Q9D428|GOG7B_MOUSE	yes	yes	2	12	11	M	R	0	1308.679	2	1.11E-06	148.18	5.97	3.51	1
295	ATGANATPLDFPSKKR	sp|Q64213-2|SF01_MOUSE	yes	no	2	17	16	M	K	0	1672.890	2;3	5.75E-12	150.37	0.98	0.83	20
296	ATGCQKLIEVDDER	sp|P62754|RS6_MOUSE	yes	yes	9	22	14	P	K	0	1632.778	2	5.15E-02	48.90	0.83	0.77	3
297	ATGQKLMR	sp|P47199|QOR_MOUSE	yes	yes	2	9	8	M	A	0	903.496	2	3.05E-02	85.67	1.11	1.04	2
298	ATIATMPVPETR	sp|Q62189|SNRPA_MOUSE	yes	yes	2	13	12	M	A	0	1285.670	2	3.27E-03	96.75	0.99	0.82	1
299	ATIGPSGLHPGER	sp|Q3TRM8|HXK3_MOUSE	yes	yes	2	14	13	M	A	0	1290.668	2	8.89E-04	107.99	NaN	NaN	0
300	ATKIDKEACR	sp|Q9CQI6|COTL1_MOUSE	yes	yes	2	11	10	M	A	0	1190.608	2;3	2.74E-02	71.09	1.15	1.11	8
301	ATNDAVLKR	sp|P31230|AIMP1_MOUSE	yes	yes	2	10	9	M	L	0	986.551	2	3.52E-14	171.33	1.07	1.00	8
302	ATNFLAHEKIWFDKFKYDDAER	sp|P57776-2|EF1D_MOUSE	yes	no	2	23	22	M	R	0	2743.340	5	2.16E-02	41.62	1.26	1.13	2
303	ATPEASGSGEKVEGSEPSVTYYR	sp|Q9CQX2|CYB5B_MOUSE	yes	yes	2	24	23	M	L	0	2400.108	2	4.00E-07	95.12	1.61	1.17	9
304	ATQICTPTFSAGSAKGLCGTSGSFS	sp|B1AQ75|KRT36_MOUSE	yes	yes	2	27	26	M	I	0	2648.232	2;3	3.32E-08	82.60	5.77	3.61	6

305	ATQVEPLLPAGAPLLQAEEHGLAF	sp|Q6ZQ58|LARP1_MOUSE	yes	yes	2	25	24	M	K	0	2480.339	2;3	2.46E-16	111.65	NaN	NaN	0
306	ATRGTVTDFPGFDGR	sp|P48036|ANXA5_MOUSE	yes	yes	2	16	15	M	A	1	1595.769	2	6.33E-04	70.20	NaN	NaN	0
307	ATSAEAPAKEAQKR	sp|Q8BGA5|KRR1_MOUSE	yes	yes	2	15	14	M	D	0	1456.763	3	1.17E-03	80.96	1.31	0.94	9
308	ATSLGSNTYNR	sp|Q8BHS3|RBM22_MOUSE	yes	yes	2	12	11	M	Q	0	1182.563	2	1.03E-02	105.46	NaN	NaN	0
309	ATTAQQSPQPVAGKR	sp|Q99J36|THUM1_MOUSE	yes	yes	2	16	15	M	K	0	1538.817	2;3	5.01E-39	208.15	1.12	1.03	14
310	ATTFLQTSSTFGGSSTR	sp|Q61414|K1C15_MOUSE	yes	no	2	18	17	M	G	0	1747.838	2;3	2.95E-29	207.39	NaN	NaN	0
311	ATVAATTKVPEIR	sp|Q9WTM5|RUVB2_MOUSE	yes	yes	2	14	13	M	D	0	1355.777	2	9.41E-13	169.04	1.26	1.04	10
312	ATVDLEKLR	sp|P12382|K6PL_MOUSE	yes	yes	2	10	9	M	M	0	1043.598	2	3.10E-14	173.37	1.11	1.07	9
313	ATYLEFIQQNEER	sp|Q9D662|SC23B_MOUSE	yes	yes	2	14	13	M	D	0	1639.784	2	5.11E-17	196.38	NaN	NaN	0
314	AVAAAAAATAMSAAGGGGASAA	sp|Q8CG72|ARHL2_MOUSE	yes	yes	2	24	23	M	S	0	1830.901	2	1.76E-03	51.88	NaN	NaN	0
315	AVAAAAVAAPAGGGGAR	sp|Q99L88-2|SNTB1_MOUSE	yes	no	2	18	17	M	A	0	1336.721	2	1.12E-04	76.76	NaN	NaN	0
316	AVAVGRPSNEELR	sp|Q8C1B7-3|SEP11_MOUSE	yes	no	2	14	13	M	N	1	1396.742	2	9.76E-04	88.02	NaN	NaN	0
317	AVEELQSIIKR	sp|Q8BZM1|GLMN_MOUSE	yes	yes	2	12	11	M	C	0	1284.740	2	1.46E-16	186.87	1.52	1.27	9
318	AVFPSIVGRPR	sp|P60710|ACTB_MOUSE	no	no	29	39	11	R	H	1	1197.698	3	5.45E-02	55.35	NaN	NaN	0
319	AVFPWHSR	sp|Q8BWQ6-2|CP062_MOUSE	yes	no	2	9	8	M	N	0	998.509	2	1.61E-02	114.28	NaN	NaN	0
320	AVNVYSTSVTSDNLSR	sp|Q61166|MARE1_MOUSE	yes	yes	2	17	16	M	H	0	1711.838	2	1.35E-02	55.01	NaN	NaN	0
321	AVPPTYADLGKSAR	sp|Q60932-2|VDAC1_MOUSE	yes	no	2	15	14	M	D	0	1444.767	2	6.53E-04	88.28	1.23	0.89	12
322	AVQISKKR	sp|P62908|RS3_MOUSE	yes	yes	2	9	8	M	K	0	928.582	3	2.65E-02	93.37	1.43	1.23	3
323	AVSDGVIKVFNDMKVR	sp|P18760|COF1_MOUSE	yes	yes	6	21	16	V	K	0	1776.956	2	1.69E-23	188.47	0.90	0.88	13
324	AVSTGVKVPR	sp|Q9D2M8-2|UB2V2_MOUSE	yes	no	2	11	10	M	N	0	1012.603	2	8.81E-11	169.99	1.27	1.10	9
325	AVTLDKDAYYR	sp|Q920B9|SP16H_MOUSE	yes	yes	2	12	11	M	R	0	1313.662	2	3.80E-16	184.03	0.64	0.59	10
326	AWKSGGASHSELIHNLR	sp|P23506|PIMT_MOUSE	yes	no	2	18	17	M	K	0	1861.955	3;4	1.86E-05	89.36	1.16	1.07	5
327	AYHSFLVEPISCHAWNKDR	sp|Q9WV32|ARC1B_MOUSE	yes	yes	2	20	19	M	T	0	2329.106	3;4	4.77E-05	81.16	1.22	0.99	11
328	AYKLVLIR	sp|Q9DBJ1|PGAM1_MOUSE	yes	yes	3	10	8	A	H	0	974.628	2	1.11E-04	144.38	1.02	0.93	6
329	AYKYIQELWR	sp|Q9CZM2|RL15_MOUSE	yes	yes	3	12	10	G	K	0	1368.719	2	3.14E-11	170.52	0.98	0.93	8
330	CDAFVGTWKLVSSENFDDYMKE\	sp|P04117|FABP4_MOUSE	yes	yes	2	31	30	M	K	0	3427.585	3	5.51E-03	42.06	0.73	0.73	1
331	CDFTEDQTAEFKEAFQLFDR	sp|Q60605-2|MYL6_MOUSE	yes	no	2	21	20	M	T	0	2496.090	2;3	9.97E-36	198.24	1.93	1.52	9
332	CESCLPALSCR	sp|Q9D646|KRT34_MOUSE	yes	no	3	13	11	S	T	0	1351.568	2	9.31E-03	105.03	NaN	NaN	0
333	CGLVASNLNLKPGECLKVR	sp|P16045|LEG1_MOUSE	yes	yes	3	21	19	A	G	0	2127.129	3	5.67E-06	84.65	0.93	0.80	8
334	CGYYGNYYGGR	sp|Q925H3|KRA65_MOUSE	yes	no	2	12	11	M	G	0	1328.524	2	4.55E-03	129.85	NaN	NaN	0
335	CNSGNYSSQSFGGFLR	sp|Q9QZU5|KR151_MOUSE	yes	yes	5	20	16	T	Q	0	1779.764	2	6.56E-08	141.55	NaN	NaN	0
336	CQAGEDYAGPAR	sp|Q3U308|CTU2_MOUSE	yes	yes	2	13	12	M	R	0	1293.541	2	9.58E-03	70.09	NaN	NaN	0
337	CSLGLFPPPPPR	sp|P58742|AAAS_MOUSE	yes	yes	2	13	12	M	G	0	1336.696	2	3.37E-03	88.60	NaN	NaN	0
338	DDDIAALVVDNGSGMCKAGFAG	sp|P60710|ACTB_MOUSE	yes	no	2	28	27	M	A	0	2736.212	2;3	8.77E-45	187.95	1.25	1.01	59
339	DELGCSHLGQSYESR	sp|P08121|CO3A1_MOUSE	yes	yes	29	43	15	V	D	0	1736.742	2	5.42E-07	131.56	NaN	NaN	0
340	DFSKLPKIR	sp|P50516-2|VATA_MOUSE	yes	no	2	10	9	M	D	0	1102.650	2	2.97E-02	79.15	1.05	1.00	7
341	DGPEQMELEEGKAGSGLR	sp|P62196|PRS8_MOUSE	yes	yes	4	21	18	L	Q	0	1901.879	2	6.15E-06	86.80	1.35	1.17	4
342	DIAIHHPWIR	sp|P23927|CRYAB_MOUSE	yes	yes	2	11	10	M	R	0	1256.678	2	1.67E-02	80.69	NaN	NaN	0
343	DIPENVEITLKGR	sp|P51410|RL9_MOUSE	yes	yes	11	23	13	V	T	0	1482.804	2	2.66E-03	79.88	1.16	1.09	1
344	DNGSGMCKAGFAGDDAPR	sp|P60710|ACTB_MOUSE	no	no	11	28	18	V	A	0	1824.752	2	5.30E-06	88.57	1.42	1.15	11
345	DPNTIIEALR	sp|Q9EPL8|IPO7_MOUSE	yes	yes	2	11	10	M	G	0	1140.614	2	4.50E-02	62.47	NaN	NaN	0
346	DSLTAANNKFCFDFFR	sp|Q9D7P9|SPB12_MOUSE	yes	yes	2	17	16	M	E	0	1951.889	2	5.66E-07	113.47	1.01	0.94	2
347	EALVETNRR	sp|Q9D646|KRT34_MOUSE	no	no	233	241	9	Y	E	1	1086.578	2	5.21E-03	128.36	NaN	NaN	0
348	EAPGVEQR	sp|Q6PFY1-2|FCSD1_MOUSE	yes	no	103	110	8	R	L	0	884.435	2	6.22E-02	77.32	NaN	NaN	0
349	EAPLNPKANR	sp|P60710|ACTB_MOUSE	no	no	107	116	10	T	E	0	1108.599	2	2.76E-03	111.46	11.37	7.86	3
350	EEEDSTALVCDNGSGLCKAGFAGI	sp|P62737|ACTA_MOUSE	yes	yes	3	30	28	C	A	0	2940.250	2;3	8.88E-44	179.20	1.34	1.12	12
351	EEEIAALVIDNGSGMCKAGFAGDI	sp|P63260|ACTG_MOUSE	yes	yes	2	28	27	M	A	0	2792.275	2;3	3.03E-52	192.75	1.10	1.02	49
352	EEIVEVKEDLLEER	sp|Q8BZ21|KAT6A_MOUSE	yes	yes	1209	1222	14	N	K	0	1728.878	3	2.92E-02	56.57	1.12	0.78	8
353	EGHDPKEPEQLR	sp|Q8BG05|ROA3_MOUSE	no	no	24	35	12	E	K	0	1433.690	2	9.31E-05	125.54	0.94	0.76	6
354	EGPLSVFGDR	sp|P11983|TCPA_MOUSE	yes	yes	2	11	10	M	S	0	1075.530	2	4.05E-02	64.10	NaN	NaN	0
355	EIAQDFKTDLR	sp|P84244|H33_MOUSE	yes	no	74	84	11	R	F	0	1334.683	2	1.37E-04	130.56	NaN	NaN	0
356	EKVIEGFSR	sp|Q8CIT9-3|SBSN_MOUSE	yes	no	30	38	9	V	G	0	1063.566	2	5.61E-02	67.08	1.17	1.09	6
357	ELAEDGYSGVEVR	sp|P62908|RS3_MOUSE	yes	yes	28	40	13	R	V	0	1422.663	2	6.47E-03	64.10	NaN	NaN	0
358	EMTALKEER	sp|A0JNT9|BICR1_MOUSE	yes	yes	446	454	9	V	D	0	1105.544	2	4.89E-02	70.40	NaN	NaN	0
359	ENAELECKIQER	sp|Q61897|KT33B_MOUSE	yes	no	80	91	12	R	N	0	1517.714	2	5.63E-02	53.45	NaN	NaN	0
360	ENSFYVDTVR	sp|Q9WVF7|DPOE1_MOUSE	yes	yes	750	759	10	R	A	0	1228.572	2	5.96E-02	59.07	1.27	0.99	7
361	EPGPDGPAAPGPAAIR	sp|Q64674|SPEE_MOUSE	yes	yes	2	17	16	M	E	0	1471.742	2	2.11E-02	49.99	NaN	NaN	0
362	ETGDAGASATFPMQCSALR	sp|P63242|IF5A1_MOUSE	yes	yes	8	26	19	F	K	0	1968.867	2	5.31E-12	133.78	NaN	NaN	0
363	FETGDAGASATFPMQCSALR	sp|P63242|IF5A1_MOUSE	yes	yes	7	26	20	D	K	0	2115.935	2	4.64E-02	39.39	NaN	NaN	0
364	FFGEVVKAPCR	sp|Q9JK23|PSMG1_MOUSE	yes	yes	5	15	11	T	A	0	1308.665	2	4.64E-04	119.27	0.98	0.90	1
365	FGEVVKAPCR	sp|Q9JK23|PSMG1_MOUSE	yes	yes	6	15	10	F	A	0	1161.597	2	2.04E-02	76.23	1.34	1.15	2
366	FGGGSGFGGGGFGGGSFGGGR	sp|Q3TTY5|K22E_MOUSE	yes	no	132	152	21	R	F	0	1734.750	2	1.74E-11	112.44	NaN	NaN	0
367	FHVNLLCGEEQGADAALHFNPR	sp|O54974|LEG7_MOUSE	yes	yes	33	54	22	R	L	0	2494.181	3;4	3.01E-17	124.20	NaN	NaN	0
368	FLEQQNQVLQTKWELLQQVDTT	sp|P04104|K2C1_MOUSE	yes	yes	208	231	24	R	T	0	2945.525	3	1.60E-04	71.65	1.00	0.70	1
369	FSWLKKGGAR	sp|Q8BH64|EHD2_MOUSE	yes	yes	2	11	10	M	G	0	1148.646	2	1.64E-02	79.15	1.17	1.14	1
370	GDAGASATFPMQCSALR	sp|P63242|IF5A1_MOUSE	yes	yes	10	26	17	T	K	0	1738.777	2	2.88E-06	87.43	NaN	NaN	0
371	GDAPSPEEKLHLITR	sp|Q91WQ3|SYYC_MOUSE	yes	yes	2	16	15	M	N	0	1661.874	3	2.82E-02	54.40	0.99	0.93	5
372	GDIKNFLYAWCGKR	sp|O70133|DHX9_MOUSE	yes	no	2	15	14	M	K	0	1726.861	3	2.90E-05	116.19	1.27	1.23	7
373	GDLPLNINIQEPR	sp|Q91V61-2|SFXN3_MOUSE	yes	no	2	14	13	M	W	0	1477.789	2	1.62E-05	150.22	NaN	NaN	0
374	GDPSKQDILAIFKR	sp|Q9D8S3|ARFG3_MOUSE	yes	yes	2	15	14	M	L	0	1586.878	3	5.76E-04	90.41	1.38	1.15	10
375	GDREQLLQR	sp|P68510|1433F_MOUSE	yes	yes	2	10	9	M	A	1	1113.589	2	3.18E-14	175.93	45.30	31.62	4
376	GEIEQKPTPASR	sp|F8VPU2|FARP1_MOUSE	yes	yes	2	13	12	M	L	0	1311.678	2	1.72E-10	153.39	1.43	1.08	9
377	GEIKVSPDYNWFR	sp|Q9CQC8-2|SPG21_MOUSE	yes	no	2	14	13	M	S	0	1609.789	2	4.11E-03	76.76	1.57	1.20	10
378	GEVAGGAAPGPPR	sp|Q61210-3|ARHG1_MOUSE	yes	no	2	14	13	M	S	0	1134.578	2	8.57E-04	109.72	NaN	NaN	0
379	GFGGLGCGCNSIR	sp|Q8C1I6|KR163_MOUSE	yes	yes	17	29	13	G	R	0	1353.592	2	8.85E-04	96.06	NaN	NaN	0
380	GGEGGVTLGQPHLSR	sp|Q9Z0N1|IF2G_MOUSE	yes	yes	3	17	15	A	Q	0	1463.748	2	2.08E-04	77.73	NaN	NaN	0
381	GGIGQPLSLLLKNSPLVSR	sp|P08249|MDHM_MOUSE	yes	yes	34	52	19	S	L	0	1948.147	2	8.83E-03	48.91	1.12	1.02	1
382	GGLGKLAAEGLAHR	sp|Q8CF02|FM25C_MOUSE	yes	yes	3	16	14	L	T	0	1348.758	2	4.88E-08	138.19	1.39	1.28	11
383	GGPGAGKGTQCAR	sp|Q9DBP5|KCY_MOUSE	yes	yes	10	22	13	L	I	0	1215.578	2	8.64E-03	66.99	1.73	1.59	3
384	GGSGFGGGQGFGGGSR	sp|Q3TTY5|K22E_MOUSE	yes	no	116	131	16	G	F	0	1340.586	2	7.10E-04	63.61	NaN	NaN	0
385	GGYSSGGFSGGSFSR	sp|P02535-3|K1C10_MOUSE	yes	no	37	51	15	G	G	0	1408.601	2	6.86E-04	69.26	NaN	NaN	0
386	GHDPKEPEQLR	sp|Q8BG05|ROA3_MOUSE	no	no	25	35	11	E	K	0	1304.647	2	1.48E-03	110.39	1.39	1.30	4
387	GIAIKLAKDR	sp|O08529|CAN2_MOUSE	yes	yes	3	12	10	A	E	0	1083.676	2	2.09E-03	113.69	1.62	1.42	7
388	GKLAAEGLAHR	sp|Q8CF02|FM25C_MOUSE	yes	yes	6	16	11	L	T	0	1121.631	2	4.61E-04	119.39	1.44	1.12	1
389	GLGKLAAEGLAHR	sp|Q8CF02|FM25C_MOUSE	yes	yes	4	16	13	G	T	0	1291.736	2	6.37E-03	71.88	1.41	1.19	4
390	GLVASNLNLKPGECLKVR	sp|P16045|LEG1_MOUSE	yes	yes	4	21	18	C	G	0	1967.099	2;3	1.12E-20	185.25	0.89	0.86	6
391	GPEGGEGYVVKLR	sp|Q9Z2X1|HNRPF_MOUSE	yes	yes	4	16	13	L	G	0	1359.715	2	8.50E-08	141.13	1.12	1.06	10
392	GPLCLQEVDEPPQHALR	sp|P70296|PEBP1_MOUSE	yes	yes	10	26	17	A	V	0	1957.968	2;3	6.15E-51	258.36	NaN	NaN	0
393	GPLSVFGDR	sp|P11983|TCPA_MOUSE	yes	yes	3	11	9	E	S	0	946.487	2	5.07E-02	55.06	NaN	NaN	0
394	GQPLSLLLKNSPLVSR	sp|P08249|MDHM_MOUSE	yes	yes	37	52	16	I	L	0	1721.020	2	5.26E-09	132.51	0.96	0.90	6
395	GSEAAQLLEAADFAAHKHR	sp|Q9D114|MESH1_MOUSE	yes	yes	2	20	19	M	Q	0	2021.008	3	2.39E-06	93.23	1.18	1.02	2
396	GSELQSDAQQLSAEAPR	sp|P07607|TYSY_MOUSE	yes	yes	5	21	17	V	H	0	1785.849	2	1.40E-02	51.50	NaN	NaN	0
397	GSFSSSSSFGGGLGSGFGGR	sp|Q61781|K1C14_MOUSE	no	no	66	84	19	G	F	0	1706.765	2	6.48E-03	52.81	NaN	NaN	0
398	GVAVSDGVIKVFNDMKVR	sp|P18760|COF1_MOUSE	yes	yes	4	21	18	S	K	0	1933.046	2;3	1.61E-09	101.05	0.79	0.73	6
399	GVTVKDVNQQEFVR	sp|Q9CZX8|RS19_MOUSE	yes	yes	3	16	14	P	A	0	1617.848	2	8.61E-06	124.62	1.01	0.91	6
400	GWAGDAGCTPRPPIRPR	sp|Q9D2V8|MFS10_MOUSE	yes	yes	2	18	17	M	P	2	1862.932	3	3.78E-06	81.63	NaN	NaN	0
401	GYFVVDIVAR	sp|Q99PF4-2|CAD23_MOUSE	yes	no	2926	2935	10	P	D	0	1137.618	2	6.35E-02	39.62	NaN	NaN	0
402	GYYGNYYGGR	sp|Q925H3|KRA65_MOUSE	yes	no	3	12	10	C	G	0	1168.494	2	1.46E-02	111.39	NaN	NaN	0
403	HEDPVEKVIEGFSR	sp|Q8CIT9-3|SBSN_MOUSE	yes	no	25	38	14	A	G	0	1640.816	2	1.36E-05	118.51	0.94	0.80	7
404	HKTSLPQGVR	sp|O54974|LEG7_MOUSE	yes	yes	6	15	10	H	V	0	1121.631	2	4.19E-04	127.83	0.95	0.75	9
405	IDNGSGMCKAGFAGDDAPR	sp|P63260|ACTG_MOUSE	yes	yes	10	28	19	V	A	0	1937.836	2	3.24E-21	166.29	1.23	1.04	12
406	IGIPDATGR	sp|Q01853|TERA_MOUSE	yes	yes	369	377	9	D	L	0	898.487	2	8.56E-02	60.02	0.73	0.69	4
407	IQGIGTVLGVAIQQR	sp|Q99PG6|TS1R1_MOUSE	yes	yes	316	330	15	G	Q	0	1551.910	3	2.71E-02	54.90	6.18	3.97	2

408	ISVYYNEATGGKYVPR	sp|P99024|TBB5_MOUSE	yes	yes	47	62	16	R	A	0	1815.916	3	2.62E-02	52.53	1.30	1.12	3
409	KAEGAALAGR	sp|Q08AT1|RASLC_MOUSE	yes	yes	146	155	10	T	F	0	942.525	2	2.63E-02	76.23	5.44	3.79	1
410	KRNSLSPPASPR	sp|Q5BKS4|ERI2_MOUSE	yes	yes	531	542	12	T	T	1	1308.726	2	4.13E-02	57.18	0.77	0.70	4
411	KTETVCTFQDGALVQHQQWDGK	sp|Q05816|FABP5_MOUSE	yes	yes	82	109	28	R	K	0	3262.568	5	2.84E-02	31.05	1.05	1.00	1
412	KTSLPQGVR	sp|O54974|LEG7_MOUSE	yes	yes	7	15	9	H	V	0	984.572	2	8.89E-02	57.53	2.06	1.35	4
413	KVGVNGFGR	sp|P16858|G3P_MOUSE	yes	yes	3	11	9	V	I	0	932.519	2	3.07E-09	160.56	1.30	1.14	5
414	LAEHLLKPLPADR	sp|Q9JL62|GLTP_MOUSE	yes	yes	4	16	13	L	Q	0	1471.851	2	6.83E-03	70.89	1.28	1.17	5
415	LASISLPR	sp|P11247|PERM_MOUSE	yes	yes	668	675	8	A	I	0	855.518	2	7.23E-02	73.25	NaN	NaN	0
416	LDGPEQMELEEGKAGSGLR	sp|P62196|PRS8_MOUSE	yes	yes	3	21	19	A	Q	0	2014.963	3	2.30E-03	62.94	1.26	1.18	2
417	LEGKWR	sp|Q05816|FABP5_MOUSE	yes	no	7	12	6	D	L	0	787.434	2	1.30E-03	94.16	1.06	0.99	3
418	LGGLGKLAAEGLAHR	sp|Q8CF02|FM25C_MOUSE	yes	yes	2	16	15	M	T	0	1461.842	2;3	4.32E-08	121.24	1.41	1.33	13
419	LGGVSEASR	sp|P35175|CYT1_MOUSE	yes	yes	3	11	9	S	A	0	874.451	2	2.32E-05	158.37	NaN	NaN	0
420	LGPEGGEGYVVKLR	sp|Q9Z2X1|HNRPF_MOUSE	yes	yes	3	16	14	M	G	0	1472.799	2	8.43E-04	83.09	0.94	0.88	5
421	LHCEKCLPR	sp|P19137|LAMA1_MOUSE	yes	yes	1544	1552	9	G	H	0	1211.590	2	7.87E-02	39.31	NaN	NaN	0
422	LKDLEGKWR	sp|Q05816|FABP5_MOUSE	yes	yes	4	12	9	S	L	0	1143.640	2	1.66E-02	94.69	0.93	0.92	7
423	LLKEYR	sp|Q8K4R4-4|PITC1_MOUSE	yes	no	2	7	6	M	I	0	820.481	2	5.58E-03	124.89	1.32	1.14	4
424	LPCVEDYLSAILNR	sp|P07724|ALBU_MOUSE	yes	yes	470	483	14	R	V	0	1661.845	2;3	3.29E-04	121.24	NaN	NaN	0
425	LPDFSYCILER	sp|Q8K284-3|TF3C1_MOUSE	yes	no	17	27	11	K	L	0	1411.681	2	7.58E-02	49.30	NaN	NaN	0
426	LPNDIGVSSLDCR	sp|Q99KK7|DPP3_MOUSE	yes	yes	8	20	13	I	E	0	1444.698	2	4.32E-03	70.89	NaN	NaN	0
427	LPPLPEYGGKVR	sp|Q9CQQ7|AT5F1_MOUSE	yes	yes	44	55	12	P	L	0	1324.750	2	1.10E-02	69.72	0.84	0.73	8
428	LTAANNKFCFDFFR	sp|Q9D7P9|SPB12_MOUSE	yes	yes	4	17	14	S	E	0	1749.830	2	3.31E-03	65.04	1.12	1.02	1
429	LVASNLNLKPGECLKVR	sp|P16045|LEG1_MOUSE	yes	yes	5	21	17	G	G	0	1910.077	2	4.09E-03	60.49	NaN	NaN	0
430	LVIDNGSGMCKAGFAGDDAPR	sp|P63260|ACTG_MOUSE	yes	yes	8	28	21	A	A	0	2149.989	2	1.84E-06	89.86	1.26	0.98	8
431	LVVDNGSGMCKAGFAGDDAPR	sp|P60710|ACTB_MOUSE	yes	no	8	28	21	A	A	0	2135.973	2	1.78E-10	109.65	1.02	0.96	4
432	LYVSPHPDAFPSLR	sp|Q9Z1Q9|SYVC_MOUSE	yes	yes	4	17	14	I	A	0	1597.825	2	1.46E-04	130.20	NaN	NaN	0
433	MDAATLTYDTLR	sp|Q8BGE6|ATG4B_MOUSE	yes	yes	1	12	12	-	F	0	1369.655	2	6.65E-11	105.65	0.04	0.04	1
434	MDAFEKVR	sp|Q8C167-4|PPCEL_MOUSE	yes	no	88	95	8	N	T	0	994.491	2	1.99E-02	103.55	1.05	0.97	5
435	MDAFGDYVWPR	sp|Q99ME2|WDR6_MOUSE	yes	yes	1	11	11	-	A	0	1355.597	2	9.30E-03	93.35	NaN	NaN	0
436	MDALKSAGR	sp|Q8C142|ARH_MOUSE	yes	yes	1	9	9	-	A	0	947.486	2	3.48E-02	77.29	1.25	0.76	3
437	MDAQSSAKVNSR	sp|P49586|PCY1A_MOUSE	yes	yes	1	12	12	-	K	0	1292.614	2	8.10E-03	74.48	1.11	0.88	6
438	MDATLTAR	sp|Q8BGQ7|SYAC_MOUSE	yes	yes	1	8	8	-	E	0	877.433	2	8.38E-03	124.08	NaN	NaN	0
439	MDDIFTQCR	sp|O55222|ILK_MOUSE	yes	yes	1	9	9	-	E	0	1184.495	2	2.80E-02	79.15	NaN	NaN	0
440	MDDREDLVYQAKLAEQAER	sp|P62259|1433E_MOUSE	yes	yes	1	19	19	-	Y	1	2279.085	3	1.54E-02	48.29	1.09	0.99	10
441	MDDYAVLSDTELAAVLR	sp|O08579|EMD_MOUSE	yes	yes	1	17	17	-	Q	0	1880.919	2	2.07E-02	45.62	NaN	NaN	0
442	MDEAVGDLKQALPCVAESPAVH\	sp|Q3UA06|PCH2_MOUSE	yes	yes	1	28	28	-	S	0	3060.537	3	1.36E-02	38.99	1.44	1.24	2
443	MDELQDVQLTEIKPLLNDKNGTR	sp|Q9QYF9|NDRG3_MOUSE	yes	yes	1	23	23	-	N	0	2669.369	3	1.19E-06	86.56	1.11	1.03	3
444	MDFEDDYVHSTCR	sp|O88291-3|ZN326_MOUSE	yes	no	1	13	13	-	G	0	1673.645	2	2.82E-05	119.25	0.29	0.21	2
445	MDFLLGNPFSSPVGQR	sp|O88746|TOM1_MOUSE	yes	yes	1	16	16	-	I	0	1763.867	2	7.08E-04	63.68	NaN	NaN	0
446	MDFNVKKLAADAGTFLSR	sp|Q9JK48|SHLB1_MOUSE	yes	no	4	21	18	I	A	0	1983.025	3	3.61E-02	62.20	1.35	1.22	4
447	MDFSKLPKIR	sp|P50516-2|VATA_MOUSE	yes	no	1	10	10	-	D	0	1233.690	2;3	6.69E-02	57.53	1.00	0.84	8
448	MDGEEKTYGGCEGPDAMYVKLIS	sp|P83940|ELOC_MOUSE	yes	yes	1	33	33	-	E	0	3717.711	5	6.36E-03	40.80	1.15	1.03	2
449	MDGIVPDIAVGTKR	sp|P17225|PTBP1_MOUSE	yes	yes	1	14	14	-	G	0	1470.786	2	1.03E-04	110.44	1.36	1.18	39
450	MDGLVAQCSAR	sp|Q9D0I9|SYRC_MOUSE	yes	yes	1	11	11	-	L	0	1206.549	2	9.69E-06	158.30	NaN	NaN	0
451	MDIAIHHPWIR	sp|P23927|CRYAB_MOUSE	yes	yes	1	11	11	-	R	0	1387.718	3	3.34E-02	61.34	NaN	NaN	0
452	MDILKSEILR	sp|Q8BM39-2|PRP18_MOUSE	yes	no	1	10	10	-	K	0	1216.685	2	1.51E-02	88.34	0.29	0.23	1
453	MDKNELVQKAKLAEQAER	sp|P63101|1433Z_MOUSE	yes	yes	1	18	18	-	Y	0	2100.100	2;3	1.80E-03	64.71	0.88	0.75	5
454	MDLAAAAEPGAGSQHPEVR	sp|P97311|MCM6_MOUSE	yes	yes	1	19	19	-	D	0	1905.900	2;3	2.44E-13	150.68	NaN	NaN	0
455	MDLEAVCKR	sp|Q9CYR6|AGM1_MOUSE	yes	yes	1	9	9	-	S	0	1120.537	2	1.46E-05	137.05	1.16	1.03	12
456	MDLSELER	sp|Q9CWY8|RNH2A_MOUSE	yes	yes	1	8	8	-	D	0	991.464	2	6.93E-02	74.46	NaN	NaN	0
457	MDMGNQHPSISR	sp|Q8CI32|BAG5_MOUSE	yes	yes	1	12	12	-	L	0	1371.602	2	3.40E-03	86.94	NaN	NaN	0
458	MDNLSPEEVQLR	sp|O09044|SNP23_MOUSE	yes	yes	1	12	12	-	A	0	1429.687	2	3.31E-03	93.62	NaN	NaN	0
459	MDNSGKQAEAMALLAEAER	sp|Q9DB05|SNAA_MOUSE	yes	yes	1	19	19	-	K	0	2033.951	2;3	1.52E-06	95.50	1.14	0.94	20
460	MDPNTIIEALR	sp|Q9EPL8|IPO7_MOUSE	yes	yes	1	11	11	-	G	0	1271.654	2	1.13E-02	111.63	NaN	NaN	0
461	MDPSGVKVLETAEDIQER	sp|P16546-2|SPTN1_MOUSE	yes	no	1	18	18	-	R	0	2015.983	2;3	4.63E-16	144.72	1.19	0.90	24
462	MDPSWATQESEAVAEKVLR	sp|Q9EPQ7|STAR5_MOUSE	yes	yes	1	19	19	-	Y	0	2146.037	2;3	1.06E-20	155.94	1.07	0.99	8
463	MDQVMQFVEPSR	sp|P60060|SC61G_MOUSE	yes	yes	1	12	12	-	Q	0	1465.669	2	2.15E-04	145.81	NaN	NaN	0
464	MDSAEELLAPLR	sp|Q9CZD3|SYG_MOUSE	yes	yes	47	58	12	S	L	0	1343.676	2	4.56E-07	116.24	NaN	NaN	0
465	MDSASQDINLNSPNKGVLSDFMT	sp|Q9CYZ2|TPD54_MOUSE	yes	yes	1	34	34	-	T	0	3653.745	3	1.10E-08	67.91	1.13	0.95	4
466	MDSEAFQHAR	sp|Q5I1X5|IASPP_MOUSE	yes	yes	1	10	10	-	D	0	1190.514	2	2.38E-03	135.55	NaN	NaN	0
467	MDSLTAANNKFCFDFFR	sp|Q9D7P9|SPB12_MOUSE	yes	yes	1	17	17	-	E	0	2082.929	2;3	4.10E-30	195.92	1.14	1.06	23
468	MDSSAVITQISKEEAR	sp|P58466|CTDS1_MOUSE	yes	yes	1	16	16	-	G	0	1763.872	2	4.45E-06	92.77	1.05	0.72	1
469	MDVGELLSYQPNR	sp|Q9CWL8|CTBL1_MOUSE	yes	yes	1	13	13	-	G	0	1520.729	2	4.11E-03	71.56	NaN	NaN	0
470	MDVLRPQIVTFDGR	sp|Q9D8Z1|ASCC1_MOUSE	yes	yes	1	14	14	-	N	1	1645.861	2	1.25E-03	76.76	NaN	NaN	0
471	MDVNLAPLR	sp|Q8R5J9|PRAF3_MOUSE	yes	yes	1	9	9	-	A	0	1027.549	2	1.21E-02	103.55	NaN	NaN	0
472	MEAALAVTR	sp|Q9CXA2|T3HPD_MOUSE	yes	yes	1	9	9	-	L	0	960.506	2	3.69E-02	74.84	NaN	NaN	0
473	MEAANCSLR	sp|Q6PIP5|NUDC1_MOUSE	yes	yes	1	9	9	-	V	0	1050.459	2	3.10E-02	77.66	NaN	NaN	0
474	MEAKGGTVKAASGFNATEDAQT	sp|P97429|ANXA4_MOUSE	yes	yes	1	24	24	-	K	0	2452.202	3	4.73E-02	34.65	1.25	1.07	3
475	MEANGFGLQNFPELKNDTFLR	sp|P70697|DCUP_MOUSE	yes	yes	1	21	21	-	A	0	2440.185	2;3	6.48E-38	206.34	1.24	1.05	12
476	MEAPLRPAADILR	sp|Q8BPM2-2|M4K5_MOUSE	yes	no	1	13	13	-	R	1	1451.792	2	2.03E-02	58.32	NaN	NaN	0
477	MEATGVLPFVR	sp|Q9JJ28|FLII_MOUSE	yes	yes	1	11	11	-	G	0	1218.643	2	8.34E-04	131.82	NaN	NaN	0
478	MEATLNLEPSGR	sp|O55137|ACOT1_MOUSE	yes	yes	1	12	12	-	S	0	1316.640	2	1.54E-04	119.21	4.03	3.71	5
479	MEDIMQLPKAR	sp|Q9CQ71|RFA3_MOUSE	yes	yes	1	11	11	-	V	0	1330.674	2	2.09E-06	143.96	1.21	1.08	15
480	MEDQEALGFEHMGLDPR	sp|Q9D0R4|DDX56_MOUSE	yes	yes	1	17	17	-	L	0	1973.861	2	3.39E-03	60.76	NaN	NaN	0
481	MEDVTLHIVER	sp|O54724|PTRF_MOUSE	yes	yes	1	11	11	-	P	0	1340.676	2	1.06E-02	107.09	NaN	NaN	0
482	MEDVTLHIVERPYSGFPDASSEGP	sp|O54724|PTRF_MOUSE	yes	yes	1	32	32	-	A	1	3500.615	3	9.52E-05	54.00	NaN	NaN	0
483	MEEAELVKGR	sp|Q9JHU2|PALMD_MOUSE	yes	yes	1	10	10	-	L	0	1160.586	2	3.69E-16	187.97	1.15	0.92	10
484	MEEAPHGCPGADSAQAGR	sp|Q9R060|NUBP1_MOUSE	yes	yes	1	18	18	-	G	0	1839.763	2	1.89E-10	104.84	NaN	NaN	0
485	MEEASGSAGNDR	sp|O70404|VAMP8_MOUSE	yes	yes	1	12	12	-	V	0	1222.488	2	3.40E-03	86.80	NaN	NaN	0
486	MEEKALEVYDLIR	sp|Q9DCL2|FA96A_MOUSE	yes	yes	33	45	13	I	T	0	1607.823	2	7.94E-06	130.72	1.08	1.03	5
487	MEFAELIKTPR	sp|Q9Z2D0|MTMR9_MOUSE	yes	yes	1	11	11	-	V	0	1333.706	2	1.94E-03	107.09	1.36	1.23	9
488	MEGHDPKEPEQLR	sp|Q8BG05-2|ROA3_MOUSE	yes	yes	1	13	13	-	K	0	1564.730	2;3	1.10E-07	137.62	1.15	0.74	28
489	MEGPLSVFGDR	sp|P11983|TCPA_MOUSE	yes	yes	1	11	11	-	S	0	1206.570	2	8.94E-03	122.33	0.07	0.05	1
490	MEIPGSLCKKVKLSNNAQNWGM	sp|Q60967|PAPS1_MOUSE	yes	yes	1	24	24	-	A	0	2788.394	4	4.56E-02	31.75	1.26	1.16	1
491	MEIPPTHYAASR	sp|P70202|LXN_MOUSE	yes	yes	1	12	12	-	A	0	1371.661	2	5.04E-03	78.32	NaN	NaN	0
492	MEKDSLSR	sp|Q64261|CDK6_MOUSE	yes	yes	1	8	8	-	A	0	964.465	2	3.93E-02	79.15	1.68	1.32	3
493	MEKPAASTEPQGSR	sp|Q9JMD3|PCTL_MOUSE	yes	yes	1	14	14	-	P	0	1487.704	2	7.21E-03	66.25	1.16	1.00	5
494	MEKPSPLLVGR	sp|P97855|G3BP1_MOUSE	yes	no	3	13	11	V	E	0	1225.685	2	1.83E-06	145.09	1.23	1.09	17
495	MEKTLETVPLER	sp|O88569|ROA2_MOUSE	yes	yes	1	12	12	-	K	0	1444.760	2	3.11E-07	148.52	1.09	1.02	18
496	MEKVPGDMEIER	sp|Q9CX80|CYGB_MOUSE	yes	yes	1	12	12	-	R	0	1432.669	2	6.71E-03	76.76	1.71	1.56	3
497	MELGELLYNKSEYIETASGNKVSR	sp|Q9QZB9|DCTN5_MOUSE	yes	yes	1	24	24	-	Q	0	2730.353	3	3.83E-02	34.22	1.12	1.10	3
498	MELITILEKTVSPDR	sp|P70168|IMB1_MOUSE	yes	yes	1	15	15	-	L	0	1743.944	2	5.82E-16	166.92	1.31	1.00	6
499	MELSADYLR	sp|Q8BGS2-2|BOLA2_MOUSE	yes	no	1	9	9	-	E	0	1096.522	2	2.80E-02	79.15	NaN	NaN	0
500	MELVEVLKR	sp|Q7TMF3|NDUAC_MOUSE	yes	yes	1	9	9	-	G	0	1115.637	2	5.95E-10	168.83	1.39	0.99	13
501	MENLFQLVR	sp|Q9CZ42-2|NNRD_MOUSE	yes	no	1	9	9	-	N	0	1148.601	2	3.36E-03	132.01	NaN	NaN	0
502	MENQLTKSVEER	sp|Q9DC50|OCTC_MOUSE	yes	yes	1	12	12	-	T	0	1462.709	2	3.07E-16	175.29	1.06	0.94	12
503	MENSQLCKLFIGGLNVQTSESGLR	sp|Q9CX86|ROA0_MOUSE	yes	yes	1	24	24	-	G	0	2680.331	2;3	1.53E-34	173.89	1.21	0.77	7
504	MEPCELQNELVSAEGR	sp|Q91X96|MSS4_MOUSE	yes	yes	1	16	16	-	N	0	1860.835	2	7.09E-02	40.49	NaN	NaN	0
505	MEPEPEVLLQEAR	sp|Q9Z2L7-2|CRLF3_MOUSE	yes	no	5	17	13	A	E	0	1539.760	2	8.21E-02	43.03	NaN	NaN	0
506	MEPGPDGPAAPGPAAIR	sp|Q64674|SPEE_MOUSE	yes	yes	1	17	17	-	E	0	1602.782	2	4.15E-02	42.95	NaN	NaN	0
507	MESAIAEGGASR	sp|Q62448-2|IF4G2_MOUSE	yes	no	1	12	12	-	F	0	1177.540	2	8.37E-03	72.29	NaN	NaN	0
508	MESEMSDPQPLQEER	sp|O89094-2|CASPE_MOUSE	yes	no	1	15	15	-	Y	0	1804.761	2	4.81E-04	72.90	NaN	NaN	0
509	MESGFTSKDTYLSHFNPR	sp|O55239|NNMT_MOUSE	yes	yes	1	18	18	-	D	0	2115.968	3	2.00E-02	47.92	1.48	1.39	4
510	METEQPEETFPNTETNGEFGKRP.	sp|P61979-3|HNRPK_MOUSE	yes	no	1	35	35	-	S	1	4130.811	4	1.59E-02	34.72	1.30	0.83	5

511	METILEQQR	sp|Q9D554|SF3A3_MOUSE	yes	yes	1	9	9	-	R	0	1146.570	2	3.04E-08	177.36	1.24	1.26	5
512	METLLKR	sp|Q8K274|KT3K_MOUSE	yes	yes	1	7	7	-	E	0	889.506	2	1.10E-13	155.51	1.28	1.13	4
513	METQSTGTEDGFTPVTHR	sp|Q9CPS7|PNO1_MOUSE	yes	yes	1	18	18	-	G	0	1992.885	2	4.97E-11	124.84	NaN	NaN	0
514	MEVHELFR	sp|P41216|ACSL1_MOUSE	yes	yes	1	8	8	-	Y	0	1059.517	2	3.79E-14	146.81	NaN	NaN	0
515	MEVKPPPGR	sp|Q8BG05|ROA3_MOUSE	yes	yes	1	9	9	-	P	0	1009.538	2	2.38E-02	82.29	1.04	0.85	6
516	MEVKPPPGRPQPDSGR	sp|Q8BG05|ROA3_MOUSE	yes	yes	1	16	16	-	R	1	1746.884	3	3.57E-03	68.48	1.13	1.09	9
517	MFLAKAILEGADR	sp|Q9D7J7|CPNS2_MOUSE	yes	yes	1	13	13	-	G	0	1433.770	2	2.63E-02	59.23	1.73	1.58	3
518	MFNVESVER	sp|Q8BUK6|HOOK3_MOUSE	yes	yes	1	9	9	-	V	0	1109.518	2	1.43E-02	96.14	NaN	NaN	0
519	MFQPAGHGQDWAMEGPR	sp|Q9Z1E3|IKBA_MOUSE	yes	yes	1	17	17	-	D	0	1913.830	2	1.16E-02	53.57	NaN	NaN	0
520	MFSEQAAQR	sp|O35654|DPOD2_MOUSE	yes	yes	1	9	9	-	A	0	1066.487	2	2.32E-02	81.97	NaN	NaN	0
521	MFSFNMFDHPIPR	sp|P70362|UFD1_MOUSE	yes	yes	1	13	13	-	V	0	1637.748	2	8.63E-04	118.24	NaN	NaN	0
522	MFSWLKKGGAR	sp|Q8BH64|EHD2_MOUSE	yes	yes	1	11	11	-	G	0	1279.686	3	2.13E-02	66.06	1.13	0.73	2
523	MFSWVSKDAR	sp|Q9WVK4|EHD1_MOUSE	yes	yes	1	10	10	-	R	0	1225.591	2	1.63E-05	115.57	1.36	1.13	12
524	MHATGLAAPAGTPR	sp|Q9CX30-2|YIF1B_MOUSE	yes	no	1	14	14	-	L	0	1349.687	2	8.62E-05	133.16	NaN	NaN	0
525	MHFSIPETESR	sp|Q8BVL3|SNX17_MOUSE	yes	yes	1	11	11	-	S	0	1332.613	2	6.24E-03	96.23	0.16	0.15	1
526	MHHQSVLHSGYFHPLLR	sp|P10518|HEM2_MOUSE	yes	yes	1	17	17	-	S	0	2058.037	5	1.47E-02	50.83	NaN	NaN	0
527	MHSLATAAPVPTALAQVDR	sp|Q9JKY0|RCD1_MOUSE	yes	yes	1	19	19	-	E	0	1948.020	2	4.03E-08	85.56	NaN	NaN	0
528	MHSLFR	sp|Q9R269|PEPL_MOUSE	yes	yes	1	6	6	-	K	0	789.396	2	4.51E-02	163.53	NaN	NaN	0
529	MIPGGLTEAR	sp|P56567|CYTA_MOUSE	yes	yes	1	10	10	-	P	0	1043.543	2	3.58E-02	67.33	NaN	NaN	0
530	MIYENLQNSR	sp|P49300|CLC10_MOUSE	yes	yes	1	10	10	-	I	0	1266.603	2	7.71E-02	54.26	NaN	NaN	0
531	MKVFVTGPLPAEGR	sp|Q91Z53|GRHPR_MOUSE	yes	yes	7	20	14	L	A	0	1500.812	2	6.81E-04	87.52	1.19	1.01	5
532	MLGGLGKLAAEGLAHR	sp|Q8CF02|FM25C_MOUSE	yes	yes	1	16	16	-	T	0	1592.882	2;3	1.37E-15	156.49	1.42	1.33	26
533	MLGPEGGGEGYVVKLR	sp|Q9Z2X1|HNRPF_MOUSE	yes	yes	2	16	15	M	G	0	1603.839	2	9.89E-12	150.11	1.07	0.94	31
534	MLGSGFKAER	sp|Q9CX00|IST1_MOUSE	yes	yes	1	10	10	-	L	0	1094.554	2	6.25E-03	99.75	1.28	1.08	16
535	MLSEAEEPR	sp|Q921Z5|TFIP8_MOUSE	yes	yes	1	9	9	-	E	0	1060.486	2	7.53E-02	59.91	NaN	NaN	0
536	MLSFQYPDVYR	sp|Q9QUR6|PPCE_MOUSE	yes	yes	1	11	11	-	D	0	1417.670	2	3.39E-06	166.14	NaN	NaN	0
537	MLVVGSELQSDAQQLSAEAPR	sp|P07607|TYSY_MOUSE	yes	yes	1	21	21	-	H	0	2228.111	3	3.52E-12	130.05	NaN	NaN	0
538	MMLGAEGGEGFVVKVR	sp|O35737|HNRH1_MOUSE	yes	yes	1	16	16	-	G	0	1678.854	2	2.01E-02	55.72	1.52	1.19	1
539	MMLGPEGGEGYVVKLR	sp|Q9Z2X1|HNRPF_MOUSE	yes	yes	1	16	16	-	G	0	1734.880	2	8.44E-04	78.69	1.15	1.00	8
540	MNAGSDPVVIVSAAR	sp|Q8CAY6|THIC_MOUSE	yes	yes	1	15	15	-	T	0	1485.761	2	1.48E-07	136.81	3.15	2.88	1
541	MNDTVTIR	sp|P62849-2|RS24_MOUSE	yes	no	1	8	8	-	T	0	948.470	1;2	1.90E-03	160.11	NaN	NaN	0
542	MNGPLHPR	sp|P56546|CTBP2_MOUSE	yes	no	26	33	8	I	P	0	920.465	2	6.43E-02	76.48	NaN	NaN	0
543	MNHTSQAFITAASGGQPPNYER	sp|Q9CQW9|IFM3_MOUSE	yes	yes	1	22	22	-	I	0	2376.092	2	3.24E-17	123.36	NaN	NaN	0
544	MNILAPVR	sp|Q64008|RAB34_MOUSE	yes	yes	1	8	8	-	R	0	912.522	2	9.02E-02	66.07	NaN	NaN	0
545	MNLLPTPESPVTR	sp|O88685|PRS6A_MOUSE	yes	yes	4	16	13	E	Q	0	1453.760	2	3.59E-02	52.58	NaN	NaN	0
546	MNSIKNVPAR	sp|Q9JKY5|HIP1R_MOUSE	yes	yes	1	10	10	-	V	0	1128.607	2	9.54E-04	118.28	1.49	1.01	4
547	MNSLEQAEDLKAFER	sp|Q3UJ81-3|NEPR1_MOUSE	yes	no	1	15	15	-	R	0	1779.846	2	2.02E-08	128.64	1.55	1.05	2
548	MNVEHEVNLLVEEIHR	sp|Q4KML4|ABRAL_MOUSE	yes	yes	1	16	16	-	L	0	1959.984	2;3	1.30E-11	147.09	0.02	0.02	1
549	MNVGTAHSEVNPNTR	sp|Q9CPZ6|ORML3_MOUSE	yes	yes	1	15	15	-	V	0	1625.758	2	7.12E-08	144.97	NaN	NaN	0
550	MNVGVAHSEVNPNTR	sp|Q9CQZ0|ORML2_MOUSE	yes	no	1	15	15	-	V	0	1623.779	2	2.66E-07	133.86	NaN	NaN	0
551	MNVNDLKQR	sp|Q91YN5-2|UAP1_MOUSE	yes	no	1	9	9	-	L	0	1116.571	2	1.35E-02	99.82	1.03	1.00	10
552	MNVVDLGR	sp|Q9DB60|PGFS_MOUSE	yes	yes	1	8	8	-	V	0	902.464	2	5.92E-02	78.52	NaN	NaN	0
553	MQPASAKWYDR	sp|Q9R0Q7|TEBP_MOUSE	yes	yes	1	11	11	-	R	0	1351.634	2	5.80E-05	116.24	1.05	0.98	23
554	MQRPEAWPR	sp|Q9JHH9|COPZ2_MOUSE	yes	yes	1	9	9	-	P	1	1169.576	2	2.92E-02	78.56	NaN	NaN	0
555	MQSAPLEQPAKRPR	sp|Q60710|SAMH1_MOUSE	yes	yes	1	14	14	-	C	1	1607.857	3	7.43E-04	85.84	1.08	0.98	5
556	MQSLAKLQER	sp|Q6NXJ0|WWC2_MOUSE	yes	yes	243	252	10	L	F	0	1202.644	2	1.52E-01	42.34	1.57	1.28	3
557	MQSPAVLR	sp|Q3TC93|H1BP3_MOUSE	yes	yes	1	8	8	-	T	0	900.485	2	7.91E-02	55.53	NaN	NaN	0
558	MSPEIALNR	sp|Q8K3W0|BRE_MOUSE	yes	no	1	9	9	-	I	0	1029.528	2	3.79E-02	74.38	NaN	NaN	0
559	MVGGEASAAVEKLVSGVR	sp|Q9D211|C2AIL_MOUSE	yes	yes	1	18	18	-	Q	0	1758.930	2	9.29E-10	107.98	1.21	1.14	4
560	MYNGIGLPTPR	sp|Q8BTI8-3|SRRM2_MOUSE	yes	no	1	11	11	-	G	0	1217.623	2	4.46E-02	58.17	NaN	NaN	0
561	MYTPIPQSGSPFPASVQDPGLHIV	sp|P24452|CAPG_MOUSE	yes	yes	1	25	25	-	V	0	2780.375	2;3	9.95E-18	118.51	NaN	NaN	0
562	NFAGTWKMR	sp|P62965|RABP1_MOUSE	yes	yes	3	11	9	P	S	0	1109.544	2	1.35E-02	99.82	0.90	0.83	2
563	NFSGNWKIIR	sp|P22935|RABP2_MOUSE	yes	yes	3	12	10	P	S	0	1233.662	2	2.42E-04	130.98	1.05	0.97	4
564	NFTAEEKTLINGLWSKVNVEEVGG	sp|P02104|HBE_MOUSE	yes	yes	3	31	29	V	L	0	3159.620	5	3.25E-04	47.73	1.85	1.67	4
565	NFTVDQIR	sp|P58252|EF2_MOUSE	yes	yes	3	10	8	V	A	0	991.509	1	2.84E-03	138.54	NaN	NaN	0
566	NPSQLLPLELVDKCIGSR	sp|P62322|LSM5_MOUSE	yes	yes	8	25	18	T	I	0	2038.088	2	1.81E-02	49.54	1.11	0.86	2
567	NPTVFFDITADDEPLGR	sp|P17742|PPIA_MOUSE	yes	yes	3	19	17	V	V	0	1905.911	2	6.01E-11	159.81	NaN	NaN	0
568	NSGNYSSQSFGGFLR	sp|Q9QZU5|KR151_MOUSE	yes	yes	6	20	15	C	Q	0	1619.733	2	5.53E-06	95.57	NaN	NaN	0
569	NYSSQSFGGFLR	sp|Q9QZU5|KR151_MOUSE	yes	yes	9	20	12	G	Q	0	1361.636	2	3.31E-03	102.40	NaN	NaN	0
570	PAAPAPAEKTPVKKKAR	sp|P43274|H14_MOUSE	yes	yes	9	25	17	A	K	0	1759.047	3	7.95E-02	37.18	NaN	NaN	0
571	PAGAPLLQAEEHGLAR	sp|Q6ZQ58|LARP1_MOUSE	yes	yes	10	25	16	L	K	0	1628.864	2	5.77E-07	113.40	1.92	1.81	3
572	PAGILNGKLVSAQIR	sp|Q922D8|C1TC_MOUSE	yes	yes	3	17	15	A	D	0	1535.915	2	9.56E-09	132.08	0.87	0.83	4
573	PAIYFKEQFLDGDAWTNR	sp|P14211|CALR_MOUSE	yes	yes	19	36	18	D	W	0	2170.048	2	5.70E-13	132.79	0.89	0.84	5
574	PANLPAVLLQPR	sp|Q61191|HCFC1_MOUSE	yes	yes	7	18	12	S	W	0	1287.766	2	4.48E-02	53.24	NaN	NaN	0
575	PAPATTFAHLDATTVLSR	sp|P56480|ATPB_MOUSE	yes	yes	370	387	18	D	A	0	1867.979	3	5.75E-08	85.56	NaN	NaN	0
576	PAPTQLSQDQLEAEER	sp|Q9CSN1|SNW1_MOUSE	yes	yes	8	23	16	L	A	0	1810.870	2	2.19E-04	75.91	NaN	NaN	0
577	PASAKWYDR	sp|Q9R0Q7|TEBP_MOUSE	yes	yes	3	11	9	Q	R	0	1092.535	2	3.55E-02	76.94	1.22	0.96	5
578	PATGCQKLIEVDDER	sp|P62754|RS6_MOUSE	yes	yes	8	22	15	F	K	0	1729.831	2;3	1.85E-06	120.63	0.96	0.88	6
579	PCNTFVR	sp|Q8K0Y2|KT33A_MOUSE	yes	yes	398	404	7	G	-	0	892.423	2	1.34E-02	150.17	NaN	NaN	0
580	PDGLAEDIDKGEVSAR	sp|P58252|EF2_MOUSE	yes	yes	610	625	16	F	Q	0	1670.811	2	2.87E-03	71.08	1.13	0.96	5
581	PDQDEIDCLPGLAKQPSFR	sp|P16675|PPGB_MOUSE	yes	yes	25	43	19	A	Q	0	2185.047	2	2.38E-02	44.79	1.12	0.98	6
582	PEGGEGYVVKLR	sp|Q9Z2X1|HNRPF_MOUSE	yes	yes	5	16	12	G	G	0	1302.693	2	3.73E-02	58.17	1.35	1.25	2
583	PEGKEVWDYVTVR	sp|Q920A5|RISC_MOUSE	yes	yes	34	46	13	E	K	0	1576.789	2	1.02E-08	151.56	1.01	0.90	6
584	PELLEQQEEDR	sp|Q9D8U8|SNX5_MOUSE	yes	yes	5	15	11	V	S	0	1384.647	2	2.36E-02	66.27	NaN	NaN	0
585	PENVEITLKGR	sp|P51410|RL9_MOUSE	yes	yes	13	23	11	I	T	0	1254.693	2	6.70E-04	116.24	1.12	1.03	3
586	PETPGYVGFANLPNQVHR	sp|P42208|SEPT2_MOUSE	yes	yes	12	29	18	N	K	0	1994.996	2	6.82E-03	55.01	NaN	NaN	0
587	PETQVSILDNGLR	sp|Q9CZ13|QCR1_MOUSE	yes	yes	46	58	13	V	V	0	1440.757	2	6.01E-04	124.07	NaN	NaN	0
588	PFFENYISILR	sp|P04104|K2C1_MOUSE	yes	yes	237	247	11	D	R	0	1397.734	2	9.81E-03	108.35	NaN	NaN	0
589	PGGDTIFGKIIR	sp|P70349|HINT1_MOUSE	yes	yes	13	24	12	Q	K	0	1272.719	2	1.94E-16	180.20	1.04	0.90	6
590	PGPDGPAAPGPAAIR	sp|Q64674|SPEE_MOUSE	yes	yes	3	17	15	E	E	0	1342.699	2	3.41E-06	103.13	NaN	NaN	0
591	PGQPVTAVVQR	sp|Q9DBG9|TX1B3_MOUSE	yes	yes	5	15	11	T	V	0	1150.646	2	6.54E-02	52.25	NaN	NaN	0
592	PIDEYTTVPGR	sp|Q60847-4|COCA1_MOUSE	yes	no	906	916	11	D	R	0	1246.619	2	9.30E-03	93.35	NaN	NaN	0
593	PIPQSGSPFPASVQDPGLHIWR	sp|P24452|CAPG_MOUSE	yes	yes	4	25	22	T	V	0	2385.223	2;3	3.52E-17	122.34	7.08	6.27	2
594	PKEPEQLR	sp|Q8BG05|ROA3_MOUSE	no	no	28	35	8	D	K	0	995.540	2	1.10E-02	113.71	1.23	1.12	22
595	PKNWDWR	sp|Q9WUU7|CATZ_MOUSE	yes	yes	65	71	7	L	N	0	1000.488	2	1.35E-02	106.36	1.02	0.96	5
596	PKSVDWR	sp|P06797|CATL1_MOUSE	yes	yes	115	121	7	I	E	0	886.466	2	1.82E-02	97.43	1.24	1.01	7
597	PKVTSELLR	sp|Q6P1B1|XPP1_MOUSE	yes	yes	3	11	9	A	Q	0	1041.618	2	8.97E-03	106.62	1.11	0.96	5
598	PKYADLPGIAR	sp|Q99KJ8|DCTN2_MOUSE	yes	yes	4	14	11	D	N	0	1199.666	2	2.21E-02	65.18	1.10	0.77	2
599	PLDLDKYVEIAR	sp|Q9CQR6|PPP6_MOUSE	yes	yes	3	14	12	A	Q	0	1430.777	2	1.02E-16	184.21	1.39	1.01	7
600	PLEDVVIER	sp|Q61576|FKB10_MOUSE	yes	yes	39	47	9	A	Y	0	1068.582	2	1.54E-02	94.31	NaN	NaN	0
601	PLLPAGAPLLQAEEHGLAR	sp|Q6ZQ58|LARP1_MOUSE	yes	yes	7	25	19	E	K	0	1952.084	2	7.85E-11	113.88	NaN	NaN	0
602	PLSLLLKNSPLVSR	sp|P08249|MDHM_MOUSE	yes	yes	39	52	14	Q	L	0	1535.940	2	8.09E-26	196.67	1.22	1.01	7
603	PLVCPAYQAYFR	sp|Q9D646|KRT34_MOUSE	no	no	97	108	12	D	T	0	1483.728	2	3.25E-03	108.70	NaN	NaN	0
604	PNDIGVSSLDCR	sp|Q99KK7|DPP3_MOUSE	yes	yes	9	20	12	L	E	0	1331.614	2	8.04E-03	72.89	NaN	NaN	0
605	PNFEANTTIGR	sp|O08709|PRDX6_MOUSE	yes	yes	12	22	11	A	I	0	1218.599	2	6.74E-07	169.52	NaN	NaN	0
606	PNTIIEALR	sp|Q9EPL8|IPO7_MOUSE	yes	yes	3	11	9	D	G	0	1025.587	2	4.98E-02	68.66	NaN	NaN	0
607	PNVLASEPEIPKGIR	sp|Q9WTP6-2|KAD2_MOUSE	yes	no	3	17	15	A	A	0	1618.904	2	1.27E-11	149.30	1.02	0.93	8
608	PPAAPAGEGGPPAPPPNLTSNR	sp|P63044|VAMP2_MOUSE	yes	yes	9	30	22	V	R	0	2064.039	2	5.38E-06	67.23	NaN	NaN	0
609	PPGASENELKKAYR	sp|Q9QYJ0|DNJA2_MOUSE	yes	yes	16	29	14	V	K	0	1558.810	2	2.92E-02	56.57	1.08	1.07	3
610	PPLPEYGGKVR	sp|Q9CQQ7|AT5F1_MOUSE	yes	yes	45	55	11	L	L	0	1211.666	2	1.80E-02	69.72	1.53	0.95	5
611	PPPEIEGEIKR	sp|P27546-3|MAP4_MOUSE	yes	no	13	23	11	E	D	0	1263.682	2	5.04E-02	62.47	1.34	1.06	3
612	PPPPNPAVSFPAPR	sp|Q8BI08|MAL2_MOUSE	yes	yes	8	21	14	V	V	0	1442.767	2	2.74E-03	68.28	NaN	NaN	0
613	PPTYADLGKSAR	sp|Q60932-2|VDAC1_MOUSE	yes	no	4	15	12	V	D	0	1274.662	2	2.53E-03	90.61	1.47	0.98	6

614	PQSGSPFPASVQDPGLHIWR	sp|P24452|CAPG_MOUSE	yes	yes	6	25	20	I	V	0	2175.086	2	3.51E-27	171.47	16.50	12.97	1
615	PRKSSPGVLR	sp|Q9CXD9|LRC17_MOUSE	yes	yes	18	27	10	E	S	1	1095.651	3	1.04E-01	28.96	NaN	NaN	0
616	PSGVKVLETAEDIQER	sp|P16546-2|SPTN1_MOUSE	yes	no	3	18	16	D	R	0	1769.916	3	2.81E-11	140.22	1.50	0.97	1
617	PSVDHGFLVTR	sp|P02463|CO4A1_MOUSE	yes	yes	1440	1450	11	T	H	0	1226.641	2	9.90E-06	158.04	NaN	NaN	0
618	PTGPATTICSSDKSCR	sp|A2A591|KRA31_MOUSE	yes	no	12	27	16	V	C	0	1736.782	2	7.46E-07	112.17	1.99	1.34	4
619	PTVFFDITADDEPLGR	sp|P17742|PPIA_MOUSE	yes	yes	4	19	16	N	V	0	1791.868	2	3.44E-07	131.56	NaN	NaN	0
620	PVAIALDTKGPEIR	sp|P53657|KPYR_MOUSE	yes	yes	150	163	14	R	T	0	1478.846	3	4.33E-02	51.73	1.10	0.99	5
621	PVDDICIAKPR	sp|P32261|ANT3_MOUSE	yes	yes	36	46	11	N	D	0	1282.670	2	8.60E-04	114.86	1.40	1.12	6
622	PVEKVIEGFSR	sp|Q8CIT9-3|SBSN_MOUSE	yes	no	28	38	11	D	G	0	1259.687	2;3	4.18E-04	120.87	1.34	0.91	9
623	PVNIFKAGADEER	sp|P80314|TCPB_MOUSE	yes	yes	8	20	13	A	A	0	1444.731	2	9.62E-04	89.23	1.58	1.20	2
624	QAAPCVLFFDELDSIAKAR	sp|Q01853|TERA_MOUSE	yes	yes	568	586	19	R	G	0	2150.083	2	3.82E-02	42.07	NaN	NaN	0
625	QADFEAHNILR	sp|Q3THK7|GUAA_MOUSE	yes	yes	590	600	11	R	E	0	1312.652	2	2.96E-03	132.56	NaN	NaN	0
626	QAEEEKVPLPELVR	sp|P56399|UBP5_MOUSE	yes	yes	511	524	14	R	A	0	1635.883	2	6.04E-04	89.62	NaN	NaN	0
627	QAEMLDDLMEKR	sp|Q9WTP6-2|KAD2_MOUSE	yes	no	107	118	12	R	K	0	1477.691	2	2.56E-03	90.41	NaN	NaN	0
628	QAGEVTFADAHR	sp|O35326|SRSF5_MOUSE	yes	yes	130	141	12	R	P	0	1300.616	2	2.96E-02	58.10	NaN	NaN	0
629	QAHLTNQYMQR	sp|P29341|PABP1_MOUSE	yes	yes	375	385	11	R	M	0	1388.662	2	8.52E-15	190.53	NaN	NaN	0
630	QAILGDHPSSFR	sp|Q921F4|HNRLL_MOUSE	yes	yes	325	336	12	R	H	0	1326.668	2	3.47E-03	81.57	NaN	NaN	0
631	QANAGLFNLR	sp|Q8C1A5|THOP1_MOUSE	yes	yes	544	553	10	R	Q	0	1102.588	2	1.89E-02	79.15	NaN	NaN	0
632	QATKDAGQISGLNVLR	sp|P38647|GRP75_MOUSE	yes	yes	203	218	16	R	V	0	1669.911	2	2.29E-02	54.28	NaN	NaN	0
633	QATKDAGTIAGLNVLR	sp|P63017|HSP7C_MOUSE	yes	yes	156	171	16	R	I	0	1626.905	2;3	2.08E-16	168.64	NaN	NaN	0
634	QATKDAGTIAGLNVMR	sp|P20029|GRP78_MOUSE	yes	yes	183	198	16	R	I	0	1644.862	2	1.40E-01	32.86	NaN	NaN	0
635	QATKDAGVIAGLNVLR	sp|Q61696|HS71A_MOUSE	yes	no	156	171	16	R	I	0	1624.926	2;3	5.51E-05	82.59	NaN	NaN	0
636	QAVDVSPLR	sp|P97461|RS5_MOUSE	yes	yes	137	145	9	R	R	0	983.540	2	6.83E-02	61.56	NaN	NaN	0
637	QCEEVAQALGKESLR	sp|Q9R0N0|GALK1_MOUSE	yes	yes	242	256	15	R	E	0	1716.847	2	1.93E-06	108.63	NaN	NaN	0
638	QDEHGFISR	sp|P23927|CRYAB_MOUSE	yes	yes	108	116	9	R	E	0	1087.505	2	1.43E-02	96.11	NaN	NaN	0
639	QDEHGYISR	sp|P14602-3|HSPB1_MOUSE	yes	no	98	106	9	R	C	0	1103.500	2	1.03E-03	143.50	NaN	NaN	0
640	QDIAFAYQR	sp|P07356|ANXA2_MOUSE	yes	yes	69	77	9	R	R	0	1110.546	2	3.44E-02	76.06	NaN	NaN	0
641	QDLGSPEGIALDHLGR	sp|P10493|NID1_MOUSE	yes	yes	1016	1031	16	R	T	0	1676.848	2	7.57E-06	83.37	NaN	NaN	0
642	QDPAMVHLPGGR	sp|Q8BPG6|SUMF2_MOUSE	yes	yes	34	45	12	A	F	0	1276.635	2	5.39E-07	105.65	NaN	NaN	0
643	QDPGSKVVADR	sp|O08543-2|EFNA5_MOUSE	yes	no	21	31	11	S	Y	0	1170.599	2	1.31E-02	75.09	NaN	NaN	0
644	QDPSVLHTEEMR	sp|Q99L47|F10A1_MOUSE	yes	yes	18	29	12	R	F	0	1440.667	2	4.03E-04	139.86	NaN	NaN	0
645	QDSLESMKFGDSNTVMR	sp|E9Q557|DESP_MOUSE	yes	yes	921	937	17	R	F	0	1943.872	2	1.71E-03	72.43	NaN	NaN	0
646	QDVDNASLAR	sp|P20152|VIME_MOUSE	yes	yes	208	217	10	R	L	0	1087.526	2	1.40E-02	103.08	NaN	NaN	0
647	QEAEEAKEALLQASR	sp|P26041|MOES_MOUSE	yes	yes	394	408	15	R	D	0	1671.843	2	5.88E-06	99.04	NaN	NaN	0
648	QEAEQLKNQIR	sp|P62874|GBB1_MOUSE	yes	yes	9	19	11	R	D	0	1355.716	2	6.24E-03	85.81	NaN	NaN	0
649	QEALEWLIR	sp|Q6P1B1|XPP1_MOUSE	yes	yes	606	614	9	R	E	0	1156.624	2	1.81E-02	90.15	NaN	NaN	0
650	QEAVALLQGQR	sp|Q64010-2|CRK_MOUSE	yes	no	21	31	11	R	H	0	1211.662	2	9.30E-03	93.35	NaN	NaN	0
651	QEDIPEVSCIHNGLR	sp|P11087-2|CO1A1_MOUSE	yes	no	23	37	15	G	V	0	1765.842	2	3.54E-06	101.53	NaN	NaN	0
652	QEFAQHANAFHQWIQETR	sp|P16546-2|SPTN1_MOUSE	yes	no	2188	2205	18	R	T	0	2240.051	3	1.88E-05	79.47	NaN	NaN	0
653	QEFLLNCLHR	sp|Q62172|RBP1_MOUSE	yes	yes	405	414	10	R	D	0	1328.666	2	1.14E-01	26.79	NaN	NaN	0
654	QEIAQEFKTLFGR	sp|P48036|ANXA5_MOUSE	yes	yes	49	61	13	R	D	0	1565.820	2	1.70E-12	167.61	NaN	NaN	0
655	QEIIKLFDER	sp|Q8BLX7|COGA1_MOUSE	yes	yes	1421	1430	10	R	M	0	1289.698	2	5.90E-03	114.86	NaN	NaN	0
656	QEIYSSHNQPSCGGR	sp|Q8K4L4|POF1B_MOUSE	yes	yes	527	541	15	R	T	0	1718.743	2	2.48E-06	114.63	NaN	NaN	0
657	QEKALLEEIER	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1153	1163	11	R	H	0	1356.725	2	1.78E-02	69.92	NaN	NaN	0
658	QEKALSAIAELLTSEHER	sp|P30999-2|CTND1_MOUSE	yes	no	702	719	18	R	V	0	2024.054	3	1.75E-03	65.23	NaN	NaN	0
659	QELEAELAKVR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1654	1664	11	R	A	0	1284.704	2	4.27E-04	120.57	NaN	NaN	0
660	QELLCLKQNHEEEVNTLR	sp|Q61897|KT33B_MOUSE	yes	no	185	202	18	R	C	0	2252.122	2;3	7.39E-06	84.25	NaN	NaN	0
661	QELQLAAGR	sp|Q6NXH9|K2C73_MOUSE	no	no	329	337	9	F	H	0	984.535	2	1.11E-02	115.86	NaN	NaN	0
662	QELSHALYQHDAACR	sp|Q99KP6|PRP19_MOUSE	yes	no	101	115	15	R	V	0	1797.822	3	4.10E-04	74.15	NaN	NaN	0
663	QEMQEVQSSR	sp|O88569|ROA2_MOUSE	yes	no	191	200	10	R	S	0	1220.546	2	1.13E-03	144.55	NaN	NaN	0
664	QEPSDSPMFIINR	sp|Q61495|DSG1A_MOUSE	yes	no	201	213	13	R	K	0	1532.729	2	9.21E-04	92.86	NaN	NaN	0
665	QEQTYVISAPKILR	sp|P06684|CO5_MOUSE	yes	yes	19	32	14	G	V	0	1644.920	2	2.05E-04	102.52	NaN	NaN	0
666	QEWESAGQQAPHPR	sp|Q62418-3|DBNL_MOUSE	yes	no	249	262	14	R	E	0	1619.744	2	9.96E-08	162.41	NaN	NaN	0
667	QFEEEKANWEAQQR	sp|O55131|SEPT7_MOUSE	yes	yes	402	415	14	R	I	0	1791.818	2	6.81E-04	87.52	NaN	NaN	0
668	QFESLPATHIR	sp|Q9R190|MTA2_MOUSE	yes	yes	93	103	11	R	G	0	1297.678	2	9.38E-03	81.63	NaN	NaN	0
669	QFLESSELPR	sp|Q9CWK8|SNX2_MOUSE	yes	yes	260	269	10	R	A	0	1204.609	2	1.58E-02	82.42	NaN	NaN	0
670	QFPFHEMFVSR	sp|P58802|TB10A_MOUSE	yes	yes	161	171	11	R	G	0	1423.671	2	1.10E-02	79.49	NaN	NaN	0
671	QFTCKPGVANR	sp|Q6NXH9|K2C73_MOUSE	yes	no	4	14	11	R	G	0	1276.635	2	1.70E-03	122.70	NaN	NaN	0
672	QFTCKSGASNR	sp|Q9R0H5|K2C71_MOUSE	yes	no	4	14	11	R	G	0	1254.578	2	9.84E-03	78.74	NaN	NaN	0
673	QFTSSSSMKGSCGIGGGSSR	sp|Q61781|K1C14_MOUSE	no	no	7	26	20	R	M	0	1976.868	2	5.02E-06	81.81	NaN	NaN	0
674	QGAAGHGGGSSLSHEDALSLLEGI	sp|Q8BJS4-3|SUN2_MOUSE	yes	no	294	320	27	R	R	0	2604.289	3	3.97E-07	79.38	NaN	NaN	0
675	QGAKINEIR	sp|Q61990-2|PCBP2_MOUSE	yes	no	272	280	9	R	Q	0	1027.577	2	2.65E-03	116.05	NaN	NaN	0
676	QGANINEIR	sp|P60335|PCBP1_MOUSE	yes	yes	298	306	9	R	Q	0	1013.525	2	8.62E-03	121.64	NaN	NaN	0
677	QGDAEFNR	sp|P57780|ACTN4_MOUSE	yes	yes	807	814	8	R	I	0	935.410	2	2.90E-02	106.60	NaN	NaN	0
678	QGSKILEGR	sp|Q61955|KLK8_MOUSE	yes	yes	29	37	9	A	E	0	986.551	2	1.47E-02	97.81	NaN	NaN	0
679	QGTGLGFR	sp|P29699|FETUA_MOUSE	yes	yes	21	28	8	P	E	0	834.435	2	9.23E-02	65.22	NaN	NaN	0
680	QGTLHVGDEIR	sp|O70589-2|CSKP_MOUSE	yes	no	527	537	11	R	E	0	1223.626	2	1.25E-02	77.89	NaN	NaN	0
681	QGVEADINGLR	sp|Q61414|K1C15_MOUSE	yes	no	196	206	11	R	R	0	1170.599	2	9.85E-03	80.69	NaN	NaN	0
682	QGVEADINGLRR	sp|Q61414|K1C15_MOUSE	yes	no	196	207	12	R	V	1	1326.700	2	3.31E-03	93.62	NaN	NaN	0
683	QGVEDAFYTLVR	sp|Q61411|RASH_MOUSE	yes	no	150	161	12	R	E	0	1396.699	2	3.36E-03	89.43	NaN	NaN	0
684	QHATNVGIMFR	sp|P35505|FAAA_MOUSE	yes	yes	132	142	11	R	G	0	1272.640	2	1.07E-02	119.39	NaN	NaN	0
685	QHCVADTATRPGR	sp|Q8CG70|P3H3_MOUSE	yes	yes	291	303	13	R	S	1	1467.700	3	3.82E-02	51.73	NaN	NaN	0
686	QHFISFDSDR	sp|Q6P069-2|SORCN_MOUSE	yes	no	92	101	10	R	S	0	1250.568	2	5.10E-06	166.69	NaN	NaN	0
687	QHFSVGGWR	sp|Q6ZPJ3|UBE2O_MOUSE	yes	yes	1126	1134	9	R	L	0	1072.520	2	1.15E-02	111.06	NaN	NaN	0
688	QHFYPSR	sp|Q6NZJ6-2|IF4G1_MOUSE	yes	no	49	55	7	R	A	0	933.446	2	3.05E-02	114.78	NaN	NaN	0
689	QHIAEKTEKILTEFLR	sp|Q8R1F1|NIBL1_MOUSE	yes	yes	15	30	16	R	F	0	1955.084	3	5.48E-02	65.37	NaN	NaN	0
690	QHLANQQALGR	sp|Q61292|LAMB2_MOUSE	yes	yes	1383	1393	11	R	L	0	1234.653	2	1.38E-03	138.22	NaN	NaN	0
691	QHLASIYEKEEDWR	sp|O88544|CSN4_MOUSE	yes	yes	108	121	14	R	N	0	1802.859	3	3.10E-04	97.69	NaN	NaN	0
692	QHQMQLVDSIVR	sp|F6ZDS4|TPR_MOUSE	yes	yes	672	683	12	R	Q	0	1452.751	2	8.32E-04	133.32	NaN	NaN	0
693	QHTSAFVPSSGR	sp|Q6PAV2-2|HERC4_MOUSE	yes	no	304	315	12	R	I	0	1272.621	2	3.43E-03	84.37	NaN	NaN	0
694	QHYKGSDFDCELR	sp|P61979-3|HNRPK_MOUSE	yes	yes	112	124	13	Y	L	0	1653.721	3	7.55E-03	69.35	NaN	NaN	0
695	QIDDVLSVASVR	sp|Q9JII6|AK1A1_MOUSE	yes	yes	168	179	12	R	P	0	1300.699	2	1.07E-02	68.00	NaN	NaN	0
696	QIEETLSHFR	sp|P17710-3|HXK1_MOUSE	yes	no	469	478	10	R	L	0	1258.631	2	1.54E-02	86.01	NaN	NaN	0
697	QIHAATAGACGETER	sp|Q9EQG3|SCEL_MOUSE	yes	yes	185	199	15	R	H	0	1570.716	2	1.17E-05	83.75	NaN	NaN	0
698	QIHIDIPR	sp|Q8R5A6|TB22A_MOUSE	yes	no	278	285	8	R	M	0	990.561	2	4.98E-02	85.68	NaN	NaN	0
699	QIHKFEELNR	sp|Q8QZY1|EIF3L_MOUSE	yes	yes	546	555	10	R	T	0	1312.689	3	5.46E-03	102.40	NaN	NaN	0
700	QILEENYGQKDPEKVAR	sp|Q920E5|FPPS_MOUSE	yes	yes	284	300	17	R	V	0	2016.028	3	2.73E-03	66.83	NaN	NaN	0
701	QINDIQLSR	sp|Q9QZD9|EIF3I_MOUSE	yes	yes	190	198	9	R	D	0	1085.583	2	2.01E-02	86.90	NaN	NaN	0
702	QIPFHDVR	sp|P35922-11|FMR1_MOUSE	yes	no	41	48	8	R	F	0	1010.530	2	6.53E-02	76.06	NaN	NaN	0
703	QITLNDLPVGR	sp|O08807|PRDX4_MOUSE	yes	yes	216	226	11	R	S	0	1224.683	2	9.29E-03	102.40	NaN	NaN	0
704	QITVNDLPVGR	sp|Q61171|PRDX2_MOUSE	yes	yes	140	150	11	R	S	0	1210.667	2	9.29E-03	121.68	NaN	NaN	0
705	QIWQNLGLDEAR	sp|Q8BGQ7|SYAC_MOUSE	yes	yes	154	165	12	R	I	0	1441.731	2	5.04E-03	78.32	NaN	NaN	0
706	QKAQVEQELTTLR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	2083	2095	13	R	L	0	1542.837	2	9.55E-03	65.04	NaN	NaN	0
707	QKGLVEDTLR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1812	1821	10	R	Q	0	1157.640	2	1.19E-02	84.48	NaN	NaN	0
708	QKHSQAVEELADQLEQTKR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	1192	1210	19	R	V	0	2237.140	4	4.61E-04	76.30	NaN	NaN	0
709	QKLQELQGR	sp|Q00623|APOA1_MOUSE	yes	yes	155	163	9	R	L	0	1098.615	2	2.09E-04	133.23	NaN	NaN	0
710	QKSTELLIR	sp|P84244|H33_MOUSE	yes	no	56	64	9	Y	K	0	1086.640	2	2.01E-02	88.60	NaN	NaN	0
711	QKTGTAEMSSILEER	sp|Q03265|ATPA_MOUSE	yes	yes	44	58	15	L	I	0	1678.820	2;3	9.12E-31	205.78	NaN	NaN	0
712	QKVAPLGAELQESAR	sp|Q00623|APOA1_MOUSE	yes	yes	140	154	15	R	Q	0	1595.863	2	3.00E-08	125.50	NaN	NaN	0
713	QKVTSLTACLVNQNLR	sp|P01831|THY1_MOUSE	yes	yes	20	35	16	G	L	0	1843.994	2;3	1.10E-39	218.78	NaN	NaN	0
714	QLAAEEEQR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1877	1885	9	R	R	0	1072.515	2	1.19E-02	106.18	NaN	NaN	0
715	QLAEEDAAR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1721	1729	9	R	Q	0	1001.478	2	2.80E-02	79.15	NaN	NaN	0
716	QLAEEDLAQQR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	2198	2208	11	R	A	0	1299.642	2	3.81E-03	131.12	NaN	NaN	0

717	QLCDNAGFDATNILNKLR	sp|P80313|TCPH_MOUSE	yes	yes	448	465	18	R	A	0	2062.027	2	7.26E-08	82.01	NaN	NaN	0
718	QLDCVSGDHGR	sp|Q99M74|KRT82_MOUSE	yes	yes	177	187	11	R	L	0	1242.541	2	1.53E-03	136.70	NaN	NaN	0
719	QLDEPKLDR	sp|Q8BGD9|IF4B_MOUSE	yes	yes	390	398	9	R	R	0	1112.583	2	2.09E-02	87.26	NaN	NaN	0
720	QLDHELR	sp|Q8VDP3-2|MICA1_MOUSE	yes	no	920	926	7	R	G	0	909.467	2	1.79E-02	137.88	NaN	NaN	0
721	QLEEAEEEAQR	sp|Q8VDD5|MYH9_MOUSE	yes	yes	1878	1888	11	R	A	0	1330.600	2	2.56E-06	167.18	NaN	NaN	0
722	QLEEAEEEATR	sp|Q61879|MYH10_MOUSE	yes	yes	1885	1895	11	R	A	0	1303.589	2	2.21E-02	65.18	NaN	NaN	0
723	QLEQENASLESR	sp|Q497I4|KRT35_MOUSE	yes	no	117	128	12	R	I	0	1402.669	2	5.65E-05	129.37	NaN	NaN	0
724	QLEQENTQLECR	sp|B1AQ75|KRT36_MOUSE	yes	yes	113	124	12	R	I	0	1546.705	2	3.38E-03	88.10	NaN	NaN	0
725	QLEQQVEEFR	sp|P06728|APOA4_MOUSE	yes	yes	295	304	10	R	R	0	1304.636	2	1.93E-03	138.76	NaN	NaN	0
726	QLEQQVEEFRR	sp|P06728|APOA4_MOUSE	yes	yes	295	305	11	R	T	1	1460.737	2	5.08E-06	164.04	NaN	NaN	0
727	QLFHPEQLITGKEDAANNYAR	sp|P68368|TBA4A_MOUSE	yes	no	85	105	21	R	G	0	2414.198	2;3	1.61E-21	160.30	NaN	NaN	0
728	QLGHLCDLTIR	sp|Q64321|ZBT7B_MOUSE	yes	yes	29	39	11	R	T	0	1324.692	2	1.20E-02	116.24	NaN	NaN	0
729	QLHDDYFYHDEL	sp|Q8BP92|RCN2_MOUSE	yes	no	309	320	12	R	-	0	1593.674	2	3.27E-03	120.87	NaN	NaN	0
730	QLHDFSSPPHLLR	sp|O88898-2|P63_MOUSE	yes	no	512	524	13	R	T	0	1545.805	3	8.77E-04	105.03	NaN	NaN	0
731	QLHEYETELEDER	sp|O08638-2|MYH11_MOUSE	yes	no	1597	1609	13	R	K	0	1689.748	2	8.64E-04	118.21	NaN	NaN	0
732	QLHLNQLIR	sp|P97310|MCM2_MOUSE	yes	yes	299	307	9	R	T	0	1133.667	2	4.00E-03	130.75	NaN	NaN	0
733	QLHQELPAHGVPLINHL	sp|Q8BTZ4-2|APC5_MOUSE	yes	no	711	727	17	R	-	0	1915.043	3	1.84E-02	47.64	NaN	NaN	0
734	QLKEEDGLR	sp|Q9QY76|VAPB_MOUSE	yes	yes	189	197	9	R	V	0	1086.567	2	6.27E-02	64.10	NaN	NaN	0
735	QLLAGLDKVASDLDR	sp|Q9R269|PEPL_MOUSE	yes	yes	504	518	15	R	Q	0	1612.878	2	4.17E-03	70.20	NaN	NaN	0
736	QLLEGELEPLRR	sp|Q9R269|PEPL_MOUSE	yes	yes	1473	1484	12	R	K	1	1451.810	2	3.25E-02	57.18	NaN	NaN	0
737	QLLHNFPPDQLTSSGAPFWSGPK	sp|Q02053|UBA1_MOUSE	yes	yes	724	747	24	R	C	0	2679.356	3	7.97E-04	60.74	NaN	NaN	0
738	QLLLTADDR	sp|P05064|ALDOA_MOUSE	yes	yes	61	69	9	R	V	0	1043.561	2	5.52E-02	66.06	NaN	NaN	0
739	QLLQANPILEAFGNAKTVKNDNS	sp|Q8VDD5|MYH9_MOUSE	yes	no	210	234	25	R	F	0	2727.430	3	1.39E-03	51.83	NaN	NaN	0
740	QLNNHFGR	sp|Q80TP3|UBR5_MOUSE	yes	yes	2252	2259	8	R	R	0	984.489	2	4.78E-02	88.95	NaN	NaN	0
741	QLQLAQEAAQKR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	1938	1949	12	R	L	0	1382.763	2	3.71E-03	81.92	NaN	NaN	0
742	QLQNIIQATSR	sp|E9Q557|DESP_MOUSE	yes	yes	283	293	11	R	E	0	1270.699	2	9.37E-03	83.18	NaN	NaN	0
743	QLSALHR	sp|Q9CZM2|RL15_MOUSE	yes	yes	32	38	7	R	A	0	823.466	2	1.74E-02	139.28	NaN	NaN	0
744	QLSSGVSEIR	sp|P14602-3|HSPB1_MOUSE	yes	no	50	59	10	R	Q	0	1074.567	2	1.41E-02	101.35	NaN	NaN	0
745	QLTEHAVEGDCDFHILKQDGQFR	sp|P29699|FETUA_MOUSE	yes	yes	104	126	23	R	V	0	2742.282	3;4	3.10E-03	52.36	NaN	NaN	0
746	QLTHENVQR	sp|Q9D554|SF3A3_MOUSE	yes	yes	339	347	9	R	K	0	1123.573	2	8.49E-03	121.90	NaN	NaN	0
747	QLVEADINGLR	sp|Q497I4|KRT35_MOUSE	no	no	194	204	11	R	R	0	1226.662	2	2.25E-02	67.39	NaN	NaN	0
748	QLVEADINSLR	sp|Q9D646|KRT34_MOUSE	no	no	153	163	11	R	R	0	1256.673	2	1.16E-05	155.99	NaN	NaN	0
749	QLVEADINSLRR	sp|Q9D646|KRT34_MOUSE	no	no	153	164	12	R	I	1	1412.774	2	3.85E-03	112.44	NaN	NaN	0
750	QLVEADTNGLR	sp|Q62168|K1H2_MOUSE	yes	no	152	162	11	R	R	0	1214.626	2	9.31E-03	99.28	NaN	NaN	0
751	QLVEQVEQIQKEQNYQR	sp|Q99KF1|TMED9_MOUSE	yes	yes	170	186	17	R	W	0	2159.097	2	1.68E-03	72.58	NaN	NaN	0
752	QLVESDLNGLR	sp|Q61897|KT33B_MOUSE	yes	no	153	163	11	R	R	0	1242.657	2	4.39E-06	164.90	NaN	NaN	0
753	QLVESDLNGLRR	sp|Q61897|KT33B_MOUSE	yes	no	153	164	12	R	I	1	1398.758	2	3.33E-03	100.93	NaN	NaN	0
754	QLVHELDEAEYQEIR	sp|P97371|PSME1_MOUSE	yes	yes	199	213	15	R	L	0	1870.906	2	3.78E-05	80.74	NaN	NaN	0
755	QLWWGHR	sp|Q9Z1Q9|SYVC_MOUSE	yes	yes	723	729	7	R	I	0	981.493	2	9.95E-02	97.07	NaN	NaN	0
756	QLYEEETR	sp|Q6IMF0|KRT83_MOUSE	yes	yes	246	253	8	R	L	0	1066.493	2	1.32E-02	116.05	NaN	NaN	0
757	QMGQPCDAYQKR	sp|E9Q557|DESP_MOUSE	yes	yes	142	153	12	R	L	0	1480.655	2	1.59E-02	63.47	NaN	NaN	0
758	QNGDDPLMTYR	sp|P48678-3|LMNA_MOUSE	yes	no	360	370	11	R	F	0	1308.577	2	2.09E-16	133.05	NaN	NaN	0
759	QNHPLPFPPPPALPFYPASVYPR	sp|Q6A0A9|F120A_MOUSE	yes	yes	849	871	23	R	H	0	2601.353	2;3	3.40E-03	45.36	NaN	NaN	0
760	QNLEPFFDTYVNDLRR	sp|Q8BGZ7|K2C75_MOUSE	yes	no	195	210	16	R	Q	1	2025.991	2	2.06E-02	50.31	NaN	NaN	0
761	QNQEYQVLLDIR	sp|Q8K0Y2|KT33A_MOUSE	yes	yes	335	346	12	R	S	0	1517.784	2	3.41E-03	119.39	NaN	NaN	0
762	QNQEYQVLLDVKAR	sp|Q61897|KT33B_MOUSE	no	no	335	348	14	R	L	0	1702.900	2	7.80E-13	167.61	NaN	NaN	0
763	QNQEYQVLLDVR	sp|Q9D646|KRT34_MOUSE	no	no	335	346	12	R	A	0	1503.768	2	1.46E-03	130.10	NaN	NaN	0
764	QNSQVPAERPR	sp|Q9ER88-2|RT29_MOUSE	yes	no	29	39	11	T	T	1	1280.659	2	9.65E-03	101.39	NaN	NaN	0
765	QNVAYEYLCHLEEAKR	sp|Q9JKF1|IQGA1_MOUSE	yes	yes	37	52	16	R	W	0	2021.963	3	3.34E-03	69.33	NaN	NaN	0
766	QNYLFEQYR	sp|Q9ER72|SYCC_MOUSE	yes	no	191	199	9	R	E	0	1259.594	2	6.14E-02	63.22	NaN	NaN	0
767	QPASAKWYDR	sp|Q9R0Q7|TEBP_MOUSE	yes	yes	2	11	10	M	R	0	1220.594	2	5.97E-03	100.69	1.10	0.92	4
768	QPDSGISSIR	sp|Q91YQ5|RPN1_MOUSE	yes	yes	270	279	10	R	S	0	1058.536	2	1.57E-02	83.18	NaN	NaN	0
769	QPFFQKR	sp|Q9EQU5-2|SET_MOUSE	yes	no	65	71	7	R	S	0	949.513	2	8.69E-03	126.24	NaN	NaN	0
770	QPGTSLVDADTFHHQVR	sp|O08579|EMD_MOUSE	yes	yes	120	136	17	R	D	0	1906.929	3	3.55E-04	66.83	NaN	NaN	0
771	QPLSLLLKNSPLVSR	sp|P08249|MDHM_MOUSE	yes	yes	38	52	15	G	L	0	1663.999	2	4.92E-05	89.62	1.53	1.43	2
772	QPPPPPDATCHQVR	sp|Q8CFZ4|GPC3_MOUSE	yes	yes	25	38	14	A	S	0	1598.762	2	2.21E-03	71.28	NaN	NaN	0
773	QPQAGHGQPSQSGYGR	sp|Q2VIS4|FILA2_MOUSE	yes	yes	1022	1037	16	R	S	0	1653.761	2	1.04E-21	203.52	NaN	NaN	0
774	QPQAGQGQPSQSGSGR	sp|Q2VIS4|FILA2_MOUSE	yes	no	1178	1193	16	R	S	0	1568.729	2	1.93E-06	107.73	NaN	NaN	0
775	QPQASQGQPSQSGSGR	sp|Q2VIS4|FILA2_MOUSE	yes	yes	1960	1975	16	S	S	0	1598.740	2	6.14E-04	66.02	NaN	NaN	0
776	QPYAVSELAGHQTSAESWGTGR	sp|Q9D8E6|RL4_MOUSE	yes	yes	50	71	22	R	A	0	2331.088	2	8.92E-19	140.59	NaN	NaN	0
777	QQEGFKGTFPDAR	sp|Q99K48|NONO_MOUSE	yes	yes	368	380	13	R	E	0	1479.711	2	2.71E-05	119.87	NaN	NaN	0
778	QQEIEEKLIEEETAR	sp|Q3UL36-2|ARGL1_MOUSE	yes	no	98	112	15	R	R	0	1843.916	2	5.08E-03	67.65	NaN	NaN	0
779	QQELKDVGNR	sp|P26231|CTNA1_MOUSE	yes	yes	195	204	10	R	D	0	1185.610	2	7.59E-03	96.11	NaN	NaN	0
780	QQELTHQEHR	sp|Q64727|VINC_MOUSE	yes	yes	179	188	10	R	V	0	1304.622	3	4.94E-02	61.34	NaN	NaN	0
781	QQHHLVEYMER	sp|Q8BK62|OLFL3_MOUSE	yes	yes	22	32	11	G	R	0	1468.688	3	9.27E-03	98.90	NaN	NaN	0
782	QQHLSSLQDYMQR	sp|Q9R269|PEPL_MOUSE	yes	yes	207	219	13	R	C	0	1632.768	2	3.16E-07	159.00	NaN	NaN	0
783	QQIVLQGPGPWGFR	sp|O70400|PDLI1_MOUSE	yes	yes	4	17	14	T	L	0	1581.842	2	2.65E-02	53.45	NaN	NaN	0
784	QQLGPNSGEVESHLSFLEKSLR	sp|P06728|APOA4_MOUSE	yes	yes	327	348	22	R	E	0	2454.250	3	2.72E-04	73.29	NaN	NaN	0
785	QQQCTNGFDLDR	sp|Q9WVH9|FBLN5_MOUSE	yes	yes	24	35	12	A	Q	0	1480.637	2	1.46E-06	164.11	NaN	NaN	0
786	QQSNVDELGCSHLGQSYESR	sp|P08121|CO3A1_MOUSE	yes	yes	24	43	20	A	D	0	2293.003	2;3	1.11E-15	154.34	NaN	NaN	0
787	QQWDGKESTITR	sp|Q05816|FABP5_MOUSE	yes	yes	98	109	12	H	K	0	1447.706	2	1.30E-02	66.39	NaN	NaN	0
788	QSCVWYGECGIATGDKR	sp|O35604|NPC1_MOUSE	yes	yes	23	39	17	S	Y	0	1985.872	2	2.16E-03	69.98	NaN	NaN	0
789	QSEELSKLR	sp|Q8K4L4|POF1B_MOUSE	yes	yes	518	526	9	R	Q	0	1088.583	2	2.09E-04	133.23	NaN	NaN	0
790	QSEQDFYDFKAVNIR	sp|Q99LJ6|GPX7_MOUSE	yes	yes	19	33	15	A	G	0	1858.885	2	4.62E-11	139.58	NaN	NaN	0
791	QSGQCLDIDECR	sp|Q9WVH9|FBLN5_MOUSE	yes	yes	36	47	12	R	T	0	1479.608	2	8.04E-02	44.51	NaN	NaN	0
792	QSIDALKDWFR	sp|Q05D44|IF2P_MOUSE	yes	yes	1185	1195	11	R	D	0	1377.704	2	7.43E-04	74.99	NaN	NaN	0
793	QSKYEELQITAGKHGDSVR	sp|P04104|K2C1_MOUSE	yes	yes	382	400	19	Y	N	0	2145.081	4	1.28E-04	64.71	NaN	NaN	0
794	QSLHTYLR	sp|Q9D6Z1|NOP56_MOUSE	yes	yes	279	286	8	R	S	0	1016.540	2	1.32E-02	116.05	NaN	NaN	0
795	QSNVDELGCSHLGQSYESR	sp|P08121|CO3A1_MOUSE	yes	yes	25	43	19	Q	D	0	2164.944	2	7.04E-03	51.88	NaN	NaN	0
796	QSSGPGASSGPGGDHSELIVR	sp|P57776-2|EF1D_MOUSE	yes	yes	39	59	21	R	I	0	1993.945	2	4.38E-09	92.10	NaN	NaN	0
797	QSTLVIAEHANDSLAPITLNTITAA	sp|Q99LC5|ETFA_MOUSE	yes	yes	20	46	27	F	L	0	2776.472	2;3	1.40E-30	160.57	NaN	NaN	0
798	QSVEADINGLR	sp|P02535-3|K1C10_MOUSE	yes	no	235	245	11	R	R	0	1200.610	2	3.87E-03	131.02	NaN	NaN	0
799	QSVEADINGLRR	sp|P02535-3|K1C10_MOUSE	yes	no	235	246	12	R	V	1	1356.711	2	1.98E-04	146.36	NaN	NaN	0
800	QSVNHQMAQEDAQR	sp|Q07076|ANXA7_MOUSE	yes	yes	310	323	14	R	L	0	1640.733	2	4.66E-06	95.07	NaN	NaN	0
801	QSVSGLHR	sp|Q505F5|LRC47_MOUSE	yes	yes	429	436	8	R	Y	0	882.467	2	1.72E-02	113.66	NaN	NaN	0
802	QSVYEEKLKQFEER	sp|P23116|EIF3A_MOUSE	yes	yes	769	782	14	R	L	0	1811.905	3	7.65E-02	44.25	NaN	NaN	0
803	QTEGFKNVSLGNVLAVAYAAKR	sp|Q99KK7|DPP3_MOUSE	yes	yes	400	421	22	R	E	0	2335.265	3	2.12E-03	58.69	NaN	NaN	0
804	QTFKSHFGR	sp|P14824|ANXA6_MOUSE	yes	yes	403	411	9	R	D	0	1106.562	3	2.37E-02	82.42	NaN	NaN	0
805	QTNLENLDQAFSVAER	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	119	134	16	R	D	0	1833.886	2	7.07E-04	63.69	NaN	NaN	0
806	QTPVLYAMLDHSR	sp|P27573|MYP0_MOUSE	yes	yes	215	227	13	R	S	0	1529.766	2	8.97E-04	109.83	NaN	NaN	0
807	QVAEEWVNQGR	sp|Q9DCJ9|NPL_MOUSE	yes	yes	65	75	11	R	N	0	1314.632	2	4.11E-03	97.45	NaN	NaN	0
808	QVCEQLISGQMSR	sp|Q60847-4|COCA1_MOUSE	yes	no	1750	1762	13	R	F	0	1534.723	2	9.57E-03	62.29	NaN	NaN	0
809	QVDQLTNDKAR	sp|P20152|VIME_MOUSE	yes	yes	160	170	11	R	V	0	1286.658	2	1.81E-10	165.58	NaN	NaN	0
810	QVEEKEDLLR	sp|Q8BP27-3|SFR1_MOUSE	yes	no	151	160	10	R	R	0	1257.657	2	8.98E-02	53.24	NaN	NaN	0
811	QVHNSFAR	sp|Q9WUP7-2|UCHL5_MOUSE	yes	no	138	145	8	R	Q	0	957.478	2	9.92E-03	120.87	NaN	NaN	0
812	QVIDCQLADVNNLGKYR	sp|Q9CPY7-2|AMPL_MOUSE	yes	no	410	426	17	R	S	0	2005.005	2	7.67E-16	153.72	NaN	NaN	0
813	QVPWTPEPR	sp|Q91V98|CD248_MOUSE	yes	yes	18	26	9	G	A	0	1108.567	2	4.51E-02	70.91	NaN	NaN	0
814	QVQHILASASPSGR	sp|Q3UPL0-2|SC31A_MOUSE	yes	no	179	192	14	R	A	0	1449.769	2	4.00E-04	107.11	NaN	NaN	0
815	QVQSLTCEVDALKGTNESLER	sp|P20152|VIME_MOUSE	yes	yes	322	342	21	R	Q	0	2376.159	2	1.38E-16	136.64	NaN	NaN	0
816	QVVTLLNELKR	sp|Q921H8|THIKA_MOUSE	yes	no	386	396	11	R	R	0	1311.787	2	3.76E-03	96.23	NaN	NaN	0
817	QWLNSGHISDVR	sp|Q9DBR7-2|MYPT1_MOUSE	yes	no	183	194	12	R	H	0	1410.700	2	3.46E-03	82.07	NaN	NaN	0
818	QWYESHYALPLGR	sp|P62242|RS8_MOUSE	yes	yes	111	123	13	R	K	0	1618.789	2	4.72E-07	153.39	NaN	NaN	0
819	QYAGLDHELAFSR	sp|O55242-2|SGMR1_MOUSE	yes	no	48	60	13	R	L	0	1505.726	2	1.05E-03	81.63	NaN	NaN	0

820	QYAKDIGFIKLD	sp|P62274|RS29_MOUSE	yes	no	45	56	12	R	-	0	1409.756	2	3.18E-03	85.84	NaN	NaN	0
821	QYDEDSHWWIQYLR	sp|P50608|FMOD_MOUSE	yes	yes	19	32	14	G	N	0	1937.870	2	3.55E-04	119.96	NaN	NaN	0
822	QYDIDDAITKNLIDR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	4104	4118	15	R	S	0	1791.900	2	2.44E-08	127.30	NaN	NaN	0
823	QYDISNPQKPR	sp|Q63836|SBP2_MOUSE	yes	no	334	344	11	R	L	0	1344.679	2	4.64E-04	119.27	NaN	NaN	0
824	QYEALVETNRR	sp|Q9D646|KRT34_MOUSE	no	no	231	241	11	C	E	1	1377.700	2	9.36E-03	110.08	NaN	NaN	0
825	QYEDEAAKAR	sp|Q9R269|PEPL_MOUSE	yes	yes	1134	1143	10	R	S	0	1179.552	2	4.08E-04	128.01	NaN	NaN	0
826	QYEKYSFR	sp|Q8K2B0|SC65_MOUSE	yes	yes	19	26	8	A	G	0	1119.535	2	1.46E-04	128.38	NaN	NaN	0
827	QYENFINR	sp|Q9R269|PEPL_MOUSE	yes	yes	252	259	8	R	N	0	1082.515	2	3.38E-02	103.74	NaN	NaN	0
828	QYEQLAEKNR	sp|P02535-3|K1C10_MOUSE	yes	no	313	322	10	N	K	0	1277.636	2	3.94E-02	64.82	1.37	0.83	1
829	QYKIPDWFLNR	sp|P62270|RS18_MOUSE	yes	yes	76	86	11	R	Q	0	1478.767	2	3.37E-16	184.55	NaN	NaN	0
830	QYLLSGQHYDFPSYR	sp|Q9CYZ6|CS060_MOUSE	yes	yes	56	70	15	R	S	0	1872.880	2	2.07E-04	77.75	NaN	NaN	0
831	QYLQSGSVR	sp|Q01149|CO1A2_MOUSE	yes	yes	23	31	9	C	K	0	1036.530	2	1.21E-02	104.39	NaN	NaN	0
832	QYNIPHGPIVGSTR	sp|O08579|EMD_MOUSE	yes	yes	18	31	14	R	K	0	1537.800	2	2.28E-03	70.89	NaN	NaN	0
833	QYPWGVAEVENGEHCDFTILR	sp|O55131|SEPT7_MOUSE	yes	yes	265	285	21	R	N	0	2519.154	2	3.34E-03	49.77	NaN	NaN	0
834	QYYTLLNQAPDMLHR	sp|P97855|G3BP1_MOUSE	yes	yes	18	32	15	R	F	0	1861.915	2	6.29E-08	145.86	NaN	NaN	0
835	RPASRR	sp|Q99KX1|MLF2_MOUSE	yes	no	52	57	6	T	M	2	741.436	2	9.83E-02	10.92	NaN	NaN	0
836	RSAEDGPR	sp|E9PZQ0|RYR1_MOUSE	yes	yes	1753	1760	8	G	R	1	886.426	2	1.16E-01	27.25	NaN	NaN	0
837	SAAEEVDGLGVVR	sp|Q9JKF1|IQGA1_MOUSE	yes	yes	2	14	13	M	P	0	1300.662	2	1.01E-02	62.09	NaN	NaN	0
838	SAAEEVDGLGVVRPHYGSVLDNE	sp|Q9JKF1|IQGA1_MOUSE	yes	yes	2	25	24	M	L	1	2568.257	3	1.21E-19	149.07	NaN	NaN	0
839	SAASGGFQPR	sp|O35130|NEP1_MOUSE	yes	yes	2	11	10	M	E	0	976.473	2	1.41E-02	101.38	NaN	NaN	0
840	SADAAAGEPLPR	sp|P70441|NHRF1_MOUSE	yes	yes	2	13	12	M	L	0	1153.573	2	8.38E-07	112.84	NaN	NaN	0
841	SAFNLLHLVTKSQPVAPR	sp|Q8BU85|MSRB3_MOUSE	yes	yes	69	86	18	M	A	0	1977.116	3	6.67E-16	141.07	1.07	1.02	5
842	SAGGDFGNPLR	sp|P61294|RAB6B_MOUSE	yes	no	2	12	11	M	K	0	1089.520	2	6.68E-03	126.19	NaN	NaN	0
843	SAHLQWMVVR	sp|P41105|RL28_MOUSE	yes	yes	2	11	10	M	N	0	1225.639	2	1.37E-05	160.53	0.68	0.65	1
844	SALKAVFQYIDENQDR	sp|Q9D1A2|CNDP2_MOUSE	yes	yes	2	17	16	M	Y	0	1895.938	2;3	2.10E-11	143.46	1.16	1.02	7
845	SALLEQKEQQER	sp|Q5SUE8-2|ANR40_MOUSE	yes	no	2	13	12	M	L	0	1457.747	2	3.05E-03	86.77	0.98	0.85	6
846	SALQIQNVNWQVPMNR	sp|Q08189|TGM3_MOUSE	yes	yes	2	17	16	M	R	0	1896.963	2;3	5.68E-15	177.88	NaN	NaN	0
847	SAMEAADVFHR	sp|Q8BFS6-3|CPPED_MOUSE	yes	no	2	12	11	M	A	0	1232.561	2	9.05E-15	189.57	NaN	NaN	0
848	SAPEGLGDAHGDADR	sp|P58137|ACOT8_MOUSE	yes	yes	2	16	15	M	G	0	1466.639	2	3.37E-06	103.60	NaN	NaN	0
849	SAPMPAVVPAAR	sp|P97823-2|LYPA1_MOUSE	yes	no	7	18	12	M	K	0	1165.628	2	1.60E-02	62.47	NaN	NaN	0
850	SASGAVQPGHPGAAVGPSPAAA/	sp|Q62384|ZPR1_MOUSE	yes	yes	2	33	32	M	P	0	2853.452	3	2.26E-02	27.42	NaN	NaN	0
851	SASVVSVISR	sp|P61804|DAD1_MOUSE	yes	yes	2	11	10	M	F	0	1003.566	2	1.37E-02	99.28	NaN	NaN	0
852	SATSVDPQR	sp|P59326|YTHD1_MOUSE	yes	yes	2	10	9	M	T	0	959.467	2	5.81E-02	64.65	NaN	NaN	0
853	SCESCLPALSCR	sp|Q9D646|KRT34_MOUSE	yes	no	2	13	12	M	T	0	1438.600	2	5.52E-10	173.72	NaN	NaN	0
854	SCQISCR	sp|Q3TTY5|K22E_MOUSE	yes	no	2	8	7	M	S	0	909.380	2	6.71E-03	161.11	NaN	NaN	0
855	SDAAVDTSSEITTKDLKEKKEVVEE	sp|P26350|PTMA_MOUSE	yes	yes	2	31	30	M	D	0	3277.616	5	2.64E-03	44.16	0.69	0.66	1
856	SDFDEFER	sp|P26369|U2AF2_MOUSE	yes	yes	2	9	8	M	Q	0	1043.420	2	4.42E-02	94.85	NaN	NaN	0
857	SDFDSNPFADPDLNNPFKDPSVT(	sp|Q8K021|SCAM1_MOUSE	yes	yes	2	28	27	M	N	0	3022.395	3	7.82E-13	105.35	1.26	1.10	7
858	SDGVIKVFNDMKVR	sp|P18760|COF1_MOUSE	yes	yes	8	21	14	V	K	0	1606.850	2	2.69E-07	134.88	1.01	0.99	4
859	SDHGDVSLPPQDR	sp|Q9CQ26|STABP_MOUSE	yes	yes	2	14	13	M	V	0	1421.654	2	3.18E-03	74.48	NaN	NaN	0
860	SDILPLDVIGR	sp|Q8CIV8|TBCE_MOUSE	yes	yes	2	12	11	M	R	0	1196.677	2	1.49E-02	75.42	NaN	NaN	0
861	SDKLPYKVADIGLAAWGR	sp|P50247|SAHH_MOUSE	yes	yes	2	19	18	M	K	0	1959.058	2;3	9.10E-04	73.14	0.94	0.95	8
862	SDKSDLKAELER	sp|O88485-2|DC1I1_MOUSE	yes	no	2	13	12	M	K	0	1389.710	2;3	2.93E-02	60.16	1.18	0.78	9
863	SDNGELEDKPPAPPVR	sp|Q8CIN4|PAK2_MOUSE	yes	yes	2	17	16	M	M	0	1719.843	2;3	2.65E-08	121.82	1.30	1.14	11
864	SDQQLDCALDLMR	sp|P47757-2|CAPZB_MOUSE	yes	no	2	14	13	M	R	0	1563.702	2	1.04E-03	81.90	NaN	NaN	0
865	SDSEKLNLDSIIGR	sp|P62137|PP1A_MOUSE	yes	yes	2	15	14	M	L	0	1545.800	2	4.27E-35	214.45	1.16	1.02	10
866	SDSLVVCEVDPELKETLR	sp|Q9ERL7|GMFG_MOUSE	yes	yes	2	19	18	M	K	0	2088.041	2	1.62E-06	96.14	1.03	0.98	6
867	SDTAVADTR	sp|O70493|SNX12_MOUSE	yes	yes	2	10	9	M	R	0	934.436	2	9.61E-03	119.68	NaN	NaN	0
868	SDTPASTFGGR	sp|Q8BH61|F13A_MOUSE	yes	yes	2	12	11	M	R	0	1094.499	2	9.29E-03	94.47	NaN	NaN	0
869	SDVGEFRAVTELGR	sp|P04231|HB23_MOUSE	yes	no	37	50	14	D	P	1	1534.774	2	3.98E-02	47.71	NaN	NaN	0
870	SEAFDCAKCNESLYGR	sp|Q9R059|FHL3_MOUSE	yes	yes	2	17	16	M	K	0	1905.799	2	1.68E-15	153.23	1.01	0.87	8
871	SEAPPLVNEDVKR	sp|Q91YQ5|RPN1_MOUSE	yes	yes	27	39	13	S	T	0	1452.757	2	2.41E-05	121.56	1.55	1.05	4
872	SEDSSALPWSINR	sp|Q6P9R2|OXSR1_MOUSE	yes	yes	2	14	13	M	D	0	1460.690	2	3.62E-04	129.37	NaN	NaN	0
873	SEGDSVGDSVHGKPSVVYR	sp|Q9CQU3|RER1_MOUSE	yes	yes	2	20	19	M	F	0	1973.944	3	7.18E-02	41.29	1.40	1.03	6
874	SEKFDCHYCR	sp|P97447-2|FHL1_MOUSE	yes	no	2	11	10	M	D	0	1400.560	3	1.07E-03	117.09	0.90	0.86	5
875	SEPELKLVAR	sp|P08030|APT_MOUSE	yes	yes	2	11	10	M	R	0	1140.650	2	6.79E-06	138.76	1.22	1.12	10
876	SEPGGGEDGSAGLEVSAVQNVAE	sp|Q9JHU4|DYHC1_MOUSE	yes	yes	2	33	32	M	K	0	3188.606	3	1.74E-02	30.60	2.20	1.53	1
877	SEQSICQAR	sp|P70429-2|EVL_MOUSE	yes	no	2	10	9	M	A	0	1077.487	2	2.25E-05	158.76	NaN	NaN	0
878	SESGHSQPGLYGIER	sp|Q9DB90-2|SMG9_MOUSE	yes	no	2	16	15	M	R	0	1615.759	2	6.53E-02	42.24	NaN	NaN	0
879	SESLVVCDVAEDLVEKLR	sp|Q9CQJ3|GMFB_MOUSE	yes	yes	2	19	18	M	K	0	2060.046	2	1.66E-20	165.90	1.27	1.00	4
880	SETVICSSR	sp|P70460|VASP_MOUSE	yes	yes	2	10	9	M	A	0	1037.481	2	1.11E-02	116.52	NaN	NaN	0
881	SFHLPVNSR	sp|Q9D1D4|TMEDA_MOUSE	yes	yes	33	41	9	I	K	0	1055.551	2	1.22E-02	102.07	NaN	NaN	0
882	SFLKSFPPPGSADGLR	sp|Q61189|ICLN_MOUSE	yes	yes	2	17	16	M	L	0	1674.873	2	5.27E-05	83.37	1.01	0.97	5
883	SFLVSKPER	sp|Q3UUJ4|STRAA_MOUSE	yes	yes	2	10	9	M	I	0	1061.587	2	2.83E-03	115.78	1.87	1.62	4
884	SFSSSSFGGGLGSGFGGR	sp|Q61781|K1C14_MOUSE	no	no	67	84	18	G	F	0	1649.743	2	5.39E-03	56.82	NaN	NaN	0
885	SGDHLHNDSQIEADFR	sp|Q04750|TOP1_MOUSE	yes	yes	2	17	16	M	L	0	1839.814	3	5.17E-08	143.88	NaN	NaN	0
886	SGEDEQQEQTIAEDLVVTKYKMG	sp|P50580|PA2G4_MOUSE	yes	yes	2	30	29	M	V	0	3223.530	3	3.15E-06	73.68	1.22	0.87	11
887	SGEDVPHR	sp|Q9CR00|PSMD9_MOUSE	yes	yes	2	9	8	M	A	0	895.415	2	2.51E-03	141.39	NaN	NaN	0
888	SGEGENPASKPTPVQDVQGDGR	sp|Q61205|PA1B3_MOUSE	yes	yes	2	23	22	M	W	0	2224.036	2;3	9.41E-35	184.35	1.22	1.03	14
889	SGEVPPNINIKEPR	sp|Q99JR1|SFXN1_MOUSE	yes	yes	2	15	14	M	W	0	1548.826	2	1.88E-02	60.16	1.45	1.00	5
890	SGFSSEER	sp|Q9D819|IPYR_MOUSE	yes	yes	2	9	8	M	A	0	897.383	2	4.52E-02	93.17	NaN	NaN	0
891	SGGEVVCSGWLR	sp|Q9QYY0|GAB1_MOUSE	yes	yes	2	13	12	M	K	0	1305.614	2	3.46E-03	108.56	0.09	0.09	1
892	SGGKYVDSEGHLYTVPIR	sp|P49817|CAV1_MOUSE	yes	yes	2	19	18	M	E	0	1976.996	2;3	1.70E-10	115.63	1.29	0.94	19
893	SGGLLKALR	sp|Q9CQ49|NCBP2_MOUSE	yes	yes	2	10	9	M	S	0	913.571	2	1.84E-09	164.68	1.17	0.88	17
894	SGLSHLESEGCR	sp|Q3TTL0|CC038_MOUSE	yes	yes	2	13	12	M	N	0	1330.594	2	3.36E-03	89.66	NaN	NaN	0
895	SGLVLGQR	sp|Q9DBS5|KLC4_MOUSE	yes	yes	2	9	8	M	D	0	828.482	2	3.21E-02	104.75	NaN	NaN	0
896	SGNNLSGNDEFDEQLR	sp|Q8BGC0-2|HTSF1_MOUSE	yes	no	2	17	16	M	M	0	1793.782	2	3.24E-04	73.28	NaN	NaN	0
897	SGPGGLHADLLR	sp|Q8BWF0|SSDH_MOUSE	yes	yes	37	48	12	A	G	0	1191.636	2	3.34E-03	108.32	NaN	NaN	0
898	SGPTTDTPAAIQICR	sp|Q91V12-2|BACH_MOUSE	yes	no	2	16	15	M	I	0	1586.772	2	1.06E-05	85.84	NaN	NaN	0
899	SGTLAKIAEIEAEMAR	sp|P32233|DRG1_MOUSE	yes	yes	2	17	16	M	T	0	1688.877	2;3	3.67E-11	136.34	1.19	0.99	8
900	SGVAVSDGVIKVFNDMKVR	sp|P18760|COF1_MOUSE	yes	yes	3	21	19	A	K	0	2020.078	2;3	6.35E-06	82.88	0.89	0.87	7
901	SGVQVADEVCR	sp|Q9R0P5|DEST_MOUSE	yes	yes	3	13	11	A	I	0	1218.566	2	9.34E-03	117.09	NaN	NaN	0
902	SGYTPDEKLR	sp|Q3UIU2|NDUB6_MOUSE	yes	yes	2	11	10	M	L	0	1164.578	2	4.08E-04	128.01	1.21	0.96	9
903	SHPSWLPPKSTGEPLGHVPAR	sp|Q8BFW7-3|LPP_MOUSE	yes	no	2	22	21	M	M	0	2249.171	4	7.91E-04	64.71	0.98	0.93	6
904	SHQTGIQASEDVKEIFAR	sp|Q91YR1|TWF1_MOUSE	yes	yes	2	19	18	M	A	0	2015.007	3	6.01E-16	142.26	1.12	1.03	7
905	SHTILLVQPTKRPEGR	sp|P84089|ERH_MOUSE	yes	yes	2	17	16	M	T	1	1831.043	3;4	2.09E-08	124.62	1.01	0.94	17
906	SHYSSYYGGLGYGYGSFGGPGCG(	sp|Q925H6|KR193_MOUSE	yes	yes	2	29	28	M	R	0	2979.234	2;3	8.82E-43	197.54	NaN	NaN	0
907	SIEKIWAR	sp|P17183|ENOG_MOUSE	yes	yes	2	9	8	M	E	0	1001.566	2	5.77E-05	148.52	0.94	0.89	6
908	SIETLLEAAR	sp|O08789|MNT_MOUSE	yes	yes	2	11	10	M	F	0	1101.603	2	1.58E-02	82.42	NaN	NaN	0
909	SIFTPTNQIR	sp|P70122|SBDS_MOUSE	yes	yes	2	11	10	M	L	0	1175.630	2	2.21E-02	76.94	NaN	NaN	0
910	SIGVPIKVLHEAEGHIVTCETNTGE	sp|P62320|SMD3_MOUSE	yes	yes	2	29	28	M	G	0	3107.571	4	6.01E-06	71.30	0.96	0.92	3
911	SIHFSSR	sp|Q9DCV7|K2C7_MOUSE	yes	no	2	8	7	M	S	0	832.419	2	2.16E-02	116.90	NaN	NaN	0
912	SILYVSPHPDAFPSLR	sp|Q9Z1Q9|SYVC_MOUSE	yes	yes	2	17	16	M	A	0	1797.941	2;3	9.56E-16	171.46	255.04	246.09	1
913	SIQRNMSAMER	sp|Q9R0Q6|ARC1A_MOUSE	yes	yes	292	302	11	Q	F	1	1321.623	2	1.27E-02	77.66	NaN	NaN	0
914	SKQQPTQFINPETPGYVGFANLP	sp|P42208|SEPT2_MOUSE	yes	yes	2	29	28	M	K	0	3166.595	3	6.94E-19	118.63	1.14	0.86	10
915	SKSESPKEPEQLR	sp|P49312-2|ROA1_MOUSE	yes	no	2	14	13	M	K	0	1513.774	2;3	2.10E-08	150.05	1.20	0.98	18
916	SKSFQQSSLGR	sp|Q8K310|MATR3_MOUSE	yes	yes	2	12	11	M	D	0	1223.626	2	7.39E-16	179.67	1.32	0.97	9
917	SKTEELNR	sp|Q61781|K1C14_MOUSE	no	no	314	321	8	F	E	0	975.499	2	1.36E-04	142.43	5.73	3.82	4
918	SLALNDLLICCR	sp|Q62388|ATM_MOUSE	yes	yes	2	13	12	M	Q	0	1446.732	2	3.25E-03	98.11	NaN	NaN	0
919	SLAPVNIFKAGADEER	sp|P80314|TCPB_MOUSE	yes	yes	5	20	16	L	A	0	1715.884	2	5.82E-04	66.83	1.29	0.78	1
920	SLDIQCEQLSDAR	sp|Q91VI7|RINI_MOUSE	yes	yes	2	14	13	M	W	0	1533.709	2	2.83E-03	75.59	NaN	NaN	0
921	SLGGVSEASR	sp|P35175|CYT1_MOUSE	yes	yes	2	11	10	M	A	0	961.483	2	1.18E-12	195.51	NaN	NaN	0
922	SLHQFLLEPITCHAWNR	sp|Q9R0Q6|ARC1A_MOUSE	yes	yes	2	18	17	M	D	0	2121.058	3	3.37E-15	174.87	NaN	NaN	0

923	SLICSISNEVPEHPCVSPVSNHVYE	sp|Q99KP6|PRP19_MOUSE	yes	no	2	27	26	M	R	0	3008.412	3;4	7.81E-18	115.01	NaN	NaN	0
924	SLKDLEGKWR	sp|Q05816|FABP5_MOUSE	yes	yes	3	12	10	A	L	0	1230.672	2	1.40E-06	150.06	0.91	0.90	9
925	SLKPQPQPPAPATGR	sp|O70305-3|ATX2_MOUSE	yes	no	152	166	15	M	K	0	1543.847	2	1.84E-06	109.07	1.46	1.39	3
926	SLQMIVENVKLAR	sp|Q9WV86|KTNA1_MOUSE	yes	yes	2	14	13	M	E	0	1499.849	2	1.71E-05	125.53	1.16	0.97	5
927	SLVDLGKR	sp|P81069-2|GABP2_MOUSE	yes	no	2	9	8	M	L	0	886.524	2	2.19E-02	101.25	1.17	0.90	8
928	SLVIKNLQR	sp|Q8CAV0|YBEY_MOUSE	yes	yes	2	10	9	M	V	0	1069.661	2	8.95E-02	59.35	0.81	0.79	1
929	SLWVDKYR	sp|Q8R323|RFC3_MOUSE	yes	yes	2	9	8	M	P	0	1065.561	2	1.05E-02	114.28	1.55	1.36	7
930	SMHTEAAEVLLER	sp|Q8QZS1|HIBCH_MOUSE	yes	yes	29	41	13	M	R	0	1484.729	2	8.68E-04	97.63	NaN	NaN	0
931	SMILSASVIR	sp|Q8BH47|SC22A_MOUSE	yes	yes	2	11	10	M	V	0	1075.606	2	1.17E-02	64.82	NaN	NaN	0
932	SMNKGPTLLDGDLPEQENVLQR	sp|Q8CGN5-4|PLIN1_MOUSE	yes	no	2	23	22	M	V	0	2453.222	2;3	1.42E-06	88.09	0.98	0.66	9
933	SNGYEDHMAEDCR	sp|P70372|ELAV1_MOUSE	yes	yes	2	14	13	M	D	0	1582.578	2	7.92E-05	141.00	NaN	NaN	0
934	SNGYEDHMAEDCRDDIGR	sp|P70372|ELAV1_MOUSE	yes	yes	2	19	18	M	T	1	2138.838	3	4.03E-11	126.84	NaN	NaN	0
935	SNISSIVNR	sp|P47739|AL3A1_MOUSE	yes	yes	2	10	9	M	A	0	988.530	2	5.26E-03	128.27	NaN	NaN	0
936	SNLNLKPGECLKVR	sp|P16045|LEG1_MOUSE	yes	yes	8	21	14	A	G	0	1626.888	2	7.82E-04	84.75	0.92	0.90	8
937	SNRPNNNPGGSLR	sp|G5E870|TRIPC_MOUSE	yes	yes	2	14	13	M	R	1	1381.681	2	1.80E-03	78.81	NaN	NaN	0
938	SNYSVSLVGPAPWGFR	sp|Q8CI51-3|PDLI5_MOUSE	yes	no	2	17	16	M	L	0	1735.868	2	7.08E-04	63.68	NaN	NaN	0
939	SPANLPAVLLQPR	sp|Q61191|HCFC1_MOUSE	yes	yes	6	18	13	V	W	0	1374.798	2	8.86E-04	107.09	NaN	NaN	0
940	SQAEFDKAAEEVKR	sp|P31786|ACBP_MOUSE	yes	yes	2	15	14	M	L	0	1606.795	3	7.82E-04	84.75	1.04	1.03	6
941	SQENLKIKGGLSEAR	sp|P35173|CYT3_MOUSE	yes	yes	2	16	15	M	P	0	1628.885	2;3	1.17E-08	131.40	1.15	1.05	19
942	SQERPTFYR	sp|P47811-2|MK14_MOUSE	yes	no	2	10	9	M	Q	1	1182.578	2	1.20E-06	169.76	NaN	NaN	0
943	SQGDSNPAAIPHAAEDIQGDDR	sp|Q61206|PA1B2_MOUSE	yes	yes	2	23	22	M	W	0	2263.010	2;3	2.44E-22	165.38	NaN	NaN	0
944	SQLQMKLLR	sp|Q8K363|DDX18_MOUSE	yes	yes	2	10	9	M	R	0	1115.649	2	1.57E-03	119.68	1.13	0.90	9
945	SQPGPKPAASPR	sp|P51125-3|ICAL_MOUSE	yes	no	2	13	12	M	P	0	1191.636	2	1.20E-02	68.00	0.38	0.30	3
946	SQWAGPLCLQEVDEPPQHALR	sp|P70296|PEBP1_MOUSE	yes	yes	6	26	21	I	V	0	2430.175	2	2.92E-16	158.00	NaN	NaN	0
947	SRPCGLPEPVR	sp|Q99P30-5|NUDT7_MOUSE	yes	no	2	12	11	M	N	1	1266.650	2	7.53E-02	49.45	NaN	NaN	0
948	SSAPTTPPSVDKVDGFSR	sp|Q61151|2A5E_MOUSE	yes	yes	2	19	18	M	K	0	1846.906	2	3.22E-12	121.82	1.31	1.11	8
949	SSEEGKLFVGGLNFNTDEQALEDF	sp|O89086|RBM3_MOUSE	yes	yes	2	41	40	M	E	0	4382.134	5	1.56E-11	74.08	1.19	1.04	3
950	SSEELACKLQR	sp|Q9D4J1|EFHD1_MOUSE	yes	yes	2	12	11	M	R	0	1319.650	2	2.15E-33	172.17	0.77	0.73	8
951	SSEPPPPPLQPPTHQTSVGLLDTP	sp|Q9CR86|CHSP1_MOUSE	yes	yes	2	26	25	M	T	0	2647.361	2;3	1.59E-03	52.90	NaN	NaN	0
952	SSFGYDPYFSTSYKR	sp|P08551|NFL_MOUSE	yes	yes	2	16	15	M	R	0	1803.810	2	1.26E-15	162.37	1.36	1.06	10
953	SSGALLPKPQMR	sp|Q9CPQ1|COX6C_MOUSE	yes	yes	2	13	12	M	G	0	1283.702	2	8.68E-05	126.19	2.35	1.49	8
954	SSGGVCGIGGGYGGSFSSSSFGGG	sp|Q9Z2K1|K1C16_MOUSE	yes	no	53	84	32	F	F	0	2815.226	2	9.97E-12	85.94	2.98	1.92	3
955	SSIGTGYDLSASTFSPDGR	sp|O70435|PSA3_MOUSE	yes	yes	2	20	19	M	V	0	1916.875	2	4.13E-03	56.72	NaN	NaN	0
956	SSIKVECVLR	sp|Q64374|RGN_MOUSE	yes	yes	2	11	10	M	E	0	1189.649	2	6.61E-06	100.93	0.94	0.81	4
957	SSILPFTPPIVKR	sp|Q8BUN5|SMAD3_MOUSE	yes	yes	2	14	13	M	L	0	1453.866	2	3.08E-05	117.79	1.08	0.85	8
958	SSILPFTPPVVKR	sp|Q62432-2|SMAD2_MOUSE	yes	no	2	14	13	M	L	0	1439.850	2	7.24E-04	96.82	0.75	0.69	7
959	SSKSMVLGYWDIR	sp|P48774|GSTM5_MOUSE	yes	yes	2	14	13	M	G	0	1540.771	2	7.81E-09	118.52	1.17	1.12	6
960	SSNECFKCGR	sp|P53996-2|CNBP_MOUSE	yes	no	2	11	10	M	S	0	1243.507	2	3.57E-30	211.64	1.04	0.96	9
961	SSQSHPDGLSGR	sp|Q6NZM9|HDAC4_MOUSE	yes	yes	2	13	12	M	D	0	1226.564	2	2.87E-03	88.08	19.21	17.00	4
962	SSSASAANGNDSKKFKGDNR	sp|P17225|PTBP1_MOUSE	yes	yes	32	51	20	M	S	0	2039.962	3;4	4.03E-04	75.55	1.02	0.60	5
963	SSTQFNKGPSYGLSAEVKNR	sp|Q08093|CNN2_MOUSE	yes	yes	2	21	20	M	L	0	2169.081	3	6.32E-03	56.12	1.31	1.08	6
964	SSVAVLTQESFAEHR	sp|Q8VDJ3|VIGLN_MOUSE	yes	yes	2	16	15	M	S	0	1659.822	2;3	4.66E-29	216.27	15.11	13.24	2
965	SSVKLWPTGASAVPLVSR	sp|Q9QZL0|RIPK3_MOUSE	yes	yes	2	19	18	M	E	0	1854.036	2	2.19E-06	94.96	1.85	1.73	7
966	SSVSPIQIPSR	sp|Q9DBN5-2|LONP2_MOUSE	yes	no	2	12	11	M	L	0	1169.640	2	1.33E-02	77.06	NaN	NaN	0
967	STEVEAAVNR	sp|P49945|FRIL2_MOUSE	yes	no	10	19	10	Y	L	0	1074.531	2	1.60E-01	41.40	1.59	1.53	3
968	STGTFVVSQPLNYR	sp|Q9JLJ2|AL9A1_MOUSE	yes	yes	2	15	14	M	G	0	1567.800	2	4.25E-04	91.62	NaN	NaN	0
969	STGVPSGSSAATGSNR	sp|P63024|VAMP3_MOUSE	yes	yes	2	17	16	M	R	0	1434.670	2	6.53E-06	86.49	NaN	NaN	0
970	STGVPSGSSAATGSNRR	sp|P63024|VAMP3_MOUSE	yes	yes	2	18	17	M	L	1	1590.771	2	2.68E-06	88.71	NaN	NaN	0
971	STKTTIKSQTSHR	sp|P50446|K2C6A_MOUSE	yes	no	2	14	13	M	G	0	1473.790	4	1.45E-03	86.94	1.68	1.11	4
972	STLLIHHPQYAWLQDLGLR	sp|Q9DBF1-2|AL7A1_MOUSE	yes	no	2	20	19	M	E	0	2260.212	2;3	1.26E-20	183.45	NaN	NaN	0
973	STNENANLPAAR	sp|P52293|IMA1_MOUSE	yes	yes	2	13	12	M	L	0	1256.611	2	3.25E-03	98.11	NaN	NaN	0
974	STNTDLSLSSYDEGQGSKFIR	sp|Q9JLR9|HIG1A_MOUSE	yes	yes	2	22	21	M	K	0	2304.087	2	1.09E-13	132.14	1.95	1.30	4
975	STPGKENFR	sp|Q60960|IMA5_MOUSE	yes	yes	2	10	9	M	L	0	1034.515	2	6.99E-05	123.79	1.30	0.96	8
976	STTTGPEAAPKPSAKSIYEQR	sp|Q8R5F8|ES8L1_MOUSE	yes	yes	2	22	21	M	K	0	2218.123	3	9.11E-02	27.13	1.12	0.99	4
977	STTTVPELKQISR	sp|Q8VHN8-3|SDOS_MOUSE	yes	no	2	14	13	M	E	0	1458.804	2	5.07E-04	100.22	1.48	1.10	10
978	SVKPYTNFDAER	sp|P07356|ANXA2_MOUSE	yes	yes	26	37	12	G	D	0	1425.689	2	2.64E-05	132.51	1.93	1.29	9
979	SVLSGLASEPR	sp|Q3UB74|TBRG1_MOUSE	yes	yes	2	12	11	M	T	0	1114.598	2	4.09E-02	59.20	NaN	NaN	0
980	SVPAFIDISEEDQAAELR	sp|Q99JX4|EIF3M_MOUSE	yes	yes	2	19	18	M	A	0	1988.969	2	1.01E-12	147.17	NaN	NaN	0
981	SVQVAAPGSTGLGPER	sp|Q91W40|KLC3_MOUSE	yes	yes	2	17	16	M	L	0	1524.790	2	2.28E-02	48.90	NaN	NaN	0
982	SVTLQTVLYSLQEEQAR	sp|Q9D8C4|IN35_MOUSE	yes	yes	2	18	17	M	L	0	1964.022	2	1.85E-02	47.55	NaN	NaN	0
983	SYDYHQSWSR	sp|Q8VHK9|DHX36_MOUSE	yes	yes	2	11	10	M	D	0	1327.558	2	9.42E-04	145.91	NaN	NaN	0
984	SYINLPTVLPSSPSKTR	sp|P04184|KITH_MOUSE	yes	yes	2	18	17	M	G	0	1859.015	2	1.69E-05	90.35	1.43	1.31	7
985	SYQGKKNIPR	sp|Q62188|DPYL3_MOUSE	yes	no	2	11	10	M	I	0	1189.657	2;3	8.27E-03	94.31	1.06	0.95	8
986	SYTCNSGNYSSQSFGGFLR	sp|Q9QZU5|KR151_MOUSE	yes	yes	2	20	19	M	Q	0	2130.907	2;3	3.95E-20	173.37	NaN	NaN	0
987	SYTLDSLGNPSAYR	sp|P08553|NFM_MOUSE	yes	yes	2	15	14	M	R	0	1542.731	2	1.93E-02	56.57	NaN	NaN	0
988	SYTPGIGGDSAQLAQR	sp|O70439|STX7_MOUSE	yes	yes	2	17	16	M	I	0	1619.790	2	4.12E-04	71.08	NaN	NaN	0
989	SYYSGYSGGLGYGYGGFGGLGCG	sp|Q8C1I6|KR163_MOUSE	yes	yes	2	29	28	M	R	0	2885.217	3	4.08E-27	140.57	NaN	NaN	0
990	SYYSGYSGGLGYGYGSSFGGLGCG	sp|Q925I0|KR192_MOUSE	yes	yes	2	30	29	M	R	0	3002.260	2;3	3.92E-36	180.88	NaN	NaN	0
991	TAAAPSQQRPAAAR	sp|Q9D0F6|RFC5_MOUSE	yes	yes	2	15	14	M	A	1	1394.738	2	4.44E-04	88.10	NaN	NaN	0
992	TAANNKFCFDFFR	sp|Q9D7P9|SPB12_MOUSE	yes	yes	5	17	13	L	E	0	1636.746	2	5.42E-08	145.43	1.31	1.17	3
993	TAGKHGDSVR	sp|P04104|K2C1_MOUSE	yes	yes	391	400	10	I	N	0	1026.521	2	1.62E-02	112.64	6.25	4.18	1
994	TAIIKEIVSR	sp|O08586|PTEN_MOUSE	yes	yes	2	11	10	M	N	0	1128.687	2	8.72E-10	162.68	1.24	1.05	9
995	TATLRPYLSAVR	sp|P59999|ARPC4_MOUSE	yes	yes	2	13	12	M	A	1	1346.767	2	3.28E-10	179.59	NaN	NaN	0
996	TCGSGFCGR	sp|Q9ERE2|KRT81_MOUSE	yes	yes	2	10	9	M	A	0	1000.386	2	1.47E-02	95.50	NaN	NaN	0
997	TCNSGNYSSQSFGGFLR	sp|Q9QZU5|KR151_MOUSE	yes	yes	4	20	17	Y	Q	0	1880.811	2	3.59E-06	82.88	NaN	NaN	0
998	TDAAVSFAKDFLAGGVAAAISKTA	sp|P51881|ADT2_MOUSE	yes	yes	2	31	30	M	V	0	2946.582	3;4	3.41E-11	81.53	NaN	NaN	0
999	TDDKDVLR	sp|Q99J83|ATG5_MOUSE	yes	yes	2	9	8	M	D	0	960.488	2	2.29E-02	100.02	1.37	1.09	1
1000	TDYGEEQR	sp|Q9CQK7|RWDD1_MOUSE	yes	yes	2	9	8	M	N	0	996.415	2	4.87E-02	87.48	NaN	NaN	0
1001	TEELITPVYCTGVSAQVQKKR	sp|O35350|CAN1_MOUSE	yes	yes	2	22	21	M	D	0	2406.258	3	5.41E-04	70.09	1.16	1.13	9
1002	TELQSALLLR	sp|P62254|UB2G1_MOUSE	yes	yes	2	11	10	M	R	0	1142.666	2	3.21E-03	133.81	NaN	NaN	0
1003	TENSTSAPAAKPKR	sp|P10922|H10_MOUSE	yes	yes	2	15	14	M	A	0	1456.763	3	2.03E-04	102.73	1.15	0.74	4
1004	TEQMTLR	sp|P68040|GBLP_MOUSE	yes	yes	2	8	7	M	G	0	877.433	2	1.93E-02	133.12	NaN	NaN	0
1005	TETDGFYKSR	sp|O08738|CASP6_MOUSE	yes	yes	2	11	10	M	E	0	1202.557	2	4.04E-30	209.97	1.01	0.95	5
1006	TEVLNRIQFR	sp|Q924Z6-2|XPO6_MOUSE	yes	no	455	464	10	L	Y	1	1274.710	2	7.29E-02	56.26	0.83	0.79	5
1007	TGDAGASATFPMQCSALR	sp|P63242|IF5A1_MOUSE	yes	yes	9	26	18	E	K	0	1839.824	2	2.38E-12	139.88	NaN	NaN	0
1008	THSVTLR	sp|P70271|PDLI4_MOUSE	yes	yes	2	8	7	M	G	0	812.450	2	5.97E-02	108.00	NaN	NaN	0
1009	THWFHR	sp|Q8K2Q7-2|BROX_MOUSE	yes	no	2	7	6	M	N	0	882.425	3	7.24E-05	88.63	NaN	NaN	0
1010	TIIDAPGHR	sp|P10126|EF1A1_MOUSE	yes	no	88	96	9	V	D	0	978.525	2	5.48E-03	111.82	1.26	0.90	3
1011	TLKDLTR	sp|Q9QYK4|H6ST3_MOUSE	yes	yes	129	135	7	F	F	0	845.497	2	1.99E-02	106.60	1.15	0.83	6
1012	TLQLMER	sp|Q7TT37|ELP1_MOUSE	yes	yes	1263	1269	7	S	A	0	889.469	2	1.67E-02	117.40	0.91	0.87	5
1013	TLWSQAVPWR	sp|Q8BUL6|PKHA1_MOUSE	yes	yes	345	354	10	A	S	0	1242.651	3	1.60E-01	41.40	1.08	0.99	5
1014	TLYDAELSQLQQDVTDTNVILSMI	sp|Q3TTY5|K22E_MOUSE	yes	no	336	362	27	R	N	0	3095.472	3	1.80E-42	193.09	NaN	NaN	0
1015	TMFENVTR	sp|Q9EST1|GSDMA_MOUSE	yes	yes	2	9	8	M	A	0	996.470	2	3.15E-03	135.83	NaN	NaN	0
1016	TMLADHAAR	sp|Q6P5F9|XPO1_MOUSE	yes	yes	6	14	9	M	Q	0	984.481	2	2.94E-03	132.84	NaN	NaN	0
1017	TNYRPDWNR	sp|Q8VHC3|SELM_MOUSE	yes	yes	25	33	9	T	L	1	1220.569	2	4.51E-02	70.91	NaN	NaN	0
1018	TPIPQSGSPFPASVQDPGLHIWR	sp|P24452|CAPG_MOUSE	yes	yes	3	25	23	Y	V	0	2486.271	3	3.58E-06	71.15	NaN	NaN	0
1019	TQSLVCPDTVSR	sp|Q3TV70|NR2CA_MOUSE	yes	yes	2	13	12	M	V	0	1361.661	2	7.47E-03	73.93	NaN	NaN	0
1020	TSALENYINR	sp|Q6ZWM4|NAA38_MOUSE	yes	yes	2	11	10	M	T	0	1179.588	2	6.19E-18	211.64	NaN	NaN	0
1021	TSALTQGLER	sp|Q8CF66|LTOR4_MOUSE	yes	yes	2	11	10	M	I	0	1074.567	2	2.01E-03	138.25	NaN	NaN	0
1022	TSIHFVVHPLPGTEDQLNDR	sp|Q80TP3|UBR5_MOUSE	yes	yes	2	21	20	M	L	0	2274.139	3	5.62E-05	69.36	NaN	NaN	0
1023	TSMASLFSFTSPAVKR	sp|P97454|SMAD5_MOUSE	yes	yes	2	17	16	M	L	0	1728.887	2	2.90E-02	51.03	0.79	0.58	1
1024	TTKDPESEHPSVTLFR	sp|Q99JW2|ACY1_MOUSE	yes	yes	2	17	16	M	Q	0	1842.911	3	2.56E-02	52.86	1.06	1.00	5
1025	TTLTELR	sp|P05784|K1C18_MOUSE	yes	no	287	293	7	E	R	0	832.465	2	2.81E-02	104.21	1.97	1.33	4

1026	TTNTVPLHPYWPR	sp|P70245|EBP_MOUSE	yes	yes	2	14	13	M	H	0	1580.810	2	8.76E-05	139.78	NaN	NaN	0
1027	TTQGGLVANR	sp|Q9CZX9|EMC4_MOUSE	yes	yes	2	11	10	M	G	0	1015.541	2	1.57E-02	83.44	NaN	NaN	0
1028	TTQQIVLQGPGPWGFR	sp|O70400|PDLI1_MOUSE	yes	yes	2	17	16	M	L	0	1783.937	2	5.14E-08	143.93	NaN	NaN	0
1029	TTSGALFPSLVPGSR	sp|Q9JKV1|ADRM1_MOUSE	yes	yes	2	16	15	M	G	0	1488.794	2	3.44E-04	75.32	NaN	NaN	0
1030	TTSLLLHPR	sp|P50207|HXC13_MOUSE	yes	yes	2	10	9	M	W	0	1036.603	2	1.59E-02	93.65	NaN	NaN	0
1031	TTYLEFIQQNEER	sp|Q01405|SC23A_MOUSE	yes	yes	2	14	13	M	D	0	1669.795	2	8.77E-04	117.93	NaN	NaN	0
1032	VASNLNLKPGECLKVR	sp|P16045|LEG1_MOUSE	yes	yes	6	21	16	L	G	0	1796.993	2;3	3.72E-16	166.92	0.89	0.85	21
1033	VAVSDGVIKVFNDMKVR	sp|P18760|COF1_MOUSE	yes	yes	5	21	17	G	K	0	1876.024	2	1.69E-05	90.35	0.86	0.81	3
1034	VDELGCSHLGQSYESR	sp|P08121|CO3A1_MOUSE	yes	yes	28	43	16	N	D	0	1835.811	2	4.82E-04	69.33	NaN	NaN	0
1035	VDHLANTEINSQR	sp|Q3TB82|PKHF1_MOUSE	yes	yes	2	14	13	M	I	0	1495.738	2	8.56E-04	99.93	NaN	NaN	0
1036	VDNGSGMCKAGFAGDDAPR	sp|P60710|ACTB_MOUSE	yes	no	10	28	19	V	A	0	1923.820	2	7.16E-28	186.56	1.21	1.01	15
1037	VFSGVVSTGLKVR	sp|P58252|EF2_MOUSE	yes	yes	416	428	13	R	I	0	1347.787	3	5.75E-02	39.01	NaN	NaN	0
1038	VIDNGSGMCKAGFAGDDAPR	sp|P63260|ACTG_MOUSE	yes	yes	9	28	20	L	A	0	2036.904	2	9.01E-13	126.26	1.21	1.06	7
1039	VKVGVNGFGR	sp|P16858|G3P_MOUSE	yes	yes	2	11	10	M	I	0	1031.588	2	4.39E-03	105.98	1.15	1.05	8
1040	VNPTVFFDITADDEPLGR	sp|P17742|PPIA_MOUSE	yes	yes	2	19	18	M	V	0	2004.979	2;3	2.68E-15	154.49	NaN	NaN	0
1041	VQGASAGGLAADASR	sp|P11088|FILA_MOUSE	yes	yes	55	69	15	G	R	0	1329.664	2	1.00E-03	63.68	NaN	NaN	0
1042	VQISKKR	sp|P62908|RS3_MOUSE	yes	yes	3	9	7	A	K	0	857.545	2	2.28E-02	110.31	0.98	0.96	2
1043	VSDGVIKVFNDMKVR	sp|P18760|COF1_MOUSE	yes	yes	7	21	15	A	K	0	1705.919	2	2.20E-08	128.06	0.78	0.77	6
1044	VSPANLPAVLLQPR	sp|Q61191|HCFC1_MOUSE	yes	yes	5	18	14	A	W	0	1473.867	2	4.22E-04	92.30	NaN	NaN	0
1045	VSPHPDAFPSLR	sp|Q9Z1Q9|SYVC_MOUSE	yes	yes	6	17	12	Y	A	0	1321.678	2	2.65E-02	59.12	NaN	NaN	0
1046	VSSVLEVSHVFCCPNR	sp|Q91WG4-2|ELP2_MOUSE	yes	no	2	17	16	M	V	0	1888.892	2	1.68E-38	228.19	NaN	NaN	0
1047	VSVMNTVDTSHEDMIHDAQMD'	sp|Q9D1M0|SEC13_MOUSE	yes	yes	2	27	26	M	L	0	3014.285	3	2.47E-30	156.70	NaN	NaN	0
1048	VTIIDAPGHR	sp|P10126|EF1A1_MOUSE	yes	yes	87	96	10	Y	D	0	1077.593	2	1.38E-02	118.71	NaN	NaN	0
1049	VVDNGSGMCKAGFAGDDAPR	sp|P60710|ACTB_MOUSE	yes	no	9	28	20	L	A	0	2022.889	2	1.59E-27	180.86	1.08	0.99	13
1050	WAGPLCLQEVDEPPQHALR	sp|P70296|PEBP1_MOUSE	yes	yes	8	26	19	Q	V	0	2215.084	2	3.95E-20	173.37	NaN	NaN	0
1051	WIKFAAACR	sp|Q61495|DSG1A_MOUSE	yes	no	51	59	9	E	E	0	1121.580	2	2.18E-02	85.68	1.38	1.08	5
1052	YEALVETNRR	sp|Q9D646|KRT34_MOUSE	no	no	232	241	10	Q	E	1	1249.642	2	9.15E-04	146.11	NaN	NaN	0
1053	YILPNDIGVSSLDCR	sp|Q99KK7|DPP3_MOUSE	yes	yes	6	20	15	Q	E	0	1720.845	2	9.48E-02	39.00	NaN	NaN	0
1054	YKYIQELWR	sp|Q9CZM2|RL15_MOUSE	yes	yes	4	12	9	A	K	0	1297.682	2	3.42E-03	114.89	0.82	0.78	2
1055	YLTVAAVFR	sp|P99024|TBB5_MOUSE	yes	no	310	318	9	R	G	0	1038.586	2	5.70E-02	65.22	NaN	NaN	0
1056	YQGKKNIPR	sp|Q62188|DPYL3_MOUSE	yes	no	3	11	9	S	I	0	1102.625	2	3.89E-02	74.92	1.17	0.98	1
1057	YTCNSGNYSSQSFGGFLR	sp|Q9QZU5|KR151_MOUSE	yes	yes	3	20	18	S	Q	0	2043.875	2	9.69E-05	72.36	NaN	NaN	0
1058	YVSPHPDAFPSLR	sp|Q9Z1Q9|SYVC_MOUSE	yes	yes	5	17	13	L	A	0	1484.741	2	1.01E-04	137.84	NaN	NaN	0

ST1E Supplementary Table 1E: **Peptides identified by TAILS with a labeled N-terminus (i.e. dimethylated with heavy (+/+) or light (Adamts9-Und4/+) formaldehyde).**

Abbreviations: aa - amino acids; PEP - Posterior Error Probability; Score - Andromeda score for the best associated MS/MS spectrum; Ratio H/L - ratio between heavy and light label partners; NaN - non-quantifiable ratio.

Index	Sequence	Leading razor protein	Unique (Groups)	Unique (Proteins)	Start position	End position	Length (# aa)	Amino acid before	Amino acid after	Missed cleavages	Mass (Da)	Charges	PEP	Score	Ratio H/L	Ratio H/L normalized	Ratio H/L count
1	AAAGAAATDLEVVR	sp|Q6PD26|PIGS_MOUSE	yes	yes	2	15	14	M	G	0	1313.694	2	3.23E-04	90.41	1.66	1.03	4
2	AAAYCTGLLLAR	sp|P47962|RL5_MOUSE	yes	yes	96	107	12	Y	R	0	1278.675	2	4.31E-05	105.03	1.88	1.21	3
3	AAEKQIPGGGSGGGGSGSGGGGGGSGGGR	sp|Q8BMA6|SRP68_MOUSE	yes	yes	2	30	29	M	S	0	2229.012	3	7.73E-03	30.36	1.05	0.76	3
4	AAGVGEFEAGISKNGQTR	sp|P10126|EF1A1_MOUSE	yes	no	117	134	18	V	E	0	1790.891	3	7.12E-04	59.73	2.34	1.51	4
5	AANINKESIIDVEGVVR	sp|Q922B2|SYDC_MOUSE	yes	yes	105	121	17	F	K	0	1825.990	3	6.75E-11	114.63	4.26	2.97	1
6	AAPGVDLTQLLNNMR	sp|P02535-3|K1C10_MOUSE	yes	no	297	311	15	N	N	0	1611.840	2	3.31E-03	71.28	2.10	1.51	3
7	AAQASAAPKAGTATGR	sp|P56480|ATPB_MOUSE	yes	yes	47	62	16	Y	I	0	1427.748	3	7.94E-05	91.36	1.15	0.92	8
8	AASIFGGAKPVDTAAR	sp|Q8BGD9|IF4B_MOUSE	yes	yes	357	372	16	R	E	0	1530.815	3	4.68E-03	59.71	1.01	0.98	5
9	ADDDYDEPTDSLDAR	sp|Q8K0E8|FIBB_MOUSE	yes	yes	20	34	15	A	G	0	1696.670	2	8.69E-04	84.51	0.90	0.78	4
10	ADDLECTPGFQR	sp|Q9WTR5|CAD13_MOUSE	yes	yes	22	33	12	S	K	0	1407.609	2	1.58E-04	95.42	1.14	0.79	7
11	ADLSEAANR	sp|P20152|VIME_MOUSE	yes	yes	296	304	9	F	N	0	945.452	2	2.04E-02	217.64	6.04	4.31	1
12	AEALTQETDFLR	sp|Q9ERE2|KRT81_MOUSE	no	no	229	240	12	N	R	0	1392.689	2	1.74E-02	69.03	2.19	1.34	1
13	AEGQVLVLDGR	sp|P19253|RL13A_MOUSE	yes	yes	2	12	11	M	G	0	1155.625	2	2.32E-07	152.47	1.16	0.92	11
14	AEQLKALR	sp|Q5SUA5|MYO1G_MOUSE	yes	no	860	867	8	F	E	0	927.550	2	5.22E-02	59.60	NaN	NaN	0
15	AFLWAGGR	sp|Q8VEK3|HNRPU_MOUSE	yes	yes	293	300	8	F	A	0	876.461	2	3.75E-02	134.66	6.27	4.30	1
16	AFSCASACGPR	sp|Q9ERE2|KRT81_MOUSE	no	no	11	21	11	R	P	0	1182.491	2	1.43E-03	97.73	1.09	0.70	4
17	AGGEGGVTLGQPHLSR	sp|Q9ZDN1|IF2G_MOUSE	yes	yes	2	17	16	M	Q	0	1534.785	3	3.96E-20	168.41	1.34	1.10	9
18	AGSSSGSGVQGASAGGLAADASR	sp|P11088|FILA_MOUSE	yes	yes	47	69	23	R	R	0	1919.893	2	8.44E-37	144.50	0.84	0.81	3
19	AHEDPVEKVIEGFSR	sp|Q8CIT9-3|SBSN_MOUSE	yes	no	24	38	15	A	G	0	1711.853	2;3;4	4.56E-15	154.69	1.25	1.16	28
20	AHGSVVKSEDYAFPTYADR	sp|P19783|COX41_MOUSE	yes	yes	23	41	19	R	R	0	2111.991	3;4	6.65E-05	71.59	1.42	0.99	7
21	AHLDATTVLSR	sp|P56480|ATPB_MOUSE	yes	yes	377	387	11	F	A	0	1182.636	2	3.38E-05	118.28	2.63	1.75	3
22	AIPGLAGAGNSVLLVSNLNPER	sp|P17225|PTBP1_MOUSE	yes	yes	325	346	22	I	V	0	2161.186	3	4.26E-08	85.74	1.87	0.95	3
23	AIVFIKEPSSQDALQGR	sp|Q8BKG3|PTK7_MOUSE	yes	yes	23	39	17	A	R	0	1857.995	2;3	6.09E-18	134.14	1.36	0.97	16
24	AIYFKEQFLDGDAWTNR	sp|P14211|CALR_MOUSE	yes	yes	20	36	17	P	W	0	2072.996	3	2.10E-02	38.78	1.37	1.17	3
25	ALEAANYQDTIGR	sp|P20152|VIME_MOUSE	yes	yes	352	364	13	F	L	0	1420.695	2	9.20E-02	64.10	NaN	NaN	0
26	ALSFLSPSLSR	sp|Q64462|CP4B1_MOUSE	yes	yes	2	12	11	M	L	0	1176.650	2	2.78E-02	66.27	1.59	0.96	1
27	ALVCDNGSGLCKAGFAGDDAPR	sp|P63268|ACTH_MOUSE	yes	no	8	29	22	T	A	0	2250.016	2	1.09E-04	49.13	1.08	1.00	5
28	ANSIGEAVSGTAR	sp|Q63870|CO7A1_MOUSE	yes	yes	313	325	13	Y	T	0	1231.616	2	5.62E-03	75.76	5.24	3.60	3
29	APAGILNGKLVSAQIR	sp|Q922D8|C1TC_MOUSE	yes	yes	2	17	16	M	D	0	1606.952	3	2.77E-03	64.57	0.77	0.78	1
30	APAPPPAASFTPAEVQR	sp|Q5MPP0-2|FA2H_MOUSE	yes	no	2	18	17	M	R	0	1705.879	3	3.73E-03	58.72	1.50	0.91	3
31	APDQDEIDCLPGLAKQPSFR	sp|P16675|PPGB_MOUSE	yes	yes	24	43	20	A	Q	0	2256.085	3	1.36E-06	85.74	1.02	0.95	7
32	APKGGSKQQSEEDLLLQDFSR	sp|Q9DCF9-2|SSRG_MOUSE	yes	no	2	22	21	M	N	0	2332.166	4	1.70E-06	67.93	1.22	0.97	5
33	APKVTSELLR	sp|Q6P1B1|XPP1_MOUSE	yes	yes	2	11	10	M	Q	0	1112.655	2;3	2.20E-02	72.20	1.16	0.97	7
34	APLDLDKYVEIAR	sp|Q9CQR6|PPP6_MOUSE	yes	yes	2	14	13	M	Q	0	1501.814	2;3	1.73E-05	100.22	1.22	1.15	13
35	APNVLASEPEIPKGIR	sp|Q9WTP6-2|KAD2_MOUSE	yes	no	2	17	16	M	A	0	1689.941	3	8.99E-17	127.30	1.15	0.93	9
36	APPPLLPVAASTPILHGEFGSYPANGPR	sp|Q9JIA7|SPHK2_MOUSE	yes	yes	2	29	28	M	F	0	2825.486	4	1.42E-02	29.86	1.23	0.75	1
37	APQGTGLGFR	sp|P29699|FETUA_MOUSE	yes	yes	19	28	10	S	E	0	1002.525	2	1.57E-08	133.81	1.08	0.93	4
38	APSPLYSVEFSEEPFGVIVR	sp|P70699|LYAG_MOUSE	yes	yes	204	223	20	Q	R	0	2222.126	2;3	3.24E-17	116.60	1.29	1.11	6
39	APSQLALFSVSDKTGLVEFAR	sp|Q9CWJ9|PUR9_MOUSE	yes	yes	2	22	21	M	S	0	2235.190	2;3	6.13E-08	86.56	0.99	0.99	4
40	APSTPLLTVR	sp|Q8BJW6|EIF2A_MOUSE	yes	yes	2	11	10	M	G	0	1053.618	2	8.81E-03	92.54	1.05	0.99	6
41	APVEHVVADAGAFLR	sp|Q8BW10|NOB1_MOUSE	yes	yes	2	16	15	M	D	0	1550.821	3	4.37E-15	159.22	1.09	0.93	8
42	AQPADLLEMLDFHNLPSGVTKTTGFCATR	sp|O88207|CO5A1_MOUSE	yes	yes	37	65	29	A	R	0	3189.559	4	2.82E-02	25.51	0.89	0.80	2
43	ASAFGSSTESLVAR	sp|Q9CQJ0|ACO15_MOUSE	yes	no	31	44	14	L	F	0	1381.684	2	2.08E-12	130.20	1.19	1.11	5
44	ASAPATPLSPTR	sp|P14733|LMNB1_MOUSE	yes	yes	16	27	12	R	L	0	1167.625	2	1.00E-04	98.11	1.47	1.04	8
45	ASASSTNLKDVLSNLIPKEQAR	sp|Q9CZU6|CISY_MOUSE	yes	yes	26	47	22	H	I	0	2341.260	3	4.81E-02	46.95	1.51	0.89	1
46	ASFFGENHLEVPVPSALTR	sp|Q8VHY0-3|CSPG4_MOUSE	yes	no	30	48	19	P	V	0	2070.053	3	1.70E-06	89.86	1.75	1.16	2
47	ASFIDKVR	sp|Q3TTY5|K22E_MOUSE	no	no	211	218	8	F	F	0	934.524	2	1.67E-01	94.85	3.69	2.35	1
48	ASGGGVPTDEEQATGLER	sp|P19536|COX5B_MOUSE	yes	yes	31	48	18	M	E	0	1772.818	2	1.00E-04	75.55	2.19	1.44	3
49	ASGPGGLHADLLR	sp|Q8BWF0|SSDH_MOUSE	yes	yes	36	48	13	Y	G	0	1262.673	3	1.09E-06	113.76	1.03	0.96	6
50	ASKPTLNEVVIVSAIR	sp|Q8QZT1|THIL_MOUSE	yes	yes	31	46	16	Y	T	0	1695.988	2;3	5.89E-21	155.79	0.96	0.97	14
51	ATVEEVDAAMNAR	sp|P49312-2|ROA1_MOUSE	yes	no	63	75	13	Y	P	0	1375.640	2;3	4.66E-09	131.06	3.32	2.16	12
52	AVFPSIVGR	sp|P63260|ACTG_MOUSE	no	no	29	37	9	R	P	0	944.544	2	2.90E-02	120.87	NaN	NaN	0
53	AVLKLCEQPPLVQAIFSGDPEEIR	sp|B2RXR6|ANR44_MOUSE	yes	yes	2	25	24	M	M	0	2708.421	3	1.90E-02	27.42	0.92	0.81	2
54	AVSELAGHQTSAESWGTGR	sp|Q9D8E6|RL4_MOUSE	yes	yes	53	71	19	Y	A	0	1942.913	3	6.42E-02	28.17	5.15	3.58	1
55	AVTVAPPGAR	sp|Q8VEK3|HNRPU_MOUSE	yes	yes	190	199	10	F	Q	0	937.535	2	9.75E-05	136.57	2.33	1.91	9
56	AVVGNAVPCGAR	sp|Q9EPE9|AT131_MOUSE	yes	yes	2	13	12	M	P	0	1169.598	2	7.72E-05	100.88	1.48	0.91	3
57	AWITAPVALR	sp|O55111|DSG2_MOUSE	yes	yes	55	64	10	R	E	0	1096.639	2	6.06E-03	101.65	1.28	0.94	5
58	AWVLDKLKAER	sp|P10126|EF1A1_MOUSE	yes	no	57	67	11	Y	E	0	1327.761	3	5.45E-02	39.63	NaN	NaN	0
59	AYGAPPPPEPR	sp|P50608|FMOD_MOUSE	yes	yes	64	74	11	Y	D	0	1150.577	2	1.31E-02	47.84	NaN	NaN	0
60	CCNYYGNSCGGCGYGSR	sp|Q925H4|KR211_MOUSE	yes	yes	2	18	17	M	Y	0	1990.682	2;3	2.99E-36	111.77	2.67	1.72	8
61	CESCDTLTCR	sp|Q62318-2|TIF1B_MOUSE	yes	no	222	231	10	F	D	0	1300.485	2	2.96E-03	108.70	5.59	3.88	3
62	CGIFAYLNYHVPR	sp|P47856-2|GFPT1_MOUSE	yes	no	2	14	13	M	T	0	1608.787	3	3.39E-09	132.32	1.12	1.06	1
63	CGYGSYYGCGYR	sp|Q925H3|KRA65_MOUSE	yes	no	31	42	12	G	G	0	1461.544	2	2.82E-02	66.27	2.27	1.51	4
64	CGYYGNYYGGR	sp|Q925H3|KRA65_MOUSE	yes	no	2	12	11	M	G	0	1328.524	2	1.70E-07	204.34	1.34	0.93	6
65	CISAAPYR	sp|Q9ERE2|KRT81_MOUSE	no	no	26	33	8	C	G	0	936.449	2	5.09E-03	86.83	NaN	NaN	0
66	CVVAEIKAQYDDIASR	sp|Q9ERE2|KRT81_MOUSE	no	no	273	288	16	D	S	0	1836.904	3	6.13E-03	60.55	1.62	1.08	2
67	DAFLASESLIKQIPR	sp|P53026|RL10A_MOUSE	yes	yes	108	122	15	Y	I	0	1686.931	2;3	5.99E-06	97.27	5.06	3.60	6
68	DCGPPPDIPNAR	sp|Q61475|DAF1_MOUSE	yes	no	35	46	12	G	P	0	1307.593	2	1.25E-02	72.29	1.41	0.92	4
69	DCILPPTRPTDKPLR	sp|P10126|EF1A1_MOUSE	yes	yes	233	247	15	L	L	1	1777.951	3;4	1.19E-02	61.41	6.19	4.36	2
70	DDEVDVDGTVEEDLGKSR	sp|P08113|ENPL_MOUSE	yes	yes	22	39	18	A	E	0	1976.881	3	1.79E-03	56.12	1.24	1.11	19
71	DEGLPPILNALEVQGR	sp|P56480|ATPB_MOUSE	yes	yes	76	91	16	F	D	0	1719.916	2;3	7.94E-05	91.36	6.55	4.35	3
72	DFCLEPPYTGPCKAR	CON_P00974|P00974	yes	yes	38	52	15	P	I	0	1809.818	3	2.29E-06	100.11	0.52	0.52	5
73	DHVKDTSFDLFSISNINR	sp|Q03350|TSP2_MOUSE	yes	yes	20	37	18	G	K	0	2107.033	3	8.43E-04	58.98	2.09	1.17	1
74	DIDLPETFDAR	sp|P10605|CATB_MOUSE	yes	yes	77	87	11	E	E	0	1290.609	2	7.54E-14	123.67	1.20	0.94	10
75	DITADDEPLGR	sp|P17742|PPIA_MOUSE	yes	yes	9	19	11	F	V	0	1200.562	2	7.94E-03	75.82	3.24	1.97	2
76	DITDGNSEHLKR	sp|Q9DBH5|LMAN2_MOUSE	yes	yes	47	58	12	A	E	0	1383.674	3	3.20E-04	89.30	1.32	0.98	8
77	DIVLTQSPASLAVSLGQR	sp|P01668|KV3AG_MOUSE	yes	no	1	18	18	-	A	0	1854.021	3	1.54E-08	99.66	1.14	0.92	3
78	DLQLDSDAGVR	sp|D3Z750|MRO2A_MOUSE	yes	yes	1643	1653	11	Q	R	0	1187.578	2	4.75E-02	61.34	2.83	1.97	4
79	DMVVERLKSR	sp|Q0VF22|CC138_MOUSE	yes	yes	12	21	10	Q	Y	1	1231.671	2	1.39E-01	28.96	NaN	NaN	0
80	DPAIYFKEQFLDGDAWTNR	sp|P14211|CALR_MOUSE	yes	yes	18	36	19	A	W	0	2285.075	2;3	1.10E-26	190.23	1.10	0.93	31
81	DPVFIPPFIR	sp|Q2MV57|TECT2_MOUSE	yes	yes	26	35	10	G	M	0	1199.670	2	3.47E-02	61.56	1.54	1.01	3
82	DREELNYWKR	sp|O70374-2|MTG8R_MOUSE	yes	no	350	359	10	S	R	1	1407.690	2	1.76E-01	14.68	NaN	NaN	0
83	DWVIPPISCPENEKGEFPKNLVQIKSNR	sp|P09803|CADH1_MOUSE	yes	yes	157	184	28	R	D	0	3293.687	5	1.27E-01	19.66	1.55	1.22	1
84	EAGPETESPVR	sp|Q9D1M7|FKB11_MOUSE	yes	yes	26	36	11	A	T	0	1170.552	2	1.66E-07	184.36	2.01	1.33	4
85	EAGPPPIQDGEFTFLLPAGR	sp|Q3V009|TMED1_MOUSE	yes	yes	23	42	20	G	K	0	2111.069	3	4.64E-04	48.91	1.60	0.98	1
86	EAIVDGGINPASLR	sp|P19096|FAS_MOUSE	yes	yes	88	101	14	Y	G	0	1410.747	2	3.92E-06	101.30	1.10	0.72	2
87	EALDCILPPTRPTDKPLR	sp|P10126|EF1A1_MOUSE	yes	yes	230	247	18	L	L	1	2091.115	3;4	1.33E-04	70.78	4.00	2.67	8
88	EAPQEPDPFTYDYHTLR	sp|Q9Z239|PLM_MOUSE	yes	yes	21	37	17	A	I	0	2077.938	3	4.10E-07	98.06	1.80	1.08	3
89	EASLTSSTYNFLHYDR	sp|Q99KG7|HPS4_MOUSE	yes	yes	557	572	16	D	I	0	1902.875	2	1.34E-01	34.43	NaN	NaN	0
90	EDIDLPETFDAR	sp|P10605|CATB_MOUSE	yes	yes	76	87	12	G	E	0	1419.652	2	2.72E-05	107.09	0.93	0.85	3
91	EDLKENLIR	sp|P48025|KSYK_MOUSE	yes	yes	120	128	9	F	E	0	1128.614	2	7.35E-02	77.73	NaN	NaN	0
92	EEAESTLQSFR	sp|P20152|VIME_MOUSE	yes	yes	197	207	11	R	Q	0	1295.599	2	1.69E-02	90.61	0.06	0.03	2
93	EEDETIPDSEQDIR	sp|Q8BFY9-2|TNPO1_MOUSE	yes	no	323	336	14	V	P	0	1674.722	2	9.34E-02	46.07	0.08	0.05	2
94	EEINELNR	sp|Q9ERE2|KRT81_MOUSE	no	no	320	327	8	R	M	0	1015.493	2	1.70E-01	93.65	0.06	0.04	1
95	EELQITAGKHGDSVR	sp|P04104|K2C1_MOUSE	yes	yes	386	400	15	Y	N	0	1638.833	3;4	1.22E-03	82.59	5.38	3.53	8
96	EELQVTAGKHGDSLR	sp|Q8VED5|K2C79_MOUSE	yes	no	338	352	15	Y	D	0	1638.833	3;4	3.18E-03	71.98	5.86	4.01	4
97	EGAVPIPVTCFTR	sp|Q62507|COCH_MOUSE	yes	yes	27	39	13	A	G	0	1445.734	2	1.08E-02	70.09	1.05	0.97	1
98	EGEPEVTDQLEWQSNQPWEQALNR	sp|P08226|APOE_MOUSE	yes	yes	19	42	24	A	F	0	2882.311	3	1.88E-29	132.72	1.30	1.22	5
99	EGLEQAALPAEESR	sp|Q8C0L0|TMX4_MOUSE	yes	yes	21	34	14	A	V	0	1498.726	2	1.82E-10	116.78	1.56	0.97	3
100	EGTLKQINFQR	sp|Q9D180|WDR65_MOUSE	yes	yes	184	194	11	A	G	0	1332.715	2	2.29E-02	94.31	NaN	NaN	0
101	EICGPGIDIR	sp|Q60751|IGF1R_MOUSE	yes	yes	31	40	10	G	N	0	1128.560	2	1.80E-02	74.84	1.42	0.87	1
102	ELPEKQIDDSR	sp|Q61739-2|ITA6_MOUSE	yes	no	903	913	11	R	K	0	1328.657	3	1.28E-02	72.29	1.74	1.13	4
103	EPEGKEVWDYVTVR	sp|Q920A5|RISC_MOUSE	yes	yes	33	46	14	R	K	0	1705.831	3	4.48E-03	74.79	1.10	0.98	5
104	EPPEPPGLAQLSPGSPPQAPDLLYADGLR	sp|Q8CG70|P3H3_MOUSE	yes	yes	20	48	29	P	A	0	2981.514	3	7.66E-11	61.53	1.34	0.93	4
105	EQDFYDFKAVNIR	sp|Q99LJ6|GPX7_MOUSE	yes	yes	21	33	13	S	G	0	1643.794	3	8.66E-06	104.41	1.38	1.13	10
106	EQEVSDNELQELSTQGSR	sp|Q06890|CLUS_MOUSE	yes	yes	22	39	18	G	Y	0	2047.929	2	8.36E-09	102.98	1.04	0.91	9
107	ESEPGWDVAAPDLLYAEGTAAYSR	sp|Q3V1T4-2|P3H1_MOUSE	yes	no	26	49	24	A	G	0	2567.182	2	5.46E-07	57.80	1.24	1.08	6

108	ESEVASSLVLER	sp|Q9CYR0|SSBP_MOUSE	yes	yes	17	28	12	H	S	0	1317.678	2	1.82E-06	110.38	1.02	0.95	4
109	ESVAVPLQQGAEQQR	sp|Q3UPL0-2|SC31A_MOUSE	yes	no	408	422	15	F	R	0	1638.833	2;3	2.37E-03	76.36	2.04	1.34	4
110	EWIKFAAACR	sp|Q7TSF0-2|DSG1C_MOUSE	yes	no	50	59	10	R	E	0	1250.623	2;3	7.03E-03	99.69	1.19	1.04	17
111	EWVMPPIFVPENGKGPFPQR	sp|P10287|CADH3_MOUSE	yes	yes	100	119	20	R	L	0	2324.178	3	7.22E-04	47.08	1.48	1.02	3
112	FAKLVRPPVQVYGIEGR	sp|Q9DB20|ATPO_MOUSE	yes	yes	24	40	17	P	Y	1	1928.100	4	3.64E-04	84.51	0.64	0.53	8
113	FANDATFEIKKCDLHR	sp|P35486|ODPA_MOUSE	yes	yes	30	45	16	N	L	0	1963.957	4	2.59E-02	41.09	1.04	1.01	5
114	FAPSNEAWENLDSDIR	sp|Q62009-5|POSTN_MOUSE	yes	no	137	152	16	Y	R	0	1862.844	2	3.14E-03	66.02	6.35	4.07	2
115	FAPSNEAWENLDSDIRR	sp|Q62009-5|POSTN_MOUSE	yes	no	137	153	17	Y	G	1	2018.945	3	1.35E-02	44.25	3.90	2.39	3
116	FAVTVAPPGAR	sp|Q8VEK3|HNRPU_MOUSE	yes	yes	189	199	11	L	Q	0	1084.603	2	5.18E-10	112.13	2.52	1.63	3
117	FCCGNYFPGYPCYGTNFHGTYR	sp|Q9D3I6|KRA71_MOUSE	yes	yes	5	26	22	Y	A	0	2737.094	3	1.87E-05	55.45	4.72	2.89	1
118	FDEESYSLLR	sp|Q62186|SSRD_MOUSE	yes	yes	106	115	10	F	K	0	1257.588	2	2.20E-02	72.20	16.53	11.88	1
119	FDITADDEPLGR	sp|P17742|PPIA_MOUSE	yes	yes	8	19	12	F	V	0	1347.631	2	9.90E-09	147.24	3.12	2.11	7
120	FHSTSISEAEPPR	sp|Q8K3F7|TDH_MOUSE	yes	yes	45	57	13	N	V	0	1456.695	3	1.17E-10	140.63	1.34	1.15	4
121	FLDFQGSAIPR	sp|Q8BGC4|ZADH2_MOUSE	yes	yes	21	31	11	H	T	0	1249.646	2	3.17E-04	110.08	1.19	1.01	6
122	FQSGQVLSALPR	sp|Q9JHH6|CBPB2_MOUSE	yes	yes	22	33	12	A	T	0	1301.709	2	6.82E-04	86.80	1.32	1.20	6
123	FSPLNPVR	sp|O35737|HNRH1_MOUSE	no	no	309	316	8	F	V	0	928.513	2	5.62E-02	58.82	NaN	NaN	0
124	FSSNPIIPSR	sp|Q7TPC1|CDSN_MOUSE	yes	yes	378	387	10	Y	G	0	1116.593	2	1.01E-02	85.81	2.13	1.36	2
125	FSTNCVEGTAR	sp|Q6PIC6|AT1A3_MOUSE	yes	no	235	245	11	F	G	0	1240.551	2	1.12E-02	73.44	2.75	1.78	4
126	FTLNPNTTGVQNPHIER	sp|P47809|MP2K4_MOUSE	yes	yes	57	73	17	R	L	0	1936.976	3	7.03E-04	70.78	1.69	1.35	4
127	FTPSLDSDFTTFLPAGR	sp|Q9CXE7|TMED5_MOUSE	yes	yes	28	44	17	G	K	0	1870.910	2	1.23E-02	47.22	1.41	0.99	1
128	FVEDLNESFKDNR	sp|Q8BXZ1|TMX3_MOUSE	yes	yes	30	42	13	G	K	0	1611.753	3	5.83E-02	54.34	1.32	0.79	1
129	GAGGALFVHR	sp|Q9D6J6|NDUV2_MOUSE	yes	yes	32	41	10	N	D	0	983.530	3	6.81E-04	120.15	1.00	0.80	8
130	GAYKYIQELWR	sp|Q9CZM2|RL15_MOUSE	yes	yes	2	12	11	M	K	0	1425.741	2;3	2.72E-07	170.04	1.24	1.05	21
131	GELETSDVVTVVLGQDAKLPCFYR	sp|Q8R007-2|PVRL4_MOUSE	yes	no	31	54	24	A	G	0	2695.353	3	1.90E-06	54.00	1.67	1.11	2
132	GFQFVSSSLPDICYR	sp|P53996-2|CNBP_MOUSE	yes	no	35	49	15	R	C	0	1774.835	2;3	2.63E-07	106.14	0.73	0.69	10
133	GGDEIPFSPYR	sp|Q8BTM8|FLNA_MOUSE	yes	yes	1623	1633	11	Y	V	0	1236.578	2	1.83E-02	93.35	4.19	2.94	2
134	GGDNIPLSPYR	sp|Q80X90|FLNB_MOUSE	yes	yes	1595	1605	11	Y	I	0	1187.594	2	2.46E-02	106.67	8.51	6.04	1
135	GGGLGSGFGGR	sp|Q61781|K1C14_MOUSE	yes	no	74	84	11	F	F	0	920.446	2	1.87E-01	61.82	3.83	2.37	1
136	GGGSGFGGGGFGGGSFGGGR	sp|Q3TTY5|K22E_MOUSE	yes	no	133	152	20	F	F	0	1587.682	2	5.39E-04	48.38	4.86	3.04	1
137	GGIGTVPVGR	sp|P10126|EF1A1_MOUSE	yes	no	257	266	10	I	V	0	911.519	2	9.37E-05	206.43	1.10	0.79	9
138	GGVGEPGGGPGPR	sp|Q9JJE7|FADS3_MOUSE	yes	yes	2	14	13	M	E	0	1092.531	2	1.61E-10	138.45	1.24	1.07	7
139	GHQQLYWSHPR	sp|P62274|RS29_MOUSE	yes	yes	2	12	11	M	K	0	1407.680	3;4	1.97E-07	143.97	1.07	1.01	9
140	GIHGLAKLIADVAPSAIR	sp|P39749|FEN1_MOUSE	yes	yes	2	19	18	M	E	0	1801.057	3	5.07E-05	71.60	1.32	1.25	1
141	GIISEVKAQYDSICQR	sp|P04104|K2C1_MOUSE	yes	yes	357	372	16	D	S	0	1865.931	3	4.42E-03	63.68	0.85	0.56	2
142	GKDYYQTLGLAR	sp|Q9QYJ3|DNJB1_MOUSE	yes	yes	2	13	12	M	G	0	1383.715	3	6.52E-02	75.74	1.17	1.16	1
143	GLLGSNPADGVAWTCFR	sp|Q8CAK1|CAF17_MOUSE	yes	yes	36	52	17	F	L	0	1819.868	2	1.35E-02	44.25	1.76	1.34	1
144	GLLSQGSPLSWEETQR	sp|P97494|GSH1_MOUSE	yes	yes	2	17	16	M	H	0	1786.885	2;3	1.06E-33	258.16	1.03	0.97	13
145	GLPKGPEGQGLPEVETR	sp|Q7TQK5|CCD93_MOUSE	yes	yes	2	18	17	M	E	0	1762.921	3	6.84E-04	71.60	1.30	0.92	3
146	GNIEIKDLMVGDEASELR	sp|P61161|ARP2_MOUSE	yes	yes	48	65	18	V	S	0	1987.989	3	8.21E-26	144.72	1.09	0.76	3
147	GNTSDRRAR	sp|Q8BLN6|UNC80_MOUSE	yes	yes	1062	1070	9	S	S	2	1031.522	2	1.11E-01	38.30	NaN	NaN	0
148	GPAGAGESKCPLMVKVLDAVR	sp|P07309|TTHY_MOUSE	yes	yes	21	41	21	A	G	0	2154.129	3	4.89E-15	112.82	1.62	1.51	1
149	GPPPIQDGEFTFLLPAGR	sp|Q3V009|TMED1_MOUSE	yes	yes	25	42	18	A	K	0	1910.989	2;3	1.82E-06	93.23	1.56	1.02	4
150	GPYPSSMDWR	sp|P49935|CATH_MOUSE	yes	yes	112	121	10	T	K	0	1194.513	2	1.34E-04	134.57	1.12	1.04	7
151	GQNDLMGTAEDFADQFLR	sp|Q64310|SURF4_MOUSE	yes	yes	2	19	18	M	V	0	2026.906	2;3	2.19E-26	176.69	1.66	1.03	3
152	GQVITIGNER	sp|P63260|ACTG_MOUSE	no	no	245	254	10	D	F	0	1085.583	2	9.14E-03	90.05	0.78	0.74	4
153	GQVVQFKLSDIGEGIR	sp|P53395|ODB2_MOUSE	yes	yes	62	77	16	Q	E	0	1744.947	3	4.22E-07	103.13	0.93	0.83	7
154	GRDFYKILGVPR	sp|Q99KV1|DJB11_MOUSE	yes	yes	23	34	12	A	S	1	1419.799	4	8.26E-05	100.22	1.10	1.05	8
155	GSGSGESSGFSQGGSGQGR	sp|Q8VHD8|HORN_MOUSE	yes	no	625	643	19	Y	S	0	1684.704	2	2.32E-07	96.39	2.90	1.83	2
156	GSLGGGYSSGGFSGGSFSR	sp|P02535-3|K1C10_MOUSE	yes	no	33	51	19	R	G	0	1722.760	2	2.00E-16	119.38	1.31	0.85	2
157	GSSTESLVAR	sp|Q9CQJ0|ACO15_MOUSE	yes	no	35	44	10	F	F	0	1005.509	2	1.54E-02	100.88	1.50	1.43	2
158	GSVKPYTNFDAER	sp|P07356|ANXA2_MOUSE	yes	yes	25	37	13	Y	D	0	1482.710	2;3	2.34E-31	184.76	1.71	1.26	14
159	GTAEDFADQFLR	sp|Q64310|SURF4_MOUSE	yes	yes	8	19	12	M	V	0	1368.631	2	3.80E-05	105.65	1.59	1.05	2
160	GTLSDPCKDPTR	sp|Q7TPC1|CDSN_MOUSE	yes	yes	36	47	12	I	I	0	1345.630	3	2.56E-03	80.69	1.93	1.20	4
161	GTTPGGSITKVLIANR	sp|Q99MR8|MCCA_MOUSE	yes	yes	38	53	16	Y	G	0	1583.900	3	6.81E-02	32.15	1.81	1.26	7
162	GVEIETISPGDGR	sp|Q9Z2I2|FKB1B_MOUSE	yes	yes	2	14	13	M	T	0	1328.657	2	2.47E-03	80.96	0.95	0.89	5
163	GVNPGPIVGTTR	sp|Q61033|LAP2A_MOUSE	yes	no	127	138	12	Y	K	0	1166.641	2	3.54E-04	88.02	4.37	2.82	4
164	GVPAFFR	sp|Q3V132|ADT4_MOUSE	yes	no	277	283	7	E	G	0	792.428	2	7.56E-03	102.98	NaN	NaN	0
165	GVQGFQDYIEKHCPSAVVPVELQKLAR	sp|Q6A0A9|F120A_MOUSE	yes	yes	2	28	27	M	G	0	3067.591	5	4.30E-03	53.48	1.33	1.23	1
166	GVQPPNFSWVLPGR	sp|Q6NT99|DUS23_MOUSE	yes	yes	2	15	14	M	L	0	1552.815	2	2.95E-02	57.43	1.11	0.97	2
167	GVQVETISPGDGR	sp|P26883|FKB1A_MOUSE	yes	yes	2	14	13	M	T	0	1313.658	2	3.49E-11	179.50	1.14	0.93	9
168	GYYGNYYGGR	sp|Q925H3|KRA65_MOUSE	yes	no	3	12	10	C	G	0	1168.494	2	9.85E-05	152.34	1.72	1.14	4
169	HSILPVDDDINGLNEEQKQLR	sp|Q9JHI5|IVD_MOUSE	yes	yes	31	51	21	A	H	0	2432.230	3;4	2.30E-09	95.50	0.90	0.89	6
170	IDLPETFDAR	sp|P10605|CATB_MOUSE	yes	yes	78	87	10	D	E	0	1175.582	2	8.58E-05	152.04	1.27	0.96	9
171	IDNIEGEWGAFNDIMR	sp|Q9JHU4|DYHC1_MOUSE	yes	yes	1209	1224	16	Y	R	0	1878.857	2	2.34E-02	46.25	5.05	3.64	1
172	IGGIGTVPVGR	sp|P10126|EF1A1_MOUSE	yes	no	256	266	11	K	V	0	1024.603	2	9.29E-03	74.84	0.79	0.69	4
173	IGGLNVQTSESGLR	sp|Q9CX86|ROA0_MOUSE	yes	yes	11	24	14	F	G	0	1429.753	2	4.86E-02	68.97	2.78	1.96	2
174	IGGLSFETTDDSLR	sp|Q8BG05-2|ROA3_MOUSE	yes	no	17	30	14	F	E	0	1509.731	2	6.98E-03	68.97	2.23	1.44	4
175	IGGLSFETTDESLR	sp|P49312-2|ROA1_MOUSE	yes	no	18	31	14	F	S	0	1523.747	2	6.57E-03	69.92	3.49	2.33	3
176	IGSVEEQLAQLR	sp|Q61781|K1C14_MOUSE	no	no	383	394	12	M	C	0	1341.725	2	5.79E-02	59.12	1.09	0.67	3
177	ILFGVYGDVQR	sp|P17225|PTBP1_MOUSE	yes	yes	354	364	11	F	V	0	1265.677	2	3.36E-02	64.82	2.39	1.64	3
178	ILGGQEAAAHAR	sp|P03953-2|CFAD_MOUSE	yes	no	25	36	12	R	P	0	1192.631	3	7.51E-07	123.95	0.81	0.77	5
179	ILNLPESWDWR	sp|P97821|CATC_MOUSE	yes	yes	227	237	11	Q	N	0	1427.720	2	6.08E-04	105.46	0.97	0.88	6
180	INPETPGYVGFANLPNQVHR	sp|P42208|SEPT2_MOUSE	yes	yes	10	29	20	F	K	0	2222.123	3	8.25E-26	138.75	1.27	1.18	7
181	INYQDDAELATR	sp|Q02257|PLAK_MOUSE	yes	no	131	142	12	L	A	0	1407.663	2	1.43E-03	84.37	2.91	1.93	4
182	IQTLHVLSGDMSQLPAGVR	sp|Q8BH04|PCKGM_MOUSE	yes	yes	27	45	19	S	D	0	2021.073	3	1.04E-08	97.49	0.98	0.89	2
183	ISFHLPVNSR	sp|Q9D1D4|TMEDA_MOUSE	yes	yes	32	41	10	G	K	0	1168.635	2;3	5.26E-03	103.26	1.42	1.09	13
184	ITHAPPGEFNEVFNDVR	sp|P47753|CAZA1_MOUSE	yes	yes	21	37	17	F	L	0	1940.938	3	4.47E-05	89.36	4.22	2.98	1
185	ITNVLQNPDLALR	sp|Q68FD5|CLH1_MOUSE	yes	yes	338	350	13	Y	M	0	1465.825	2	6.50E-02	52.53	1.55	1.01	2
186	IVGGHEASESKWPWQVSLR	sp|P21845-2|TRYB2_MOUSE	yes	no	32	50	19	G	F	0	2165.102	4	7.59E-09	100.02	0.97	0.83	8
187	IVQAEEAASMSIEER	sp|Q8BVE8|NSD2_MOUSE	yes	no	326	340	15	G	K	0	1661.793	2	3.18E-02	50.81	1.42	0.98	4
188	KELKFVTLVFR	sp|Q8CE08|PPAP_MOUSE	yes	no	32	42	11	A	H	0	1378.834	3	9.68E-04	56.21	NaN	NaN	0
189	KGSDFDCELR	sp|P61979-3|HNRPK_MOUSE	yes	yes	115	124	10	Y	L	0	1225.540	3	1.50E-02	76.84	1.42	1.35	5
190	KHFVQYYLAR	sp|Q920A7-2|AFG31_MOUSE	yes	no	168	177	10	W	G	0	1323.709	2	1.77E-01	1.75	NaN	NaN	0
191	KIGGIGTVPVGR	sp|P10126|EF1A1_MOUSE	yes	no	255	266	12	Y	V	0	1152.698	3	1.89E-02	68.54	0.64	0.63	4
192	KKLLEGEEIR	sp|P04104|K2C1_MOUSE	yes	yes	491	500	10	Y	M	0	1213.703	3	1.19E-01	33.09	NaN	NaN	0
193	KLFIGGLNVQTSESGLR	sp|Q9CX86|ROA0_MOUSE	yes	yes	8	24	17	C	G	0	1818.000	3	1.20E-02	48.22	1.88	1.24	2
194	KLNISFPATGCQKLIEVDDER	sp|P62754|RS6_MOUSE	yes	yes	2	22	21	M	K	0	2432.237	4	7.24E-07	73.67	1.00	0.92	1
195	KLSLEGDHSTPPSAYGSVKPYTNFDAER	sp|P07356|ANXA2_MOUSE	yes	yes	10	37	28	C	D	0	3065.473	5	9.50E-17	93.24	1.12	1.02	5
196	KTLVSTVGSMVFSEGEAQR	sp|Q99PL5|RRBP1_MOUSE	yes	yes	854	872	19	Y	L	0	2025.020	3	7.27E-04	57.37	2.12	1.41	2
197	LAAEILELAGNAAR	sp|Q8CCK0|H2AW_MOUSE	yes	yes	56	69	14	Y	D	0	1410.783	2	2.43E-07	106.58	2.99	1.86	3
198	LAEFATGNDR	sp|P62259|1433E_MOUSE	yes	yes	132	141	10	Y	K	0	1092.520	2	4.68E-02	63.62	13.56	10.14	1
199	LASEGAPDFLCPEELEHVSR	sp|Q148V8|FA83H_MOUSE	yes	yes	47	66	20	F	H	0	2255.053	3	3.30E-06	82.01	4.11	2.61	2
200	LDAVDTYIPVPTR	sp|Q8BFR5-2|EFTU_MOUSE	yes	no	240	252	13	L	D	0	1458.772	2;3	3.49E-11	164.68	1.08	0.97	7
201	LDLQNNDISELR	sp|P28653|PGS1_MOUSE	yes	yes	96	107	12	L	K	0	1428.721	2	1.58E-02	70.09	5.10	3.65	1
202	LDNVKALEEANSELER	sp|A6BLY7|K1C28_MOUSE	yes	yes	99	114	16	Y	K	0	1828.917	3	2.81E-02	39.91	5.18	3.62	1
203	LEAEDDLSSFR	sp|Q62009-5|POSTN_MOUSE	yes	no	243	253	11	F	A	0	1280.589	2	3.21E-02	65.18	6.19	4.04	2
204	LEAQAATGGIDPHR	sp|E9Q557|DESP_MOUSE	yes	yes	2061	2075	15	L	N	0	1547.806	3	2.35E-02	54.81	7.08	4.64	2
205	LECYSCVQKADDGCSPHR	sp|Q91YK8|LYPD3_MOUSE	yes	yes	33	50	18	A	M	0	2180.904	3;4	4.78E-16	117.84	1.60	1.07	12
206	LEFIQQNEER	sp|Q01405|SC23A_MOUSE	yes	no	5	14	10	Y	D	0	1304.636	2	2.96E-03	108.70	1.58	1.03	4
207	LEFQFLTGGLVDPEVHGR	sp|E9Q557|DESP_MOUSE	yes	yes	2739	2756	18	F	I	0	2013.032	3	4.50E-26	162.76	3.74	2.41	3
208	LENEIQTYR	sp|P02535-3|K1C10_MOUSE	yes	no	431	439	9	R	S	0	1164.578	2	2.51E-02	113.93	0.15	0.09	2
209	LEQEIATYR	sp|Q61781|K1C14_MOUSE	no	no	414	422	9	R	R	0	1121.572	2	4.88E-03	133.23	0.16	0.10	1
210	LEQQNQVLQTKWELLQQVDTTTR	sp|P04104|K2C1_MOUSE	yes	yes	209	231	23	F	T	0	2798.456	2;3;4	9.98E-41	149.07	5.52	3.40	6
211	LEQQNQVLR	sp|Q3TTY5|K22E_MOUSE	yes	no	220	228	9	F	T	0	1126.610	2	3.06E-02	214.83	8.42	5.55	4
212	LESLPEEEQQR	sp|P25976-2|UBF1_MOUSE	yes	no	325	335	11	F	V	0	1356.652	2	1.08E-04	114.86	2.10	1.27	3
213	LGTLDNPSSLDETAYER	sp|O35943|FRDA_MOUSE	yes	yes	78	94	17	N	L	0	1879.880	2	5.74E-04	76.38	1.02	0.89	2
214	LHLGVTPSVLR	sp|O89023|TPP1_MOUSE	yes	yes	195	205	11	S	Q	0	1190.714	3	1.62E-05	123.79	1.23	0.97	9
215	LHTVYQSVELPETHQMLR	sp|Q07417|ACADS_MOUSE	yes	yes	25	42	18	R	Q	0	2180.105	4	2.03E-04	67.90	1.30	1.20	3
216	LKTLLPVPTFENVSIPER	sp|Q99N93|RM16_MOUSE	yes	yes	30	47	18	G	S	0	2052.162	3	4.39E-11	100.97	1.40	0.99	4
217	LLSAAYVDSHQWEAR	sp|Q8BK72|RT27_MOUSE	yes	yes	29	43	15	C	E	0	1744.853	3	1.61E-15	146.20	1.50	1.28	6
218	LLVVYPWTQR	sp|P02088|HBB1_MOUSE	no	no	32	41	10	R	Y	0	1273.718	2	1.24E-02	79.15	0.27	0.22	4
219	LMASDPNLQVLGAAYIQHR	sp|Q9QY23|PKP3_MOUSE	yes	no	328	346	19	Y	C	0	2096.084	3	1.57E-02	35.63	2.54	1.74	3

220	LNLPESWDWR	sp|P97821|CATC_MOUSE	yes	yes	228	237	10	I	N	0	1314.636	2	2.37E-04	131.82	1.16	0.93	8
221	LNSTAGASGGAYEHR	sp|O35737|HNRH1_MOUSE	yes	yes	361	375	15	F	Y	0	1489.691	3	1.22E-02	61.13	1.81	1.17	4
222	LQCYECYGVPIETSCPAVTCR	sp|P0CW03|LY6C2_MOUSE	yes	no	27	47	21	G	A	0	2562.101	2	1.61E-04	49.13	1.65	1.08	2
223	LQTSSTFGGSSTR	sp|Q61414|K1C15_MOUSE	yes	no	6	18	13	F	G	0	1327.637	2	1.27E-06	113.25	4.31	2.85	4
224	LRPGDCEVCISYLGR	sp|Q9CXI5|MANF_MOUSE	yes	yes	22	36	15	A	F	1	1793.855	3	6.47E-05	95.07	1.21	1.05	7
225	LSGIPETVPLSTVNR	sp|Q921H8|THIKA_MOUSE	yes	no	107	121	15	F	Q	0	1581.873	2	3.50E-02	48.90	2.58	1.58	3
226	LSPTNCDASEPLAEKVLDLINKGR	sp|Q9ESB3|HRG_MOUSE	yes	yes	19	42	24	A	R	0	2639.359	4	1.04E-01	15.05	1.23	1.08	1
227	LTAEILELAGNAAR	sp|Q8CGP6|H2A1H_MOUSE	yes	no	59	72	14	Y	D	0	1440.794	2	3.57E-02	54.90	3.67	2.35	2
228	LTGGLIEPDTPGR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	4295	4307	13	Y	V	0	1324.699	2	5.01E-02	56.57	1.83	1.22	3
229	LTPTHYLTKQDVER	sp|Q9DBG6|RPN2_MOUSE	yes	yes	23	36	14	A	L	0	1699.889	4	4.70E-03	74.30	1.37	0.91	4
230	LVCDNGSGLCKAGFAGDDAPR	sp|P63268|ACTH_MOUSE	yes	no	9	29	21	A	A	0	2178.979	2	7.50E-02	26.74	1.09	1.04	2
231	LVEGLYCGTR	sp|A2ALW5|DJC25_MOUSE	yes	yes	38	47	10	A	D	0	1166.575	2	9.14E-03	90.05	1.51	0.97	4
232	LVLDEADGLLSQGYSDFINR	sp|Q91VR5|DDX1_MOUSE	yes	yes	367	386	20	F	M	0	2224.101	3	5.95E-08	95.21	1.78	1.13	1
233	LYSSSDDVIELTPSNFNR	sp|Q922R8|PDIA6_MOUSE	yes	yes	20	37	18	G	E	0	2055.975	2;3	2.54E-26	183.77	1.23	1.00	20
234	MAHLEITTER	sp|P21812|MCPT4_MOUSE	yes	yes	35	44	10	Y	G	0	1199.597	3	1.65E-02	102.52	19.66	14.14	1
235	MCGYYGNYYGGR	sp|Q925H3|KRA65_MOUSE	yes	no	1	12	12	-	G	0	1459.565	2	1.46E-08	140.49	1.62	1.14	11
236	MELLEPLSER	sp|Q62261-2|SPTB2_MOUSE	yes	no	1455	1464	10	F	K	0	1215.617	2	5.63E-03	102.52	1.85	1.16	4
237	MFLYNLTLQR	sp|Q921M3-2|SF3B3_MOUSE	yes	no	1	10	10	-	A	0	1297.685	2	4.87E-02	42.34	NaN	NaN	0
238	MKALILVGGYGTR	sp|Q8BT27|GMPPB_MOUSE	yes	yes	1	13	13	-	L	0	1377.780	3	7.81E-03	73.39	0.95	0.95	5
239	MKDSLVLQSR	sp|Q99KN2|CIAO1_MOUSE	yes	yes	1	10	10	-	V	0	1175.633	3	9.06E-03	90.61	1.04	1.00	5
240	MKDVPAFLQQSQSSGPGQAAVWHR	sp|Q9WVJ2|PSD13_MOUSE	yes	yes	1	24	24	-	L	0	2624.292	4	2.13E-23	120.32	1.08	1.04	4
241	MKFNPFVTSDR	sp|P61255|RL26_MOUSE	yes	yes	1	11	11	-	S	0	1340.655	2;3	3.79E-03	80.69	0.94	0.89	8
242	MKLNISFPATGCQKLIEVDDER	sp|P62754|RS6_MOUSE	yes	yes	1	22	22	-	K	0	2563.277	2;3;4	2.82E-08	86.56	1.15	1.09	13
243	MKLTDSVLR	sp|Q8BFQ4|WDR82_MOUSE	yes	yes	1	9	9	-	S	0	1061.590	3	1.72E-02	61.16	NaN	NaN	0
244	MKPILLQGHER	sp|Q9QZD9|EIF3I_MOUSE	yes	yes	1	11	11	-	S	0	1320.734	3;4	3.17E-04	110.08	0.99	0.86	9
245	MKPLVVFVLGGPGAGKGTQCAR	sp|Q9DBP5|KCY_MOUSE	yes	yes	1	22	22	-	I	0	2242.208	4	4.81E-02	46.95	0.84	0.74	4
246	MKPPAACAGDVVDAASPASTVNHLR	sp|Q8C1A5|THOP1_MOUSE	yes	yes	1	25	25	-	W	0	2534.237	4	5.07E-36	136.24	1.18	1.17	6
247	MKTILSNQTVDIPENVEITLKGR	sp|P51410|RL9_MOUSE	yes	yes	1	23	23	-	T	0	2598.405	2;4	1.13E-13	117.62	1.28	1.12	6
248	MKVFVTGPLPAEGR	sp|Q91Z53|GRHPR_MOUSE	yes	yes	7	20	14	L	A	0	1500.812	3	1.91E-08	107.35	0.81	0.73	6
249	MLGGLGKLAAEGLAHR	sp|Q8CF02|FM25C_MOUSE	yes	yes	1	16	16	-	T	0	1592.882	4	2.44E-02	44.25	2.60	2.49	1
250	MLPLTEENKHVAQLLFSSGTCPR	sp|Q9D3U0|PUS10_MOUSE	yes	yes	1	23	23	-	C	0	2627.320	4	5.36E-03	38.27	1.29	1.28	1
251	MLSLDFLDDVR	sp|Q9R0P6|SC11A_MOUSE	yes	yes	1	11	11	-	R	0	1322.654	2	2.73E-07	142.08	1.59	1.10	12
252	MLWFQGAIPAAIASAKR	sp|Q8VCH8|UBXN4_MOUSE	yes	yes	1	17	17	-	S	0	1829.997	3	2.37E-10	110.12	1.52	1.09	3
253	MQPASAKWYDR	sp|Q9R0Q7|TEBP_MOUSE	yes	yes	1	11	11	-	R	0	1351.634	3	2.95E-02	65.84	1.21	0.97	3
254	MRKDTPPPLVPPAAR	sp|Q99J09|MEP50_MOUSE	yes	yes	1	15	15	-	E	1	1644.913	3	9.43E-03	63.68	1.20	1.07	3
255	MSAGLQPVPIVFR	sp|Q9D051|ODPB_MOUSE	yes	yes	133	145	13	Y	G	0	1413.780	2	1.08E-02	70.09	2.05	1.45	1
256	MSPDLNCISSSLLR	sp|Q8CE93|FA26D_MOUSE	yes	yes	1	14	14	-	S	0	1591.770	2	3.90E-09	114.64	2.51	1.58	3
257	MSTGTFVVSQPLNYR	sp|Q9JLJ2|AL9A1_MOUSE	yes	yes	1	15	15	-	G	0	1698.840	2;3	1.95E-15	173.44	1.05	0.95	10
258	MSYYGSYYGGLGSGIR	sp|O08632|KR195_MOUSE	yes	yes	1	16	16	-	G	0	1729.777	2	7.14E-14	118.21	2.49	1.66	4
259	MYIKQVIIQGFR	sp|Q9CW03|SMC3_MOUSE	yes	yes	1	12	12	-	S	0	1494.838	3	8.95E-02	53.24	1.52	1.31	3
260	NAAPGVDLTQLLNNMR	sp|P02535-3|K1C10_MOUSE	yes	no	296	311	16	M	N	0	1725.883	2	6.09E-10	109.79	2.22	1.43	2
261	NANVLLQIDNAR	sp|P02535-3|K1C10_MOUSE	no	no	206	217	12	D	L	0	1339.721	2	1.43E-03	84.37	1.44	0.96	2
262	NASVSVPDSSGPER	sp|P61979-3|HNRPK_MOUSE	yes	no	73	86	14	Y	I	0	1400.653	2	4.63E-11	123.76	2.61	1.71	4
263	NATLSVEPEGR	sp|Q9QYR9|ACOT2_MOUSE	yes	yes	43	53	11	T	S	0	1171.583	2	3.57E-04	109.16	0.98	0.91	5
264	NCWLALTDPR	sp|Q9Z2V4|PCKGC_MOUSE	yes	yes	74	83	10	D	D	0	1244.597	2	5.78E-03	55.06	NaN	NaN	0
265	NDFINKELILFSNSDNER	sp|Q01320|TOP2A_MOUSE	yes	no	695	712	18	Y	S	0	2167.055	3	1.29E-04	71.38	1.61	1.01	3
266	NDPENKNDPFYYDWYSLR	sp|Q61835|FXYD3_MOUSE	yes	yes	21	38	18	A	V	0	2335.018	3	6.03E-04	61.48	1.76	1.16	6
267	NDSILQATEQR	sp|E9QS57|DESP_MOUSE	yes	yes	1269	1279	11	L	R	0	1273.626	2	7.37E-04	104.24	8.18	5.83	1
268	NDVITVQTPAFAESVTEGDVR	sp|Q9D2G2|ODO2_MOUSE	yes	yes	69	89	21	K	W	0	2247.102	2;3	3.18E-19	117.35	1.10	1.00	10
269	NEATGGKYVPR	sp|P99024|TBB5_MOUSE	no	no	52	62	11	Y	A	0	1190.604	3	8.68E-02	53.24	1.18	0.77	4
270	NEEEVEKRFEGR	sp|Q08943|SSRP1_MOUSE	yes	no	290	301	12	M	L	1	1520.722	2	2.89E-02	105.20	0.02	0.02	3
271	NEEHIPDSPFVVPVASPSGDAR	sp|Q8BTM8|FLNA_MOUSE	yes	yes	2312	2333	22	F	R	0	2319.113	3	4.45E-02	29.06	3.47	2.22	3
272	NEITELTR	sp|Q9R0H5|K2C71_MOUSE	yes	no	347	354	8	K	F	0	974.503	2	1.15E-01	46.00	NaN	NaN	0
273	NIIVEALQNQR	sp|P11276|FINC_MOUSE	yes	yes	2259	2269	11	Y	R	0	1296.715	2	8.46E-04	103.21	3.81	2.53	3
274	NLPLPPPPPPR	sp|P61979-3|HNRPK_MOUSE	yes	no	282	292	11	R	G	0	1193.692	2	1.49E-03	96.34	0.97	0.86	6
275	NTKNEITELTR	sp|Q9R0H5|K2C71_MOUSE	yes	no	344	354	11	K	F	0	1317.689	3	4.45E-02	62.09	1.72	1.31	2
276	PGPVGPAGPR	sp|Q01149|CO1A2_MOUSE	yes	yes	1050	1059	10	A	G	0	903.493	2	2.62E-03	61.68	NaN	NaN	0
277	PGQCCPVCDGCKYQGHEYRSQETFTLQENGRCLR	sp|Q3U492-2|KCP_MOUSE	yes	no	362	395	34	I	C	2	4189.803	4	1.08E-01	0.03	NaN	NaN	0
278	PLIATPTFVADKDGAR	sp|P49117|NR2C2_MOUSE	yes	yes	220	235	16	S	Q	0	1670.899	3	1.75E-01	16.18	NaN	NaN	0
279	QAEVESTGR	sp|Q8BI79-3|CCD40_MOUSE	yes	no	205	213	9	P	A	0	975.462	2	1.37E-01	70.91	NaN	NaN	0
280	QALGITTKISR	sp|P14869|RLA0_MOUSE	yes	yes	139	149	11	F	G	0	1186.703	3	6.09E-02	58.27	3.21	2.12	2
281	QELCQLAAER	sp|Q62261-2|SPTB2_MOUSE	yes	no	608	617	10	Y	R	0	1216.587	2	1.65E-02	75.82	1.84	1.19	4
282	QETQAELPRGSIPR	sp|P97311|MCM6_MOUSE	yes	yes	209	222	14	I	S	1	1580.827	2	6.05E-02	45.28	1.38	1.08	3
283	QHYLATPRMHHFPR	sp|E9QAU8|RN165_MOUSE	yes	yes	186	199	14	Y	N	1	1789.895	2	5.03E-03	43.30	NaN	NaN	0
284	QKTGTAEMSSILEER	sp|Q03265|ATPA_MOUSE	yes	yes	44	58	15	L	I	0	1678.820	2;3	1.49E-16	151.80	1.24	0.82	25
285	QLVEADINSLR	sp|Q9D646|KRT34_MOUSE	no	no	153	163	11	R	R	0	1256.673	2	7.94E-03	75.82	0.23	0.14	1
286	QLVESDLNGLR	sp|Q61897|KT33B_MOUSE	yes	no	153	163	11	R	R	0	1242.657	2	2.15E-02	43.90	NaN	NaN	0
287	QQLLDIKTR	sp|P02535-3|K1C10_MOUSE	yes	no	422	430	9	Y	L	0	1113.651	3	3.59E-02	88.50	8.50	4.87	1
288	QSKYEELQITAGKHGDSVR	sp|P04104|K2C1_MOUSE	yes	yes	382	400	19	Y	N	0	2145.081	4;5	2.20E-03	49.19	5.56	4.15	2
289	QSNVDELGCSHLGQSYESR	sp|P08121|CO3A1_MOUSE	yes	yes	25	43	19	Q	D	0	2164.944	3	1.48E-04	66.64	0.95	0.65	4
290	QSTLVIAEHANDSLAPITLNTITAAGR	sp|Q99LC5|ETFA_MOUSE	yes	yes	20	46	27	F	L	0	2776.472	3	2.94E-50	162.47	0.91	0.87	5
291	QSVEADINGLR	sp|P02535-3|K1C10_MOUSE	no	no	235	245	11	R	R	0	1200.610	2	4.11E-07	138.63	0.28	0.18	2
292	QTKFQELQLAAGR	sp|Q9R0H5|K2C71_MOUSE	no	no	325	337	13	Y	H	0	1488.805	3	1.44E-02	120.57	2.87	1.66	3
293	RAAAITSDLLESLGR	sp|Q62009-5|POSTN_MOUSE	yes	no	253	267	15	F	D	1	1571.863	2;3	2.52E-09	113.40	6.39	4.31	3
294	RAGGKGLSGGFGSR	sp|Q9R0H5|K2C71_MOUSE	yes	no	32	45	14	Y	S	1	1305.690	4	6.88E-02	42.32	1.77	1.07	3
295	RAGSSSGSGVQGASAGGLAADASR	sp|P11088|FILA_MOUSE	yes	yes	46	69	24	R	R	1	2075.994	3	3.89E-25	125.83	0.92	0.84	8
296	REDSWLKSLFVR	sp|O55126|NIPS2_MOUSE	yes	yes	36	47	12	A	K	1	1534.826	4	1.07E-03	85.55	1.81	1.79	1
297	REVAAFAQFGSDLDAATQQLLSR	sp|Q03265|ATPA_MOUSE	yes	yes	441	463	23	Y	G	1	2493.261	3	9.84E-36	139.47	1.65	1.09	2
298	RGLSGGFGSQSVCGAFR	sp|Q9ERE2|KRT81_MOUSE	yes	no	39	55	17	Y	S	1	1741.832	2;3	9.17E-07	97.29	3.12	1.99	10
299	RGLSGGFGSR	sp|Q6IMF0|KRT83_MOUSE	yes	yes	44	53	10	Y	S	1	992.515	3	1.12E-02	82.80	3.03	2.15	3
300	RIIYSPTVGDPIDEYTTVPGR	sp|Q60847-2|COCA1_MOUSE	yes	no	2058	2078	21	Y	R	1	2348.201	3	3.99E-33	147.67	7.04	4.48	3
301	RITYQPSTGEGNEQTITVGGR	sp|Q60847-2|COCA1_MOUSE	yes	no	1786	1806	21	Y	Q	1	2263.119	3	9.97E-35	220.28	4.11	2.57	3
302	RIVYSPVAGTRPSESIVVPGNTR	sp|Q60847-2|COCA1_MOUSE	yes	no	1967	1989	23	Y	T	2	2454.334	4	3.96E-02	29.45	2.59	1.72	3
303	RKLLEGEECR	sp|Q3TTY5|K22E_MOUSE	no	no	502	511	10	Y	M	1	1288.656	3	3.68E-02	66.27	8.15	5.37	4
304	RLLLPQQAGFGECDR	sp|Q8C522|ENDD1_MOUSE	yes	yes	22	36	15	A	F	1	1758.884	3	3.01E-03	72.90	1.21	1.13	7
305	RNLLEGQDAKMAGIGVR	sp|Q61414|K1C15_MOUSE	yes	no	400	416	17	Y	E	1	1826.979	4	2.13E-04	84.65	8.08	4.78	3
306	RPLPPSPPVR	sp|Q9ESY9|GILT_MOUSE	yes	yes	51	60	10	P	V	1	1114.661	3	4.87E-02	42.34	NaN	NaN	0
307	RSLLEGEGSSSGGGGGR	sp|P02535-3|K1C10_MOUSE	yes	no	439	455	17	Y	P	1	1561.745	3	2.86E-11	115.66	6.23	4.06	4
308	RTPGGDGFSLHPPYFNLAEGAR	sp|Q61001|LAMA5_MOUSE	yes	yes	41	62	22	A	I	1	2358.151	4	7.90E-04	42.64	1.35	0.84	2
309	SAAATSAVPAPNHQPEVFCNQIFINNEWHDAVSR	sp|P47738|ALDH2_MOUSE	yes	yes	20	53	34	L	K	0	3776.775	4	1.08E-06	47.38	1.06	1.01	3
310	SAASAITPSVSR	sp|Q922U2|K2C5_MOUSE	yes	no	18	29	12	F	T	0	1145.604	2	2.68E-08	156.36	2.62	1.66	8
311	SALQQTLPAENTDNRR	sp|Q6NZJ6-2|IF4G1_MOUSE	yes	no	1112	1127	16	F	V	1	1812.908	3	6.61E-05	92.38	2.11	1.30	3
312	SANLGGVPSKR	sp|P62342|SELT_MOUSE	yes	yes	20	30	11	A	L	0	1084.599	3	1.48E-03	96.75	1.83	1.18	4
313	SATFPKEIQMLAR	sp|Q62095|DDX3Y_MOUSE	yes	no	381	393	13	F	D	0	1490.792	3	4.87E-02	56.96	2.18	1.41	2
314	SCQAEIIELR	sp|Q61897|KT33B_MOUSE	no	no	267	276	10	Q	R	0	1217.607	2	5.82E-04	122.70	2.35	1.44	4
315	SCVEEVDAAMCAR	sp|Q8BG05-2|ROA3_MOUSE	yes	no	62	74	13	Y	P	0	1496.606	2	4.60E-11	146.79	2.01	1.33	8
316	SCVGVFQHGKVEIIANDQGNR	sp|P17156|HSP72_MOUSE	yes	no	17	37	21	Y	T	0	2327.144	4	2.83E-05	56.72	1.38	0.91	2
317	SDAPPLTLDGIKDR	sp|Q9CR21|ACPM_MOUSE	yes	yes	69	82	14	Y	V	0	1496.784	3	2.84E-03	78.81	1.39	0.84	10
318	SDEVGGEALGR	sp|P02088|HBB1_MOUSE	yes	yes	21	31	11	N	L	0	1088.510	2	3.87E-05	116.74	1.53	1.47	5
319	SDFSEGQAVGAHR	sp|P11088|FILA_MOUSE	yes	yes	118	130	13	H	Q	0	1359.617	3	9.48E-08	119.39	1.40	0.91	4
320	SDGGITALIAAAKYPSYIR	sp|Q8R164|BPHL_MOUSE	yes	yes	139	157	19	W	K	0	1966.052	3	3.78E-03	42.07	0.86	0.86	2
321	SDGNSQGATAEAIEKAVQEAQR	sp|Q04857|CO6A1_MOUSE	yes	yes	940	961	22	F	A	0	2259.073	3	1.86E-07	77.96	3.26	1.95	3
322	SDITENAATVSWR	sp|Q80YX1-5|TENA_MOUSE	yes	no	1083	1095	13	F	A	0	1448.690	2	2.99E-04	119.87	4.86	3.47	3
323	SDLEAQVESLR	sp|Q61897|KT33B_MOUSE	no	no	174	184	11	K	Q	0	1245.620	2	2.78E-02	66.27	2.79	1.86	2
324	SDLELHPPSYPWSHR	sp|Q9D0M3-2|CY1_MOUSE	yes	no	26	40	15	A	G	0	1819.864	3;4	1.39E-03	81.63	1.51	1.05	9
325	SDQVEVFSPPGSDR	sp|Q02788|CO6A2_MOUSE	yes	yes	117	130	14	F	A	0	1518.695	2	2.99E-02	57.29	2.41	1.56	4
326	SDSQVHSGVQVEGR	sp|P11088|FILA_MOUSE	yes	yes	23	36	14	S	R	0	1483.702	3	2.80E-04	91.36	1.35	0.89	4
327	SDVLELTDENFESR	sp|P27773|PDIA3_MOUSE	yes	yes	25	38	14	A	V	0	1652.753	2;3	1.70E-18	232.50	1.20	0.96	21
328	SEDFVDPWTVR	sp|P32921-2|SYWC_MOUSE	yes	no	85	95	11	A	T	0	1349.625	2	2.73E-07	142.08	1.06	0.87	8
329	SEGDSVGDSVHGKPSVVYR	sp|Q9CQU3|RER1_MOUSE	yes	yes	2	20	19	M	F	0	1973.944	4	3.16E-04	61.48	1.56	1.00	4
330	SEIGGLSEQIR	sp|P62334|PRS10_MOUSE	yes	yes	133	143	11	Y	E	0	1187.615	2	2.04E-07	80.69	1.31	0.80	2
331	SELASTPSGAFFQGISFPEISTRPPLGR	sp|Q61033|LAP2A_MOUSE	yes	yes	206	233	28	F	T	1	2948.503	3	3.26E-08	58.81	2.13	1.35	3

332	SELKNMQDLVEEYR	sp|P04104|K2C1_MOUSE	yes	yes	262	275	14	D	T	0	1752.835	3	6.15E-02	44.93	1.34	0.81	1
333	SELVQSGKSEISELR	sp|Q61781|K1C14_MOUSE	no	no	327	341	15	N	R	0	1660.863	3	2.16E-02	55.72	2.31	1.49	4
334	SEPEIPKGIR	sp|Q9WTP6-2|KAD2_MOUSE	yes	no	8	17	10	A	A	0	1124.619	3	6.97E-03	99.82	1.22	0.97	9
335	SEPLAATSTGDFNR	sp|Q9Z1T2|TSP4_MOUSE	yes	yes	210	223	14	Q	Q	0	1464.685	2	1.40E-08	118.52	0.87	0.82	3
336	SEQQGEAALADAR	sp|Q9ERE2|KRT81_MOUSE	yes	no	353	365	13	Q	C	0	1344.627	2	1.41E-03	142.45	1.75	1.21	2
337	SESAQELAEGQR	sp|Q8CI51-3|PDLI5_MOUSE	yes	no	105	116	12	C	R	0	1303.600	2	3.75E-07	127.02	1.11	0.92	5
338	SEVASSLVLER	sp|Q9CYR0|SSBP_MOUSE	yes	yes	18	28	11	E	S	0	1188.635	2	3.21E-02	65.18	1.22	1.09	3
339	SEVPGAAAEGPGGSGVGLGDR	sp|Q9EP72|EMC7_MOUSE	yes	yes	23	43	21	S	F	0	1838.876	2	1.04E-24	126.02	1.50	1.00	4
340	SFGGGLGSGFGGR	sp|Q61781|K1C14_MOUSE	yes	no	72	84	13	S	F	0	1154.547	2	6.09E-05	96.46	1.35	0.96	3
341	SFGGGTGSGFTSLLMER	sp|P68373|TBA1C_MOUSE	no	no	140	156	17	H	L	0	1702.799	2	2.87E-05	92.26	1.49	1.42	3
342	SFSAASAITPSVSR	sp|Q922U2|K2C5_MOUSE	yes	no	16	29	14	R	T	0	1379.705	2	6.11E-15	172.57	1.88	1.23	4
343	SFSSSSFGGGLGSGFGGR	sp|Q61781|K1C14_MOUSE	yes	no	67	84	18	G	F	0	1649.743	2	1.09E-11	106.93	1.66	1.03	3
344	SFVNDIFER	sp|Q9D2U9|H2B3A_MOUSE	yes	no	65	73	9	N	I	0	1125.546	2	5.09E-09	114.89	1.28	0.88	1
345	SGAQASSTPLSPTR	sp|P48678-2|LMNA_MOUSE	yes	no	12	25	14	R	I	0	1358.679	2	1.29E-10	119.54	1.16	1.01	9
346	SGEEFWPGQSAADILSGAASR	sp|Q8VHI3|OFUT2_MOUSE	yes	yes	22	42	21	A	R	0	2134.992	2;3	2.81E-33	162.32	1.03	0.97	9
347	SGFGGGQGFGGGSR	sp|Q3TTY5|K22E_MOUSE	yes	no	118	131	14	G	F	0	1226.543	2	1.55E-10	118.21	2.62	1.71	4
348	SGFGSKSLMNLGGGR	sp|P04104|K2C1_MOUSE	yes	yes	61	75	15	G	S	0	1466.730	3	6.41E-02	37.61	2.22	1.32	1
349	SGGFGGGSGFGGGQGFGGGSR	sp|Q3TTY5|K22E_MOUSE	yes	no	111	131	21	G	F	0	1745.751	2	3.17E-19	117.38	2.84	1.85	4
350	SGGFSGGSFSR	sp|P02535-3|K1C10_MOUSE	yes	no	41	51	11	S	G	0	1044.463	2	2.78E-02	66.27	2.11	1.37	4
351	SGGPLLCAGVAHGIVSYGR	sp|P21812|MCPT4_MOUSE	yes	yes	202	220	19	D	G	0	1869.952	3	3.88E-12	109.87	1.90	1.36	3
352	SGLEIVPNGITLPVDFQGR	sp|O35737|HNRH1_MOUSE	yes	yes	132	150	19	F	S	0	2011.074	2	1.16E-02	48.91	0.89	0.55	1
353	SGLSDGYGFTTDLFGR	sp|Q9Z2X1-2|HNRPF_MOUSE	yes	no	227	242	16	Y	D	0	1691.779	2	3.96E-20	168.41	3.44	2.29	4
354	SGNYSSQSFGGFLR	sp|Q9QZU5|KR151_MOUSE	yes	yes	7	20	14	N	Q	0	1505.690	2	1.02E-02	67.14	2.15	1.30	3
355	SGVQGASAGGLAADASR	sp|P11088|FILA_MOUSE	yes	yes	53	69	17	G	R	0	1473.717	2	4.92E-15	124.63	1.37	0.89	4
356	SHTDVKVPDFSDYR	sp|Q9CR68|UCRI_MOUSE	yes	yes	79	92	14	F	R	0	1664.779	3;4	2.21E-06	103.76	1.47	0.93	13
357	SHTDVKVPDFSDYRR	sp|Q9CR68|UCRI_MOUSE	yes	yes	79	93	15	F	A	1	1820.881	4	5.07E-02	39.63	1.29	0.93	1
358	SHYSSYYGGLGYGYGSFGGPGCGCNSIR	sp|Q925H6|KR193_MOUSE	yes	yes	2	29	28	M	R	0	2979.234	2;3	2.56E-50	198.67	1.90	1.26	12
359	SIGTLSDPCKDPTR	sp|Q7TPC1|CDSN_MOUSE	yes	yes	34	47	14	K	I	0	1545.746	2;3	1.56E-04	94.09	1.52	0.96	8
360	SIVVSPILIPENQR	sp|Q9WTR5|CAD13_MOUSE	yes	yes	139	152	14	R	Q	0	1563.898	2;3	5.33E-15	146.96	1.33	1.02	12
361	SKDSEGSWFR	sp|O55125|NIPS1_MOUSE	yes	yes	36	45	10	Y	S	0	1197.542	3	5.27E-04	124.12	1.57	1.29	3
362	SLADAINTEFKNTR	sp|P20152|VIME_MOUSE	yes	yes	87	100	14	F	T	0	1578.800	3	4.94E-02	49.30	2.06	1.23	1
363	SLEASLAETEGR	sp|P02535-3|K1C10_MOUSE	yes	no	377	388	12	Q	Y	0	1261.615	2	8.37E-03	74.99	0.78	0.61	2
364	SLEGDHSTPPSAYGSVKPYTNFDAER	sp|P07356|ANXA2_MOUSE	yes	yes	12	37	26	L	D	0	2824.294	4	1.23E-11	70.35	1.30	1.31	3
365	SLGGGTGSGMGTLLISKIR	sp|P99024|TBB5_MOUSE	no	no	138	156	19	H	E	0	1803.988	3	1.94E-04	65.23	1.35	1.31	5
366	SLGGGYSSGGFSGGSFSR	sp|P02535-3|K1C10_MOUSE	yes	no	34	51	18	G	G	0	1665.738	2	1.27E-05	86.80	1.39	0.97	2
367	SLGGVSEASR	sp|P35175|CYT1_MOUSE	yes	yes	2	11	10	M	A	0	961.483	2	6.85E-04	120.06	0.85	0.74	4
368	SLGNAGNEIGR	sp|Q6P253-2|DMKN_MOUSE	yes	no	97	107	11	R	Q	0	1086.542	2	1.39E-03	98.11	1.28	1.19	8
369	SLHLGVTPSVLR	sp|O89023|TPP1_MOUSE	yes	yes	194	205	12	V	Q	0	1277.746	3	4.90E-02	61.23	1.26	1.18	4
370	SLPPHQKVPLPSLSPTMQAGTIAR	sp|Q8BMF4|ODP2_MOUSE	yes	yes	86	109	24	Y	W	0	2525.379	4	6.61E-04	60.74	0.97	0.95	1
371	SLVFDPVQKTLLADQGEIR	sp|Q9R190|MTA2_MOUSE	yes	yes	130	148	19	Y	V	0	2128.153	3	7.55E-05	69.08	2.29	1.53	3
372	SLVMPSEHAILDNDGLYDPECDDKGR	sp|Q8BGV3|TACD2_MOUSE	yes	yes	82	107	26	R	F	0	2945.317	4	7.52E-04	40.09	1.73	1.02	3
373	SLYNVGGSKR	sp|Q922U2|K2C5_MOUSE	yes	no	61	70	10	R	I	0	1079.572	3	8.29E-02	55.31	1.56	0.93	4
374	SLYSSSPGGAYVTR	sp|P20152|VIME_MOUSE	yes	yes	51	64	14	R	S	0	1443.699	2	4.24E-15	206.49	0.86	0.70	15
375	SMGGHGALICALKNPGKYR	sp|Q9R0P3|ESTD_MOUSE	yes	yes	149	167	19	H	S	0	2029.035	4	4.13E-03	40.49	0.81	0.75	1
376	SNIEANESEEVR	sp|O88456|CPNS1_MOUSE	yes	yes	89	100	12	Y	Q	0	1375.622	2	5.73E-02	59.23	2.88	1.88	3
377	SNIPFITVPLSR	sp|Q9Z110-2|P5CS_MOUSE	yes	no	44	55	12	W	A	0	1342.761	2	1.75E-06	117.93	1.28	1.03	7
378	SNISAAKAVADAIR	sp|P80315|TCPD_MOUSE	yes	yes	36	49	14	F	T	0	1385.763	2;3	3.98E-03	75.97	2.92	1.95	7
379	SNMAVVTCGSVVKLLNTR	sp|Q9DCT5|SDF2_MOUSE	yes	yes	19	36	18	A	H	0	1948.023	3	1.76E-02	36.64	1.34	0.90	4
380	SNMEPLFEGYIEALR	sp|Q9ERE2|KRT81_MOUSE	no	no	149	163	15	E	R	0	1767.850	2	4.30E-02	42.95	1.05	0.62	1
381	SNSCKQTVITCGEGER	sp|Q9Z1Q3|LY66D_MOUSE	yes	yes	32	47	16	P	C	0	1824.809	3	9.72E-17	126.63	2.13	1.37	4
382	SNTSFSCISR	sp|Q3TTY5|K22E_MOUSE	yes	no	38	47	10	R	H	0	1157.514	2	3.80E-03	80.25	0.97	0.67	2
383	SNVEEADAAMAASPHAVDGNTVELKR	sp|Q9CX86|ROA0_MOUSE	yes	yes	56	81	26	Y	A	0	2681.272	4	9.96E-05	47.81	1.75	1.13	2
384	SNWLSKDYIPVDQEELR	sp|Q9JHU4|DYHC1_MOUSE	yes	yes	2872	2888	17	Y	D	0	2091.027	3	1.50E-07	103.66	2.57	1.70	4
385	SPADLPKNWDWR	sp|Q9WUU7|CATZ_MOUSE	yes	yes	60	71	12	L	N	0	1483.721	3	4.13E-02	63.09	1.17	1.15	3
386	SPAGAPLEDVVIER	sp|Q61576|FKB10_MOUSE	yes	yes	34	47	14	A	Y	0	1451.762	2	1.55E-08	109.07	1.56	1.35	8
387	SPLPTANGR	sp|Q91X72|HEMO_MOUSE	yes	yes	24	32	9	A	V	0	911.482	2	2.66E-02	56.26	NaN	NaN	0
388	SPPPAATPTPTPPTR	sp|Q80VP1|EPN1_MOUSE	yes	no	453	467	15	G	K	0	1486.778	2	4.38E-02	42.32	1.55	0.98	9
389	SPTPALFSLPEAR	sp|Q8R3N6|THOC1_MOUSE	yes	yes	2	14	13	M	T	0	1384.735	2	2.61E-04	91.62	1.41	0.93	2
390	SQDLQVIDLLTVGESR	sp|Q05895|TSP3_MOUSE	yes	yes	22	37	16	G	Q	0	1771.932	2	2.21E-37	180.88	1.34	0.90	7
391	SQIQSQISALEEQLQQIR	sp|P02535-3|K1C10_MOUSE	yes	no	394	411	18	L	A	0	2098.102	2;3	2.22E-26	191.64	5.45	3.48	4
392	SQISALEEQLQQIR	sp|P02535-3|K1C10_MOUSE	yes	no	398	411	14	Q	A	0	1641.869	2;3	1.17E-14	153.23	0.83	0.55	1
393	SQNAAAKASATAPEVR	sp|Q9D0G0|RT30_MOUSE	yes	yes	17	32	16	L	D	0	1570.806	3	3.28E-02	39.00	1.47	0.92	2
394	SQQSASGAPVLLR	sp|Q9DCM0|ETHE1_MOUSE	yes	yes	14	26	13	L	Q	0	1312.710	2	1.26E-10	173.06	0.92	0.85	6
395	SQVHSGVQVEGR	sp|P11088|FILA_MOUSE	yes	yes	25	36	12	D	R	0	1281.643	3	2.26E-08	135.91	0.88	0.59	4
396	SSEAPPLVNEDVKR	sp|Q91YQ5|RPN1_MOUSE	yes	yes	26	39	14	A	T	0	1539.789	2;3	5.33E-15	163.99	1.65	1.07	13
397	SSFENVEGLPAFR	sp|O35114|SCRB2_MOUSE	yes	yes	282	294	13	F	Y	0	1451.705	2	8.26E-03	72.89	4.38	2.96	1
398	SSFGGGLGSGFGGR	sp|Q61781|K1C14_MOUSE	yes	no	71	84	14	S	F	0	1241.579	2	4.20E-04	88.28	1.68	1.17	3
399	SSFGPISEVVVVKDR	sp|O89086|RBM3_MOUSE	yes	yes	27	41	15	F	E	0	1617.873	3	1.19E-02	61.44	2.38	1.43	1
400	SSGGACGIGGGYGGSFSSSSFGGGLGSGFGGR	sp|Q61781|K1C14_MOUSE	yes	yes	53	84	32	F	F	0	2787.194	2;3	2.95E-48	139.85	2.95	1.86	6
401	SSGGFSGGSFSR	sp|P02535-3|K1C10_MOUSE	yes	no	40	51	12	Y	G	0	1131.495	2	6.00E-05	102.97	4.11	2.76	4
402	SSGPGSPLTGNAATEEVR	sp|Q60847-2|COCA1_MOUSE	yes	no	797	814	18	Y	G	0	1728.828	2	5.22E-29	228.39	4.29	2.85	4
403	SSGSAGLVSFQR	sp|P04104|K2C1_MOUSE	yes	yes	21	32	12	F	R	0	1194.599	2	1.74E-08	171.26	3.62	2.36	4
404	SSLACNIALDAVKTVQFEENGR	sp|P80318|TCPG_MOUSE	yes	yes	169	190	22	W	K	0	2421.196	3	1.63E-04	48.62	2.09	1.35	2
405	SSLENIFSR	sp|Q8BYJ6-4|TBCD4_MOUSE	yes	no	575	583	9	T	G	0	1051.530	2	2.41E-02	66.69	1.77	1.07	1
406	SSMAEVDAAMAAR	sp|O88569-3|ROA2_MOUSE	yes	no	58	70	13	F	P	0	1308.580	2	6.33E-03	74.99	2.65	1.67	2
407	SSQSFGGFLR	sp|Q9QZU5|KR151_MOUSE	yes	yes	11	20	10	Y	Q	0	1084.530	2	3.21E-03	107.79	3.35	2.08	1
408	SSSAPVASPNVR	sp|Q05920|PYC_MOUSE	yes	yes	19	30	12	R	R	0	1170.599	2	9.90E-09	159.44	1.00	0.82	8
409	SSSFGGGLGSGFGGR	sp|Q61781|K1C14_MOUSE	yes	no	70	84	15	S	F	0	1328.611	2	1.64E-06	88.77	1.61	1.01	2
410	SSSGSGVQGASAGGLAADASR	sp|P11088|FILA_MOUSE	yes	yes	49	69	21	G	R	0	1791.835	2	5.56E-09	92.79	1.48	0.95	4
411	SSSLPDICYR	sp|P53996-2|CNBP_MOUSE	yes	no	40	49	10	V	C	0	1196.550	2	9.36E-05	137.98	1.57	1.13	9
412	SSSPGGAYVTR	sp|P20152|VIME_MOUSE	yes	yes	54	64	11	Y	S	0	1080.520	2	2.40E-07	142.89	1.46	1.11	8
413	SSSSFGGGLGSGFGGR	sp|Q61781|K1C14_MOUSE	yes	no	69	84	16	F	F	0	1415.643	2	9.55E-38	138.05	2.55	1.59	3
414	SSWWTHVEMGPPDPILGVTEAFKR	sp|P05202|AATM_MOUSE	yes	yes	30	53	24	A	D	0	2739.348	3;4	4.20E-41	179.42	1.07	1.05	10
415	STDITSLDQYVER	sp|P08113|ENPL_MOUSE	yes	yes	518	530	13	H	M	0	1525.726	2	3.11E-04	90.41	1.41	1.13	8
416	STEVSCGGPVCLPSSCR	sp|A2A5X5|KR161_MOUSE	yes	yes	20	36	17	C	S	0	1851.791	2	1.61E-02	46.89	NaN	NaN	0
417	STQAAPQVVLNVPETQVTCLENGLR	sp|Q9CXT8|MPPB_MOUSE	yes	yes	44	68	25	R	V	0	2723.391	3	1.06E-01	13.88	1.60	1.10	1
418	STSVTSDNLSR	sp|Q61166|MARE1_MOUSE	yes	yes	7	17	11	Y	H	0	1165.558	2	1.97E-07	159.99	1.42	1.16	7
419	STSVTSENLSR	sp|Q6PER3|MARE3_MOUSE	yes	yes	7	17	11	Y	H	0	1179.573	2	1.53E-03	94.77	1.23	1.16	4
420	STVEEAVATR	sp|Q9JIX8-3|ACINU_MOUSE	yes	no	283	292	10	Y	T	0	1061.535	2	2.96E-03	108.70	2.25	1.47	4
421	STVLGPLR	sp|Q6J1H4-2|UTF1_MOUSE	yes	no	246	253	8	I	D	0	841.502	2	1.78E-01	89.55	0.43	0.27	1
422	STVTAQFPGACGLR	sp|Q921F2|TADBP_MOUSE	yes	yes	29	42	14	L	Y	0	1463.719	2	7.02E-15	148.62	4.96	3.19	2
423	SVASKTGFGSGGQSSGGR	sp|Q3TTY5|K22E_MOUSE	yes	no	532	549	18	S	G	0	1625.776	3	3.28E-03	51.59	2.97	1.81	3
424	SVDADINGLR	sp|Q9Z320|K1C27_MOUSE	yes	yes	176	185	10	Q	R	0	1058.536	2	1.16E-12	112.36	NaN	NaN	0
425	SVEADINGLR	sp|P02535-3|K1C10_MOUSE	no	no	236	245	10	Q	R	0	1072.551	2	8.32E-03	96.34	2.02	1.37	4
426	SVEEQLAQLR	sp|Q61781|K1C14_MOUSE	no	no	385	394	10	G	C	0	1171.620	2	5.63E-03	102.52	1.81	1.15	4
427	SVVAGGPEVTLTPER	sp|Q8CIM3|D2HDH_MOUSE	yes	yes	51	65	15	Y	Y	0	1510.799	2	1.03E-02	62.86	1.05	0.99	5
428	SYSEIGGLSEQIR	sp|P62334|PRS10_MOUSE	yes	yes	131	143	13	V	E	0	1437.710	2	4.73E-06	106.32	1.28	1.20	6
429	SYTCNSGNYSSQSFGGFLR	sp|Q9QZU5|KR151_MOUSE	yes	yes	2	20	19	M	Q	0	2130.907	2	3.73E-05	79.49	2.04	1.26	3
430	SYYGSYYGGLGSGIR	sp|O08632|KR195_MOUSE	yes	yes	2	16	15	M	G	0	1598.737	2;3	1.37E-15	189.10	3.24	1.98	23
431	SYYSGYSGGLGYGYGGFGGLGCGCNSIR	sp|Q8C1I6|KR163_MOUSE	yes	yes	2	29	28	M	R	0	2885.217	2;3	1.11E-50	172.32	2.87	1.76	26
432	SYYSGYSGGLGYGYGSSFGGLGCGCNSIR	sp|Q925I0|KR192_MOUSE	yes	yes	2	30	29	M	R	0	3002.260	3	6.99E-20	100.70	2.67	1.66	3
433	TAEILELAGNAAR	sp|Q8CGP6|H2A1H_MOUSE	yes	no	60	72	13	L	D	0	1327.710	2	3.34E-08	124.12	2.59	1.66	4
434	TAFLGYKAGMTHIVR	sp|P27659|RL3_MOUSE	yes	yes	44	58	15	L	E	0	1663.887	4	2.66E-02	53.30	2.95	2.09	1
435	TATFAQALQSVPETQVSILDNGLR	sp|Q9CZ13|QCR1_MOUSE	yes	yes	35	58	24	G	V	0	2558.334	2;3	4.57E-41	161.53	1.39	0.97	13
436	TCVATGVPTPIINWR	sp|Q05793|PGBM_MOUSE	yes	yes	427	441	15	F	L	0	1683.877	2	4.16E-15	163.99	8.19	5.38	4
437	TDEDSILNLLTSR	sp|P48036|ANXA5_MOUSE	yes	yes	31	43	13	G	S	0	1475.747	2	6.80E-08	121.45	1.16	0.91	3
438	TDILFTEQER	sp|O08810|U5S1_MOUSE	yes	yes	167	176	10	Y	G	0	1250.614	2	8.29E-02	55.31	5.43	3.71	1
439	TDKFSSQDSIVR	sp|Q08189|TGM3_MOUSE	yes	yes	22	33	12	H	R	0	1381.684	3	2.11E-02	68.00	1.13	1.10	4
440	TDLEEALQQCR	sp|Q3TTY5|K22E_MOUSE	yes	no	464	474	11	L	E	0	1361.625	2	1.08E-04	114.86	2.51	1.60	3
441	TDNANVLLQIDNAR	sp|P02535-3|K1C10_MOUSE	yes	no	204	217	14	T	L	0	1555.795	2	1.38E-06	104.95	2.71	1.65	3
442	TDQNFYSLLGVSKTASSR	sp|Q9DC23|DJC10_MOUSE	yes	yes	32	49	18	G	E	0	1972.985	3	4.34E-03	48.29	1.20	0.76	3
443	TEAELPSAPAELPGGAACLSR	sp|Q9R097|SPIT1_MOUSE	yes	yes	27	47	21	A	F	0	2096.021	2;3	2.54E-15	114.55	1.45	1.09	10

444	TEAPLNPKANR	sp|P63260|ACTG_MOUSE	no	no	106	116	11	L	E	0	1209.647	3	2.81E-05	120.06	1.15	1.11	9
445	TEEDAASYVR	sp|Q9DBC7|KAP0_MOUSE	yes	yes	106	115	10	Y	K	0	1139.510	2	2.57E-02	69.72	1.32	1.15	4
446	TEGAELVDSVLDVVR	sp|P99024|TBB5_MOUSE	no	no	107	121	15	Y	K	0	1600.831	2	1.83E-15	174.62	1.15	1.01	8
447	TGFGAFGFGSSGIR	sp|Q9QZU5|KR151_MOUSE	yes	yes	100	113	14	N	S	0	1359.657	2	1.83E-08	107.74	2.51	1.50	2
448	TGGDAAAPGAAGTQAELPHR	sp|Q9D0F3|LMAN1_MOUSE	yes	yes	33	52	20	G	R	0	1846.892	3	2.12E-27	165.17	1.36	1.04	9
449	TGLPVDIDECR	sp|Q61554|FBN1_MOUSE	yes	yes	1761	1771	11	Y	E	0	1273.597	2	1.67E-03	89.30	3.81	2.50	4
450	TGPAGPAGPIGPAGAR	sp|P11087-2|CO1A1_MOUSE	yes	no	830	845	16	E	G	0	1345.710	2	2.00E-02	50.81	2.56	1.56	3
451	TGSGFTSLLMER	sp|P68373|TBA1C_MOUSE	no	no	145	156	12	G	L	0	1297.634	2	6.32E-02	76.07	0.09	0.07	1
452	TGSGMGTLLISKIR	sp|P99024|TBB5_MOUSE	no	no	143	156	14	G	E	0	1432.807	3	4.68E-06	100.22	1.42	1.28	6
453	TICNPCGPVQR	sp|Q8R081|HNRPL_MOUSE	yes	yes	210	220	11	Y	I	0	1300.602	2	1.11E-02	73.50	1.82	1.19	4
454	TIGKEIIDLVLDR	sp|P68373|TBA1C_MOUSE	yes	no	109	121	13	Y	I	0	1483.861	2;3	1.59E-04	94.09	1.23	1.03	3
455	TISPLDLAKLNQVAR	sp|P60335|PCBP1_MOUSE	yes	yes	229	243	15	H	Q	0	1637.947	3	1.72E-01	17.25	NaN	NaN	0
456	TISSSVASKTGFGSGGQSSGGR	sp|Q3TTY5|K22E_MOUSE	yes	no	528	549	22	S	G	0	2013.972	3	1.63E-04	48.62	3.46	2.03	3
457	TITVVPVYTEGDGGR	sp|Q60847-2|COCA1_MOUSE	yes	no	1912	1926	15	Y	T	0	1562.794	2	1.81E-04	90.71	3.22	2.24	2
458	TKFETEQSLR	sp|Q61781|K1C14_MOUSE	yes	yes	208	217	10	R	M	0	1237.630	3	1.78E-02	78.34	1.52	1.01	4
459	TKLEAAVTQSEQQGEAALADAR	sp|Q9ERE2|KRT81_MOUSE	yes	no	344	365	22	N	C	0	2286.145	3	1.71E-33	202.43	1.01	0.67	4
460	TKLEAAVTQSEQQGEAALTDAR	sp|Q6IMF0|KRT83_MOUSE	yes	yes	349	370	22	N	C	0	2316.156	3	1.87E-33	185.41	2.05	1.29	3
461	TKMEISELNR	sp|P04104|K2C1_MOUSE	yes	yes	402	411	10	N	M	0	1219.623	3	2.49E-03	110.39	1.27	0.92	3
462	TKNEITELTR	sp|Q9R0H5|K2C71_MOUSE	yes	no	345	354	10	N	F	0	1203.646	3	1.98E-02	73.63	1.86	1.05	3
463	TKWELLQQLDVGSR	sp|Q3TTY5|K22E_MOUSE	yes	no	229	242	14	R	T	0	1671.894	3	4.71E-02	60.55	1.44	0.85	1
464	TKWELLQQVDTTTR	sp|P04104|K2C1_MOUSE	yes	yes	218	231	14	Q	T	0	1717.900	3	7.59E-05	95.85	1.11	0.69	2
465	TKYEELQQTAGR	sp|Q922U2|K2C5_MOUSE	yes	no	357	368	12	Q	H	0	1422.710	3	8.57E-05	99.84	1.92	1.27	4
466	TLCKSDLEAQVESLR	sp|Q61897|KT33B_MOUSE	no	no	170	184	15	L	Q	0	1747.877	3	5.18E-03	86.50	2.18	1.55	1
467	TLTTDNANVLLQIDNAR	sp|P02535-3|K1C10_MOUSE	yes	no	201	217	17	L	L	0	1870.975	2	1.65E-02	39.91	2.67	1.64	1
468	TNLAPSLWLHR	sp|Q09PK2|APRV1_MOUSE	yes	yes	108	118	11	G	F	0	1306.715	3	2.33E-02	67.39	1.26	1.09	4
469	TNQELQEINR	sp|P07356|ANXA2_MOUSE	yes	yes	136	145	10	R	V	0	1243.616	2	5.27E-04	124.12	0.25	0.24	5
470	TNVILSMDNNR	sp|Q3TTY5|K22E_MOUSE	no	no	352	362	11	D	N	0	1275.624	2	1.34E-02	47.71	NaN	NaN	0
471	TPSVDHGFLVTR	sp|P02463|CO4A1_MOUSE	yes	yes	1439	1450	12	G	H	0	1327.688	3	1.83E-05	110.38	1.04	0.98	6
472	TQAGSEVSALLGR	sp|P56480|ATPB_MOUSE	yes	yes	312	324	13	F	I	0	1287.678	2	2.03E-02	66.00	2.01	1.33	2
473	TQKAPQVSTPTLVEAAR	sp|P07724|ALBU_MOUSE	yes	yes	436	452	17	Y	N	0	1795.979	3	1.02E-02	51.09	1.35	1.29	5
474	TREEINELNR	sp|Q9ERE2|KRT81_MOUSE	no	no	318	327	10	R	M	1	1272.642	3	8.21E-03	97.16	0.56	0.37	4
475	TRGSLGGGYSSGGFSGGSFSR	sp|P02535-3|K1C10_MOUSE	yes	no	31	51	21	S	G	1	1979.909	3	3.64E-08	87.21	1.52	1.05	3
476	TRLENEIQTYR	sp|P02535-3|K1C10_MOUSE	yes	no	429	439	11	K	S	1	1421.726	3	6.15E-02	58.17	1.85	1.21	2
477	TRPLEQAVAAIVCTFQEYAGR	sp|P62818|S10A3_MOUSE	yes	yes	2	22	21	M	C	1	2379.201	3	1.78E-25	133.84	1.32	1.03	1
478	TRYFCCGNYFPGYPCYGTNFHGTYR	sp|Q9D3I6|KRA71_MOUSE	yes	yes	2	26	25	M	A	1	3157.306	3;4	2.09E-07	58.47	2.31	1.51	6
479	TSGLETLLNIPIKR	sp|E9Q557|DESP_MOUSE	yes	yes	981	994	14	Y	T	0	1553.914	3	6.42E-21	95.42	NaN	NaN	0
480	TSLCFVYPLDFAR	sp|P51881|ADT2_MOUSE	yes	no	126	138	13	A	T	0	1587.776	2	1.21E-05	102.73	2.21	1.35	3
481	TSLEVENQNLR	sp|P57776-2|EF1D_MOUSE	yes	no	61	71	11	I	G	0	1301.658	2	4.49E-04	107.06	0.58	0.54	5
482	TSSYSALSEPSR	sp|Q9DCS3|MECR_MOUSE	yes	yes	31	42	12	T	V	0	1283.599	2	7.21E-09	188.91	1.03	0.89	9
483	TSVATKKTEQGPPSSEYIFER	sp|P29758|OAT_MOUSE	yes	yes	26	46	21	A	E	0	2354.175	4	1.02E-19	123.19	1.20	0.96	8
484	TSVVLSMDNNR	sp|Q922U2|K2C5_MOUSE	yes	no	315	325	11	D	S	0	1234.598	2	4.41E-07	137.89	1.81	1.18	4
485	TTAIAEAWAR	sp|P68373|TBA1C_MOUSE	no	no	381	390	10	N	L	0	1088.562	2	2.20E-02	72.20	1.35	1.07	2
486	TTDNANVLLQIDNAR	sp|P02535-3|K1C10_MOUSE	yes	no	203	217	15	L	L	0	1656.843	2	4.58E-11	119.46	2.48	1.53	3
487	TTFNVQDGPDFQDR	sp|P97493|THIOM_MOUSE	yes	yes	60	73	14	L	V	0	1638.727	2	2.38E-32	263.83	1.11	0.97	9
488	TTIAGVVYKDGIVLGADTR	sp|P70195|PSB7_MOUSE	yes	yes	44	62	19	G	A	0	1948.063	3	9.15E-17	122.94	1.05	1.02	12
489	TTLLEALDCILPPTRPTDKPLR	sp|P10126|EF1A1_MOUSE	yes	yes	226	247	22	G	L	1	2519.378	4	3.68E-02	48.05	1.24	1.23	1
490	TTMYPGIADR	sp|P63260|ACTG_MOUSE	no	no	303	312	10	G	M	0	1123.533	2	8.23E-04	116.52	0.95	0.81	4
491	TTNYRPDWNR	sp|Q8VHC3|SELM_MOUSE	yes	yes	24	33	10	S	L	1	1321.616	3	2.39E-02	70.94	1.11	1.04	5
492	TTPALLPLSGR	sp|P39098-2|MA1A2_MOUSE	yes	no	2	12	11	M	R	0	1124.655	2	6.15E-02	58.17	1.49	1.04	2
493	TVEGDVNTDPWAGYR	sp|Q8BP48|MAP11_MOUSE	yes	yes	68	82	15	W	Y	0	1678.759	2	4.77E-13	132.08	1.98	1.34	5
494	TVHNLYLFDR	sp|Q5NCF2|TPPC1_MOUSE	yes	yes	2	11	10	M	N	0	1276.656	3	4.88E-02	63.09	1.49	1.30	5
495	TVLSGGTTMYPGIADR	sp|P63260|ACTG_MOUSE	yes	no	297	312	16	N	M	0	1637.808	2	8.12E-04	81.66	1.46	1.16	6
496	TVSGPETPEPR	sp|Q99KD5|UN45A_MOUSE	yes	yes	2	12	11	M	P	0	1168.572	2	8.60E-04	103.08	1.20	0.83	4
497	TYHGDSDLQLDR	sp|P99024|TBB5_MOUSE	yes	yes	35	46	12	G	I	0	1418.643	3	4.67E-05	104.59	1.48	1.35	5
498	TYHGDSDLQLER	sp|P68372|TBB4B_MOUSE	yes	no	35	46	12	G	I	0	1432.658	3	2.67E-03	80.32	1.32	1.25	5
499	VAAGVGEFEAGISKNGQTR	sp|P10126|EF1A1_MOUSE	yes	no	116	134	19	I	E	0	1889.960	3	4.06E-03	40.80	2.18	1.51	3
500	VALDFEQEMATAASSSSLEKSYELPDGQVITIGNER	sp|P63260|ACTG_MOUSE	yes	no	219	254	36	Y	F	0	3884.863	3;4	3.44E-24	80.65	2.27	1.36	3
501	VAPMKGQVCVVTGASR	sp|Q99L04|DHRS1_MOUSE	yes	yes	2	17	16	M	G	0	1658.860	3	2.50E-02	42.95	2.17	1.42	2
502	VAVMHGETEGTVPGNALVVDPEKPFR	sp|Q8BH64|EHD2_MOUSE	yes	yes	98	123	26	F	K	0	2748.391	4	1.03E-06	51.83	1.93	1.35	1
503	VAVPEAAEER	sp|Q8JZQ9|EIF3B_MOUSE	yes	yes	7	16	10	N	A	0	1069.540	2	2.39E-02	70.94	1.13	0.79	9
504	VDLEPTVIDEIR	sp|P68368|TBA4A_MOUSE	yes	yes	68	79	12	F	N	0	1397.740	2	4.55E-02	62.09	1.56	1.00	2
505	VDLEPTVIDEVR	sp|P68373|TBA1C_MOUSE	yes	no	68	79	12	F	T	0	1383.725	2	6.08E-05	102.87	1.08	0.69	3
506	VDSEGHLYTVPIR	sp|P49817|CAV1_MOUSE	yes	yes	7	19	13	Y	E	0	1484.762	3	4.37E-02	58.32	5.05	3.63	1
507	VDVSSVPLAIGLTGQR	sp|Q8VH51-3|RBM39_MOUSE	yes	no	45	60	16	F	V	0	1610.899	2	2.25E-03	67.65	1.76	1.21	1
508	VDYYEVLGVQR	sp|O54946-2|DNJB6_MOUSE	yes	no	2	12	11	M	H	0	1339.677	2	1.52E-09	87.18	NaN	NaN	0
509	VEFVDVSSVPLAIGLTGQR	sp|Q8VH51-3|RBM39_MOUSE	yes	no	42	60	19	Y	V	0	1986.079	2;3	1.44E-06	92.47	3.44	2.46	5
510	VEKEEAGGGGGGGISEEEAAQYDR	sp|Q9R1T2-2|SAE1_MOUSE	yes	no	2	25	24	M	Q	0	2394.057	3	1.87E-09	68.45	1.07	1.01	5
511	VELLMDAEGKSR	sp|Q9D0E1-2|HNRPM_MOUSE	yes	no	100	111	12	Y	G	0	1346.686	3	5.34E-02	60.16	2.07	1.44	3
512	VGGGGSGGGLLENANPLIYER	sp|Q9D187|MIP18_MOUSE	yes	yes	2	22	21	M	S	0	2029.023	2	1.02E-06	69.77	1.06	0.88	7
513	VGSLNLEELSEMR	sp|Q8K2C7-2|OS9_MOUSE	yes	no	28	40	13	G	Y	0	1475.729	2	3.25E-06	107.74	1.13	0.74	2
514	VGVKPVGSDPDFQPELSGAGSR	sp|Q8CDN6|TXNL1_MOUSE	yes	yes	2	23	22	M	L	0	2198.097	3	7.84E-20	121.33	1.11	1.01	8
515	VHLTDAEKAAVSCLWGKVNSDEVGGEALGR	sp|P02088|HBB1_MOUSE	yes	yes	2	31	30	M	L	0	3167.567	4;5	1.45E-21	89.66	1.93	1.60	8
516	VHLTDAEKSAVSCLWAKVNPDEVGGEALGR	sp|P02089|HBB2_MOUSE	yes	yes	2	31	30	M	L	0	3207.598	3;4;5	7.71E-25	101.34	1.58	1.30	10
517	VKLFIGNLPR	sp|Q8C7Q4-2|RBM4_MOUSE	yes	no	2	11	10	M	E	0	1155.713	3	6.06E-03	101.65	1.24	1.10	7
518	VKLTAELIEQAAQYTNAVR	sp|P57784|RU2A_MOUSE	yes	yes	2	20	19	M	D	0	2117.148	2;3	1.84E-25	143.04	0.97	0.82	10
519	VKMAAAGGGGGGGR	sp|Q8R081|HNRPL_MOUSE	yes	yes	33	46	14	M	Y	0	1144.577	3	1.37E-02	65.30	1.10	0.84	5
520	VKVGVNGFGR	sp|P16858|G3P_MOUSE	yes	yes	2	11	10	M	I	0	1031.588	2;3	9.37E-05	160.36	1.15	1.02	20
521	VLAELYVSDR	sp|Q8BP47|SYNC_MOUSE	yes	yes	13	22	10	M	E	0	1163.619	2	1.13E-02	82.42	1.13	1.04	5
522	VLESTMVCVDNSEYMR	sp|O35226-5|PSMD4_MOUSE	yes	no	2	17	16	M	N	0	1931.843	3	8.15E-04	81.63	0.77	0.67	2
523	VLESVVADLLNR	sp|Q8BX70-2|VP13C_MOUSE	yes	no	2	13	12	M	F	0	1326.751	2	4.01E-02	94.12	NaN	NaN	0
524	VLLESEQFLTELTR	sp|P16254|SRP14_MOUSE	yes	yes	2	15	14	M	L	0	1676.899	2	1.07E-03	85.49	1.13	0.94	3
525	VLRPPGGGSNFSLGFDEPAEQPVR	sp|P97825|HN1_MOUSE	yes	yes	20	43	24	R	K	1	2525.266	3	1.41E-29	133.41	1.67	1.59	4
526	VLSGEDKSNIKAAWGKIGGHGAEYGAEALER	sp|P01942|HBA_MOUSE	yes	yes	2	32	31	M	M	0	3212.621	5;6	1.12E-06	64.21	1.40	1.43	4
527	VLSNEPAASAAEEEVEDDALVR	sp|Q8BYA0|TBCD_MOUSE	yes	yes	2	23	22	M	A	0	2313.097	2	2.82E-08	86.56	1.29	1.13	4
528	VLTLGESWPVLVGKR	sp|Q6PCM1|KDM3A_MOUSE	yes	yes	2	16	15	M	F	0	1652.961	3	2.19E-02	38.40	NaN	NaN	0
529	VMAEGTAVLR	sp|Q6PEB6|PHOCN_MOUSE	yes	yes	2	11	10	M	R	0	1045.559	2	1.93E-02	49.30	NaN	NaN	0
530	VMEKPSPLLVGR	sp|P97855|G3BP1_MOUSE	yes	no	2	13	12	M	E	0	1324.754	3	1.91E-05	110.08	1.22	1.00	16
531	VNFQQPADAER	sp|P29341|PABP1_MOUSE	yes	yes	57	67	11	Y	A	0	1273.605	2	2.30E-03	85.81	1.29	0.84	4
532	VNHPQVSALLGEEDEEALHYLTR	sp|Q9EQU5-2|SET_MOUSE	yes	no	87	109	23	F	V	0	2619.293	4	5.37E-10	77.58	1.90	1.21	2
533	VNPTVFDITADDEPLGR	sp|P17742|PPIA_MOUSE	yes	yes	2	19	18	M	V	0	2004.979	2;3	7.53E-26	156.73	1.07	0.93	46
534	VPGVPLPPEIQLAQR	sp|P56183-2|RRP1_MOUSE	yes	no	2	16	15	M	L	0	1612.930	3	3.32E-02	50.09	1.48	1.15	2
535	VQAWYMDESTADPR	sp|Q99JT9|MTND_MOUSE	yes	yes	2	15	14	M	K	0	1667.725	2	3.07E-06	102.52	1.01	0.95	3
536	VQKESQAALEER	sp|Q9EQQ9|NCOAT_MOUSE	yes	no	2	13	12	M	E	0	1386.710	3	2.26E-04	92.86	1.46	1.25	4
537	VRAPQVYILPPPAEQLSR	sp|P01867-2|IGG2B_MOUSE	yes	no	231	248	18	L	K	1	2033.142	3	4.77E-03	46.89	1.20	1.04	6
538	VRINGDGQEVMYLAEGDNVR	sp|Q6P3A4|VSIG8_MOUSE	yes	yes	22	41	20	A	L	1	2234.075	3	4.63E-06	79.46	1.41	1.00	6
539	VRLVLPNPGLEER	sp|Q9D687|S6A19_MOUSE	yes	yes	2	14	13	M	I	1	1490.857	3	8.37E-02	47.62	1.63	1.01	1
540	VRPLNCIVAVSQNMGIGKNGDLPWPPLR	sp|P00375|DYR_MOUSE	yes	yes	2	29	28	M	N	1	3100.643	4	6.16E-05	62.03	1.09	0.89	1
541	VRSWSNIPFITVPLSR	sp|Q9Z110-2|P5CS_MOUSE	yes	no	40	55	16	H	A	1	1871.042	3	1.52E-03	70.78	1.53	1.21	1
542	VSEPTTVPFDVR	sp|Q9CPT4|CS010_MOUSE	yes	yes	25	36	12	A	P	0	1345.688	2	1.31E-06	120.57	1.12	0.97	6
543	VSLHLGVTPSVLR	sp|O89023|TPP1_MOUSE	yes	yes	193	205	13	T	Q	0	1376.814	3	2.80E-03	79.88	0.86	0.79	3
544	VSNELLEEAFSQFGPIER	sp|Q8VIJ6|SFPQ_MOUSE	yes	yes	374	391	18	Y	A	0	2064.016	3	1.44E-03	57.17	2.91	2.07	1
545	VSSELQIQQSFVPDECPR	sp|Q9Z247|FKBP9_MOUSE	yes	yes	32	49	18	A	T	0	2118.005	2;3	4.71E-03	47.08	1.45	1.31	11
546	VSSLYDAMPR	sp|Q9QXS1-15|PLEC_MOUSE	yes	no	161	170	10	Y	V	0	1137.549	2	1.19E-02	80.71	5.48	3.79	2
547	VSSSLPDICYR	sp|P53996-2|CNBP_MOUSE	yes	no	39	49	11	F	C	0	1295.618	2	2.57E-14	162.26	0.91	0.87	6
548	VSSVLEVSHVFCCPNR	sp|Q91WG4-2|ELP2_MOUSE	yes	no	2	17	16	M	V	0	1888.892	3	3.96E-03	64.52	1.27	1.04	6
549	VTIIDAPGHR	sp|P10126|EF1A1_MOUSE	yes	yes	87	96	10	Y	D	0	1077.593	2;3	7.06E-04	119.53	2.20	1.47	8
550	VVEHPEFLKAGKEPGLQIWR	sp|P13020-2|GELS_MOUSE	yes	no	2	21	20	M	V	0	2332.269	5	3.67E-02	44.79	1.12	1.05	1
551	VYISNGQVLDSR	sp|Q9JLJ1|SELK_MOUSE	yes	yes	2	13	12	M	N	0	1349.694	2	4.13E-02	63.09	2.03	1.36	4
552	WLLNGVPVQDTER	sp|Q8BKG3|PTK7_MOUSE	yes	yes	57	69	13	Y	R	0	1525.789	2	3.74E-02	60.20	3.52	2.24	2
553	YAPTSGGPEELVPIPGNTNYAILR	sp|Q60847-2|COCA1_MOUSE	yes	no	1880	1903	24	F	N	0	2528.291	2	1.00E-09	83.40	4.54	2.85	3
554	YEANFPANVMDVIAR	sp|Q61656|DDX5_MOUSE	yes	yes	97	111	15	F	Q	0	1708.824	2	6.38E-09	108.63	3.96	2.52	2
555	YNCCLPALSCR	sp|Q61765|K1H1_MOUSE	yes	no	3	13	11	P	T	0	1412.600	2	1.12E-02	73.44	1.36	0.97	3

556	YNCCLPAMSCR	sp|Q61897|KT33B_MOUSE	no	no	3	13	11	P	T	0	1430.556	2	1.63E-03	90.61	2.19	1.44	2
557	YNEATGGKYVPR	sp|P99024|TBB5_MOUSE	no	no	51	62	12	Y	A	0	1353.668	3	3.07E-04	89.81	0.91	0.54	3
558	YSDGEGNPSPSQGR	sp|Q60847-2|COCA1_MOUSE	yes	no	2010	2023	14	L	T	0	1449.612	2	5.53E-15	173.44	3.99	2.69	4
559	YSLVFDPVQKTLLADQGEIR	sp|Q9R190|MTA2_MOUSE	yes	yes	129	148	20	F	V	0	2291.216	3	1.51E-03	41.51	1.50	0.89	1
560	YSSSPGGAYVTR	sp|P20152|VIME_MOUSE	yes	yes	53	64	12	L	S	0	1243.583	2	2.72E-05	107.09	2.02	1.74	4
561	YSVPIQIQDR	sp|P55849-2|DSC1_MOUSE	yes	no	642	651	10	Y	H	0	1217.640	2	2.49E-03	110.39	3.22	2.15	4
562	YTLLNQAPDMLHR	sp|P97855|G3BP1_MOUSE	yes	yes	20	32	13	Y	F	0	1570.793	3	2.86E-02	63.18	3.10	2.04	2
563	YVLDDSDGLGR	sp|P54818|GALC_MOUSE	yes	yes	43	53	11	A	E	0	1208.567	2	1.69E-03	88.60	1.32	1.07	9
564	YVTIIDAPGHR	sp|P10126|EF1A1_MOUSE	yes	yes	86	96	11	Y	D	0	1240.656	2;3	3.90E-06	131.82	2.24	1.41	10
565	YYGCPSECTCSR	sp|Q80X72|LRC15_MOUSE	yes	yes	22	33	12	A	A	0	1538.559	2	2.49E-06	116.24	1.49	1.21	8