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The Molecular Mechanisms of Longevity Promotion by Alpha-Ketobutyrate in *Caenorhabditis elegans* and mice

A dissertation submitted in partial satisfaction of the requirements for the degree Doctor of Philosophy in Molecular, Cellular, and Integrative Physiology

by

Chieh Chen

2024

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ABSTRACT OF THE DISSERTATION

The Molecular Mechanisms of Longevity Promotion by Alpha-Ketobutyrate in *Caenorhabditis elegans* and mice

by

Chieh Chen

Doctor of Philosophy in Molecular, Cellular, and Integrative Physiology
University of California, Los Angeles, 2024
Professor Jing Huang, Chair

Abstract

As organisms age, they often experience declining health and an increased risk of debilitating diseases, ultimately leading to mortality. With the aging population growing rapidly in the United States and globally, medical expenditures for treating age-related conditions are skyrocketing. Decades of research into aging have accumulated vast knowledge, paving the way for the development of treatments and therapeutic strategies to combat these issues. The extraordinary findings have shown that aging processes can be regulated, as evidenced by model organisms whose lifespan has been doubled through specific gene mutations, offering promising avenues for

controlling aging and associated diseases. Here we show that supplementation with the endogenous metabolite α-ketobutyrate (α-KB) prolongs the healthspans and lifespans of *C. elegans* and mice. Using an unbiased biochemical approach, drug affinity responsive target stability (DARTS), we identified microtubule-actin cross-linking factor (MACF1) protein to be the target of α-KB, as MACF1 exhibited resistance to proteolysis in the presence of α-KB. MACF1, a cytoskeletal linker protein critical for cellular and tissue integrity, has not previously been studied for its influence on longevity pathways. Our research revealed that α-KB's longevity effects require VAB-10, the worm ortholog of mammalian MACF1. Knockdown of VAB-10 via RNA interference increased the phosphorylation of AMP-activated protein kinase (AMPK), a sensor and regulator of cellular energy balance. We found that AMPK was also activated by α-KB treatment in wildtype animals. Furthermore, AMPK downstream effectors CRTC-1 and NHR-49 were found to be essential for lifespan extension by α-KB in this study. AMPK activation has been shown to preserve mitochondrial homeostasis during aging, and we found that α-KB treated worms had maintained youthful mitochondrial network during aging. α-KB’s longevity effect is abrogated by loss-of-function mutation of mitochondrial fusion component. These findings collectively propose a model wherein α-KB promotes longevity by modulating AMPK via VAB-10/MACF1 interaction. Crucially, our study demonstrated that α-KB prolonged the lifespan of aged male mice and enhanced the healthspan of both male and female mice. Our findings provide hope for developing therapeutic strategies that utilize endogenous metabolites to target longevity pathways linked to cellular energy metabolism and mitochondrial dynamics.

The dissertation of Chieh Chen is approved.

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1. Gourgou, E., **Chen, C**., *et al*. "*Caenorhabditis elegans learning in a structured maze is a multisensory behavior.*" 2021, iScience.
2. **Chen, C**., *et al*., "*The metabolite α-ketobutyrate increases health and life spans by activating AMPK*." 2022, bioRxiv.
3. Lyu, YX., **Chen, C**., *et al*. "*Longevity Biotechnology: Bridging AI, Biomarkers, Geroscience and Clinical Applications for Healthy Longevity*." *manuscript submitted to Aging.*
4. **Chieh Chen** and Ao-Lin Hsu**, "***RIL-1 influences life span through suppression of mitochondrial electron transport chain in C. elegans." manuscript in preparation.*

Chapter 1

Introduction

Chronological aging is the greatest risk factor for major life-threatening diseases and disorders [1]. With the global aging population on the rise, there is an urgent need to develop effective interventions to ameliorate aging-related health declines and diseases [2, 3]. One way to treat the modern epidemic of aging-related diseases is to target the aging process itself. Aging-related genes and pathways are remarkably evolutionarily conserved across many species including yeast, worms, flies, mice, and even primates [1, 2]. Interventions that target such pathways not only promote lifespan, but also increase overall fitness and decrease incidence of aging-related chronic disease [4-7].

Insulin/Insulin-like growth factor-1 signaling (IIS) pathway

Insulin-like signaling (IIS) pathway is the first established longevity signaling pathway [8, 9]. In 1988, a break-through study reported that mutation on a single gene, *age-1*, can significantly prolong the lifespan of the nematode *Caenorhabditis elegans* by 40-60% [2, 10]. In 1993, another remarkable study reported that two genes *daf-2* and *daf-16* function through same pathway to regulate the rate of aging [11]. DAF-2 mutants live

twice as long as wild type, and such lifespan extension can be abolished by mutation of DAF-16 [11]. AGE-1 was found out to be a phosphatidylinositol-3 kinase (PI-3 kinase), DAF-2 as an insulin-like receptor and DAF-16 as an a FOXO-like transcription factor, and they are the important components participating in insulin signalling pathway in mammals [2, 12-15]. Phosphorylation of DAF-2 receptor activates AGE-1 and triggers downstream kinase cascade to regulate lifespan [12, 15-17]. The activated PI-3 kinase signaling pathway ultimately leads to inhibition of DAF-16 by phosphorylation [18]. Phosphorylated DAF-16 then gets sequestrated and lose its activity in cytoplasm [19].

The insulin/IGF-1 pathway regulates metabolism, development, and longevity and is evolutionarily conserved from nematodes to mammals [17, 20]. Inhibition of IIS pathway such as DAF-2 mutation, stress, can trigger translocation of DAF-16 into the nucleus and DAF-16 thereby acts as a transcriptional factor to regulate its downstream target genes to prolong longevity [19, 21]. DAF-16 has diverse roles in the regulation of aging, since it can respond to signals from multiple longevity pathways independently from DAF-2/IIS pathway [19]. A specific form of dietary restriction with diluted bacteria on solid plates, solid DR, activates DAF-16 without triggering its nuclear localization [22]. Under solid DR (sDR) condition, the AMP:ATP ratio is increased and thereby activate AMP-activated protein kinase (AMPK) [22]. AMPK regulates DAF-16 and the downstream genes potentially by direct phosphorylation to increase longevity [22]. AMPK-DAF-16 interaction may form a positive feedback loop since DAF-16 regulates the transcription of 2 AMPK subunits, aakg-4 and possibly aakb-1 [19, 23].

Forkhead box (FOXO) transcription factors control the expressions of genes involved in stress resistance and protein homeostasis, and there are more than 100 members of this subgroup of proteins in human [24, 25]. The forkhead box O3A (FOXO3A) transcription factor contains polymorphisms associated with long life in human populations [1, 26]. FOXO3A was also shown to promote stem cell maintenance by a protective autophagy program [24, 27]. In addition, it has been reported that the offspring of centenarians had lower circulating IGF-1 bioactivity [28]. Considering the IIS pathway is evolutionarily conserved across species, treatments targeting the components in the pathway may be a solid strategy to delay the rate of aging in humans.

Dietary restrictions (DR)

In 1939, a study reported that restriction of calories increased the lifespan in rodents [29]. Later, dietary restrictions have been shown to induce lifespan extension in wide range of species, from invertebrates to primates [30]. The key element of dietary restrictions is not simply decreasing the overall calories, since caloric restriction with high-protein diets or libitum feeding diluted diets does not extend life in mice [31]. Instead, limitation on the feeding frequency or specific nutrients intake are sufficient to promote longevity [30, 32].

In *C. elegans*, different dietary-restriction regimens function through different downstream effectors to achieve lifespan extension [33, 34]. *eat-2* mutant is one of the

most extensively studied DR models in *C. elegans* [33]. The *eat-2* gene encodes a nicotinic acetyl-choline receptor, which functions in the pharyngeal muscle [33]. Worms carrying *eat-2* mutation exhibit lower rate of pumping behavior, thereby reduce the intake of bacteria through pharynx [33, 35]. This DR model is subject to dietary reduction chronically though their whole life and across generations, and have an lifespan extension around 30% [33, 35]. *eat-2* mutations inhibit feeding, thereby suppress the target of rapamycin (TOR) protein signaling and this phenomenon is crucial for the lifespan extension [17]. TOR acts as a kinase and as a nutrient sensor, controls important cellular events such as cell growth, proliferation and survival via regulation of protein synthesis and autophagy [2, 9]. Under DR condition, inhibition of TOR leads to activation of PHA-4/FoxA, a transcription factor promotes autophagy and results in long life [9, 17, 36]. Pharmacological inhibition of mTOR (mammalian target of rapamycin) also mimicked the effects of dietary restriction and extended the lifespan in mammalians [2, 9, 37].

Another method of dietary restriction in *C. elegans*, solid DR (sDR), achieves DR by seeding plates with restrictive amounts of feeding bacteria [22]. Different from *eat-2* model, which undergoes low food intake throughout life, sDR only started at day 4 of adulthood of the worms in the study [22]. The sDR treated worms exhibited longer lifespan and higher resistance to ROS stress [22]. AMPK is required for sDR to prolong lifespan, and the activity of AMPK is mediated by DAF-16 in such condition [22]. In contrast, *eat-2* longevity pathway is independent of AMPK activity [38]. Together, these

studies showed that different methods and timings of DR may achieve enhanced longevity by different mechanisms.

Mitochondria

The free radical theory of aging can be tracked back to 1956, which hypothesized that aging is the result of cumulative free radical damage [2, 39, 40]. Oxygen has been known to be toxic if at high concentrations, since it can lead to elevated highly reactive chemical species through aerobic respiration [39]. In the free radical theory, this phenomenon then results in cumulative oxidative damage to the cells after long-term exposure to oxygen, eventually leads to aging [2, 39]. Inhibition of mitochondrial electron transport chain (ETC) has been shown to increase longevity in multiple species, which appears to be the evidence for the free radical theory of aging [41-47]. However, the studies on the theory remained controversial, since overexpression of key antioxidant enzymes was found to be beneficial for lifespan in some studies [48, 49], while others research groups reported no effects on longevity [2, 50]. And, surprisingly, short-term or low levels of oxidative stress were shown to increase longevity [43, 51]. The modest increase of reactive oxygen species (ROS) induces stress responses involving AMPK and HIF-1, and thereby promote longevity [38, 43]. Inhibition of mitochondrial respiration has been shown to elevate the levels of ROS, and the ROS-induced protective stress responses lengthen the lifespan [51, 52]. Together, these studies showed that ROS plays a more complex role in the regulation of aging.

Besides respiration, mitochondrial network homeostasis is also linked to health and longevity [3, 53-55]. In *C. elegans*, mitochondria lose their contents and have elevated level of fragmentation during aging [3, 54]. Mitochondrial fission increases the fragmentation of the mitochondrial morphology, and dynamin-related protein 1 (DRP-1) is responsible for the process [3]. Mitochondrial fusion requires FZO-1 (ortholog of mitofusins MFN1 and MFN2) to increase the mitochondrial connectivity, and it is critical for mitochondria quality control since the components are allowed be reconstituted during the fusion process [3, 56]. Phosphorylation of AMPK preserves youthful mitochondrial network by mediating fusion and fission [54, 57]. Exercise has been known to increase healthspan and lifespan [3, 58, 59]. AMPK plays a crucial role in the increase of physical fitness during aging by exercise [3]. Exercise, dietary restrictions and constitutive activation of AMPK all function through FZO-1 and DRP-1 to prevent impaired mitochondrial dynamics during aging, with outcomes of improved fitness or lifespan extension [3, 54]. These findings support exercise and dietary restrictions to be powerful nonpharmacological tools for fighting aging, through maintaining mitochondria network homeostasis.

In this dissertation, we present the endogenous metabolite α-ketobutyrate as a novel anti-aging molecule. We demonstrate that supplement of α-KB increases the lifespans of adult *C. elegans* and mice. This study used drug affinity responsive target stability (DARTS), an unbiased and label-free biochemical approach to identify the target protein of α-KB. We discovered MACF1/VAB-10 protein to be the target protein of α-KB. Combined with lifespan analysis, we found that α-KB's longevity effect depends upon

AMPK and VAB-10. Here we further show that knockdown of VAB-10 increases the phosphorylation of AMPK. Based on the findings, we have built a model in which α-KB activates AMPK by binding to MACF1/VAB-10. We also explore the roles of AMPK downstream effectors in the mechanism of α-KB-induced longevity in the latter chapter.

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CHAPTER 2

The metabolite α-ketobutyrate increases health and life spans by activating AMPK

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The metabolite α-ketobutyrate increases health and life spans by activating AMPK

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Abstract

Aging is a complex process that is directly related to human health and disease. The extraordinary finding that aging is malleable, as shown in model organisms whose life and health spans are extended by specific gene mutations or dietary or pharmacological perturbations [1-3], has offered enormous hope for our understanding and treatment of aging and related diseases. Although many molecules have been identified that can extend the lifespan of model organisms, few have been shown to alleviate age-related symptoms or illness in mammals [4]. Here we show that supplementation with the endogenous metabolite α-ketobutyrate (α-KB) increases the lifespan of adult *C. elegans*. Using Gelfree DARTS-PROTOMAP, we identified microtubule-actin cross-linking factor (MACF1) that was protected against proteolysis in the presence of α-KB. MACF1 belongs to the spectraplakin family of giant, evolutionarily conserved proteins with versatile functions [5], but their link to longevity regulation has not been explored. α-KB's longevity effect in *C. elegans* is abrogated by loss-of-function mutation in *vab-10*, encoding the worm ortholog of mammalian MACF1 [6]. Like α-KB treatment, *vab-10* knockdown activates AMP-activated protein kinase (AMPK), and AMPK is required for α-KB effects on longevity. The findings suggest a model in which α-KB increases longevity by activating AMPK via VAB-10/MACF1 modulation. α-KB also delays aging in mammals, increasing the lifespan of aged male mice and the healthspan of both male and female animals. Targeting of broadly expressed scaffolding proteins in connection to cellular energy homeostasis seems to be a clever way that nature has devised for metabolite signals to impinge upon multiple organ and tissue systems, which may have utility for controlling aging and related diseases.

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Metabolism plays important roles in aging and disease. In fact, two of the most robust ways to increase lifespan and protect against aging-related degeneration across diverse organisms are modulation of metabolism through dietary restriction or restrained insulin-like growth factor-1 (IGF-1) signaling [2]. The finding that supplementation of endogenous metabolites, some as common as α-ketoglutarate (α-KG) and nicotinamide adenine dinucleotide (NAD+), may likewise deter aging opens new avenues for understanding and counteracting aging [7,8].

α-keto acids are important intermediates in metabolic pathways, e.g., α-ketoglutarate (α-KG) in the tricarboxylic acid (TCA) cycle and pyruvate as the end product of glycolysis. α-KG is elevated upon starvation [7,9] and increases lifespan and healthspan in organisms ranging from *C. elegans* to mice [7,10,11]. Intriguingly, several other α-keto acids, including α-keto-3-methylvalerate, α-ketoisocaproic acid and α-ketobutyrate, were found to accumulate in the exometabolome of long-lived *C. elegans* mitochondrial respiratory mutants [12], but their relation to longevity has not been studied.

Here we report the anti-aging effects of α-ketobutyrate (α-KB; Fig. 1a) in *C. elegans* and in mice. α-KB is a short-chain α-keto acid found in all cells, and a metabolite in the catabolism of methionine, threonine, and homocysteine. α-KB can be used as a substrate by both the pyruvate dehydrogenase complex (PDC) and branched-chain α-keto acid dehydrogenase complex (BCKDC) [13,14], and by lactate dehydrogenase (LDH) [15]. Unlike its analogs ketone body β-hydroxybutyrate and short-chain fatty acid butyrate [16], α-KB's biological function is not well understood. We discovered that α-KB increases the lifespan of adult *C. elegans* by up to ~60% (Fig. 1b; Extended Data Table 1). Moreover, α-KB delays age-related decline in rapid, coordinated body movement, indicating improved healthspan. α-KB also offsets a major conserved hallmark of aging – loss of proteostasis [17] – delaying the paralysis in *C. elegans* induced by Aβ expression (Fig. 1c). The optimal concentration of α-KB for longevity in worms is ~4 mM (Fig. 1d), which was used in all subsequent *C. elegans* experiments unless otherwise stated.

Dietary restriction and IGF-1 signaling have emerged as two key longevity regulatory mechanisms conserved in evolution. Dietary restriction and reduced IGF-1 receptor activity can both result in longer lifespan and healthspan in diverse organisms [2], and IGF-1 receptor pathway gene variants have been associated with exceptional human longevity [18,19]. α-KB does not affect food intake of worms (Extended Data Fig. 1) and still significantly increases longevity in the *eat-2* (Fig. 1e) genetic model of dietary restriction [20], suggesting that α-KB's longevity effect may be largely independent of dietary restriction. The lifespan of the very long-lived insulin/IGF-1 receptor *daf-2(e1370)* mutant worms [1], on the other hand, is not increased by α-KB (Fig. 1f;

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Extended Data Table 1), indicating an involvement of *daf-2*/IGF-I receptor pathway in the longevity by α-KB.

Since long-lived *C. elegans* mitochondrial respiratory mutants accumulate and excrete α-KB [12], we initially examined α-KB interaction with mitochondria using coupling and electron flow assays [21]. In this setting, α-KB decreases pyruvate-driven complex I respiration (Extended Data Fig. 2a-b). As may be expected from the close structural similarity between α-KB and pyruvate, this decrease can be explained by an inhibition of pyruvate dehydrogenase (PDH) by α-KB (Extended Data Fig. 2c). However, lifespan increase by α-KB is unaffected in PDH/*pdhb-1* RNAi worms (Extended Data Fig. 2d; Extended Data Table 1), suggesting a PDH-independent effect.

To help understand the molecular mechanisms of α-KB in longevity, we made use of an unbiased biochemical approach, drug affinity responsive target stability, or DARTS [22], to identify cellular proteins with which α-KB interacts. To this end, we digested DMSO– and α-KB–treated mouse liver mitochondrial lysates with Pronase and performed in-solution molecular weight-based fractionation of the DARTS samples followed by trypsin digestion and liquid chromatography-mass spectrometry (LC-MS) (Fig. 2a). This next generation Gelfree DARTS approach eliminates the need to visualize the protected proteins on a stained gel and relies solely on the mass spectrometer for identification and quantification. For data analysis, we utilized the Protein Topography and Migration Analysis Platform (PROTOMAP) [23], which was initially developed to identify protease substrates based on their altered molecular weight after proteolysis and detects differences in overall protein abundance and digestion efficiency. DARTS-PROTOMAP identified MACF1 among the most strongly protected proteins present in the α-KB–treated sample (Fig. 2b-c; Extended Data Table 2 and Extended Data Table 3).

MACF1 (also known as ACF7), originally named for its microtubule and actin crosslinking functions, is a member of the spectraplakin family of plakins [5,24,25]. Plakins are large proteins with multiple domains that link cytoskeletal components to each other and to other organelles in the cell. They are essential for maintaining cell and tissue integrity; mutations in the plakin genes are linked to inherited human disorders ranging from hair and skin abnormalities to heart disease [25]. *C. elegans* contains a single plakin gene, *vab-10*, orthologous to mammalian MACF1 [6]. To determine the functional significance of VAB-10 in α-KB–promoted longevity, we assessed the lifespan of *vab-10* RNAi *C. elegans* treated with α-KB (Fig. 2d). Relative to control RNAi, *vab-10* RNAi worms have an increased lifespan but their lifespan increase by α-KB is substantially smaller than in control RNAi worms (8.3% vs. 35.5%), indicating an important role of VAB-10 in the longevity effect of α-KB. We also analyzed the lifespan of loss-of-function *vab-10* mutants treated with α-KB. *vab-10(e698)* is a strong hypomorphic allele carrying

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a missense mutation (P1666S) [6]. The longevity-enhancing activity of α-KB is completely lost in *vab-10(e698)* mutant worms compared to wild-type worms in the same experiment (Fig. 2e). This effect is specific since silent intronic deletion control *vab-10(gk45)* worms remain responsive to lifespan increase by α-KB (Extended Data Fig. 2e; Extended Data Table 1) . These analyses indicate a specific requirement of VAB-10 for the longevity effect by α-KB and provide genetic validation of VAB-10 as a target of α-KB in longevity.

Plectin scaffolds have been shown to recruit AMPK in differentiated myofibres and plectin-deficient myocytes exhibit enhanced levels of activated AMPK [26]. Since AMPK is a highly conserved master regulator of energy homeostasis [27] and constitutively active *aak-2*/AMPK mutants have increased lifespan [28], we examined whether AMPK may be involved in α-KB longevity. Indeed, lifespan increase by α-KB is abrogated in *aak-2* mutant worms (Fig. 3a; Extended Data Table 1), indicating a dependence on AMPK for α-KB–induced longevity.

The failure of α-KB to increase lifespan of *aak-2* worms suggests two possible models. In the first model, α-KB and AMPK may act on the same pathway with α-KB acting upstream of AMPK (e.g., by means of *vab-10*), to promote longevity. Alternatively, α-KB may function through an independent pathway(s) in parallel with AMPK but converge downstream on a common effector. The first model predicts that α-KB treatment will activate AMPK, whereas the latter model predicts that AMPK activity would not be altered by α-KB treatment. In support of the first model, we found that α-KB increases phosphorylated active AMPK [29] in *C. elegans* (Fig. 3b-c) and in mice (Fig. 3d).

In *C. elegans*, *vab-10* knockdown also results in AMPK activation, as indicated by increased phosphorylation of AAK-2 (Fig. 3c). Moreover, VAB-10 is required for mitochondrial maintenance [30], and MACF1 and plectin deficient mice exhibit increased mitochondrial biogenesis or mitochondrial network connectivity [31-33]. AMPK plays a vital role in both sensing and regulating mitochondrial function [34,35]. Previous studies discovered that aging in *C. elegans* progresses with loss of mitochondrial network connectivity [36,37] and AMPK maintains youthful mitochondrial network structure, delaying mitochondrial fragmentation and loss of mitochondrial content during aging [36]. We found that while aged control worms have disrupted mitochondrial networks compared to young worms, as reported [36,37], α-KB-treated aged worms maintain greater mitochondrial content and network connectivity (Fig. 3e). Together these findings suggest that α-KB may act through VAB-10 to activate AMPK. In support of this model, α-KB induced AMPK activation is diminished in *vab-10* RNAi worms (Fig. 3c).

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As an important downstream component in insulin/IGF-1 signaling, *aak-2*/AMPK is required for the longevity effect of *daf-2*/IGF-1 receptor mutations [38]. This is in line with our observation that the lifespan of long-lived *daf-2* mutants is not further increased by α-KB (Fig. 1f). The DAF-16/FoxO transcription factor, which mediates lifespan increase induced by *daf-2* mutations, also plays a role in lifespan extension by constitutively active AMPK [28,39]. We measured the lifespan of *daf-16* mutant *C. elegans* treated with α-KB. As shown in Fig. 3f, α-KB increases the mean (11.2%), but not maximum (0%), lifespan of *daf-16* mutants, whereas it increases both the mean (22.0%) and maximum (30.4%) lifespan of N2 worms in the same experiment. These results indicate that α-KB–enhanced longevity involves *daf-16*. The dependence on both *aak-2*/AMPK (Fig. 3a) and intact *daf-2*/IGF-1 receptor (Fig. 1f) for α-KB effects on longevity are consistent with the reported importance of *aak-2* in *daf-2* mutant longevity [38]. Furthermore, both *aak-2* and *daf-16* are necessary for lifespan increase by sDR, a dietary restriction method involving bacterial food dilution [39], consistent with our finding that α-KB does not increase lifespan of *C. elegans* under sDR (Fig. 3g). In contrast, the longevity of *eat-2* dietary restriction mutants does not require *aak-2*/AMPK [40] and can be further increased by α-KB (Fig. 1e). Taken together, our data support a model in which α-KB regulates longevity through activating AMPK (Fig. 3h).

Additionally, we found that α-KB exhibits notable longevity effects in mice. We treated aged C57BL/6J mice (89-101 weeks of age) with α-KB in the drinking water and monitored their healthspan and lifespan. α-KB treatment did not alter body weight or fat/lean body composition (Extended Data Fig. 3a). α-KB increased the lifespan of male mice by 36.5% from inception of treatment (Fig. 4a). α-KB did not increase the survival of female mice (Fig. 4b), although it did alleviate various aging related phenotypes (see below). Sex-dependent longevity effects have previously been observed. For example, late-life targeting of IGF-1 receptor [41] and mid-life supplementation of α-KG [11] increase lifespan only in female mice, whereas a branched-chain amino acid (BCAA) restricted diet benefits male mice only [42]. The precise underlying reasons for the interaction between sex and α-KB effects on lifespan remain to be determined; it is possible that optimal dosage and/or treatment age may differ for males and females.

Despite the lack of α-KB effects on female mouse longevity, the healthspan of female mice was improved. For studies of healthspan, independent mouse cohorts were treated for 30 weeks (from age 101 to 131 weeks) and assessed for aging phenotypes, including cataracts, hair loss, and mobility and motility. These analyses showed that 75% of control female mice developed cataracts, but none of the α-KB treated mice did (Fig. 4c-d). Additionally, α-KB-treated mice did not suffer hair graying (Fig. 4c) or hair loss (Extended Data Fig. 3b-c) or reduced motility (Fig. 4e), which were prevalent in control mice. Control mice were also prone to enlarged livers, which were rare in α-KB

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treated mice (Fig. 4f; Extended Data Fig. 3b, d). Together, our results indicate that α-KB can increase mammalian healthspan and lifespan even when treatment is initiated in late life.

In addition to dietary restriction strategies which require strict self-control or timing, such as fasting and time-restricted feeding, restriction of dietary amino acids has demonstrated exciting longevity benefits [2,42,43]. We postulate that dietary supplementation of related keto acids may serve as convenient alternatives. Here in this study, we discovered that supplementation of the keto-acid α-KB has favorable anti-aging effects and increases longevity in both *C. elegans* and mice. Aging is associated with reductions in AMPK activity and mitochondrial biogenesis [44]. α-KB treatment activates AMPK in both worms and mice, likely by modulating VAB-10/MACF1 and mitochondrial networks. It has emerged that besides structural functions, cytoskeletal and cell junction machineries also possess signaling and regulatory capabilities [45]. Targeting of such multipurpose, universally expressed anchoring proteins with pro-longevity small molecules may represent a new way to facilitate healthy aging.

Beyond longevity regulation, MACF1 has a role in Wnt signaling and is required for the activation of Wnt-responsive genes [46]. MACF1 interacts with Axin, which regulates energy metabolism through mitochondrial function and Wnt signaling [47]. Transgenic mice overexpressing plakoglobin (γ-catenin) , which is upregulated by Wnt-1, exhibit stunted hair growth due to premature termination of anagen [48]. Topical application of α-KB, on the other hand, induces anagen and stimulates hair regrowth [49], consistent with inhibited Wnt signaling upon MACF1 perturbation by α-KB. Whether this and other seemingly pleiotropic actions of α-KB may also be mediated by VAB-10/MACF1 and/or additional factors remains to be studied.

Figure Legends

Fig. 1. α-KB increases the adult lifespan of *C. elegans*. a, Structure of α-KB. **b**, α-KB increases the lifespan of adult worms, mean lifespan (days of adulthood) with vehicle treatment (m_{veh}) = 14.1 (n = 111 animals tested), $m_{\alpha\text{-KB}}$ = 22.4 (n = 66), $P < 0.0001$. **c**, α-KB delays paralysis in the $A\beta_{1\text{-}42}$ expressing GMC101 *C. elegans* strain [50]. m_{veh} = 2.5 (n = 248), $m_{\alpha\text{-KB}}$ = 3.5 (n = 150), $P < 0.0001$. **d**, Dose–response curve of the α-KB effect on longevity. **e**, α-KB increases the lifespan of *eat-2(ad1116)* mutant *C. elegans* strain, m_{veh} = 20.4 (n = 99), $m_{\alpha\text{-KB}}$ = 23.0 (n = 116), P = 0.0054. **f**, α-KB does not further increase the lifespan of *daf-2(e1370)*, m_{veh} = 33.3 (n = 103), $m_{\alpha\text{-KB}}$ = 35.3 (n = 102), P = 0.7804; $m_{\alpha\text{-KG}}$ = 47.3 (n = 110), $P < 0.0001$. P values were determined by the log-rank test.

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Fig. 2. Gelfree DARTS-PROTOMAP identifies MACF1/VAB-10 as a target of α-KB in promoting longevity in *C. elegans*. a, Schematic of Gelfree DARTS-PROTOMAP method. **b**, DARTS identifies MACF1 as an α-KB-binding protein. Data represent 3 biological replicates. Bars indicate the mean. Mean ± s.d. is plotted. **c**, Peptides protected in DARTS (red) relative to the full length of the mouse MACF1 isoform 1 (aka MACF1b) protein (https://www.uniprot.org/uniprot/Q9QXZ0#Q9QXZ0-1). Plectin repeats (blue, unique to isoform 1) and spectrin repeats (green, common to all isoforms) are shown. Protein domains are according to UniProt. **d**-**e**, Lifespan effect of α-KB upon loss-of-function of the *C. elegans* homolog VAB-10 via RNAi and mutation. **d**, *vab-10* RNAi, m_{veh} = 22.8 (n = 99), $m_{\alpha\text{-KB}}$ = 24.7 (n = 99), 8.3%, P = 0.0012; RNAi control, m_{veh} = 19.9 (n = 84), $m_{\alpha\text{-KB}}$ = 26.9 (n = 69), 35.5%, P < 0.0001. **e**, *vab-10(e698)*, m_{veh} = 15.4 (n = 67), $m_{\alpha\text{-KB}}$ = 16.3 (n = 69), P = 0.1344; N2, m_{veh} = 13.9 (n = 72), $m_{\alpha\text{-KB}}$ = 20.9 (n = 65), P < 0.0001.

Fig. 3. α-KB–induced longevity in *C. elegans* is mediated through AMPK. a, Effect of α-KB on the lifespan of *aak-2* mutant *C. elegans*. *aak-2(gt33)*, m_{veh} = 14.2 (n = 118), $m_{\alpha\text{-KB}}$ = 15.0 (n = 118), 5.5%, P = 0.0368; N2, m_{veh} = 14.5 (n = 116), $m_{\alpha\text{-KB}}$ = 17.7 (n = 118), 22%, P < 0.0001. **b**, Increased phosphorylated active AAK-2 in *C. elegans* treated with α-KB. P, phospho. **c**, Increased phosphorylated active AAK-2 in *C. elegans* treated with RNAi for *vab-10*. **d**, Increased AMPK activation in α-KB–treated mice. 120-day old male mice were orally supplemented with α-KB for 6 days before spleens were harvested for Western blot analysis for phosphorylated active AMPK. **e**, Fluorescence images at ξ63 magnification showing mitochondrial networks in body wall muscle cells of *C. elegans* treated with vehicle control or α-KB. SJ4103 (*zcIs14 [myo-3::GFP(mit)]*) expresses mitochondrial targeted GFP under control of the muscle-specific *myo-3* promoter (Benedetti et al., 2006) . At least 10 animals were analyzed for each condition in at least 2 independent experiments. **f**, Effect of α-KB on the lifespan of *daf-16* mutant *C. elegans*. *daf-16(mu86)*, m_{veh} = 13.9 (n = 116), $m_{\alpha\text{-KB}}$ = 15.4 (n = 112), 11.2%, P < 0.0001; N2, m_{veh} = 14.5 (n = 116), $m_{\alpha\text{-KB}}$ = 17.7 (n = 118), 22.0%, P < 0.0001. **g**, Effect of α-KB on the lifespan of *C. elegans* under sDR. 0.4X OP50, m_{veh} = 23.6 (n = 50), $m_{\alpha\text{-KB}}$ = 20.2 (n = 69), –14.6%, P = 0.0002; 4X OP50, m_{veh} = 14.1 (n = 111), $m_{\alpha\text{-KB}}$ = 22.4 (n = 66), 58.9%, P < 0.0001; 40X OP50, m_{veh} = 15.7 (n = 96), $m_{\alpha\text{-KB}}$ = 20.4 (n = 100), %, P < 0.0001. **h**, Model of α-KB–mediated longevity.

Fig. 4. α-KB administered in late life increases healthy lifespan and alleviates aging-related symptoms in mice. a, α-KB increases the lifespan of old male mice. Data show results of 3 pooled experiments performed at different times. n_{veh} = 16, $n_{\alpha\text{-KB}}$ = 13, *P = 0.0448 (log-rank test). **b**, α-KB does not increase the lifespan of old female mice. Data show results of 2 pooled experiments done at different times. n_{veh} = 10, $n_{\alpha\text{-KB}}$ = 8, P = 0.3356 (log-rank test). **c**, α-KB confers protection against hair graying and

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cataracts in old female mice. **d**, α-KB-treated female mice have lower cataract incidence compared to control mice. n_{veh} = 11, $n_{\alpha\text{-KB}}$ = 5, *P* = 5.3102e-05 (*t*-test, two-tailed, two-sample unequal variance). Mean ± SEM is plotted. No cataracts were found in control or treated male mice. **e**, α-KB supplementation diminishes the rapid decline in motility/activity in female mice during advanced aging at ~90-95% of maximum lifespan. Vehicle, *n* = 8, *P* = 0.0013; α-KB, *n* = 4, *P* = 0.4363; by two-way ANOVA. Mean ± s.d. is plotted. **f**, α-KB reduces hepatomegaly in aged mice. n_{veh} = 4, $n_{\alpha\text{-KB}}$ = 5, *P* = 0.0274 (*t*-test, two-tailed, two-sample unequal variance). Mean ± s.d. is plotted. See also Extended Data Fig. 3b and d.

METHODS

Nematode strains. The following strains were used (strain, genotype): Bristol N2, wild type; CB698, *vab-10(e698)*I; VC117, *vab-10(gk45)*I; TG38, *aak-2(gt33)*X; DA1116, *eat-2(ad1116)*II; CB1370, *daf-2(e1370)*III; CF1038, *daf-16(mu86)*I; SJ4103, *zcIs14 [myo-3::GFP(mit)]*. All strains were obtained from the Caenorhabditis Genetics Center (CGC).

Lifespan analysis. *C. elegans* lifespan assays were conducted as described [7] at 20 °C on solid nematode growth media (NGM) using standard protocols and were replicated in at least two independent experiments. All lifespan data are available in Extended Data Table 1. The sample size was chosen on the basis of standards done in the field in published manuscripts. No statistical method was used to predetermine the sample size. Animals were assigned randomly to the experimental groups. Worms that ruptured, bagged (that is, exhibited internal progeny hatching), or crawled off the plates were censored. Lifespan data were analyzed using GraphPad Prism; *P* values were calculated using the log-rank (Mantel–Cox) test.

RNAi in *C. elegans*. RNAi in *C. elegans* was accomplished by feeding worms HT115(DE3) bacteria expressing target-gene double-stranded RNA (dsRNA) from the pL4440 vector [51]. dsRNA production was induced overnight on plates containing 1mM isopropyl-b-D-thiogalactoside (IPTG). All RNAi feeding clones were obtained from the *C. elegans* ORF-RNAi Library (Thermo Scientific/Open Biosystems).

Assay for *C. elegans* paralysis in Alzheimer's disease model. The GMC101 *C. elegans* strain [50] expresses the full length human amyloid-beta 1-42 protein in the body wall muscle cells, leading to a fully-penetrant age-progressive paralysis. Worms were age-synchronized by performing a timed egg lay for 3 h with ~100 gravid adults and the eggs placed in a 20°C incubator. Once the eggs had developed to the L4 stage at 42 h post egg lay, they were picked onto NGM treatment plates containing 49.5 µM 5-fluoro-

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2'-deoxyuridine (FUDR, Sigma F0503) to prevent progeny production and either α-KB or vehicle (water) control. The worms were then shifted to 30°C to induce amyloid-beta aggregation and paralysis. Worms were assessed for paralysis daily, beginning on the second day of treatment, by the failure to perform whole body bends and significantly move forwards and backwards upon gentle prodding with a platinum wire. Most paralyzed worms could still move their heads and part of their body. All worms were transferred to fresh treatment plates on day 4.

Measurement of mitochondrial respiration. Mitochondria were isolated from mouse liver as described [7]. The final mitochondrial pellet was resuspended in 30 µl of MAS buffer (70 mM sucrose, 220 mM mannitol, 10 mM KH_2PO_4, 5 mM $MgCl_2$, 2 mM HEPES, 1 mM EGTA, and 0.2% fatty acid free BSA, pH 7.2).

Mitochondrial respiration was measured by running coupling assays. 20 µg of mitochondria in complete MAS buffer (MAS buffer supplemented with 10 mM pyruvate/2 mM malate, 10 mM glutamate/10 mM malate, or 10 mM succinate and 2 µM rotenone) were seeded into a XF24 Seahorse plate by centrifugation at 2,000*g* for 20 min at 4 °C. Just before the assay, the mitochondria were supplemented with complete MAS buffer for a total of 500 µl (with 1% DMSO or α-KB) and warmed at 37 °C for 30 min before starting the OCR measurements. Mitochondrial respiration begins in a coupled state 2; state 3 is initiated by 2 mM ADP; state 4o (oligomycin insensitive, that is, complex V independent) is induced by 2.5 µM oligomycin; and state 3u (FCCP-uncoupled maximal respiratory capacity) by 4 µM FCCP. Finally, 1.5 µg/mL antimycin A was injected at the end of the assay.

Target identification using Gelfree DARTS-MS and PROTOMAP. Mouse liver mitochondria were isolated as described previously [7]. Protein contents of mitochondrial pellets were extracted by adding 4X volume of 1x MAS buffer followed by 1/9 volume of 10% *n*-dodecyl ß-D-maltoside (DDM; Sigma D4641) for a final 1% DDM concentration, followed by incubation on ice for 30 min. Lysates were clarified at 20,000*g* for 30 min at 4°C. Aliquots of clarified lysate (~10 µg/µL) were treated with 1/50 volume of H_2O or 10 mM α-KB (200 µM final), mixed, and incubated for 30 min at room temperature. Samples were then digested with 1:200 Pronase:lysate ratio for 10 min at room temperature, and the digests stopped by addition of 2 µL 100x protease inhibitor and placing on ice. Digested samples were desalted with Zeba 7K MWCO spin columns (Thermo Scientific, 89882) and then fractionated in a 10% Tris Acetate cartridge using a Gelfree 8100 system (Expedeon) as follows: load sample at 50 V for 16 min, collect fraction 1 at 50 V for 36 min, fraction 2 at 50 V for 3 min, fraction 3 at 50 V for 4 min, fraction 4 at 100 V for 5 min, fraction 5 at 100 V for 8 min, fraction 6 at 100 V for 18 min, and fraction 7 at 100 V for 59 min. Detergent removal was performed with 50 µL of each

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fraction using 0.1 mL HIPPR resin (Thermo Scientific, 88305) followed by TCA precipitation of the samples. The pellets were then resuspended in 50 µL 8 M urea/0.1 M Tris pH 8.5 and reduced, alkylated, and digested with LysC and trypsin as described previously [52]. Digests were desalted on C18 spin tips (Nest Group, SUM SS18V) and the dried peptides resuspended in 20 µL 1% formic acid.

Fractions from the DARTS experiment using 200 µM α-KB in triplicate were analyzed on an Easy-nLC1000 and QExactive mass spectrometer (Thermo Scientific). 2 µL of each fraction was injected onto a 20 x 0.075 mm Acclaim PepMap RSLC Nano-Trap C18 column with 3 µm particles and 100 Å pore size, followed by separation on a 250 x 0.075 mm Acclaim PepMap RSLC EasySpray C18 column (Thermo Scientific) with 2 µm particles and 100 Å pore size with the following gradient: 5 – 40%B over 120 min, 40 – 100%B over 10 min, and stay at 100%B for 10 min, with a flow rate of 300 nL/min. Buffer A consisted of 0.1% formic acid in water and buffer B consisted of 0.1% formic acid in acetonitrile. Top-10 DDA analysis in positive mode in the QExactive consisted of 70k resolution ms1 scans with an AGC target of 1e6 and scan range of 200-2000 m/z, and ms2 scans at 17.5k resolution with an AGC target of 2e5. Dynamic exclusion was set to 30 sec.

Raw data were extracted with RawXtract v1.9 and the ms2 files were searched against a Uniprot Mouse nonredundant FASTA file (downloaded May 2015) using Mascot 2.5.1 with the following parameters: Trypsin set to full with up to 2 missed cleavages, precursor mass tolerance of 10 ppm, fragment mass tolerance of 0.02 Da, use average precursor mass set to false, maximum deltaCn of 0.05, and carbamidomethylation of cysteine and oxidation of methionine set as dynamic modifications. Search results were further filtered with DTASelect v1.9 for a 1% FDR. Spectral counts of all proteins for fractions 2-6 (renamed bands 5-1 to reflect the low to high molecular weight order presentation) were then analyzed with PROTOMAP as described [23]. Fractions 1 and 7 had few protein identifications and were therefore excluded from the analysis. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE [53] partner repository with the dataset identifier PXD035341.

Western blot analysis.

Worms. N2 worms were egg-prepped onto solid NGM with 50 µg/ml carbenicillin (GoldBio, C-103-5) and HT115(DE3) bacteria expressing empty vector dsRNA. The eggs were placed in a 20 °C incubator to develop. Once most of the worms had reached the L4 stage, L4 staged worms were picked onto NGM plates containing 49.5 µM 5-fluoro-2'-deoxyuridine (FUDR, Sigma F0503), 50 µg/ml carbenicillin, 1mM isopropyl-b-D-thiogalactoside (IPTG, Fisher Scientific BP1755-10), 1.5% DMSO, and HT115(DE3) bacteria expressing dsRNA for either empty vector or vab-10 for RNAi

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treatment. After 24 h of empty vector or vab-10 RNAi treatment, worms from each RNAi treatment plate were moved onto similar respective RNAi treatment plates with the addition of either vehicle (water) control or 4 mM α-KB. After 24 h of treatment, worms were quickly washed off from their solid NGM plates with liquid NGM, collected in Lysing Matrix C tubes, and immediately flash frozen in liquid N_2. 2X sample buffer (50 mM Tris-HCl pH 6.8, 2 mM EDTA, 4% Glycerol, 4% SDS, 2% β-mercaptoethanol, and bromophenol blue) along with protease and phosphatase inhibitors (Sigma P8340 and Sigma P5726, respectively) were added to each of the samples. Next, the samples were lysed using Lysing Matrix C tubes and the FastPrep-24 high speed bench top homogenizer in a 4 °C room. For 3 times, the worms were disrupted for 20 s at 6.5 m/s and rested on ice for 1 min. The lysed worms were centrifuged for 30 s at 600 X *g* at 22 °C to collect the lysates and the lysates were centrifuged for 10 min at 18,000 X *g* at 22 °C to separate the supernatants from the worm debris. The supernatants were collected, heated for 10 min at 70 °C, subjected to SDS-Page on NuPage Novex 4-12% Bis-Tris gradient gels (Invitrogen, NP0323BOX) in MES SDS Running Buffer (Invitrogen, NP0002), and transferred to PVDF membranes for western blotting. Antibodies used: P-AMPK T172 (Cell Signaling, 2535S), GAPDH (Thermo Fisher Scientific, AM4300), and α-Tubulin.

Mice. Male C57BL/6J mice (Jackson Laboratories) were treated at 120 days of age with either water (vehicle control) or α-KB (90 mg/kg or 180 mg/kg bodyweight) in drinking water for 6 days. Mice were sacrificed, and organs were harvested and frozen immediately in liquid nitrogen. Tissues were homogenized in T-PER tissue protein extraction reagent (Thermo Scientific, 78510) with protease inhibitors (Roche, 11836153001) and phosphatase inhibitors (Sigma-Aldrich, P5726) using Lysing Matrix A tubes with a FastPrep-24 instrument (MP Biomedicals). Tissue and cell debris was removed by centrifugation and lysates were boiled for 5 min in 1 x SDS (Fisher Scientific, BP166) loading buffer containing 5% 2-mercaptoethanol (Fisher Scientific, O3446I-100). Samples were then subjected to SDS-PAGE on NuPAGE Novex 12% Bis-Tris gels (Invitrogen, NP0343BOX) in MOPS SDS Running Buffer (Invitrogen, B0001). Proteins were transferred to PVDF membranes (Millipore, IPVH00010) for Western blotting. Antibodies used: P-AMPKα T172 (Cell Signaling, 2535S), AMPKα (Cell Signaling, 2603), and GAPDH (Santa Cruz Biotechnology, 25778).

Microscopy. *C. elegans* mitochondrial network structure was assessed using protocols adapted from published work [36,54]. SJ4103 (*zcIs14 [myo-3::GFP(mit)]*) expresses mitochondrial targeted GFP under control of the muscle-specific *myo-3* promoter (Benedetti et al., 2006). Worms were anesthetized in 10 mM NaN_3 in M9 buffer at 4 °C, mounted on 2% agarose pads on glass slides under coverslips and imaged on a confocal laser scanning microscope (Zeiss, LSM 880).

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Aged mice study.
C57BL/6J mice were obtained at 20 months (i.e., 89 weeks) of age (NIA aged rodent colonies) and treatment started at 20-23 months (i.e., 89-101 weeks), with the exception of one male cohort obtained at 15 months (i.e., 64 weeks) of age but started treatment at a similar age (22 months, or 95 weeks, in this case). Mice were housed in a controlled SPF facility (22 ± 2 °C, 6:00-18:00, 12 h/12 h light/dark cycle) at UCLA. Mice were fed a standard chow diet and provided ad libitum access to food and water throughout the study. Treatments were with either water (vehicle control) or α-KB (90 mg/kg bodyweight) in drinking water. Mice were inspected daily for signs of ill health; severely sick or immobilized mice were terminated. The principal endpoint was age at death (for mice found dead at daily inspections) or age at euthanasia (for mice deemed unlikely to survive for additional 48 hours). All experiments were approved by the UCLA Chancellor's Animal Research Committee. Lifespan data were analyzed using GraphPad Prism; *P* values were calculated using the log-rank (Mantel–Cox) test.

Mouse activity level assessment. Mice were monitored every 10 days and video recorded for activity assessment and assigned a number on a scale of 0.5~4 based on their activity levels, with 4 representing the highest level of activity (fast, nonstop movement), and 0.5 representing the lowest level of activity (alive, but barely moving). Only living mice were assigned activity levels; mice that were found dead upon inspection were excluded (rather than assigned an activity level of 0). Activity levels were monitored throughout the study until all mice reached death. Activity levels data were analyzed using GraphPad Prism.

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Author contributions

C. elegans lifespan assays were performed by C.C., B.L., M.C., W.H., J.C., R.M.C., H.H. and X.Y.; mouse lifespan experiments by M.C., J.C. and M.J.; DARTS-MS and PROTOMAP by B.L., R.O.J., M.M.D., G.S., B.F.C., J.A.W. and J.A.L.; mitochondrial respiration studies by L.V. and K.R.; enzymatic assays by X.F.; Western blotting by M.C., W.H., J.C., and X.F.; confocal microscopy by C.C. L.V., M.M.D., G.S., S.C.B., D.B., N.H.D.K., Y.W., S.M.D., M.A.T., O.F., M.J., B.F.C., J.A.W., J.A.L. and K.R. provided guidance, specialized reagents and expertise. C.C., B.L., M.C., J.C., X.F., K.R. and J.H. wrote the paper. C.C., B.L., M.C., W.H., J.C., L.R., R.M.C., X.F. and J.H. analyzed data. All authors discussed the results, commented on the studies and contributed to aspects of preparing the manuscript.

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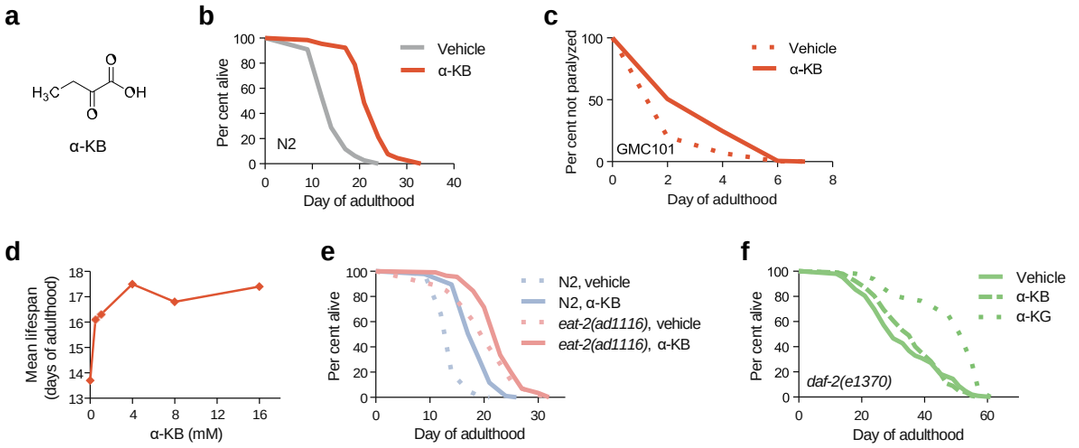
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Figure



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Figure

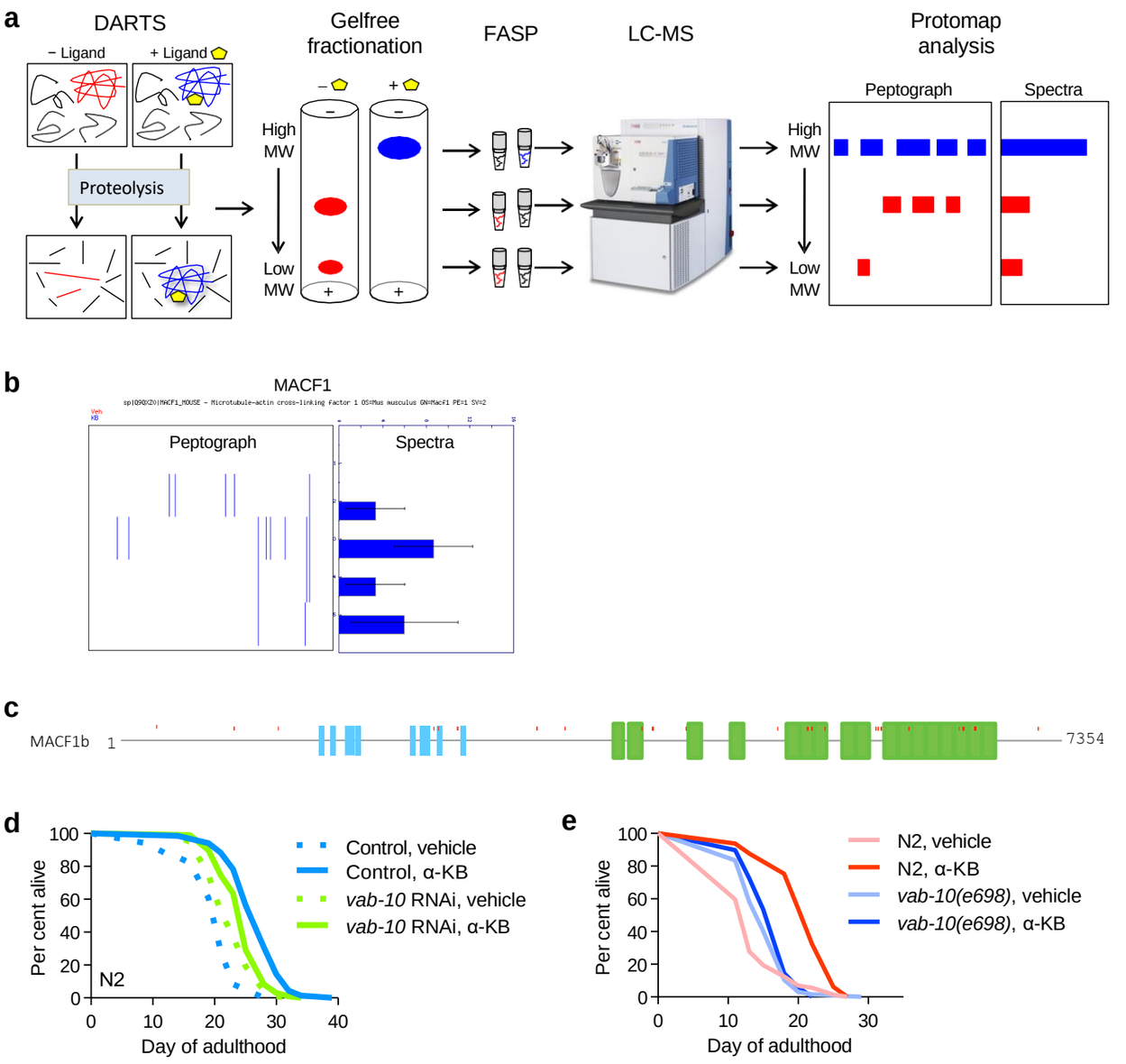


Figure 3

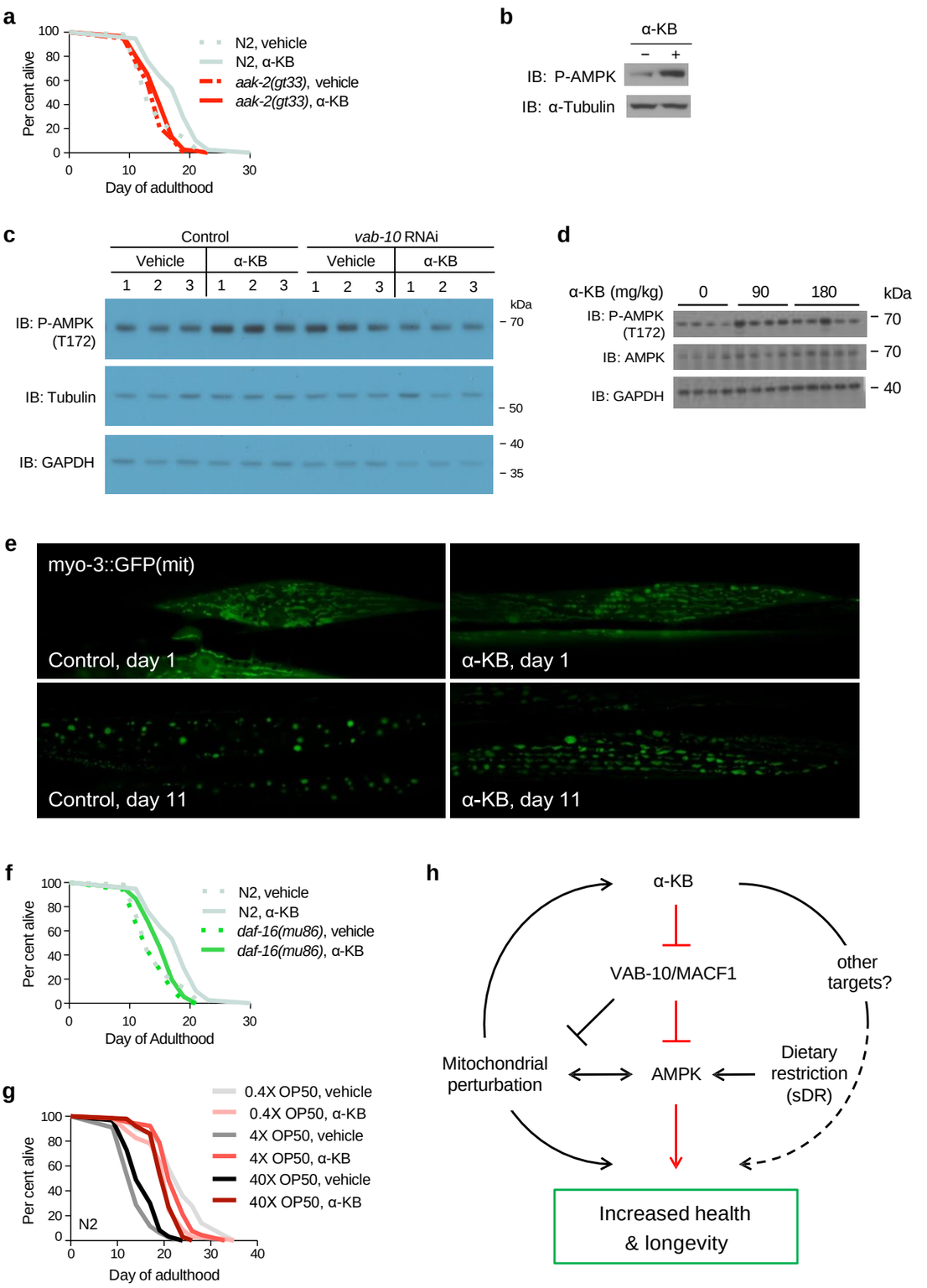
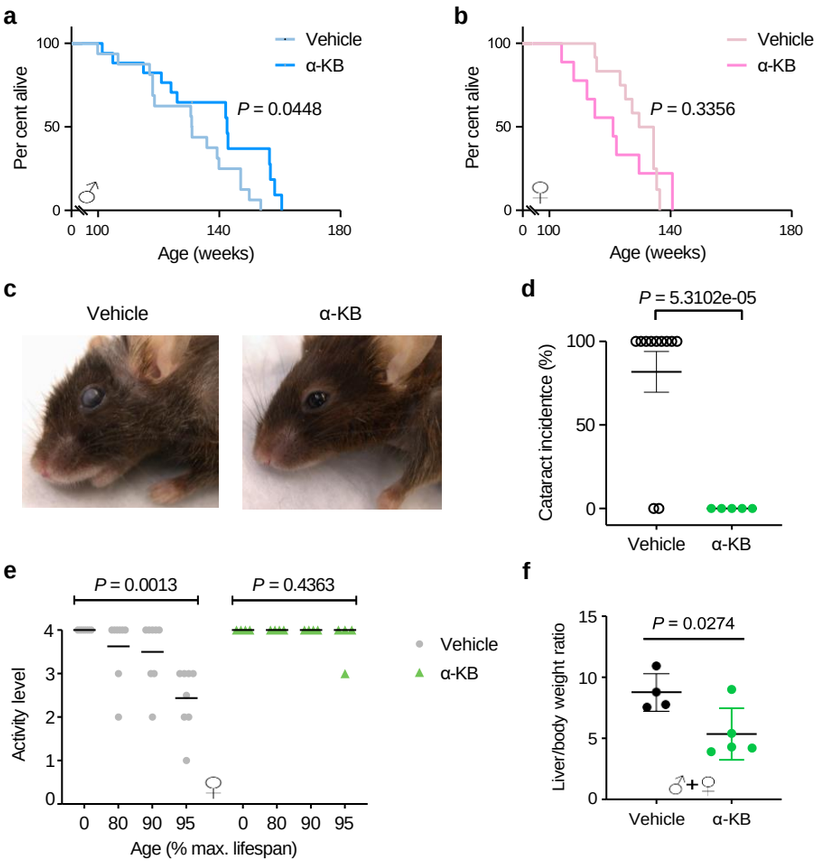
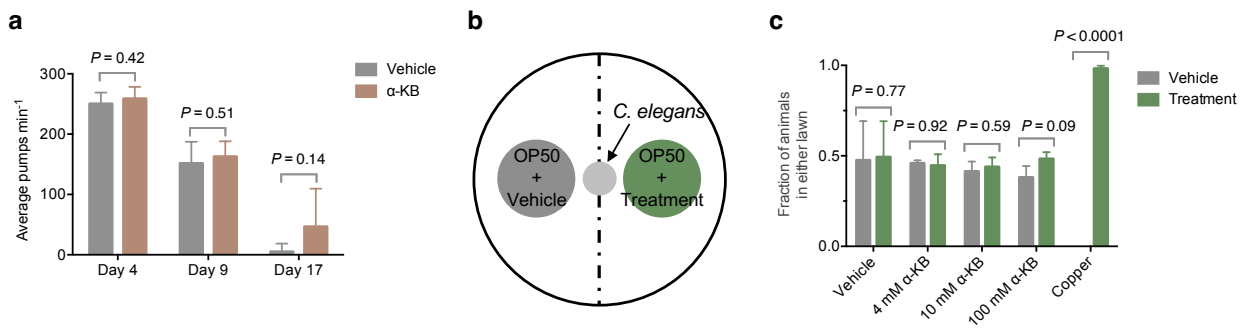
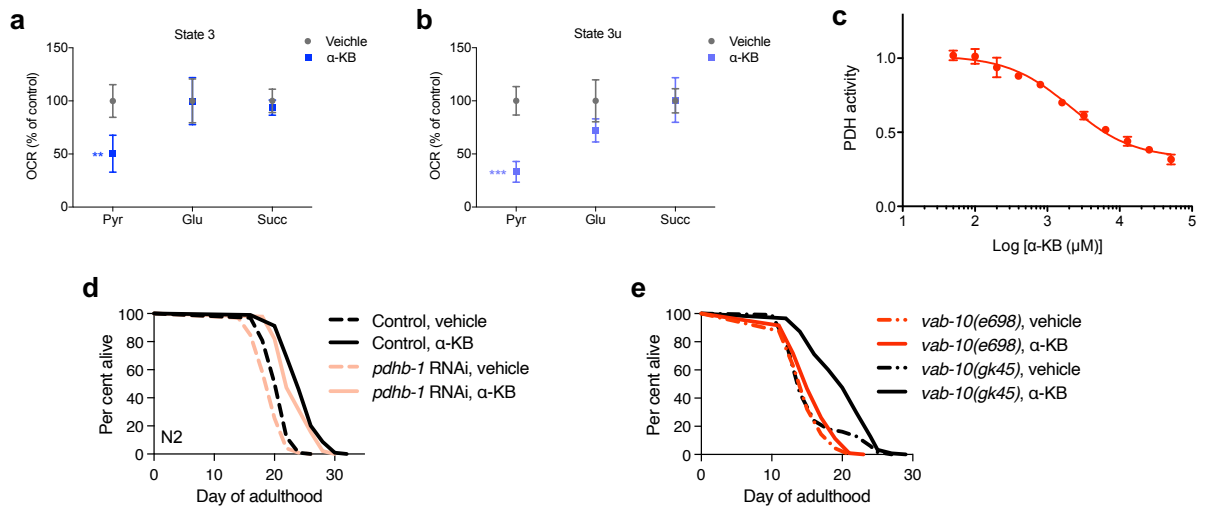

a
Per cent alive
Day of adulthood
N2, vehicle
N2, α-KB
aak-2(gt33), vehicle
aak-2(gt33), α-KB
b
α-KB
IB: P-AMPK
IB: α-Tubulin
c
Control
vab-10 RNAi
Vehicle
α-KB
IB: P-AMPK (T172)
IB: Tubulin
IB: GAPDH
kDa
d
α-KB (mg/kg)
IB: P-AMPK (T172)
IB: AMPK
IB: GAPDH
e
myo-3::GFP(mit)
Control, day 1
α-KB, day 1
Control, day 11
α-KB, day 11
f
Day of Adulthood
daf-16(mu86), vehicle
daf-16(mu86), α-KB
g
N2
0.4X OP50, vehicle
0.4X OP50, α-KB
4X OP50, vehicle
4X OP50, α-KB
40X OP50, vehicle
40X OP50, α-KB
h
α-KB
VAB-10/MACF1
other targets?
Mitochondrial perturbation
AMPK
Dietary restriction (sDR)
Increased health & longevity

Figure 4


a
Per cent alive
100
50
0
Vehicle
α-KB
P = 0.0448
♂
0 100 140 180
Age (weeks)
b
Per cent alive
100
50
0
Vehicle
α-KB
P = 0.3356
♀
0 100 140 180
Age (weeks)
c
Vehicle
α-KB
d
P = 5.3102e-05
Cataract incidentce (%)
100
50
0
Vehicle
α-KB
e
P = 0.0013
P = 0.4363
Activity level
4
3
2
1
0
♀
0 80 90 95 0 80 90 95
Age (% max. lifespan)
Vehicle
α-KB
f
P = 0.0274
Liver/body weight ratio
15
10
5
0
♂+♀
Vehicle
α-KB



Extended Data Fig. 1. α-KB does not decrease food intake of the worms. a, Pharyngeal pumping rate of *C. elegans* on 4 mM α-KB is not significantly altered (by *t*-test, two-tailed, two-sample unequal variance). **b**, Schematic representation of food preference assay. **c**, N2 worms show no preference between OP50 *E. coli* food treated with vehicle control or α-KB (P = 0.7666, by *t*-test, two-tailed, two-sample unequal variance), nor preference between identically treated OP50 *E. coli.*



Extended Data Fig. 2. α-KB inhibits pyruvate-driven complex I respiration. a-b, Isolated mitochondria from mouse liver are incubated with different respiratory substrates. Upon α-KB treatment (500 μM), both state 3 (a) and state 3u (b) respiration are decreased when pyruvate (Pyr) is used as a substrate (∗∗p < 0.01, ∗∗∗p < 0.001). Unpaired t test, two-tailed, two-sample unequal variance is used. Mean ± s.d. is plotted. Glu, glutamate; Succ, succinate. **c**, Inhibition of pyruvate dehydrogenase complex (PDC) activity by α-KB with pyruvate (1 mM) provided as the substrate. PDH activity was assayed using the Abcam Pyruvate dehydrogenase (PDH) Enzyme Activity Microplate Assay Kit (ab109902) with bovine heart mitochondrial lysate (ab110338) according to the manufacturer's instructions. **d**, Effect of α-KB on the lifespan of *C. elegans* with knockdown of pyruvate dehydrogenase E1 subunit beta *pdhb-1*. N2 treated with *pdhb-1* RNAi, m_{veh} = 19.4 (n = 98), $m_{\alpha\text{-KB}}$ = 23.6 (n = 96), P <0.0001; N2 treated with empty vector control, m_{veh} = 20.8 (n = 99), $m_{\alpha\text{-KB}}$ = 24.7 (n = 104), P <0.0001. P values were determined by the log-rank test. **e**, Effect of α-KB on the lifespan of *vab-10* mutant *C. elegans*. Loss-of-function *vab-10(e698)*, m_{veh} = 15.0 (n = 90), $m_{\alpha\text{-KB}}$ = 16.0 (n = 107), 6.2%, P = 0.016; silent *vab-10(gk45)*, m_{veh} = 16.0 (n = 117), $m_{\alpha\text{-KB}}$ = 20.1 (n = 118), 25.6%, P < 0.0001. P values were determined by the log-rank test.

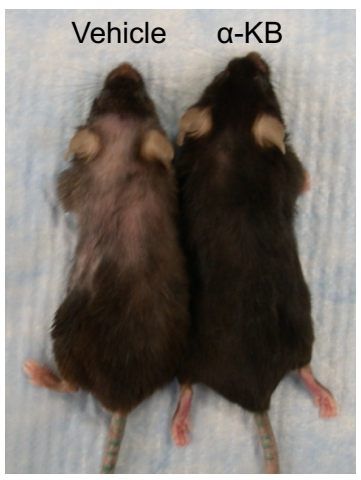
a

	Male		Female	
	Vehicle	α-KB	Vehicle	α-KB
Weight (g)	33.3 ± 2.7	30.4 ± 2.0	27.8 ± 3.3	27.4 ± 0.6
Plasma glucose (mg/dL)	147.0 ± 20.0	132.5 ± 13.0	155.3 ± 24.0	116.5 ± 36.1
% fat	10.5 ± 3.7	8.8 ± 1.0	13.1 ± 4.5	13.4 ± 6.2
% lean	83.9 ± 3.0	86.7 ± 1.5	80.1 ± 3.3	79.8 ± 5.4

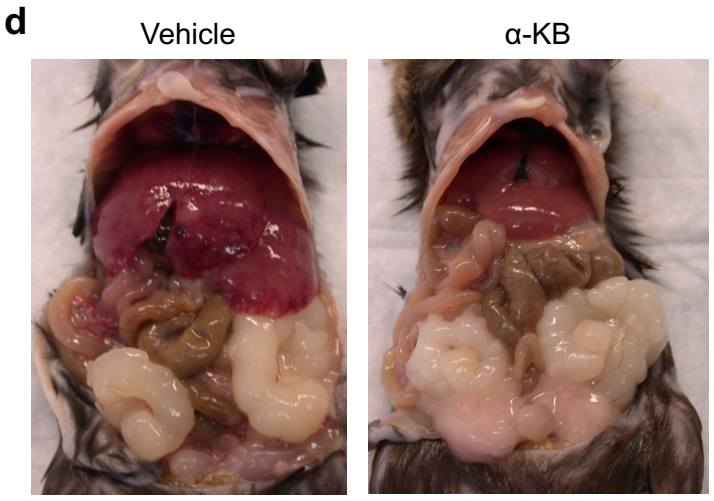
b

Sex	Treatment	No.	Hair	Liver	Body weight (g)	Liver weight (g)	% Liver
M	Vehicle	C4	Lesser hair	Enlarged	27.40	3.00	10.9
M	α-KB	T2	Lesser hair	Normal	27.50	1.19	4.3
M	α-KB	T3	Normal	Enlarged	28.42	2.57	9.0
M	α-KB	T4	Normal	Normal	28.87	1.14	3.9
M	α-KB	T5	Normal	Normal	29.80	1.25	4.2
F	Vehicle	C1	No hair	Ascites	22.43	1.98	8.8
F	Vehicle	C2	No hair	Enlarged	23.10	1.80	7.8
F	Vehicle	C3	No hair	Enlarged	26.33	2.00	7.6
F	α-KB	T1	Normal	Normal	24.27	1.32	5.4

c



d



Extended Data Fig. 3. α-KB supplementation protects aged mice against hair loss and liver disease. Aged C57BL/6J mice were treated with either vehicle control or α-KB starting at 23 months of age. The experiments were completed at 131 weeks of age, by which time 2 of 3 untreated females had developed large cataracts; 4 of 5 α-KB treated males were alive, whereas 3 of 4 vehicle control males had died and the remaining control male was terminated due to severely impaired motility. **a**, Table showing body weight, plasma glucose, and fat/lean body composition of vehicle control and α-KB–treated mice. **b**, Table showing hair and liver conditions of vehicle control and α-KB–treated male and female mice. **c**, Photo showing vehicle control (left) and α-KB–

treated (right) female mice side by side. α-KB–treated aged mice had better hair coating conditions and less hair loss than control mice. **d**, Photos showing enlarged liver in a control male mouse (left) and normal liver in an α-KB–treated (right) male mouse. α-KB–treated mice had a lower incidence of hepatomegaly.

Extended Data Table 1. Summary of lifespan data

Strain	*m* (mean lifespan, days) vehicle	α-KB	% difference	*p*-value	*n* (number of animals) vehicle	α-KB
N2	14.1	22.4	58.9	< 0.0001	111	66
N2	13.1	18.3	39.8	< 0.0001	83	99
N2	17.6	20.1	14.0	0.0037	95	71
N2	15.9	19.1	20.3	< 0.0001	98	94
N2	16.2	20.4	26.0	< 0.0001	73	64
N2	12.8	15.9	24.4	< 0.0001	105	107
N2	12.2	15.5	27.1	< 0.0001	101	103
N2	16.0	17.6	10.3	0.0016	110	107
N2	14.0	18.6	32.9	< 0.0001	92	95
eat-2(ad1116)	20.4	23.0	12.7	0.0054	99	116
N2	16.9	19.7	16.2	< 0.0001	117	116
daf-2 (e1370)	32.0	32.2	0.7	0.7379	108	109
N2	16.5	18.8	13.9	< 0.0001	108	110
daf-2 (e1370)	33.3	35.3	6.0	0.7804	103	102
N2	13.9	20.9	50.5	< 0.0001	72	65
vab-10(e698)	15.4	16.3	5.5	0.1344	67	69
N2	16.3	20.1	23.9	< 0.0001	98	98
vab-10(e698)	16.1	16.8	4.3	0.1507	85	87
N2	18.4	21.0	14.0	< 0.0001	117	112
vab-10(e698)	15.0	16.0	6.2	0.016	90	107
vab-10(gk45)	16.0	20.1	25.6	< 0.0001	117	118
N2	14.5	17.7	22.0	< 0.0001	116	118
aak-2 (gt33)	14.2	15.0	5.5	0.0368	118	118
N2	13.2	18.6	40.9	< 0.0001	121	127
aak-2 (gt33)	14.7	15.9	8.2	0.0111	127	127
N2	14.9	16.5	10.9	0.0002	97	91
aak-2 (gt33)	13.3	12.6	-5.1	0.0379	85	95
N2	20.8	26.6	27.9	< 0.0001	95	111
aak-2(gt33)	17.7	18.9	6.8	0.0076	99	100
N2	14.9	16.5	10.7	0.0002	97	91
aak-2(gt33)	13.3	12.6	-5.3	0.0379	85	95
aak-2(gt33)	15.9	15.1	-5.0	0.0029	120	138
N2	13.2	18.6	40.9	< 0.0001	121	127
daf-16 (mu86)	13.5	16.5	22.2	< 0.0001	124	128
N2	14.9	16.5	11.0	0.0002	97	91
daf-16 (mu86)	14.7	16.3	10.9	< 0.0001	94	90
N2	14.5	17.7	22.0	< 0.0001	116	118
daf-16 (mu86)	13.9	15.4	11.2	< 0.0001	116	112
EV RNAi control	19.9	26.9	35.5	< 0.0001	84	69
vab-10(RNAi)	22.8	24.7	8.3	0.0012	99	99
EV RNAi control	20.8	24.7	18.6	< 0.0001	99	104
pdhb-1(RNAi)	19.4	23.6	21.6	< 0.0001	98	96
gfp RNAi control	19.4	23.0	18.6	< 0.0001	86	49
pdhb-1(RNAi)	17.8	21.6	21.3	< 0.0001	45	49

Extended Data Table 2. Enriched proteins in the α-KB DARTS samples

Protein	Control			α-KB			Enrichment	*P*-value	Total SCs
	1	2	3	1	2	3			
sp|Q9ERU9|RBP2_MOUSE - E3 SUMO-protein ligase RanBP2	0	0	0	4	8	9	Inf	0.0101	21
sp|Q6DFV3|RHG21_MOUSE - Rho GTPase-activating protein 21	0	0	0	4	6	2	Inf	0.0257	12
sp|Q9QXZ0|MACF1_MOUSE - Microtubule-actin cross-linking factor 1	0	0	0	10	22	32	Inf	0.0284	64
sp|P56395|CYB5_MOUSE - Cytochrome b5	6	18	0	39	49	67	6.5	0.011	179
sp|P19783|COX41_MOUSE - Cytochrome c oxidase subunit 4 isoform 1	12	19	0	37	74	66	5.7	0.0178	208

Only showing those proteins with $p < 0.05$ in the 3 biological replicates and at least 15 spectra in α-KB samples. Full information is available in Extended Data Table 3.

Extended Data Table 3. Proteins in the vehicle control and α-KB DARTS samples

Protein	Ctrl 1	Ctrl 2	Ctrl 3	α-KB 1	α-KB 2	α-KB 3	Fold Change	*P*-value	SCs
sp|Q3UPH1|PRRC1_MOUSE - Protein PRRC1 OS=Mus musculus GN=Prrc1 PE=2 SV=1	3	0	0	0	0	0	Inf	0.3739	3
sp|O88898|P63_MOUSE - Tumor protein 63 OS=Mus musculus GN=Tp63 PE=1 SV=1	3	11	2	0	0	0	Inf	0.1344	16
sp|Q3URU2|PEG3_MOUSE - Paternally-expressed gene 3 protein OS=Mus musculus GN=Pe	2	0	0	0	0	0	Inf	0.3739	2
sp|Q6GQT1|A2MP_MOUSE - Alpha-2-macroglobulin-P OS=Mus musculus GN=A2mp PE=2 SV=2	4	9	0	0	0	0	Inf	0.1713	13
sp|Q80WC3|TNC18_MOUSE - Trinucleotide repeat-containing gene 18 protein OS=Mus m	2	0	0	0	0	0	Inf	0.3739	2
sp|Q6PCM2|INT6_MOUSE - Integrator complex subunit 6 OS=Mus musculus GN=Ints6 PE=	4	0	0	0	0	0	Inf	0.3739	4
sp|Q8K259|GIN1_MOUSE - Gypsy retrotransposon integrase-like protein 1 OS=Mus mus	6	3	0	0	0	0	Inf	0.1583	9
sp|Q14B71|CDCA2_MOUSE - Cell division cycle-associated protein 2 OS=Mus musculus	2	0	0	0	0	0	Inf	0.3739	2
sp|P48972|MYBB_MOUSE - Myb-related protein B OS=Mus musculus GN=Mybl2 PE=1 SV=1	2	18	0	0	0	0	Inf	0.3068	20
sp|Q0VGT4|ZGRF1_MOUSE - Protein ZGRF1 OS=Mus musculus GN=Zgrf1 PE=2 SV=2	3	0	0	0	0	0	Inf	0.3739	3
sp|Q8CGM1|BAI2_MOUSE - Brain-specific angiogenesis inhibitor 2 OS=Mus musculus G	2	5	0	0	0	0	Inf	0.1835	7
sp|Q9CZU3|SK2L2_MOUSE - Superkiller viralicidic activity 2-like 2 OS=Mus musculu	2	18	15	0	0	0	Inf	0.0763	35
sp|Q05144|RAC2_MOUSE - Ras-related C3 botulinum toxin substrate 2 OS=Mus musculu	2	7	0	0	0	0	Inf	0.2229	9
sp|P48774|GSTM5_MOUSE - Glutathione S-transferase Mu 5 OS=Mus musculus GN=Gstm5	2	0	0	0	0	0	Inf	0.3739	2
sp|Q9Z2L7|CRLF3_MOUSE - Cytokine receptor-like factor 3 OS=Mus musculus GN=Crlf3	3	0	0	0	0	0	Inf	0.3739	3
sp|Q8C3I9|DIA1R_MOUSE - Deleted in autism-related protein 1 homolog OS=Mus muscu	2	0	0	0	0	0	Inf	0.3739	2
sp|Q9ERH8|S28A3_MOUSE - Solute carrier family 28 member 3 OS=Mus musculus GN=Slc	3	8	0	0	0	0	Inf	0.1911	11
sp|P25976|UBF1_MOUSE - Nucleolar transcription factor 1 OS=Mus musculus GN=Ubtf	3	0	0	0	0	0	Inf	0.3739	3
sp|P48281|VDR_MOUSE - Vitamin D3 receptor OS=Mus musculus GN=Vdr PE=1 SV=2	3	0	0	0	0	0	Inf	0.3739	3
sp|Q80WQ9|ZBED4_MOUSE - Zinc finger BED domain-containing protein 4 OS=Mus muscu	2	0	0	0	0	0	Inf	0.3739	2
sp|Q9QY06|MYO9B_MOUSE - Unconventional myosin-IXb OS=Mus musculus GN=Myo9b PE=1	3	24	0	0	0	0	Inf	0.2991	27
sp|Q3V1H3|HPHL1_MOUSE - Hephaestin-like protein 1 OS=Mus musculus GN=Hephl1 PE=2	2	0	0	0	0	0	Inf	0.3739	2
sp|Q9D125|RT25_MOUSE - 28S ribosomal protein S25, mitochondrial OS=Mus musculus	4	0	0	0	0	0	Inf	0.3739	4
sp|Q8BU88|RM22_MOUSE - 39S ribosomal protein L22, mitochondrial OS=Mus musculus	2	2	0	0	0	0	Inf	0.1161	4
sp|P62281|RS11_MOUSE - 40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=1 S	2	4	0	0	0	0	Inf	0.1583	6
sp|Q9CPU0|LGUL_MOUSE - Lactoylglutathione lyase OS=Mus musculus GN=Glo1 PE=1 SV=	2	0	0	0	0	0	Inf	0.3739	2
sp|P70245|EBP_MOUSE - 3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase OS=Mus m	2	22	5	0	0	0	Inf	0.1955	29
sp|A4Q9E4|TTLL2_MOUSE - Probable tubulin polyglutamylase TTLL2 OS=Mus musculus G	2	0	0	0	0	0	Inf	0.3739	2
sp|Q80YR4|ZN598_MOUSE - Zinc finger protein 598 OS=Mus musculus GN=Znf598 PE=2 S	2	0	0	0	0	0	Inf	0.3739	2
sp|O08810|U5S1_MOUSE - 116 kDa U5 small nuclear ribonucleoprotein component OS=M	4	2	4	0	0	0	Inf	0.0074	10
sp|Q62468|VILI_MOUSE - Villin-1 OS=Mus musculus GN=Vil1 PE=1 SV=3	4	0	0	0	0	0	Inf	0.3739	4
sp|Q8BGF7|PAN2_MOUSE - PAB-dependent poly(A)-specific ribonuclease subunit PAN2	2	0	0	0	0	0	Inf	0.3739	2
sp|Q80TR8|VPRBP_MOUSE - Protein VPRBP OS=Mus musculus GN=Vprbp PE=1 SV=4	3	0	0	0	0	0	Inf	0.3739	3
sp|A2AJ76|HMCN2_MOUSE - Hemicentin-2 OS=Mus musculus GN=Hmcn2 PE=2 SV=1	4	9	10	0	0	0	Inf	0.0144	23
sp|O09111|NDUBB_MOUSE - NADH dehydrogenase [ubiquinone] 1 beta subcomplex subuni	2	2	0	0	0	0	Inf	0.1161	4
sp|P62852|RS25_MOUSE - 40S ribosomal protein S25 OS=Mus musculus GN=Rps25 PE=1 S	2	2	0	0	0	0	Inf	0.1161	4
sp|P56384|AT5G3_MOUSE - ATP synthase F(0) complex subunit C3, mitochondrial OS=M	2	0	0	0	0	0	Inf	0.3739	2
sp|Q6X7S9|EID2_MOUSE - EP300-interacting inhibitor of differentiation 2 OS=Mus m	2	0	0	0	0	0	Inf	0.3739	2
sp|P62751|RL23A_MOUSE - 60S ribosomal protein L23a OS=Mus musculus GN=Rpl23a PE=	3	0	0	0	0	0	Inf	0.3739	3

sp|Q9Z2Y8|PROSC_MOUSE - Proline synthase co-transcribed bacterial homolog protei	2	2	0	0	0	0	Inf	0.1161	4
sp|P70441|NHRF1_MOUSE - Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Mus m	2	0	0	0	0	0	Inf	0.3739	2
sp|Q8CGC4|LS14B_MOUSE - Protein LSM14 homolog B OS=Mus musculus GN=Lsm14b PE=2 S	2	2	2	0	0	0	Inf	0	6
sp|Q923B1|DBR1_MOUSE - Lariat debranching enzyme OS=Mus musculus GN=Dbr1 PE=1 SV	2	0	0	0	0	0	Inf	0.3739	2
sp|Q922W5|P5CR1_MOUSE - Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Mu	2	0	0	0	0	0	Inf	0.3739	2
sp|Q3URD3|SLMAP_MOUSE - Sarcolemmal membrane-associated protein OS=Mus musculus	4	0	0	0	0	0	Inf	0.3739	4
sp|Q8BZ03|KPCD2_MOUSE - Serine/threonine-protein kinase D2 OS=Mus musculus GN=Pr	2	0	0	0	0	0	Inf	0.3739	2
sp|A3KG59|P20D2_MOUSE - Peptidase M20 domain-containing protein 2 OS=Mus musculu	2	0	0	0	0	0	Inf	0.3739	2
sp|Q9Z110|P5CS_MOUSE - Delta-1-pyrroline-5-carboxylate synthase OS=Mus musculus	3	0	0	0	0	0	Inf	0.3739	3
sp|Q9D783|KLH40_MOUSE - Kelch-like protein 40 OS=Mus musculus GN=Klhl40 PE=1 SV=	2	0	0	0	0	0	Inf	0.3739	2
sp|Q6A068|CDC5L_MOUSE - Cell division cycle 5-like protein OS=Mus musculus GN=Cd	3	0	0	0	0	0	Inf	0.3739	3
sp|Q8K2J9|BTBD6_MOUSE - BTB/POZ domain-containing protein 6 OS=Mus musculus GN=B	2	7	0	0	0	0	Inf	0.2229	9
sp|A2CI98|DYTN_MOUSE - Dystrotelin OS=Mus musculus GN=Dytn PE=2 SV=1	2	0	0	0	0	0	Inf	0.3739	2
sp|Q6A025|PPR26_MOUSE - Protein phosphatase 1 regulatory subunit 26 OS=Mus muscu	3	0	0	0	0	0	Inf	0.3739	3
sp|O08582|GTPB1_MOUSE - GTP-binding protein 1 OS=Mus musculus GN=Gtpbp1 PE=1 SV=	2	0	0	0	0	0	Inf	0.3739	2
sp|P15116|CADH2_MOUSE - Cadherin-2 OS=Mus musculus GN=Cdh2 PE=1 SV=2	2	2	0	0	0	0	Inf	0.1161	4
sp|P28658|ATX10_MOUSE - Ataxin-10 OS=Mus musculus GN=Atxn10 PE=1 SV=2	2	0	0	0	0	0	Inf	0.3739	2
sp|Q8BRG8|TM209_MOUSE - Transmembrane protein 209 OS=Mus musculus GN=Tmem209 PE=	2	0	0	0	0	0	Inf	0.3739	2
sp|Q8CH25|SLTM_MOUSE - SAFB-like transcription modulator OS=Mus musculus GN=Sltm	3	0	16	0	0	0	Inf	0.2666	19
sp|Q8CDV6|CCD63_MOUSE - Coiled-coil domain-containing protein 63 OS=Mus musculus	3	0	0	0	0	0	Inf	0.3739	3
sp|Q5U4C1|GASP1_MOUSE - G-protein coupled receptor-associated sorting protein 1	2	0	0	0	0	0	Inf	0.3739	2
sp|O35231|KIFC3_MOUSE - Kinesin-like protein KIFC3 OS=Mus musculus GN=Kifc3 PE=1	3	0	0	0	0	0	Inf	0.3739	3
sp|Q9QXY6|EHD3_MOUSE - EH domain-containing protein 3 OS=Mus musculus GN=Ehd3 PE	2	0	0	0	0	0	Inf	0.3739	2
sp|Q3UU96|MRCKA_MOUSE - Serine/threonine-protein kinase MRCK alpha OS=Mus muscul	4	0	0	0	0	0	Inf	0.3739	4
sp|Q80YR5|SAFB2_MOUSE - Scaffold attachment factor B2 OS=Mus musculus GN=Safb2 P	3	0	16	0	0	0	Inf	0.2666	19
sp|Q9CS00|CATIN_MOUSE - Cactin OS=Mus musculus GN=Cactin PE=1 SV=2	2	5	4	0	0	0	Inf	0.0141	11
sp|A1EGX6|FSCB_MOUSE - Fibrous sheath CABYR-binding protein OS=Mus musculus GN=F	2	0	0	0	0	0	Inf	0.3739	2
sp|Q66X03|NAL9A_MOUSE - NACHT, LRR and PYD domains-containing protein 9A OS=Mus	3	0	0	0	0	0	Inf	0.3739	3
sp|Q07139|ECT2_MOUSE - Protein ECT2 OS=Mus musculus GN=Ect2 PE=1 SV=2	2	0	0	0	0	0	Inf	0.3739	2
sp|Q0VF58|COJA1_MOUSE - Collagen alpha-1(XIX) chain OS=Mus musculus GN=Col19a1 P	2	0	0	0	0	0	Inf	0.3739	2
sp|Q99MS7|EH1L1_MOUSE - EH domain-binding protein 1-like protein 1 OS=Mus muscul	2	0	0	0	0	0	Inf	0.3739	2
sp|O54990|PROM1_MOUSE - Prominin-1 OS=Mus musculus GN=Prom1 PE=1 SV=1	2	0	0	0	0	0	Inf	0.3739	2
sp|Q7TT50|MRCKB_MOUSE - Serine/threonine-protein kinase MRCK beta OS=Mus musculu	2	0	0	0	0	0	Inf	0.3739	2
sp|E9Q414|APOB_MOUSE - Apolipoprotein B-100 OS=Mus musculus GN=Apob PE=1 SV=1	4	16	7	0	0	0	Inf	0.067	27
sp|P0DM40|FR1L5_MOUSE - Fer-1-like protein 5 OS=Mus musculus GN=Fer1l5 PE=1 SV=1	2	0	0	0	0	0	Inf	0.3739	2
sp|Q5H8C4|VP13A_MOUSE - Vacuolar protein sorting-associated protein 13A OS=Mus m	2	6	0	0	0	0	Inf	0.2051	8
sp|Q30KP5|DFB18_MOUSE - Beta-defensin 18 OS=Mus musculus GN=Defb18 PE=3 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BQ47|CNPY4_MOUSE - Protein canopy homolog 4 OS=Mus musculus GN=Cnpy4 PE=1 S	0	2	0	0	0	0	Inf	0.3739	2
sp|P43276|H15_MOUSE - Histone H1.5 OS=Mus musculus GN=Hist1h1b PE=1 SV=2	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9D7X8|GGCT_MOUSE - Gamma-glutamylcyclotransferase OS=Mus musculus GN=Ggct PE	0	8	0	0	0	0	Inf	0.3739	8
sp|O89013|OBRG_MOUSE - Leptin receptor gene-related protein OS=Mus musculus GN=L	0	4	0	0	0	0	Inf	0.3739	4

sp|O08583|THOC4_MOUSE - THO complex subunit 4 OS=Mus musculus GN=Alyref PE=1 SV=	0	5	0	0	0	0	Inf	0.3739	5
sp|Q9CPT0|B2L14_MOUSE - Apoptosis facilitator Bcl-2-like protein 14 OS=Mus muscu	0	13	0	0	0	0	Inf	0.3739	13
sp|Q91Z49|UIF_MOUSE - UAP56-interacting factor OS=Mus musculus GN=Fyttd1 PE=1 SV	0	10	0	0	0	0	Inf	0.3739	10
sp|Q8BJF9|CHM2B_MOUSE - Charged multivesicular body protein 2b OS=Mus musculus G	0	5	4	0	0	0	Inf	0.121	9
sp|Q9JJU9|CRBB3_MOUSE - Beta-crystallin B3 OS=Mus musculus GN=Crybb3 PE=2 SV=3	0	8	0	0	0	0	Inf	0.3739	8
sp|Q80Y61|BI2L2_MOUSE - Brain-specific angiogenesis inhibitor 1-associated prote	0	3	0	0	0	0	Inf	0.3739	3
sp|P11438|LAMP1_MOUSE - Lysosome-associated membrane glycoprotein 1 OS=Mus muscu	0	14	3	0	0	0	Inf	0.2538	17
sp|Q91VL8|TE2IP_MOUSE - Telomeric repeat-binding factor 2-interacting protein 1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q80Y20|ALKB8_MOUSE - Alkylated DNA repair protein alkB homolog 8 OS=Mus muscu	0	5	0	0	0	0	Inf	0.3739	5
sp|P12790|CP2B9_MOUSE - Cytochrome P450 2B9 OS=Mus musculus GN=Cyp2b9 PE=2 SV=2	0	8	0	0	0	0	Inf	0.3739	8
sp|P52800|EFNB2_MOUSE - Ephrin-B2 OS=Mus musculus GN=Efnb2 PE=1 SV=1	0	5	0	0	0	0	Inf	0.3739	5
sp|Q9R069|BCAM_MOUSE - Basal cell adhesion molecule OS=Mus musculus GN=Bcam PE=2	0	2	0	0	0	0	Inf	0.3739	2
sp|P20152|VIME_MOUSE - Vimentin OS=Mus musculus GN=Vim PE=1 SV=3	0	14	13	0	0	0	Inf	0.1166	27
sp|Q921X9|PDIA5_MOUSE - Protein disulfide-isomerase A5 OS=Mus musculus GN=Pdia5	0	10	0	0	0	0	Inf	0.3739	10
sp|Q60967|PAPS1_MOUSE - Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synth	0	6	7	0	0	0	Inf	0.1184	13
sp|P03995|GFAP_MOUSE - Glial fibrillary acidic protein OS=Mus musculus GN=Gfap P	0	3	0	0	0	0	Inf	0.3739	3
sp|P70158|ASM3A_MOUSE - Acid sphingomyelinase-like phosphodiesterase 3a OS=Mus m	0	6	5	0	0	0	Inf	0.1193	11
sp|Q61616|DRD1_MOUSE - D(1A) dopamine receptor OS=Mus musculus GN=Drd1 PE=2 SV=2	0	4	0	0	0	0	Inf	0.3739	4
sp|Q9EPX5|FXL12_MOUSE - F-box/LRR-repeat protein 12 OS=Mus musculus GN=Fbxl12 PE	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BVU0|LRCH3_MOUSE - Leucine-rich repeat and calponin homology domain-contain	0	5	0	0	0	0	Inf	0.3739	5
sp|Q0VBV7|K1377_MOUSE - Uncharacterized protein KIAA1377 OS=Mus musculus GN=Kiaa	0	26	0	0	0	0	Inf	0.3739	26
sp|O55071|CP2BJ_MOUSE - Cytochrome P450 2B19 OS=Mus musculus GN=Cyp2b19 PE=2 SV=	0	3	0	0	0	0	Inf	0.3739	3
sp|Q91YD9|WASL_MOUSE - Neural Wiskott-Aldrich syndrome protein OS=Mus musculus G	0	9	0	0	0	0	Inf	0.3739	9
sp|Q8BMA5|NPAT_MOUSE - Protein NPAT OS=Mus musculus GN=Npat PE=2 SV=2	0	7	13	0	0	0	Inf	0.1506	20
sp|Q02819|NUCB1_MOUSE - Nucleobindin-1 OS=Mus musculus GN=Nucb1 PE=1 SV=2	0	15	0	0	0	0	Inf	0.3739	15
sp|Q9D1P2|KAT8_MOUSE - Histone acetyltransferase KAT8 OS=Mus musculus GN=Kat8 PE	0	2	0	0	0	0	Inf	0.3739	2
sp|Q80ZJ8|EFC4A_MOUSE - EF-hand calcium-binding domain-containing protein 4A OS=	0	5	0	0	0	0	Inf	0.3739	5
sp|Q60675|LAMA2_MOUSE - Laminin subunit alpha-2 OS=Mus musculus GN=Lama2 PE=1 SV	0	15	0	0	0	0	Inf	0.3739	15
sp|A2ACJ2|FP100_MOUSE - Fanconi anemia-associated protein of 100 kDa OS=Mus musc	0	7	0	0	0	0	Inf	0.3739	7
sp|Q99J79|DDB2_MOUSE - DNA damage-binding protein 2 OS=Mus musculus GN=Ddb2 PE=1	0	5	2	0	0	0	Inf	0.1835	7
sp|Q9JME5|AP3B2_MOUSE - AP-3 complex subunit beta-2 OS=Mus musculus GN=Ap3b2 PE=	0	16	0	0	0	0	Inf	0.3739	16
sp|A6H6E2|MMRN2_MOUSE - Multimerin-2 OS=Mus musculus GN=Mmrn2 PE=2 SV=1	0	19	0	0	0	0	Inf	0.3739	19
sp|Q61771|KIF3B_MOUSE - Kinesin-like protein KIF3B OS=Mus musculus GN=Kif3b PE=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BT60|CPNE3_MOUSE - Copine-3 OS=Mus musculus GN=Cpne3 PE=2 SV=2	0	10	0	0	0	0	Inf	0.3739	10
sp|Q6PGA0|RCOR3_MOUSE - REST corepressor 3 OS=Mus musculus GN=Rcor3 PE=2 SV=2	0	8	0	0	0	0	Inf	0.3739	8
sp|Q8VC03|EMAL3_MOUSE - Echinoderm microtubule-associated protein-like 3 OS=Mus	0	15	21	0	0	0	Inf	0.127	36
sp|P03921|NU5M_MOUSE - NADH-ubiquinone oxidoreductase chain 5 OS=Mus musculus GN	0	4	0	0	0	0	Inf	0.3739	4
sp|Q03311|CHLE_MOUSE - Cholinesterase OS=Mus musculus GN=Bche PE=2 SV=2	0	4	0	0	0	0	Inf	0.3739	4
sp|Q811C2|ATG4C_MOUSE - Cysteine protease ATG4C OS=Mus musculus GN=Atg4c PE=1 SV	0	7	0	0	0	0	Inf	0.3739	7
sp|Q5DTT3|F208B_MOUSE - Protein FAM208B OS=Mus musculus GN=Fam208b PE=2 SV=2	0	15	0	0	0	0	Inf	0.3739	15
sp|Q6P542|ABCF1_MOUSE - ATP-binding cassette sub-family F member 1 OS=Mus muscul	0	6	0	0	0	0	Inf	0.3739	6

sp|Q6ZQ11|CHSS1_MOUSE - Chondroitin sulfate synthase 1 OS=Mus musculus GN=Chsy1	0	6	0	0	0	0	Inf	0.3739	6
sp|P51125|ICAL_MOUSE - Calpastatin OS=Mus musculus GN=Cast PE=1 SV=2	0	12	0	0	0	0	Inf	0.3739	12
sp|Q8CG48|SMC2_MOUSE - Structural maintenance of chromosomes protein 2 OS=Mus mu	0	27	15	0	0	0	Inf	0.1475	42
sp|Q61056|TRPC1_MOUSE - Short transient receptor potential channel 1 OS=Mus musc	0	5	0	0	0	0	Inf	0.3739	5
sp|Q8K212|PACS1_MOUSE - Phosphofurin acidic cluster sorting protein 1 OS=Mus mus	0	8	0	0	0	0	Inf	0.3739	8
sp|Q91X43|SH319_MOUSE - SH3 domain-containing protein 19 OS=Mus musculus GN=Sh3d	0	12	0	0	0	0	Inf	0.3739	12
sp|Q8BMP4|GPER1_MOUSE - G-protein coupled estrogen receptor 1 OS=Mus musculus GN	0	0	18	0	0	0	Inf	0.3739	18
sp|O70410|V2R1_MOUSE - Vomeronasal type-2 receptor 1 OS=Mus musculus GN=Vmn2r1 P	0	6	0	0	0	0	Inf	0.3739	6
sp|Q8C052|MAP1S_MOUSE - Microtubule-associated protein 1S OS=Mus musculus GN=Map	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9JHD1|KAT2B_MOUSE - Histone acetyltransferase KAT2B OS=Mus musculus GN=Kat2b	0	6	0	0	0	0	Inf	0.3739	6
sp|P42230|STA5A_MOUSE - Signal transducer and activator of transcription 5A OS=M	0	5	0	0	0	0	Inf	0.3739	5
sp|Q80TI0|GRM1B_MOUSE - GRAM domain-containing protein 1B OS=Mus musculus GN=Gra	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9Z0J4|NOS1_MOUSE - Nitric oxide synthase, brain OS=Mus musculus GN=Nos1 PE=1	0	8	0	0	0	0	Inf	0.3739	8
sp|Q69ZZ9|K0754_MOUSE - Uncharacterized protein KIAA0754 OS=Mus musculus GN=Kiaa	0	10	0	0	0	0	Inf	0.3739	10
sp|Q61161|M4K2_MOUSE - Mitogen-activated protein kinase kinase kinase kinase 2 O	0	11	0	0	0	0	Inf	0.3739	11
sp|Q923A2|SPDLY_MOUSE - Protein Spindly OS=Mus musculus GN=Spdl1 PE=1 SV=2	0	8	0	0	0	0	Inf	0.3739	8
sp|Q9WTS6|TEN3_MOUSE - Teneurin-3 OS=Mus musculus GN=Tenm3 PE=1 SV=1	0	17	0	0	0	0	Inf	0.3739	17
sp|Q9Z1T1|AP3B1_MOUSE - AP-3 complex subunit beta-1 OS=Mus musculus GN=Ap3b1 PE=	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9QX47|SON_MOUSE - Protein SON OS=Mus musculus GN=Son PE=1 SV=2	0	9	0	0	0	0	Inf	0.3739	9
sp|Q9ESF1|OTOF_MOUSE - Otoferlin OS=Mus musculus GN=Otof PE=1 SV=1	0	11	0	0	0	0	Inf	0.3739	11
sp|P13597|ICAM1_MOUSE - Intercellular adhesion molecule 1 OS=Mus musculus GN=Ica	0	2	0	0	0	0	Inf	0.3739	2
sp|P19137|LAMA1_MOUSE - Laminin subunit alpha-1 OS=Mus musculus GN=Lama1 PE=1 SV	0	12	0	0	0	0	Inf	0.3739	12
sp|Q5SUR0|PUR4_MOUSE - Phosphoribosylformylglycinamidine synthase OS=Mus musculu	0	5	0	0	0	0	Inf	0.3739	5
sp|Q9Z1B3|PLCB1_MOUSE - 1-phosphatidylinositol 4,5-bisphosphate phosphodiesteras	0	5	0	0	0	0	Inf	0.3739	5
sp|A2A891|CMTA1_MOUSE - Calmodulin-binding transcription activator 1 OS=Mus musc	0	6	0	0	0	0	Inf	0.3739	6
sp|Q3UHK6|TEN4_MOUSE - Teneurin-4 OS=Mus musculus GN=Tenm4 PE=1 SV=2	0	24	0	0	0	0	Inf	0.3739	24
sp|Q9QY81|PO210_MOUSE - Nuclear pore membrane glycoprotein 210 OS=Mus musculus G	0	2	0	0	0	0	Inf	0.3739	2
sp|Q61037|TSC2_MOUSE - Tuberin OS=Mus musculus GN=Tsc2 PE=1 SV=1	0	5	0	0	0	0	Inf	0.3739	5
sp|P97450|ATP5J_MOUSE - ATP synthase-coupling factor 6, mitochondrial OS=Mus mus	0	10	0	0	0	0	Inf	0.3739	10
sp|P63260|ACTG_MOUSE - Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1	0	14	0	0	0	0	Inf	0.3739	14
sp|Q9WUL7|ARL3_MOUSE - ADP-ribosylation factor-like protein 3 OS=Mus musculus GN	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9QYF1|RDH11_MOUSE - Retinol dehydrogenase 11 OS=Mus musculus GN=Rdh11 PE=2 S	0	8	0	0	0	0	Inf	0.3739	8
sp|P13516|ACOD1_MOUSE - Acyl-CoA desaturase 1 OS=Mus musculus GN=Scd1 PE=1 SV=2	0	6	0	0	0	0	Inf	0.3739	6
sp|Q8CHY3|DYM_MOUSE - Dymeclin OS=Mus musculus GN=Dym PE=2 SV=1	0	10	0	0	0	0	Inf	0.3739	10
sp|P07361|A1AG2_MOUSE - Alpha-1-acid glycoprotein 2 OS=Mus musculus GN=Orm2 PE=1	0	4	0	0	0	0	Inf	0.3739	4
sp|Q283N4|URAD_MOUSE - 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxyla	0	4	0	0	0	0	Inf	0.3739	4
sp|Q6PEB4|OSGP2_MOUSE - Probable tRNA N6-adenosine threonylcarbamoyltransferase,	0	4	0	0	0	0	Inf	0.3739	4
sp|P35980|RL18_MOUSE - 60S ribosomal protein L18 OS=Mus musculus GN=Rpl18 PE=2 S	0	2	0	0	0	0	Inf	0.3739	2
sp|Q91V51|TTLL1_MOUSE - Probable tubulin polyglutamylase TTLL1 OS=Mus musculus G	0	11	0	0	0	0	Inf	0.3739	11
sp|O70200|AIF1_MOUSE - Allograft inflammatory factor 1 OS=Mus musculus GN=Aif1 P	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9EQX4|AIF1L_MOUSE - Allograft inflammatory factor 1-like OS=Mus musculus GN=	0	2	0	0	0	0	Inf	0.3739	2

sp|Q9D9C6|CC182_MOUSE - Coiled-coil domain-containing protein 182 OS=Mus musculu	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8R235|TM203_MOUSE - Transmembrane protein 203 OS=Mus musculus GN=Tmem203 PE=	0	2	0	0	0	0	Inf	0.3739	2
sp|P03911|NU4M_MOUSE - NADH-ubiquinone oxidoreductase chain 4 OS=Mus musculus GN	0	3	0	0	0	0	Inf	0.3739	3
sp|Q5M8N4|D39U1_MOUSE - Epimerase family protein SDR39U1 OS=Mus musculus GN=Sdr3	0	2	0	0	0	0	Inf	0.3739	2
sp|Q3TR08|FNDC4_MOUSE - Fibronectin type III domain-containing protein 4 OS=Mus	0	4	0	0	0	0	Inf	0.3739	4
sp|Q6GQS1|SCMC3_MOUSE - Calcium-binding mitochondrial carrier protein SCaMC-3 OS	0	5	0	0	0	0	Inf	0.3739	5
sp|Q9ERE2|KRT81_MOUSE - Keratin, type II cuticular Hb1 OS=Mus musculus GN=Krt81	0	4	0	0	0	0	Inf	0.3739	4
sp|P47802|MTX1_MOUSE - Metaxin-1 OS=Mus musculus GN=Mtx1 PE=1 SV=1	0	13	0	0	0	0	Inf	0.3739	13
sp|Q8CAT8|FBX48_MOUSE - F-box only protein 48 OS=Mus musculus GN=Fbxo48 PE=2 SV=	0	5	0	0	0	0	Inf	0.3739	5
sp|Q9CQU5|ZWINT_MOUSE - ZW10 interactor OS=Mus musculus GN=Zwint PE=2 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|P15948|K1B22_MOUSE - Kallikrein 1-related peptidase b22 OS=Mus musculus GN=Kl	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8CEZ0|KCTD2_MOUSE - BTB/POZ domain-containing protein KCTD2 OS=Mus musculus	0	4	0	0	0	0	Inf	0.3739	4
sp|O35841|API5_MOUSE - Apoptosis inhibitor 5 OS=Mus musculus GN=Api5 PE=1 SV=2	0	7	0	0	0	0	Inf	0.3739	7
sp|P50516|VATA_MOUSE - V-type proton ATPase catalytic subunit A OS=Mus musculus	0	7	0	0	0	0	Inf	0.3739	7
sp|Q8K2I3|FMO2_MOUSE - Dimethylaniline monooxygenase [N-oxide-forming] 2 OS=Mus	0	9	0	0	0	0	Inf	0.3739	9
sp|P68254|1433T_MOUSE - 14-3-3 protein theta OS=Mus musculus GN=Ywhaq PE=1 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8VBY2|KKCC1_MOUSE - Calcium/calmodulin-dependent protein kinase kinase 1 OS=	0	2	0	0	0	0	Inf	0.3739	2
sp|Q99MI6|GIMA3_MOUSE - GTPase IMAP family member 3 OS=Mus musculus GN=Gimap3 PE	0	2	0	0	0	0	Inf	0.3739	2
sp|Q6P8X1|SNX6_MOUSE - Sorting nexin-6 OS=Mus musculus GN=Snx6 PE=1 SV=2	0	3	0	0	0	0	Inf	0.3739	3
sp|Q6PGC7|S35E3_MOUSE - Solute carrier family 35 member E3 OS=Mus musculus GN=Sl	0	2	0	0	0	0	Inf	0.3739	2
sp|P05132|KAPCA_MOUSE - cAMP-dependent protein kinase catalytic subunit alpha OS	0	6	0	0	0	0	Inf	0.3739	6
sp|Q9Z0F8|ADA17_MOUSE - Disintegrin and metalloproteinase domain-containing prot	0	4	0	0	0	0	Inf	0.3739	4
sp|P28862|MMP3_MOUSE - Stromelysin-1 OS=Mus musculus GN=Mmp3 PE=2 SV=2	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9Z2X2|PSD10_MOUSE - 26S proteasome non-ATPase regulatory subunit 10 OS=Mus m	0	2	0	0	0	0	Inf	0.3739	2
sp|O88554|PARP2_MOUSE - Poly [ADP-ribose] polymerase 2 OS=Mus musculus GN=Parp2	0	5	0	0	0	0	Inf	0.3739	5
sp|P50428|ARSA_MOUSE - Arylsulfatase A OS=Mus musculus GN=Arsa PE=2 SV=2	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9QWZ1|RAD1_MOUSE - Cell cycle checkpoint protein RAD1 OS=Mus musculus GN=Rad	0	2	0	0	0	0	Inf	0.3739	2
sp|Q80US4|ARP5_MOUSE - Actin-related protein 5 OS=Mus musculus GN=Actr5 PE=2 SV=	0	4	0	0	0	0	Inf	0.3739	4
sp|P38585|TTL_MOUSE - Tubulin--tyrosine ligase OS=Mus musculus GN=Ttl PE=2 SV=2	0	4	0	0	0	0	Inf	0.3739	4
sp|Q8HW98|IGLO5_MOUSE - IgLON family member 5 OS=Mus musculus GN=Iglon5 PE=2 SV=	0	2	0	0	0	0	Inf	0.3739	2
sp|O54891|LEG6_MOUSE - Galectin-6 OS=Mus musculus GN=Lgals6 PE=2 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9CZB3|THUM2_MOUSE - THUMP domain-containing protein 2 OS=Mus musculus GN=Thu	0	7	0	0	0	0	Inf	0.3739	7
sp|Q8BZW8|NHLC2_MOUSE - NHL repeat-containing protein 2 OS=Mus musculus GN=Nhlrc	0	5	0	0	0	0	Inf	0.3739	5
sp|Q8R180|ERO1A_MOUSE - ERO1-like protein alpha OS=Mus musculus GN=Ero1l PE=1 SV	0	5	0	0	0	0	Inf	0.3739	5
sp|Q8K409|DPOLB_MOUSE - DNA polymerase beta OS=Mus musculus GN=Polb PE=1 SV=3	0	2	0	0	0	0	Inf	0.3739	2
sp|Q924D0|RT4I1_MOUSE - Reticulon-4-interacting protein 1, mitochondrial OS=Mus	0	6	0	0	0	0	Inf	0.3739	6
sp|P59900|EMIL3_MOUSE - EMILIN-3 OS=Mus musculus GN=Emilin3 PE=2 SV=1	0	4	0	0	0	0	Inf	0.3739	4
sp|P45700|MA1A1_MOUSE - Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA OS=Mus	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8VEB4|PAG15_MOUSE - Group XV phospholipase A2 OS=Mus musculus GN=Pla2g15 PE=	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9R1J0|NSDHL_MOUSE - Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylat	0	8	0	0	0	0	Inf	0.3739	8
sp|Q99M31|HSP7E_MOUSE - Heat shock 70 kDa protein 14 OS=Mus musculus GN=Hspa14 P	0	3	0	0	0	0	Inf	0.3739	3

sp|Q8C6P8|ZFP57_MOUSE - Zinc finger protein 57 OS=Mus musculus GN=Zfp57 PE=1 SV=	0	2	0	0	0	0	Inf	0.3739	2
sp|O70570|PIGR_MOUSE - Polymeric immunoglobulin receptor OS=Mus musculus GN=Pigr	0	4	0	0	0	0	Inf	0.3739	4
sp|Q9DCP2|S38A3_MOUSE - Sodium-coupled neutral amino acid transporter 3 OS=Mus m	0	2	0	0	0	0	Inf	0.3739	2
sp|Q91YA2|KPSH1_MOUSE - Serine/threonine-protein kinase H1 OS=Mus musculus GN=Ps	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8CGE8|IFI5A_MOUSE - Interferon-activable protein 205-A OS=Mus musculus GN=If	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BRM2|GORAB_MOUSE - RAB6-interacting golgin OS=Mus musculus GN=Gorab PE=1 SV	0	2	0	0	0	0	Inf	0.3739	2
sp|A2ARS0|ANR63_MOUSE - Ankyrin repeat domain-containing protein 63 OS=Mus muscu	0	3	0	0	0	0	Inf	0.3739	3
sp|O55087|MEF2B_MOUSE - Myocyte-specific enhancer factor 2B OS=Mus musculus GN=M	0	5	0	0	0	0	Inf	0.3739	5
sp|Q8C1B1|CAMP2_MOUSE - Calmodulin-regulated spectrin-associated protein 2 OS=Mu	0	7	0	0	0	0	Inf	0.3739	7
sp|Q61586|GPAT1_MOUSE - Glycerol-3-phosphate acyltransferase 1, mitochondrial OS	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8BG89|ZN365_MOUSE - Protein ZNF365 OS=Mus musculus GN=Znf365 PE=2 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q6NZP1|ZRAB3_MOUSE - DNA annealing helicase and endonuclease ZRANB3 OS=Mus mu	0	4	0	0	0	0	Inf	0.3739	4
sp|P41438|S19A1_MOUSE - Folate transporter 1 OS=Mus musculus GN=Slc19a1 PE=1 SV=	0	2	0	0	0	0	Inf	0.3739	2
sp|P35583|FOXA2_MOUSE - Hepatocyte nuclear factor 3-beta OS=Mus musculus GN=Foxa	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BKN6|HS3SA_MOUSE - Heparan sulfate glucosamine 3-O-sulfotransferase 3A1 OS=	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8CJG1|AGO1_MOUSE - Protein argonaute-1 OS=Mus musculus GN=Ago1 PE=1 SV=2	0	5	0	0	0	0	Inf	0.3739	5
sp|Q8VEB1|GRK5_MOUSE - G protein-coupled receptor kinase 5 OS=Mus musculus GN=Gr	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8K297|GT251_MOUSE - Procollagen galactosyltransferase 1 OS=Mus musculus GN=C	0	2	0	0	0	0	Inf	0.3739	2
sp|Q3UK37|CN080_MOUSE - Uncharacterized protein C14orf80 homolog OS=Mus musculus	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BGA5|KRR1_MOUSE - KRR1 small subunit processome component homolog OS=Mus mu	0	3	0	0	0	0	Inf	0.3739	3
sp|P23242|CXA1_MOUSE - Gap junction alpha-1 protein OS=Mus musculus GN=Gja1 PE=1	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8BHI7|ELOV5_MOUSE - Elongation of very long chain fatty acids protein 5 OS=M	0	2	0	0	0	0	Inf	0.3739	2
sp|A1IGU4|ARH37_MOUSE - Rho guanine nucleotide exchange factor 37 OS=Mus musculu	0	3	0	0	0	0	Inf	0.3739	3
sp|Q5RKZ7|MOCS1_MOUSE - Molybdenum cofactor biosynthesis protein 1 OS=Mus muscul	0	2	0	0	0	0	Inf	0.3739	2
sp|Q80W47|WIPI2_MOUSE - WD repeat domain phosphoinositide-interacting protein 2	0	2	0	0	0	0	Inf	0.3739	2
sp|Q5SSF7|FA46C_MOUSE - Protein FAM46C OS=Mus musculus GN=Fam46c PE=2 SV=1	0	4	0	0	0	0	Inf	0.3739	4
sp|Q99PT3|IN80B_MOUSE - INO80 complex subunit B OS=Mus musculus GN=Ino80b PE=1 S	0	3	0	0	0	0	Inf	0.3739	3
sp|P58069|RASA2_MOUSE - Ras GTPase-activating protein 2 OS=Mus musculus GN=Rasa2	0	4	0	0	0	0	Inf	0.3739	4
sp|P47857|PFKAM_MOUSE - ATP-dependent 6-phosphofructokinase, muscle type OS=Mus	0	3	0	0	0	0	Inf	0.3739	3
sp|Q5RJI5|BRSK1_MOUSE - Serine/threonine-protein kinase BRSK1 OS=Mus musculus GN	0	2	0	0	0	0	Inf	0.3739	2
sp|A6H611|MIPEP_MOUSE - Mitochondrial intermediate peptidase OS=Mus musculus GN=	0	7	0	0	0	0	Inf	0.3739	7
sp|Q04891|SOX13_MOUSE - Transcription factor SOX-13 OS=Mus musculus GN=Sox13 PE=	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9Z179|SHCBP_MOUSE - SHC SH2 domain-binding protein 1 OS=Mus musculus GN=Shcb	0	8	0	0	0	0	Inf	0.3739	8
sp|Q80WP8|GADL1_MOUSE - Acidic amino acid decarboxylase GADL1 OS=Mus musculus GN	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9CQ26|STABP_MOUSE - STAM-binding protein OS=Mus musculus GN=Stambp PE=2 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q7TQH0|ATX2L_MOUSE - Ataxin-2-like protein OS=Mus musculus GN=Atxn2l PE=1 SV=	0	3	6	0	0	0	Inf	0.1583	9
sp|Q8C0C4|CCSE1_MOUSE - Serine-rich coiled-coil domain-containing protein 1 OS=M	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9Z218|DPP6_MOUSE - Dipeptidyl aminopeptidase-like protein 6 OS=Mus musculus	0	3	0	0	0	0	Inf	0.3739	3
sp|P81117|NUCB2_MOUSE - Nucleobindin-2 OS=Mus musculus GN=Nucb2 PE=1 SV=2	0	2	0	0	0	0	Inf	0.3739	2
sp|Q921Q7|RIN1_MOUSE - Ras and Rab interactor 1 OS=Mus musculus GN=Rin1 PE=1 SV=	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9R190|MTA2_MOUSE - Metastasis-associated protein MTA2 OS=Mus musculus GN=Mta	0	3	0	0	0	0	Inf	0.3739	3

sp|Q8BZ97|PRDM8_MOUSE - PR domain zinc finger protein 8 OS=Mus musculus GN=Prdm8	0	10	0	0	0	0	Inf	0.3739	10
sp|Q0MW30|NEU1B_MOUSE - E3 ubiquitin-protein ligase NEURL1B OS=Mus musculus GN=N	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9ERH4|NUSAP_MOUSE - Nucleolar and spindle-associated protein 1 OS=Mus muscul	0	3	0	0	0	0	Inf	0.3739	3
sp|Q6ZPI3|LCOR_MOUSE - Ligand-dependent corepressor OS=Mus musculus GN=Lcor PE=2	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8CHG3|GCC2_MOUSE - GRIP and coiled-coil domain-containing protein 2 OS=Mus m	0	16	0	0	0	0	Inf	0.3739	16
sp|Q05D44|IF2P_MOUSE - Eukaryotic translation initiation factor 5B OS=Mus muscul	0	4	0	0	0	0	Inf	0.3739	4
sp|O88908|SOAT2_MOUSE - Sterol O-acyltransferase 2 OS=Mus musculus GN=Soat2 PE=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9D306|MGT4C_MOUSE - Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosami	0	5	0	0	0	0	Inf	0.3739	5
sp|Q9DA37|SAMD8_MOUSE - Sphingomyelin synthase-related protein 1 OS=Mus musculus	0	6	0	0	0	0	Inf	0.3739	6
sp|Q3URQ0|TEX10_MOUSE - Testis-expressed sequence 10 protein OS=Mus musculus GN=	0	3	3	0	0	0	Inf	0.1161	6
sp|Q8BG79|C19L2_MOUSE - CWF19-like protein 2 OS=Mus musculus GN=Cwf19l2 PE=2 SV=	0	2	0	0	0	0	Inf	0.3739	2
sp|Q811T9|DISC1_MOUSE - Disrupted in schizophrenia 1 homolog OS=Mus musculus GN=	0	3	0	0	0	0	Inf	0.3739	3
sp|Q587J6|LITD1_MOUSE - LINE-1 type transposase domain-containing protein 1 OS=M	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9JMH6|TRXR1_MOUSE - Thioredoxin reductase 1, cytoplasmic OS=Mus musculus GN=	0	5	0	0	0	0	Inf	0.3739	5
sp|Q91W98|S15A4_MOUSE - Solute carrier family 15 member 4 OS=Mus musculus GN=Slc	0	3	0	0	0	0	Inf	0.3739	3
sp|Q3UIK4|MET14_MOUSE - N6-adenosine-methyltransferase subunit METTL14 OS=Mus mu	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8CFE5|BTBD7_MOUSE - BTB/POZ domain-containing protein 7 OS=Mus musculus GN=B	0	7	0	0	0	0	Inf	0.3739	7
sp|Q8R429|AT2A1_MOUSE - Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=M	0	6	0	0	0	0	Inf	0.3739	6
sp|B2RY56|RBM25_MOUSE - RNA-binding protein 25 OS=Mus musculus GN=Rbm25 PE=1 SV=	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8BLN5|ERG7_MOUSE - Lanosterol synthase OS=Mus musculus GN=Lss PE=2 SV=2	0	8	0	0	0	0	Inf	0.3739	8
sp|Q9QXK7|CPSF3_MOUSE - Cleavage and polyadenylation specificity factor subunit	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BYW9|EOGT_MOUSE - EGF domain-specific O-linked N-acetylglucosamine transfer	0	13	0	0	0	0	Inf	0.3739	13
sp|Q3TJZ6|FA98A_MOUSE - Protein FAM98A OS=Mus musculus GN=Fam98a PE=2 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q4QY64|ATAD5_MOUSE - ATPase family AAA domain-containing protein 5 OS=Mus mus	0	5	0	0	0	0	Inf	0.3739	5
sp|Q64318|ZEB1_MOUSE - Zinc finger E-box-binding homeobox 1 OS=Mus musculus GN=Z	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8BWA5|KLH31_MOUSE - Kelch-like protein 31 OS=Mus musculus GN=Klhl31 PE=1 SV=	0	2	0	0	0	0	Inf	0.3739	2
sp|O88495|MTR1L_MOUSE - Melatonin-related receptor OS=Mus musculus GN=Gpr50 PE=2	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8BP47|SYNC_MOUSE - Asparagine--tRNA ligase, cytoplasmic OS=Mus musculus GN=N	0	2	0	0	0	0	Inf	0.3739	2
sp|Q6URW6|MYH14_MOUSE - Myosin-14 OS=Mus musculus GN=Myh14 PE=1 SV=1	0	9	0	0	0	0	Inf	0.3739	9
sp|Q9JHR7|IDE_MOUSE - Insulin-degrading enzyme OS=Mus musculus GN=Ide PE=1 SV=1	0	19	0	0	0	0	Inf	0.3739	19
sp|Q6P9J5|KANK4_MOUSE - KN motif and ankyrin repeat domain-containing protein 4	0	3	0	0	0	0	Inf	0.3739	3
sp|Q91WG4|ELP2_MOUSE - Elongator complex protein 2 OS=Mus musculus GN=Elp2 PE=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BUE7|MUC20_MOUSE - Mucin-20 OS=Mus musculus GN=Muc20 PE=1 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|A2AL36|CNTRL_MOUSE - Centriolin OS=Mus musculus GN=Cntrl PE=2 SV=2	0	13	0	0	0	0	Inf	0.3739	13
sp|Q9JM61|THSD1_MOUSE - Thrombospondin type-1 domain-containing protein 1 OS=Mus	0	2	0	0	0	0	Inf	0.3739	2
sp|A2AI08|TPRN_MOUSE - Taperin OS=Mus musculus GN=Tprn PE=1 SV=1	0	8	0	0	0	0	Inf	0.3739	8
sp|B2RY83|HPSE2_MOUSE - Inactive heparanase-2 OS=Mus musculus GN=Hpse2 PE=2 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BTW9|PAK4_MOUSE - Serine/threonine-protein kinase PAK 4 OS=Mus musculus GN=	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8CHE4|PHLP1_MOUSE - PH domain leucine-rich repeat-containing protein phospha	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9CPW0|CNTP2_MOUSE - Contactin-associated protein-like 2 OS=Mus musculus GN=C	0	4	0	0	0	0	Inf	0.3739	4
sp|O35604|NPC1_MOUSE - Niemann-Pick C1 protein OS=Mus musculus GN=Npc1 PE=1 SV=2	0	5	0	0	0	0	Inf	0.3739	5

sp|Q91V83|TTI1_MOUSE - TELO2-interacting protein 1 homolog OS=Mus musculus GN=Tt	0	3	0	0	0	0	Inf	0.3739	3
sp|P53569|CEBPZ_MOUSE - CCAAT/enhancer-binding protein zeta OS=Mus musculus GN=C	0	3	0	0	0	0	Inf	0.3739	3
sp|P35710|SOX5_MOUSE - Transcription factor SOX-5 OS=Mus musculus GN=Sox5 PE=1 S	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9D5U8|CNBD2_MOUSE - Cyclic nucleotide-binding domain-containing protein 2 OS	0	2	0	0	0	0	Inf	0.3739	2
sp|Q6V595|KLHL6_MOUSE - Kelch-like protein 6 OS=Mus musculus GN=Klhl6 PE=2 SV=2	0	3	5	0	0	0	Inf	0.1403	8
sp|Q8CJ40|CROCC_MOUSE - Rootletin OS=Mus musculus GN=Crocc PE=1 SV=2	0	8	0	0	0	0	Inf	0.3739	8
sp|P48754|BRCA1_MOUSE - Breast cancer type 1 susceptibility protein homolog OS=M	0	4	0	0	0	0	Inf	0.3739	4
sp|Q8K268|ABCF3_MOUSE - ATP-binding cassette sub-family F member 3 OS=Mus muscul	0	2	0	0	0	0	Inf	0.3739	2
sp|Q6PD19|CJ076_MOUSE - UPF0668 protein C10orf76 homolog OS=Mus musculus PE=2 SV	0	6	0	0	0	0	Inf	0.3739	6
sp|Q641K5|NUAK1_MOUSE - NUAK family SNF1-like kinase 1 OS=Mus musculus GN=Nuak1	0	2	0	0	0	0	Inf	0.3739	2
sp|A2RSQ0|DEN5B_MOUSE - DENN domain-containing protein 5B OS=Mus musculus GN=Den	0	12	0	0	0	0	Inf	0.3739	12
sp|Q5DU41|LRC8B_MOUSE - Volume-regulated anion channel subunit LRRC8B OS=Mus mus	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8C5W3|TBCEL_MOUSE - Tubulin-specific chaperone cofactor E-like protein OS=Mu	0	3	0	0	0	0	Inf	0.3739	3
sp|O70305|ATX2_MOUSE - Ataxin-2 OS=Mus musculus GN=Atxn2 PE=1 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|P47713|PA24A_MOUSE - Cytosolic phospholipase A2 OS=Mus musculus GN=Pla2g4a PE	0	3	0	0	0	0	Inf	0.3739	3
sp|Q61285|ABCD2_MOUSE - ATP-binding cassette sub-family D member 2 OS=Mus muscul	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8BWW9|PKN2_MOUSE - Serine/threonine-protein kinase N2 OS=Mus musculus GN=Pkn	0	2	0	0	0	0	Inf	0.3739	2
sp|P22682|CBL_MOUSE - E3 ubiquitin-protein ligase CBL OS=Mus musculus GN=Cbl PE=	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8BY46|ZN574_MOUSE - Zinc finger protein 574 OS=Mus musculus GN=Znf574 PE=2 S	0	3	0	0	0	0	Inf	0.3739	3
sp|O54951|SEM6B_MOUSE - Semaphorin-6B OS=Mus musculus GN=Sema6b PE=2 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9JL18|BACE2_MOUSE - Beta-secretase 2 OS=Mus musculus GN=Bace2 PE=2 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8VI56|LRP4_MOUSE - Low-density lipoprotein receptor-related protein 4 OS=Mus	0	7	0	0	0	0	Inf	0.3739	7
sp|Q6ZQH8|NU188_MOUSE - Nucleoporin NUP188 homolog OS=Mus musculus GN=Nup188 PE=	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BZ05|ARAP2_MOUSE - Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-co	0	6	0	0	0	0	Inf	0.3739	6
sp|Q60610|TIAM1_MOUSE - T-lymphoma invasion and metastasis-inducing protein 1 OS	0	5	0	0	0	0	Inf	0.3739	5
sp|Q9R1S7|MRP6_MOUSE - Multidrug resistance-associated protein 6 OS=Mus musculus	0	3	0	0	0	0	Inf	0.3739	3
sp|Q80V94|AP4E1_MOUSE - AP-4 complex subunit epsilon-1 OS=Mus musculus GN=Ap4e1	0	3	0	0	0	0	Inf	0.3739	3
sp|P13595|NCAM1_MOUSE - Neural cell adhesion molecule 1 OS=Mus musculus GN=Ncam1	0	6	0	0	0	0	Inf	0.3739	6
sp|Q8R554|OTU7A_MOUSE - OTU domain-containing protein 7A OS=Mus musculus GN=Otud	0	2	12	0	0	0	Inf	0.277	14
sp|P09803|CADH1_MOUSE - Cadherin-1 OS=Mus musculus GN=Cdh1 PE=1 SV=1	0	5	0	0	0	0	Inf	0.3739	5
sp|P58681|TLR7_MOUSE - Toll-like receptor 7 OS=Mus musculus GN=Tlr7 PE=1 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q6B966|NAL14_MOUSE - NACHT, LRR and PYD domains-containing protein 14 OS=Mus	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BHY8|SNX14_MOUSE - Sorting nexin-14 OS=Mus musculus GN=Snx14 PE=2 SV=1	0	4	0	0	0	0	Inf	0.3739	4
sp|Q99MQ1|BICC1_MOUSE - Protein bicaudal C homolog 1 OS=Mus musculus GN=Bicc1 PE	0	3	0	0	0	0	Inf	0.3739	3
sp|P13542|MYH8_MOUSE - Myosin-8 OS=Mus musculus GN=Myh8 PE=2 SV=2	0	12	0	0	0	0	Inf	0.3739	12
sp|P97868|RBBP6_MOUSE - E3 ubiquitin-protein ligase RBBP6 OS=Mus musculus GN=Rbb	0	2	0	0	0	0	Inf	0.3739	2
sp|O35954|PITM1_MOUSE - Membrane-associated phosphatidylinositol transfer protei	0	2	0	0	0	0	Inf	0.3739	2
sp|Q6NWV3|IF122_MOUSE - Intraflagellar transport protein 122 homolog OS=Mus musc	0	4	0	0	0	0	Inf	0.3739	4
sp|Q3UVV9|VWA3A_MOUSE - von Willebrand factor A domain-containing protein 3A OS=	0	2	0	0	0	0	Inf	0.3739	2
sp|Q924A2|CIC_MOUSE - Protein capicua homolog OS=Mus musculus GN=Cic PE=1 SV=2	0	3	0	0	0	0	Inf	0.3739	3
sp|P70208|PLXA3_MOUSE - Plexin-A3 OS=Mus musculus GN=Plxna3 PE=1 SV=2	0	4	0	0	0	0	Inf	0.3739	4

sp|Q8CHC4|SYNJ1_MOUSE - Synaptojanin-1 OS=Mus musculus GN=Synj1 PE=1 SV=3	0	3	0	0	0	0	Inf	0.3739	3
sp|Q0VBN2|DSEL_MOUSE - Dermatan-sulfate epimerase-like protein OS=Mus musculus G	0	2	0	0	0	0	Inf	0.3739	2
sp|P16283|B3A3_MOUSE - Anion exchange protein 3 OS=Mus musculus GN=Slc4a3 PE=1 S	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BMJ2|SYLC_MOUSE - Leucine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Lars	0	2	11	0	0	0	Inf	0.2694	13
sp|P15379|CD44_MOUSE - CD44 antigen OS=Mus musculus GN=Cd44 PE=1 SV=3	0	6	0	0	0	0	Inf	0.3739	6
sp|Q8C4A5|ASXL3_MOUSE - Putative Polycomb group protein ASXL3 OS=Mus musculus GN	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8R4H2|ARHGC_MOUSE - Rho guanine nucleotide exchange factor 12 OS=Mus musculu	0	4	0	0	0	0	Inf	0.3739	4
sp|Q8BZ32|ASXL2_MOUSE - Putative Polycomb group protein ASXL2 OS=Mus musculus GN	0	2	0	0	0	0	Inf	0.3739	2
sp|Q3UHR0|BAHC1_MOUSE - BAH and coiled-coil domain-containing protein 1 OS=Mus m	0	3	0	0	0	0	Inf	0.3739	3
sp|Q3UHF7|ZEP2_MOUSE - Transcription factor HIVEP2 OS=Mus musculus GN=Hivep2 PE=	0	19	14	0	0	0	Inf	0.1251	33
sp|P70207|PLXA2_MOUSE - Plexin-A2 OS=Mus musculus GN=Plxna2 PE=1 SV=2	0	3	0	0	0	0	Inf	0.3739	3
sp|P35917|VGFR3_MOUSE - Vascular endothelial growth factor receptor 3 OS=Mus mus	0	2	0	0	0	0	Inf	0.3739	2
sp|P19639|GSTM4_MOUSE - Glutathione S-transferase Mu 3 OS=Mus musculus GN=Gstm3	0	12	0	0	0	0	Inf	0.3739	12
sp|Q8K2C6|SIR5_MOUSE - NAD-dependent protein deacylase sirtuin-5, mitochondrial	0	4	0	0	0	0	Inf	0.3739	4
sp|P53026|RL10A_MOUSE - 60S ribosomal protein L10a OS=Mus musculus GN=Rpl10a PE=	0	3	0	0	0	0	Inf	0.3739	3
sp|P63101|1433Z_MOUSE - 14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1	0	7	0	0	0	0	Inf	0.3739	7
sp|Q91V64|ISOC1_MOUSE - Isochorismatase domain-containing protein 1 OS=Mus muscu	0	6	0	0	0	0	Inf	0.3739	6
sp|Q80X85|RT07_MOUSE - 28S ribosomal protein S7, mitochondrial OS=Mus musculus G	0	2	0	0	0	0	Inf	0.3739	2
sp|P60766|CDC42_MOUSE - Cell division control protein 42 homolog OS=Mus musculus	0	4	0	0	0	0	Inf	0.3739	4
sp|P09925|SURF1_MOUSE - Surfeit locus protein 1 OS=Mus musculus GN=Surf1 PE=2 SV	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8JZV9|BDH2_MOUSE - 3-hydroxybutyrate dehydrogenase type 2 OS=Mus musculus GN	0	3	0	0	0	0	Inf	0.3739	3
sp|P40936|INMT_MOUSE - Indolethylamine N-methyltransferase OS=Mus musculus GN=In	0	2	0	0	0	0	Inf	0.3739	2
sp|P14869|RLA0_MOUSE - 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0	0	4	0	0	0	0	Inf	0.3739	4
sp|Q9Z0S1|BPNT1_MOUSE - 3'(2'),5'-bisphosphate nucleotidase 1 OS=Mus musculus GN	0	2	0	0	0	0	Inf	0.3739	2
sp|Q99N93|RM16_MOUSE - 39S ribosomal protein L16, mitochondrial OS=Mus musculus	0	4	0	0	0	0	Inf	0.3739	4
sp|P01899|HA11_MOUSE - H-2 class I histocompatibility antigen, D-B alpha chain O	0	6	0	0	0	0	Inf	0.3739	6
sp|P06797|CATL1_MOUSE - Cathepsin L1 OS=Mus musculus GN=Ctsl PE=1 SV=2	0	4	0	0	0	0	Inf	0.3739	4
sp|P15626|GSTM2_MOUSE - Glutathione S-transferase Mu 2 OS=Mus musculus GN=Gstm2	0	3	0	0	0	0	Inf	0.3739	3
sp|O55242|SGMR1_MOUSE - Sigma non-opioid intracellular receptor 1 OS=Mus musculu	0	3	0	0	0	0	Inf	0.3739	3
sp|O35660|GSTM6_MOUSE - Glutathione S-transferase Mu 6 OS=Mus musculus GN=Gstm6	0	4	0	0	0	0	Inf	0.3739	4
sp|Q9CXW4|RL11_MOUSE - 60S ribosomal protein L11 OS=Mus musculus GN=Rpl11 PE=1 S	0	6	0	0	0	0	Inf	0.3739	6
sp|P57759|ERP29_MOUSE - Endoplasmic reticulum resident protein 29 OS=Mus musculu	0	9	0	0	0	0	Inf	0.3739	9
sp|Q8R238|SDSL_MOUSE - Serine dehydratase-like OS=Mus musculus GN=Sdsl PE=2 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9QXD6|F16P1_MOUSE - Fructose-1,6-bisphosphatase 1 OS=Mus musculus GN=Fbp1 PE	0	3	0	0	0	0	Inf	0.3739	3
sp|P01898|HA10_MOUSE - H-2 class I histocompatibility antigen, Q10 alpha chain O	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9D710|TMX2_MOUSE - Thioredoxin-related transmembrane protein 2 OS=Mus muscul	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9CRD2|EMC2_MOUSE - ER membrane protein complex subunit 2 OS=Mus musculus GN=	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9D1B9|RM28_MOUSE - 39S ribosomal protein L28, mitochondrial OS=Mus musculus	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9DBW0|CP4V2_MOUSE - Cytochrome P450 4V2 OS=Mus musculus GN=Cyp4v2 PE=1 SV=1	0	3	0	0	0	0	Inf	0.3739	3
sp|Q64481|CP3AG_MOUSE - Cytochrome P450 3A16 OS=Mus musculus GN=Cyp3a16 PE=2 SV=	0	6	0	0	0	0	Inf	0.3739	6
sp|Q9D7N3|RT09_MOUSE - 28S ribosomal protein S9, mitochondrial OS=Mus musculus G	0	3	0	0	0	0	Inf	0.3739	3

sp|Q9D9F8|MIPO1_MOUSE - Mirror-image polydactyly gene 1 protein homolog OS=Mus m	0	3	0	0	0	0	Inf	0.3739	3
sp|Q80XI7|VOME_MOUSE - Vomeromodulin OS=Mus musculus PE=2 SV=1	0	5	0	0	0	0	Inf	0.3739	5
sp|Q8R323|RFC3_MOUSE - Replication factor C subunit 3 OS=Mus musculus GN=Rfc3 PE	0	7	0	0	0	0	Inf	0.3739	7
sp|O89091|KLF10_MOUSE - Krueppel-like factor 10 OS=Mus musculus GN=Klf10 PE=1 SV	0	5	0	0	0	0	Inf	0.3739	5
sp|P01867|IGG2B_MOUSE - Ig gamma-2B chain C region OS=Mus musculus GN=Igh-3 PE=1	0	2	0	0	0	0	Inf	0.3739	2
sp|P42586|NKX22_MOUSE - Homeobox protein Nkx-2.2 OS=Mus musculus GN=Nkx2-2 PE=1	0	2	0	0	0	0	Inf	0.3739	2
sp|P00158|CYB_MOUSE - Cytochrome b OS=Mus musculus GN=Mt-Cyb PE=2 SV=1	0	9	0	0	0	0	Inf	0.3739	9
sp|Q9Z2X1|HNRPF_MOUSE - Heterogeneous nuclear ribonucleoprotein F OS=Mus musculu	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9CYV5|TM135_MOUSE - Transmembrane protein 135 OS=Mus musculus GN=Tmem135 PE=	0	5	0	0	0	0	Inf	0.3739	5
sp|Q9CRA4|MSMO1_MOUSE - Methylsterol monooxygenase 1 OS=Mus musculus GN=Msmo1 PE	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8BM88|CATO_MOUSE - Cathepsin O OS=Mus musculus GN=Ctso PE=2 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q91YY4|ATPF2_MOUSE - ATP synthase mitochondrial F1 complex assembly factor 2	0	3	0	0	0	0	Inf	0.3739	3
sp|Q91ZU1|ASB6_MOUSE - Ankyrin repeat and SOCS box protein 6 OS=Mus musculus GN=	0	2	0	0	0	0	Inf	0.3739	2
sp|P16125|LDHB_MOUSE - L-lactate dehydrogenase B chain OS=Mus musculus GN=Ldhb P	0	2	0	0	0	0	Inf	0.3739	2
sp|Q99M01|SYFM_MOUSE - Phenylalanine--tRNA ligase, mitochondrial OS=Mus musculus	0	3	0	0	0	0	Inf	0.3739	3
sp|O54833|CSK22_MOUSE - Casein kinase II subunit alpha' OS=Mus musculus GN=Csnk2	0	3	0	0	0	0	Inf	0.3739	3
sp|Q07456|AMBP_MOUSE - Protein AMBP OS=Mus musculus GN=Ambp PE=2 SV=2	0	5	0	0	0	0	Inf	0.3739	5
sp|P62141|PP1B_MOUSE - Serine/threonine-protein phosphatase PP1-beta catalytic s	0	2	0	0	0	0	Inf	0.3739	2
sp|Q07174|M3K8_MOUSE - Mitogen-activated protein kinase kinase kinase 8 OS=Mus m	0	6	6	0	0	0	Inf	0.1161	12
sp|Q8BH01|TMCO3_MOUSE - Transmembrane and coiled-coil domain-containing protein	0	6	0	0	0	0	Inf	0.3739	6
sp|Q8BJW6|EIF2A_MOUSE - Eukaryotic translation initiation factor 2A OS=Mus muscu	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8BGS7|CEPT1_MOUSE - Choline/ethanolaminephosphotransferase 1 OS=Mus musculus	0	2	0	0	0	0	Inf	0.3739	2
sp|P70387|HFE_MOUSE - Hereditary hemochromatosis protein homolog OS=Mus musculus	0	2	0	0	0	0	Inf	0.3739	2
sp|O35658|C1QBP_MOUSE - Complement component 1 Q subcomponent-binding protein, m	0	7	0	0	0	0	Inf	0.3739	7
sp|Q9JM76|ARPC3_MOUSE - Actin-related protein 2/3 complex subunit 3 OS=Mus muscu	0	2	0	0	0	0	Inf	0.3739	2
sp|Q3UMW8|CLN5_MOUSE - Ceroid-lipofuscinosis neuronal protein 5 homolog OS=Mus m	0	2	0	0	0	0	Inf	0.3739	2
sp|P58389|PTPA_MOUSE - Serine/threonine-protein phosphatase 2A activator OS=Mus	0	2	0	0	0	0	Inf	0.3739	2
sp|Q99N16|CP4F3_MOUSE - Leukotriene-B(4) omega-hydroxylase 2 OS=Mus musculus GN=	0	2	0	0	0	0	Inf	0.3739	2
sp|Q6KAU4|MB12B_MOUSE - Multivesicular body subunit 12B OS=Mus musculus GN=Mvb12	0	3	0	0	0	0	Inf	0.3739	3
sp|O08811|ERCC2_MOUSE - TFIIH basal transcription factor complex helicase XPD su	0	7	0	0	0	0	Inf	0.3739	7
sp|P00397|COX1_MOUSE - Cytochrome c oxidase subunit 1 OS=Mus musculus GN=Mtco1 P	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8R2E9|ERO1B_MOUSE - ERO1-like protein beta OS=Mus musculus GN=Ero1lb PE=1 SV	0	3	0	0	0	0	Inf	0.3739	3
sp|P80314|TCPB_MOUSE - T-complex protein 1 subunit beta OS=Mus musculus GN=Cct2	0	2	0	0	0	0	Inf	0.3739	2
sp|O35719|RA51B_MOUSE - DNA repair protein RAD51 homolog 2 OS=Mus musculus GN=Ra	0	2	0	0	0	0	Inf	0.3739	2
sp|Q810U5|CCD50_MOUSE - Coiled-coil domain-containing protein 50 OS=Mus musculus	0	2	0	0	0	0	Inf	0.3739	2
sp|O70250|PGAM2_MOUSE - Phosphoglycerate mutase 2 OS=Mus musculus GN=Pgam2 PE=2	0	2	0	0	0	0	Inf	0.3739	2
sp|P04202|TGFB1_MOUSE - Transforming growth factor beta-1 OS=Mus musculus GN=Tgf	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9R1T2|SAE1_MOUSE - SUMO-activating enzyme subunit 1 OS=Mus musculus GN=Sae1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BM39|PRP18_MOUSE - Pre-mRNA-splicing factor 18 OS=Mus musculus GN=Prpf18 PE	0	3	0	0	0	0	Inf	0.3739	3
sp|Q91V01|MBOA5_MOUSE - Lysophospholipid acyltransferase 5 OS=Mus musculus GN=Lp	0	2	0	0	0	0	Inf	0.3739	2
sp|O88947|FA10_MOUSE - Coagulation factor X OS=Mus musculus GN=F10 PE=1 SV=1	0	2	0	0	0	0	Inf	0.3739	2

sp|Q9CQJ4|RING2_MOUSE - E3 ubiquitin-protein ligase RING2 OS=Mus musculus GN=Rnf	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9Z0G2|SRPK3_MOUSE - SRSF protein kinase 3 OS=Mus musculus GN=Srpk3 PE=2 SV=1	0	3	0	0	0	0	Inf	0.3739	3
sp|O55103|PRAX_MOUSE - Periaxin OS=Mus musculus GN=Prx PE=2 SV=1	0	5	0	0	0	0	Inf	0.3739	5
sp|Q60737|CSK21_MOUSE - Casein kinase II subunit alpha OS=Mus musculus GN=Csnk2a	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8C119|NDNF_MOUSE - Protein NDNF OS=Mus musculus GN=Ndnf PE=1 SV=2	0	4	0	0	0	0	Inf	0.3739	4
sp|Q8K1J6|TRNT1_MOUSE - CCA tRNA nucleotidyltransferase 1, mitochondrial OS=Mus	0	2	0	0	0	0	Inf	0.3739	2
sp|P63005|LIS1_MOUSE - Platelet-activating factor acetylhydrolase IB subunit alp	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9WU01|KHDR2_MOUSE - KH domain-containing, RNA-binding, signal transduction-a	0	13	0	0	0	0	Inf	0.3739	13
sp|P04186|CFAB_MOUSE - Complement factor B OS=Mus musculus GN=Cfb PE=1 SV=2	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9ESV0|DDX24_MOUSE - ATP-dependent RNA helicase DDX24 OS=Mus musculus GN=Ddx2	0	3	0	0	0	0	Inf	0.3739	3
sp|Q6PGK7|CHSTA_MOUSE - Carbohydrate sulfotransferase 10 OS=Mus musculus GN=Chst	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9JL96|CATM_MOUSE - Cathepsin M OS=Mus musculus GN=Ctsm PE=2 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BQM4|HEAT3_MOUSE - HEAT repeat-containing protein 3 OS=Mus musculus GN=Heat	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9ET30|TM9S3_MOUSE - Transmembrane 9 superfamily member 3 OS=Mus musculus GN=	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9D5E4|LRC48_MOUSE - Leucine-rich repeat-containing protein 48 OS=Mus musculu	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9WV91|FPRP_MOUSE - Prostaglandin F2 receptor negative regulator OS=Mus muscu	0	6	0	0	0	0	Inf	0.3739	6
sp|O08795|GLU2B_MOUSE - Glucosidase 2 subunit beta OS=Mus musculus GN=Prkcsh PE=	0	7	0	0	0	0	Inf	0.3739	7
sp|E9Q816|CP2W1_MOUSE - Cytochrome P450 2W1 OS=Mus musculus GN=Cyp2w1 PE=2 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8C1A9|CD029_MOUSE - Uncharacterized protein C4orf29 homolog OS=Mus musculus	0	2	0	0	0	0	Inf	0.3739	2
sp|P70333|HNRH2_MOUSE - Heterogeneous nuclear ribonucleoprotein H2 OS=Mus muscul	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8CEZ4|CB054_MOUSE - Uncharacterized protein C2orf54 homolog OS=Mus musculus	0	2	0	0	0	0	Inf	0.3739	2
sp|Q3USZ8|DIA1_MOUSE - Deleted in autism protein 1 homolog OS=Mus musculus PE=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8K442|ABC8A_MOUSE - ATP-binding cassette sub-family A member 8-A OS=Mus musc	0	5	0	0	0	0	Inf	0.3739	5
sp|A6X935|ITIH4_MOUSE - Inter alpha-trypsin inhibitor, heavy chain 4 OS=Mus musc	0	7	0	0	0	0	Inf	0.3739	7
sp|Q8VBZ3|CLPT1_MOUSE - Cleft lip and palate transmembrane protein 1 homolog OS=	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8CFB4|GBP5_MOUSE - Guanylate-binding protein 5 OS=Mus musculus GN=Gbp5 PE=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q91WG2|RABE2_MOUSE - Rab GTPase-binding effector protein 2 OS=Mus musculus GN	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9CYQ7|NARF_MOUSE - Nuclear prelamin A recognition factor OS=Mus musculus GN=	0	2	0	0	0	0	Inf	0.3739	2
sp|Q6VGS5|DAPLE_MOUSE - Protein Daple OS=Mus musculus GN=Ccdc88c PE=1 SV=1	0	11	0	0	0	0	Inf	0.3739	11
sp|Q8K093|TRHDE_MOUSE - Thyrotropin-releasing hormone-degrading ectoenzyme OS=Mu	0	3	0	0	0	0	Inf	0.3739	3
sp|A2APC3|TTLL9_MOUSE - Probable tubulin polyglutamylase TTLL9 OS=Mus musculus G	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8CHH5|GSC1L_MOUSE - GLTSCR1-like protein OS=Mus musculus GN=Gltscr1l PE=2 SV	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8VEJ4|NLE1_MOUSE - Notchless protein homolog 1 OS=Mus musculus GN=Nle1 PE=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8C456|FRITZ_MOUSE - WD repeat-containing and planar cell polarity effector p	0	2	0	0	0	0	Inf	0.3739	2
sp|D3YX43|VSI10_MOUSE - V-set and immunoglobulin domain-containing protein 10 OS	0	2	0	0	0	0	Inf	0.3739	2
sp|Q61247|A2AP_MOUSE - Alpha-2-antiplasmin OS=Mus musculus GN=Serpinf2 PE=1 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q810I2|TRI50_MOUSE - E3 ubiquitin-protein ligase TRIM50 OS=Mus musculus GN=Tr	0	4	0	0	0	0	Inf	0.3739	4
sp|P30280|CCND2_MOUSE - G1/S-specific cyclin-D2 OS=Mus musculus GN=Ccnd2 PE=2 SV	0	4	0	0	0	0	Inf	0.3739	4
sp|Q810A7|DDX42_MOUSE - ATP-dependent RNA helicase DDX42 OS=Mus musculus GN=Ddx4	0	4	0	0	0	0	Inf	0.3739	4
sp|Q68ED3|PAPD5_MOUSE - Non-canonical poly(A) RNA polymerase PAPD5 OS=Mus muscul	0	2	0	0	0	0	Inf	0.3739	2
sp|Q149C3|LIGO4_MOUSE - Leucine-rich repeat and immunoglobulin-like domain conta	0	2	0	0	0	0	Inf	0.3739	2

sp|Q6P5U8|CC148_MOUSE - Coiled-coil domain-containing protein 148 OS=Mus musculu	0	3	0	0	0	0	Inf	0.3739	3
sp|Q7TNT2|FACR2_MOUSE - Fatty acyl-CoA reductase 2 OS=Mus musculus GN=Far2 PE=2	0	3	8	0	0	0	Inf	0.1911	11
sp|Q9JHP7|KDEL1_MOUSE - KDEL motif-containing protein 1 OS=Mus musculus GN=Kdelc	0	2	0	0	0	0	Inf	0.3739	2
sp|Q3TZ89|SC31B_MOUSE - Protein transport protein Sec31B OS=Mus musculus GN=Sec3	0	4	0	0	0	0	Inf	0.3739	4
sp|Q9JKY5|HIP1R_MOUSE - Huntingtin-interacting protein 1-related protein OS=Mus	0	2	0	0	0	0	Inf	0.3739	2
sp|P70218|M4K1_MOUSE - Mitogen-activated protein kinase kinase kinase kinase 1 O	0	2	0	0	0	0	Inf	0.3739	2
sp|O88705|HCN3_MOUSE - Potassium/sodium hyperpolarization-activated cyclic nucle	0	2	0	0	0	0	Inf	0.3739	2
sp|Q921N6|DDX27_MOUSE - Probable ATP-dependent RNA helicase DDX27 OS=Mus musculu	0	2	0	0	0	0	Inf	0.3739	2
sp|Q920Q8|NS1BP_MOUSE - Influenza virus NS1A-binding protein homolog OS=Mus musc	0	2	0	0	0	0	Inf	0.3739	2
sp|G3UYX5|RGS22_MOUSE - Regulator of G-protein signaling 22 OS=Mus musculus GN=R	0	3	0	0	0	0	Inf	0.3739	3
sp|Q5U464|ASAP3_MOUSE - Arf-GAP with SH3 domain, ANK repeat and PH domain-contai	0	2	0	0	0	0	Inf	0.3739	2
sp|Q3V1V3|ESF1_MOUSE - ESF1 homolog OS=Mus musculus GN=Esf1 PE=1 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8CDM1|ATAD2_MOUSE - ATPase family AAA domain-containing protein 2 OS=Mus mus	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9DBB4|NAA16_MOUSE - N-alpha-acetyltransferase 16, NatA auxiliary subunit OS=	0	2	0	0	0	0	Inf	0.3739	2
sp|Q80UM3|NAA15_MOUSE - N-alpha-acetyltransferase 15, NatA auxiliary subunit OS=	0	2	0	0	0	0	Inf	0.3739	2
sp|Q3UMT1|PP12C_MOUSE - Protein phosphatase 1 regulatory subunit 12C OS=Mus musc	0	4	0	0	0	0	Inf	0.3739	4
sp|Q99PV0|PRP8_MOUSE - Pre-mRNA-processing-splicing factor 8 OS=Mus musculus GN=	0	7	0	0	0	0	Inf	0.3739	7
sp|P41234|ABCA2_MOUSE - ATP-binding cassette sub-family A member 2 OS=Mus muscul	0	7	0	0	0	0	Inf	0.3739	7
sp|Q6P4T2|U520_MOUSE - U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Mu	0	7	0	0	0	0	Inf	0.3739	7
sp|Q99K23|UFSP2_MOUSE - Ufm1-specific protease 2 OS=Mus musculus GN=Ufsp2 PE=1 S	0	2	0	0	0	0	Inf	0.3739	2
sp|P97479|MYO7A_MOUSE - Unconventional myosin-VIIa OS=Mus musculus GN=Myo7a PE=1	0	6	0	0	0	0	Inf	0.3739	6
sp|Q9Z277|BAZ1B_MOUSE - Tyrosine-protein kinase BAZ1B OS=Mus musculus GN=Baz1b P	0	3	0	0	0	0	Inf	0.3739	3
sp|O35071|KIF1C_MOUSE - Kinesin-like protein KIF1C OS=Mus musculus GN=Kif1c PE=2	0	5	0	0	0	0	Inf	0.3739	5
sp|Q91XY4|PCDG4_MOUSE - Protocadherin gamma-A4 OS=Mus musculus GN=Pcdhga4 PE=2 S	0	3	0	0	0	0	Inf	0.3739	3
sp|E9PZM4|CHD2_MOUSE - Chromodomain-helicase-DNA-binding protein 2 OS=Mus muscul	0	4	0	0	0	0	Inf	0.3739	4
sp|Q9ES00|UBE4B_MOUSE - Ubiquitin conjugation factor E4 B OS=Mus musculus GN=Ube	0	8	0	0	0	0	Inf	0.3739	8
sp|Q9QZW0|AT11C_MOUSE - Phospholipid-transporting ATPase 11C OS=Mus musculus GN=	0	2	0	0	0	0	Inf	0.3739	2
sp|Q91YE6|IPO9_MOUSE - Importin-9 OS=Mus musculus GN=Ipo9 PE=1 SV=3	0	5	0	0	0	0	Inf	0.3739	5
sp|Q9Z0T6|PKDRE_MOUSE - Polycystic kidney disease and receptor for egg jelly-rel	0	3	0	0	0	0	Inf	0.3739	3
sp|P0C6F1|DYH2_MOUSE - Dynein heavy chain 2, axonemal OS=Mus musculus GN=Dnah2 P	0	6	0	0	0	0	Inf	0.3739	6
sp|Q9QWK5|BIR1A_MOUSE - Baculoviral IAP repeat-containing protein 1a OS=Mus musc	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9R016|BIR1E_MOUSE - Baculoviral IAP repeat-containing protein 1e OS=Mus musc	0	2	0	0	0	0	Inf	0.3739	2
sp|A2CG49|KALRN_MOUSE - Kalirin OS=Mus musculus GN=Kalrn PE=1 SV=1	0	3	0	0	0	0	Inf	0.3739	3
sp|A2AF47|DOC11_MOUSE - Dedicator of cytokinesis protein 11 OS=Mus musculus GN=D	0	2	0	0	0	0	Inf	0.3739	2
sp|P40201|CHD1_MOUSE - Chromodomain-helicase-DNA-binding protein 1 OS=Mus muscul	0	2	0	0	0	0	Inf	0.3739	2
sp|P70398|USP9X_MOUSE - Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=	0	2	0	0	0	0	Inf	0.3739	2
sp|P60764|RAC3_MOUSE - Ras-related C3 botulinum toxin substrate 3 OS=Mus musculu	0	5	0	0	0	0	Inf	0.3739	5
sp|P46638|RB11B_MOUSE - Ras-related protein Rab-11B OS=Mus musculus GN=Rab11b PE	0	6	0	0	0	0	Inf	0.3739	6
sp|Q8R035|ICT1_MOUSE - Peptidyl-tRNA hydrolase ICT1, mitochondrial OS=Mus muscul	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9ER71|RHOJ_MOUSE - Rho-related GTP-binding protein RhoJ OS=Mus musculus GN=R	0	2	0	0	0	0	Inf	0.3739	2
sp|P35290|RAB24_MOUSE - Ras-related protein Rab-24 OS=Mus musculus GN=Rab24 PE=1	0	2	0	0	0	0	Inf	0.3739	2

sp|P84096|RHOG_MOUSE - Rho-related GTP-binding protein RhoG OS=Mus musculus GN=R	0	5	0	0	0	0	Inf	0.3739	5
sp|Q8CIC2|NUPL2_MOUSE - Nucleoporin-like protein 2 OS=Mus musculus GN=Nupl2 PE=2	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8VEH3|ARL8A_MOUSE - ADP-ribosylation factor-like protein 8A OS=Mus musculus	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9D1N9|RM21_MOUSE - 39S ribosomal protein L21, mitochondrial OS=Mus musculus	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9JJR9|NRIP3_MOUSE - Nuclear receptor-interacting protein 3 OS=Mus musculus G	0	3	0	0	0	0	Inf	0.3739	3
sp|P61255|RL26_MOUSE - 60S ribosomal protein L26 OS=Mus musculus GN=Rpl26 PE=1 S	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BKT2|HES7_MOUSE - Transcription factor HES-7 OS=Mus musculus GN=Hes7 PE=1 S	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9CWG1|GLIP1_MOUSE - Glioma pathogenesis-related protein 1 OS=Mus musculus GN	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8R5C5|ACTY_MOUSE - Beta-centractin OS=Mus musculus GN=Actr1b PE=1 SV=1	0	9	0	0	0	0	Inf	0.3739	9
sp|Q9JLR1|S61A2_MOUSE - Protein transport protein Sec61 subunit alpha isoform 2	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9JLZ8|SIGIR_MOUSE - Single Ig IL-1-related receptor OS=Mus musculus GN=Sigir	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8R326|PSPC1_MOUSE - Paraspeckle component 1 OS=Mus musculus GN=Pspc1 PE=1 SV	0	4	0	0	0	0	Inf	0.3739	4
sp|Q80Y75|DJB13_MOUSE - DnaJ homolog subfamily B member 13 OS=Mus musculus GN=Dn	0	4	0	0	0	0	Inf	0.3739	4
sp|P58468|F207A_MOUSE - Protein FAM207A OS=Mus musculus GN=Fam207a PE=1 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|P23813|HXD11_MOUSE - Homeobox protein Hox-D11 OS=Mus musculus GN=Hoxd11 PE=2	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9CXI5|MANF_MOUSE - Mesencephalic astrocyte-derived neurotrophic factor OS=Mu	0	6	0	0	0	0	Inf	0.3739	6
sp|P30554|MAS_MOUSE - Proto-oncogene Mas OS=Mus musculus GN=Mas1 PE=1 SV=2	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9WTP3|SPDEF_MOUSE - SAM pointed domain-containing Ets transcription factor O	0	2	0	0	0	0	Inf	0.3739	2
sp|Q91VN6|DDX41_MOUSE - Probable ATP-dependent RNA helicase DDX41 OS=Mus musculu	0	4	0	0	0	0	Inf	0.3739	4
sp|Q80X56|TRI69_MOUSE - E3 ubiquitin-protein ligase TRIM69 OS=Mus musculus GN=Tr	0	3	0	0	0	0	Inf	0.3739	3
sp|Q91WK0|LRRF2_MOUSE - Leucine-rich repeat flightless-interacting protein 2 OS=	0	4	0	0	0	0	Inf	0.3739	4
sp|Q8C739|F110B_MOUSE - Protein FAM110B OS=Mus musculus GN=Fam110b PE=2 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9JMC3|DNJA4_MOUSE - DnaJ homolog subfamily A member 4 OS=Mus musculus GN=Dna	0	2	0	0	0	0	Inf	0.3739	2
sp|P63037|DNJA1_MOUSE - DnaJ homolog subfamily A member 1 OS=Mus musculus GN=Dna	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9EST5|AN32B_MOUSE - Acidic leucine-rich nuclear phosphoprotein 32 family mem	0	5	0	0	0	0	Inf	0.3739	5
sp|Q80Z10|ASTN2_MOUSE - Astrotactin-2 OS=Mus musculus GN=Astn2 PE=2 SV=2	0	5	6	0	0	0	Inf	0.1193	11
sp|Q8BJY1|PSMD5_MOUSE - 26S proteasome non-ATPase regulatory subunit 5 OS=Mus mu	0	2	0	0	0	0	Inf	0.3739	2
sp|Q7TS68|NSUN6_MOUSE - Putative methyltransferase NSUN6 OS=Mus musculus GN=Nsun	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9CWR1|WDR73_MOUSE - WD repeat-containing protein 73 OS=Mus musculus GN=Wdr73	0	4	0	0	0	0	Inf	0.3739	4
sp|Q149L6|DJB14_MOUSE - DnaJ homolog subfamily B member 14 OS=Mus musculus GN=Dn	0	2	0	0	0	0	Inf	0.3739	2
sp|B2RWW0|TAGAP_MOUSE - T-cell activation Rho GTPase-activating protein OS=Mus m	0	3	2	0	0	0	Inf	0.1317	5
sp|Q9CR14|FANCL_MOUSE - E3 ubiquitin-protein ligase FANCL OS=Mus musculus GN=Fan	0	3	0	0	0	0	Inf	0.3739	3
sp|Q91WL0|ES8L3_MOUSE - Epidermal growth factor receptor kinase substrate 8-like	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9D4H1|EXOC2_MOUSE - Exocyst complex component 2 OS=Mus musculus GN=Exoc2 PE=	0	5	0	0	0	0	Inf	0.3739	5
sp|Q921C5|BICD2_MOUSE - Protein bicaudal D homolog 2 OS=Mus musculus GN=Bicd2 PE	0	5	0	0	0	0	Inf	0.3739	5
sp|Q8C3X4|GUF1_MOUSE - Translation factor Guf1, mitochondrial OS=Mus musculus GN	0	9	0	0	0	0	Inf	0.3739	9
sp|Q99PP9|TRI16_MOUSE - Tripartite motif-containing protein 16 OS=Mus musculus G	0	5	0	0	0	0	Inf	0.3739	5
sp|Q8QZR5|ALAT1_MOUSE - Alanine aminotransferase 1 OS=Mus musculus GN=Gpt PE=2 S	0	2	0	0	0	0	Inf	0.3739	2
sp|P0C605|KGP1_MOUSE - cGMP-dependent protein kinase 1 OS=Mus musculus GN=Prkg1	0	4	0	0	0	0	Inf	0.3739	4
sp|Q8BW88|PKHS1_MOUSE - Pleckstrin homology domain-containing family S member 1	0	3	0	0	0	0	Inf	0.3739	3
sp|Q80YD1|SUV3_MOUSE - ATP-dependent RNA helicase SUPV3L1, mitochondrial OS=Mus	0	3	0	0	0	0	Inf	0.3739	3

sp|Q8BSN3|CC151_MOUSE - Coiled-coil domain-containing protein 151 OS=Mus musculu	0	7	0	0	0	0	Inf	0.3739	7
sp|Q3U095|NXPE2_MOUSE - NXPE family member 2 OS=Mus musculus GN=Nxpe2 PE=2 SV=1	0	8	0	0	0	0	Inf	0.3739	8
sp|B2RUP2|UN13D_MOUSE - Protein unc-13 homolog D OS=Mus musculus GN=Unc13d PE=1	0	6	0	0	0	0	Inf	0.3739	6
sp|Q5RJH2|MCTP2_MOUSE - Multiple C2 and transmembrane domain-containing protein	0	16	0	0	0	0	Inf	0.3739	16
sp|Q640M6|GDPD5_MOUSE - Glycerophosphodiester phosphodiesterase domain-containin	0	5	0	0	0	0	Inf	0.3739	5
sp|Q3U6K5|SPAT6_MOUSE - Spermatogenesis-associated protein 6 OS=Mus musculus GN=	0	4	0	0	0	0	Inf	0.3739	4
sp|Q9JIW4|DPOLM_MOUSE - DNA-directed DNA/RNA polymerase mu OS=Mus musculus GN=Po	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9WTM5|RUVB2_MOUSE - RuvB-like 2 OS=Mus musculus GN=Ruvbl2 PE=2 SV=3	0	2	0	0	0	0	Inf	0.3739	2
sp|Q6ZPJ0|TEX2_MOUSE - Testis-expressed sequence 2 protein OS=Mus musculus GN=Te	0	4	0	0	0	0	Inf	0.3739	4
sp|Q8BGQ7|SYAC_MOUSE - Alanine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Aars	0	3	0	0	0	0	Inf	0.3739	3
sp|Q6NS57|MABP1_MOUSE - Mitogen-activated protein kinase-binding protein 1 OS=Mu	0	4	0	0	0	0	Inf	0.3739	4
sp|Q68ED2|GRM7_MOUSE - Metabotropic glutamate receptor 7 OS=Mus musculus GN=Grm7	0	3	0	0	0	0	Inf	0.3739	3
sp|P68404|KPCB_MOUSE - Protein kinase C beta type OS=Mus musculus GN=Prkcb PE=1	0	6	0	0	0	0	Inf	0.3739	6
sp|Q8BSK8|KS6B1_MOUSE - Ribosomal protein S6 kinase beta-1 OS=Mus musculus GN=Rp	0	7	0	0	0	0	Inf	0.3739	7
sp|P38532|HSF1_MOUSE - Heat shock factor protein 1 OS=Mus musculus GN=Hsf1 PE=1	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9WUU8|TNIP1_MOUSE - TNFAIP3-interacting protein 1 OS=Mus musculus GN=Tnip1 P	0	4	0	0	0	0	Inf	0.3739	4
sp|Q62074|KPCI_MOUSE - Protein kinase C iota type OS=Mus musculus GN=Prkci PE=1	0	3	0	0	0	0	Inf	0.3739	3
sp|Q3UYK3|TBCD9_MOUSE - TBC1 domain family member 9 OS=Mus musculus GN=Tbc1d9 PE	0	3	0	0	0	0	Inf	0.3739	3
sp|Q91ZT5|FGD4_MOUSE - FYVE, RhoGEF and PH domain-containing protein 4 OS=Mus mu	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8K1M6|DNM1L_MOUSE - Dynamin-1-like protein OS=Mus musculus GN=Dnm1l PE=1 SV=	0	4	0	0	0	0	Inf	0.3739	4
sp|O08858|SSR5_MOUSE - Somatostatin receptor type 5 OS=Mus musculus GN=Sstr5 PE=	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BRT1|CLAP2_MOUSE - CLIP-associating protein 2 OS=Mus musculus GN=Clasp2 PE=	0	4	0	0	0	0	Inf	0.3739	4
sp|Q8BRB7|KAT6B_MOUSE - Histone acetyltransferase KAT6B OS=Mus musculus GN=Kat6b	0	7	0	0	0	0	Inf	0.3739	7
sp|Q8BR07|BICD1_MOUSE - Protein bicaudal D homolog 1 OS=Mus musculus GN=Bicd1 PE	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9ERK0|RIPK4_MOUSE - Receptor-interacting serine/threonine-protein kinase 4 O	0	5	0	0	0	0	Inf	0.3739	5
sp|O70582|LX12B_MOUSE - Arachidonate 12-lipoxygenase, 12R-type OS=Mus musculus G	0	2	0	0	0	0	Inf	0.3739	2
sp|P23298|KPCL_MOUSE - Protein kinase C eta type OS=Mus musculus GN=Prkch PE=1 S	0	6	0	0	0	0	Inf	0.3739	6
sp|P20444|KPCA_MOUSE - Protein kinase C alpha type OS=Mus musculus GN=Prkca PE=1	0	7	0	0	0	0	Inf	0.3739	7
sp|Q6JPI3|MD13L_MOUSE - Mediator of RNA polymerase II transcription subunit 13-l	0	4	0	0	0	0	Inf	0.3739	4
sp|Q3URK3|TET1_MOUSE - Methylcytosine dioxygenase TET1 OS=Mus musculus GN=Tet1 P	0	4	6	0	0	0	Inf	0.1317	10
sp|Q9QY01|ULK2_MOUSE - Serine/threonine-protein kinase ULK2 OS=Mus musculus GN=U	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8CCE9|E4F1_MOUSE - Transcription factor E4F1 OS=Mus musculus GN=E4f1 PE=1 SV	0	2	0	0	0	0	Inf	0.3739	2
sp|Q6WKZ8|UBR2_MOUSE - E3 ubiquitin-protein ligase UBR2 OS=Mus musculus GN=Ubr2	0	2	0	0	0	0	Inf	0.3739	2
sp|Q60949|TBCD1_MOUSE - TBC1 domain family member 1 OS=Mus musculus GN=Tbc1d1 PE	0	3	0	0	0	0	Inf	0.3739	3
sp|O88343|S4A4_MOUSE - Electrogenic sodium bicarbonate cotransporter 1 OS=Mus mu	0	9	0	0	0	0	Inf	0.3739	9
sp|Q8CD54|PIEZ2_MOUSE - Piezo-type mechanosensitive ion channel component 2 OS=M	0	10	0	0	0	0	Inf	0.3739	10
sp|Q71LX4|TLN2_MOUSE - Talin-2 OS=Mus musculus GN=Tln2 PE=1 SV=3	0	4	0	0	0	0	Inf	0.3739	4
sp|P16056|MET_MOUSE - Hepatocyte growth factor receptor OS=Mus musculus GN=Met P	0	2	0	0	0	0	Inf	0.3739	2
sp|Q80WJ6|MRP9_MOUSE - Multidrug resistance-associated protein 9 OS=Mus musculus	0	4	0	0	0	0	Inf	0.3739	4
sp|Q812A2|SRGP3_MOUSE - SLIT-ROBO Rho GTPase-activating protein 3 OS=Mus musculu	0	3	0	0	0	0	Inf	0.3739	3
sp|Q99K30|ES8L2_MOUSE - Epidermal growth factor receptor kinase substrate 8-like	0	2	0	0	0	0	Inf	0.3739	2

sp|O88379|BAZ1A_MOUSE - Bromodomain adjacent to zinc finger domain protein 1A OS	0	4	0	0	0	0	Inf	0.3739	4
sp|Q6Y7W8|PERQ2_MOUSE - PERQ amino acid-rich with GYF domain-containing protein	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8K371|AMOL2_MOUSE - Angiomotin-like protein 2 OS=Mus musculus GN=Amotl2 PE=2	0	3	4	0	0	0	Inf	0.1241	7
sp|Q8C3Y4|KNTC1_MOUSE - Kinetochore-associated protein 1 OS=Mus musculus GN=Kntc	0	3	0	0	0	0	Inf	0.3739	3
sp|Q3U7R1|ESYT1_MOUSE - Extended synaptotagmin-1 OS=Mus musculus GN=Esyt1 PE=1 S	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9JLG8|CAN15_MOUSE - Calpain-15 OS=Mus musculus GN=Capn15 PE=1 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|P33173|KIF1A_MOUSE - Kinesin-like protein KIF1A OS=Mus musculus GN=Kif1a PE=1	0	2	0	0	0	0	Inf	0.3739	2
sp|A2AAE1|K1109_MOUSE - Uncharacterized protein KIAA1109 OS=Mus musculus GN=Kiaa	0	5	0	0	0	0	Inf	0.3739	5
sp|P62075|TIM13_MOUSE - Mitochondrial import inner membrane translocase subunit	0	3	0	0	0	0	Inf	0.3739	3
sp|P56391|CX6B1_MOUSE - Cytochrome c oxidase subunit 6B1 OS=Mus musculus GN=Cox6	0	6	6	0	0	0	Inf	0.1161	12
sp|P41105|RL28_MOUSE - 60S ribosomal protein L28 OS=Mus musculus GN=Rpl28 PE=1 S	0	7	0	0	0	0	Inf	0.3739	7
sp|P62204|CALM_MOUSE - Calmodulin OS=Mus musculus GN=Calm1 PE=1 SV=2	0	4	0	0	0	0	Inf	0.3739	4
sp|P03930|ATP8_MOUSE - ATP synthase protein 8 OS=Mus musculus GN=Mtatp8 PE=1 SV=	0	4	0	0	0	0	Inf	0.3739	4
sp|P15532|NDKA_MOUSE - Nucleoside diphosphate kinase A OS=Mus musculus GN=Nme1 P	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9WV85|NDK3_MOUSE - Nucleoside diphosphate kinase 3 OS=Mus musculus GN=Nme3 P	0	3	0	0	0	0	Inf	0.3739	3
sp|P61358|RL27_MOUSE - 60S ribosomal protein L27 OS=Mus musculus GN=Rpl27 PE=1 S	0	8	0	0	0	0	Inf	0.3739	8
sp|O35972|RM23_MOUSE - 39S ribosomal protein L23, mitochondrial OS=Mus musculus	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9CZX8|RS19_MOUSE - 40S ribosomal protein S19 OS=Mus musculus GN=Rps19 PE=1 S	0	4	0	0	0	0	Inf	0.3739	4
sp|P47758|SRPRB_MOUSE - Signal recognition particle receptor subunit beta OS=Mus	0	6	0	0	0	0	Inf	0.3739	6
sp|Q9CQ40|RM49_MOUSE - 39S ribosomal protein L49, mitochondrial OS=Mus musculus	0	3	0	0	0	0	Inf	0.3739	3
sp|O70325|GPX41_MOUSE - Phospholipid hydroperoxide glutathione peroxidase, mitoc	0	3	0	0	0	0	Inf	0.3739	3
sp|P67984|RL22_MOUSE - 60S ribosomal protein L22 OS=Mus musculus GN=Rpl22 PE=1 S	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9CQ91|NDUA3_MOUSE - NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subun	0	2	0	0	0	0	Inf	0.3739	2
sp|P01896|HA1Z_MOUSE - H-2 class I histocompatibility antigen, alpha chain (Frag	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9CR57|RL14_MOUSE - 60S ribosomal protein L14 OS=Mus musculus GN=Rpl14 PE=1 S	0	2	0	0	0	0	Inf	0.3739	2
sp|P35282|RAB21_MOUSE - Ras-related protein Rab-21 OS=Mus musculus GN=Rab21 PE=1	0	3	4	0	0	0	Inf	0.1241	7
sp|P01901|HA1B_MOUSE - H-2 class I histocompatibility antigen, K-B alpha chain O	0	3	0	0	0	0	Inf	0.3739	3
sp|P35279|RAB6A_MOUSE - Ras-related protein Rab-6A OS=Mus musculus GN=Rab6a PE=1	0	3	0	0	0	0	Inf	0.3739	3
sp|P46656|ADX_MOUSE - Adrenodoxin, mitochondrial OS=Mus musculus GN=Fdx1 PE=1 SV	0	2	0	0	0	0	Inf	0.3739	2
sp|P09528|FRIH_MOUSE - Ferritin heavy chain OS=Mus musculus GN=Fth1 PE=1 SV=2	0	6	0	0	0	0	Inf	0.3739	6
sp|Q9CQL4|RM20_MOUSE - 39S ribosomal protein L20, mitochondrial OS=Mus musculus	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BHC1|RB39B_MOUSE - Ras-related protein Rab-39B OS=Mus musculus GN=Rab39b PE	0	3	0	0	0	0	Inf	0.3739	3
sp|Q923S9|RAB30_MOUSE - Ras-related protein Rab-30 OS=Mus musculus GN=Rab30 PE=2	0	3	0	0	0	0	Inf	0.3739	3
sp|P01897|HA1L_MOUSE - H-2 class I histocompatibility antigen, L-D alpha chain O	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9CR62|M2OM_MOUSE - Mitochondrial 2-oxoglutarate/malate carrier protein OS=Mu	0	2	0	0	0	0	Inf	0.3739	2
sp|P43275|H11_MOUSE - Histone H1.1 OS=Mus musculus GN=Hist1h1a PE=1 SV=2	0	2	4	0	0	0	Inf	0.1583	6
sp|Q9D9V4|RSPH9_MOUSE - Radial spoke head protein 9 homolog OS=Mus musculus GN=R	0	2	0	0	0	0	Inf	0.3739	2
sp|P01900|HA12_MOUSE - H-2 class I histocompatibility antigen, D-D alpha chain O	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9JIZ0|CMLO1_MOUSE - Probable N-acetyltransferase CML1 OS=Mus musculus GN=Cml	0	2	0	0	0	0	Inf	0.3739	2
sp|P20918|PLMN_MOUSE - Plasminogen OS=Mus musculus GN=Plg PE=1 SV=3	0	5	0	0	0	0	Inf	0.3739	5
sp|Q9CWP6|MSPD2_MOUSE - Motile sperm domain-containing protein 2 OS=Mus musculus	0	8	0	0	0	0	Inf	0.3739	8

sp|P14426|HA13_MOUSE - H-2 class I histocompatibility antigen, D-K alpha chain O	0	2	0	0	0	0	Inf	0.3739	2
sp|P10630|IF4A2_MOUSE - Eukaryotic initiation factor 4A-II OS=Mus musculus GN=Ei	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9WVD5|ORNT1_MOUSE - Mitochondrial ornithine transporter 1 OS=Mus musculus GN	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9QZ49|UBXN8_MOUSE - UBX domain-containing protein 8 OS=Mus musculus GN=Ubxn8	0	2	0	0	0	0	Inf	0.3739	2
sp|Q5XJY5|COPD_MOUSE - Coatomer subunit delta OS=Mus musculus GN=Arcn1 PE=1 SV=2	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8BWM0|PGES2_MOUSE - Prostaglandin E synthase 2 OS=Mus musculus GN=Ptges2 PE=	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8CDN8|CCD38_MOUSE - Coiled-coil domain-containing protein 38 OS=Mus musculus	0	2	0	0	0	0	Inf	0.3739	2
sp|Q3UHB8|CC177_MOUSE - Coiled-coil domain-containing protein 177 OS=Mus musculu	0	5	0	0	0	0	Inf	0.3739	5
sp|Q8K2C9|HACD3_MOUSE - Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3 OS=	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8BJU0|SGTA_MOUSE - Small glutamine-rich tetratricopeptide repeat-containing	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BHE8|CB047_MOUSE - Uncharacterized protein C2orf47 homolog, mitochondrial O	0	2	0	0	0	0	Inf	0.3739	2
sp|Q91WR5|AK1CL_MOUSE - Aldo-keto reductase family 1 member C21 OS=Mus musculus	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8R3J5|CHAC1_MOUSE - Glutathione-specific gamma-glutamylcyclotransferase 1 OS	0	2	0	0	0	0	Inf	0.3739	2
sp|P55302|AMRP_MOUSE - Alpha-2-macroglobulin receptor-associated protein OS=Mus	0	2	0	0	0	0	Inf	0.3739	2
sp|P20801|TNNC2_MOUSE - Troponin C, skeletal muscle OS=Mus musculus GN=Tnnc2 PE=	0	2	0	0	0	0	Inf	0.3739	2
sp|Q91YJ5|IF2M_MOUSE - Translation initiation factor IF-2, mitochondrial OS=Mus	0	5	0	0	0	0	Inf	0.3739	5
sp|Q9JLV1|BAG3_MOUSE - BAG family molecular chaperone regulator 3 OS=Mus musculu	0	3	0	0	0	0	Inf	0.3739	3
sp|Q7TNE1|SUCHY_MOUSE - Succinate--hydroxymethylglutarate CoA-transferase OS=Mus	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8BM55|TM214_MOUSE - Transmembrane protein 214 OS=Mus musculus GN=Tmem214 PE=	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9DCL9|PUR6_MOUSE - Multifunctional protein ADE2 OS=Mus musculus GN=Paics PE=	0	3	0	0	0	0	Inf	0.3739	3
sp|O88520|SHOC2_MOUSE - Leucine-rich repeat protein SHOC-2 OS=Mus musculus GN=Sh	0	3	0	0	0	0	Inf	0.3739	3
sp|P97357|TAF1A_MOUSE - TATA box-binding protein-associated factor RNA polymeras	0	6	0	0	0	0	Inf	0.3739	6
sp|Q9WU40|MAN1_MOUSE - Inner nuclear membrane protein Man1 OS=Mus musculus GN=Le	0	5	0	0	0	0	Inf	0.3739	5
sp|Q8C129|LCAP_MOUSE - Leucyl-cystinyl aminopeptidase OS=Mus musculus GN=Lnpep P	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8R3P7|CLUA1_MOUSE - Clusterin-associated protein 1 OS=Mus musculus GN=Cluap1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8K330|SSH3_MOUSE - Protein phosphatase Slingshot homolog 3 OS=Mus musculus G	0	4	0	0	0	0	Inf	0.3739	4
sp|O70373|XIRP1_MOUSE - Xin actin-binding repeat-containing protein 1 OS=Mus mus	0	2	0	0	0	0	Inf	0.3739	2
sp|Q91ZS8|RED1_MOUSE - Double-stranded RNA-specific editase 1 OS=Mus musculus GN	0	2	0	0	0	0	Inf	0.3739	2
sp|Q91X17|UROM_MOUSE - Uromodulin OS=Mus musculus GN=Umod PE=1 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9WVL4|RK_MOUSE - Rhodopsin kinase OS=Mus musculus GN=Grk1 PE=1 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|B2RRE7|OTUD4_MOUSE - OTU domain-containing protein 4 OS=Mus musculus GN=Otud4	0	3	0	0	0	0	Inf	0.3739	3
sp|Q3UVK0|ERMP1_MOUSE - Endoplasmic reticulum metallopeptidase 1 OS=Mus musculus	0	3	0	0	0	0	Inf	0.3739	3
sp|P53995|APC1_MOUSE - Anaphase-promoting complex subunit 1 OS=Mus musculus GN=A	0	6	0	0	0	0	Inf	0.3739	6
sp|Q99MR1|PERQ1_MOUSE - PERQ amino acid-rich with GYF domain-containing protein	0	3	0	0	0	0	Inf	0.3739	3
sp|Q8BZI0|AF1L1_MOUSE - Actin filament-associated protein 1-like 1 OS=Mus muscul	0	2	0	0	0	0	Inf	0.3739	2
sp|Q9WUN2|TBK1_MOUSE - Serine/threonine-protein kinase TBK1 OS=Mus musculus GN=T	0	2	0	0	0	0	Inf	0.3739	2
sp|P28867|KPCD_MOUSE - Protein kinase C delta type OS=Mus musculus GN=Prkcd PE=1	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9D2R0|AACS_MOUSE - Acetoacetyl-CoA synthetase OS=Mus musculus GN=Aacs PE=2 S	0	3	0	0	0	0	Inf	0.3739	3
sp|P58871|TB182_MOUSE - 182 kDa tankyrase-1-binding protein OS=Mus musculus GN=T	0	3	9	0	0	0	Inf	0.2051	12
sp|Q9R0R1|TRFM_MOUSE - Melanotransferrin OS=Mus musculus GN=Mfi2 PE=2 SV=1	0	2	0	0	0	0	Inf	0.3739	2
sp|D3Z5L9|WISP3_MOUSE - WNT1-inducible-signaling pathway protein 3 OS=Mus muscul	0	2	0	0	0	0	Inf	0.3739	2

sp|Q9QYK9|KCC1B_MOUSE - Calcium/calmodulin-dependent protein kinase type 1B OS=M	0	4	0	0	0	0	Inf	0.3739	4
sp|Q61143|TRPC6_MOUSE - Short transient receptor potential channel 6 OS=Mus musc	0	2	4	0	0	0	Inf	0.1583	6
sp|Q9ERV7|PIDD1_MOUSE - p53-induced death domain-containing protein 1 OS=Mus mus	0	3	0	0	0	0	Inf	0.3739	3
sp|Q0KK55|VKIND_MOUSE - Protein very KIND OS=Mus musculus GN=Kndc1 PE=1 SV=2	0	3	0	0	0	0	Inf	0.3739	3
sp|Q9WVB4|SLIT3_MOUSE - Slit homolog 3 protein OS=Mus musculus GN=Slit3 PE=2 SV=	0	6	0	0	0	0	Inf	0.3739	6
sp|Q7M6Z4|KIF27_MOUSE - Kinesin-like protein KIF27 OS=Mus musculus GN=Kif27 PE=1	0	7	0	0	0	0	Inf	0.3739	7
sp|Q6PFD9|NUP98_MOUSE - Nuclear pore complex protein Nup98-Nup96 OS=Mus musculus	0	4	0	0	0	0	Inf	0.3739	4
sp|Q920F6|SMC1B_MOUSE - Structural maintenance of chromosomes protein 1B OS=Mus	0	3	0	0	0	0	Inf	0.3739	3
sp|P43406|ITAV_MOUSE - Integrin alpha-V OS=Mus musculus GN=Itgav PE=1 SV=2	0	3	0	0	0	0	Inf	0.3739	3
sp|A2A690|TANC2_MOUSE - Protein TANC2 OS=Mus musculus GN=Tanc2 PE=1 SV=1	0	3	4	0	0	0	Inf	0.1241	7
sp|Q3UPH7|ARH40_MOUSE - Rho guanine nucleotide exchange factor 40 OS=Mus musculu	0	2	0	0	0	0	Inf	0.3739	2
sp|Q8K441|ABCA6_MOUSE - ATP-binding cassette sub-family A member 6 OS=Mus muscul	0	2	0	0	0	0	Inf	0.3739	2
sp|Q80TY5|VP13B_MOUSE - Vacuolar protein sorting-associated protein 13B OS=Mus m	0	2	0	0	0	0	Inf	0.3739	2
sp|Q91V09|WDR13_MOUSE - WD repeat-containing protein 13 OS=Mus musculus GN=Wdr13	0	0	7	0	0	0	Inf	0.3739	7
sp|D3YV10|CCD13_MOUSE - Coiled-coil domain-containing protein 13 OS=Mus musculus	0	0	17	0	0	0	Inf	0.3739	17
sp|P59242|CING_MOUSE - Cingulin OS=Mus musculus GN=Cgn PE=1 SV=1	0	0	15	0	0	0	Inf	0.3739	15
sp|O35691|PININ_MOUSE - Pinin OS=Mus musculus GN=Pnn PE=1 SV=4	0	0	7	0	0	0	Inf	0.3739	7
sp|Q9DBR3|ARMC8_MOUSE - Armadillo repeat-containing protein 8 OS=Mus musculus GN	0	0	2	0	0	0	Inf	0.3739	2
sp|Q6PAL7|AHDC1_MOUSE - AT-hook DNA-binding motif-containing protein 1 OS=Mus mu	0	0	4	0	0	0	Inf	0.3739	4
sp|Q6PIJ4|NFRKB_MOUSE - Nuclear factor related to kappa-B-binding protein OS=Mus	0	0	4	0	0	0	Inf	0.3739	4
sp|Q9D8W7|OCAD2_MOUSE - OCIA domain-containing protein 2 OS=Mus musculus GN=Ocia	0	0	3	0	0	0	Inf	0.3739	3
sp|P01868|IGHG1_MOUSE - Ig gamma-1 chain C region secreted form OS=Mus musculus	0	0	2	0	0	0	Inf	0.3739	2
sp|Q9QZ10|ANX10_MOUSE - Annexin A10 OS=Mus musculus GN=Anxa10 PE=2 SV=2	0	0	7	0	0	0	Inf	0.3739	7
sp|Q8C5N5|PDD2L_MOUSE - Programmed cell death protein 2-like OS=Mus musculus GN=	0	0	7	0	0	0	Inf	0.3739	7
sp|P31324|KAP3_MOUSE - cAMP-dependent protein kinase type II-beta regulatory sub	0	0	2	0	0	0	Inf	0.3739	2
sp|Q99N96|RM01_MOUSE - 39S ribosomal protein L1, mitochondrial OS=Mus musculus G	0	0	10	0	0	0	Inf	0.3739	10
sp|Q8QZV7|ASUN_MOUSE - Protein asunder homolog OS=Mus musculus GN=Asun PE=1 SV=2	0	0	5	0	0	0	Inf	0.3739	5
sp|O35659|GLP1R_MOUSE - Glucagon-like peptide 1 receptor OS=Mus musculus GN=Glp1	0	0	6	0	0	0	Inf	0.3739	6
sp|P97784|CRY1_MOUSE - Cryptochrome-1 OS=Mus musculus GN=Cry1 PE=1 SV=1	0	0	13	0	0	0	Inf	0.3739	13
sp|P97504|BMX_MOUSE - Cytoplasmic tyrosine-protein kinase BMX OS=Mus musculus GN	0	0	2	0	0	0	Inf	0.3739	2
sp|Q9WVH6|ANGP4_MOUSE - Angiopoietin-4 OS=Mus musculus GN=Angpt4 PE=1 SV=1	0	0	6	0	0	0	Inf	0.3739	6
sp|Q76MZ3|2AAA_MOUSE - Serine/threonine-protein phosphatase 2A 65 kDa regulatory	0	0	12	0	0	0	Inf	0.3739	12
sp|Q03267|IKZF1_MOUSE - DNA-binding protein Ikaros OS=Mus musculus GN=Ikzf1 PE=1	0	0	5	0	0	0	Inf	0.3739	5
sp|Q8VDC1|FYCO1_MOUSE - FYVE and coiled-coil domain-containing protein 1 OS=Mus	0	0	5	0	0	0	Inf	0.3739	5
sp|Q04750|TOP1_MOUSE - DNA topoisomerase 1 OS=Mus musculus GN=Top1 PE=1 SV=2	0	0	12	0	0	0	Inf	0.3739	12
sp|P61406|EST1A_MOUSE - Telomerase-binding protein EST1A OS=Mus musculus GN=Smg6	0	0	10	0	0	0	Inf	0.3739	10
sp|Q9D4H7|LONF3_MOUSE - LON peptidase N-terminal domain and RING finger protein	0	0	7	0	0	0	Inf	0.3739	7
sp|Q91Y44|BRDT_MOUSE - Bromodomain testis-specific protein OS=Mus musculus GN=Br	0	0	3	0	0	0	Inf	0.3739	3
sp|Q99N50|SYTL2_MOUSE - Synaptotagmin-like protein 2 OS=Mus musculus GN=Sytl2 PE	0	0	8	0	0	0	Inf	0.3739	8
sp|Q8VE19|MIO_MOUSE - WD repeat-containing protein mio OS=Mus musculus GN=Mios P	0	0	14	0	0	0	Inf	0.3739	14
sp|P58281|OPA1_MOUSE - Dynamin-like 120 kDa protein, mitochondrial OS=Mus muscul	0	0	8	0	0	0	Inf	0.3739	8

sp|Q6P2L6|NSD3_MOUSE - Histone-lysine N-methyltransferase NSD3 OS=Mus musculus G	0	0	2	0	0	0	Inf	0.3739	2
sp|A6X8Z5|RHG31_MOUSE - Rho GTPase-activating protein 31 OS=Mus musculus GN=Arhg	0	0	4	0	0	0	Inf	0.3739	4
sp|Q9EPL8|IPO7_MOUSE - Importin-7 OS=Mus musculus GN=Ipo7 PE=1 SV=2	0	0	4	0	0	0	Inf	0.3739	4
sp|P27546|MAP4_MOUSE - Microtubule-associated protein 4 OS=Mus musculus GN=Map4	0	0	14	0	0	0	Inf	0.3739	14
sp|O08808|DIAP1_MOUSE - Protein diaphanous homolog 1 OS=Mus musculus GN=Diaph1 P	0	0	18	0	0	0	Inf	0.3739	18
sp|Q8BJ34|MARF1_MOUSE - Meiosis arrest female protein 1 OS=Mus musculus GN=Marf1	0	0	4	0	0	0	Inf	0.3739	4
sp|Q7TPH6|MYCB2_MOUSE - E3 ubiquitin-protein ligase MYCBP2 OS=Mus musculus GN=My	0	0	9	0	0	0	Inf	0.3739	9
sp|Q99J47|DRS7B_MOUSE - Dehydrogenase/reductase SDR family member 7B OS=Mus musc	0	0	6	0	0	0	Inf	0.3739	6
sp|P58500|M3KCL_MOUSE - MAP3K7 C-terminal-like protein OS=Mus musculus GN=Map3k7	0	0	6	0	0	0	Inf	0.3739	6
sp|Q9D1F4|AKTS1_MOUSE - Proline-rich AKT1 substrate 1 OS=Mus musculus GN=Akt1s1	0	0	3	0	0	0	Inf	0.3739	3
sp|Q80U56|AVL9_MOUSE - Late secretory pathway protein AVL9 homolog OS=Mus muscul	0	0	3	0	0	0	Inf	0.3739	3
sp|B2RW38|CFA58_MOUSE - Cilia- and flagella-associated protein 58 OS=Mus musculu	0	0	16	0	0	0	Inf	0.3739	16
sp|Q8K363|DDX18_MOUSE - ATP-dependent RNA helicase DDX18 OS=Mus musculus GN=Ddx1	0	0	7	0	0	0	Inf	0.3739	7
sp|Q7M6Y3|PICAL_MOUSE - Phosphatidylinositol-binding clathrin assembly protein O	0	0	2	0	0	0	Inf	0.3739	2
sp|Q03717|KCNB1_MOUSE - Potassium voltage-gated channel subfamily B member 1 OS=	0	0	10	0	0	0	Inf	0.3739	10
sp|Q9EQP2|EHD4_MOUSE - EH domain-containing protein 4 OS=Mus musculus GN=Ehd4 PE	0	0	12	0	0	0	Inf	0.3739	12
sp|Q8BZR9|CQ085_MOUSE - Uncharacterized protein C17orf85 homolog OS=Mus musculus	0	0	5	0	0	0	Inf	0.3739	5
sp|Q8BU27|PPM1M_MOUSE - Protein phosphatase 1M OS=Mus musculus GN=Ppm1m PE=2 SV=	0	0	2	0	0	0	Inf	0.3739	2
sp|Q99KR6|RNF34_MOUSE - E3 ubiquitin-protein ligase RNF34 OS=Mus musculus GN=Rnf	0	0	6	0	0	0	Inf	0.3739	6
sp|Q3UXZ9|KDM5A_MOUSE - Lysine-specific demethylase 5A OS=Mus musculus GN=Kdm5a	0	0	6	0	0	0	Inf	0.3739	6
sp|Q8VHG2|AMOT_MOUSE - Angiomotin OS=Mus musculus GN=Amot PE=1 SV=3	0	0	5	0	0	0	Inf	0.3739	5
sp|Q8K2A8|ALG3_MOUSE - Dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransf	0	0	6	0	0	0	Inf	0.3739	6
sp|Q8CI32|BAG5_MOUSE - BAG family molecular chaperone regulator 5 OS=Mus musculu	0	0	4	0	0	0	Inf	0.3739	4
sp|Q8BPY9|FIGL1_MOUSE - Fidgetin-like protein 1 OS=Mus musculus GN=Fignl1 PE=2 S	0	0	10	0	0	0	Inf	0.3739	10
sp|O88962|CP8B1_MOUSE - 7-alpha-hydroxycholest-4-en-3-one 12-alpha-hydroxylase O	0	0	15	0	0	0	Inf	0.3739	15
sp|Q9D300|RGF1C_MOUSE - Ras-GEF domain-containing family member 1C OS=Mus muscul	0	0	10	0	0	0	Inf	0.3739	10
sp|O08934|UNC4_MOUSE - Homeobox protein unc-4 homolog OS=Mus musculus GN=Uncx PE	0	0	9	0	0	0	Inf	0.3739	9
sp|Q5I043|UBP28_MOUSE - Ubiquitin carboxyl-terminal hydrolase 28 OS=Mus musculus	0	0	13	0	0	0	Inf	0.3739	13
sp|Q8R4P5|TMC1_MOUSE - Transmembrane channel-like protein 1 OS=Mus musculus GN=T	0	0	13	0	0	0	Inf	0.3739	13
sp|Q8VCR8|MYLK2_MOUSE - Myosin light chain kinase 2, skeletal/cardiac muscle OS=	0	0	13	0	0	0	Inf	0.3739	13
sp|Q8CGB3|UACA_MOUSE - Uveal autoantigen with coiled-coil domains and ankyrin re	0	0	6	0	0	0	Inf	0.3739	6
sp|Q8BGW0|THMS1_MOUSE - Protein THEMIS OS=Mus musculus GN=Themis PE=1 SV=1	0	0	3	0	0	0	Inf	0.3739	3
sp|Q8K337|I5P2_MOUSE - Type II inositol 1,4,5-trisphosphate 5-phosphatase OS=Mus	0	0	4	0	0	0	Inf	0.3739	4
sp|Q6P9J9|ANO6_MOUSE - Anoctamin-6 OS=Mus musculus GN=Ano6 PE=1 SV=1	0	0	9	0	0	0	Inf	0.3739	9
sp|P97414|KCNQ1_MOUSE - Potassium voltage-gated channel subfamily KQT member 1 O	0	0	6	0	0	0	Inf	0.3739	6
sp|Q08857|CD36_MOUSE - Platelet glycoprotein 4 OS=Mus musculus GN=Cd36 PE=1 SV=2	0	0	6	0	0	0	Inf	0.3739	6
sp|Q4KUS2|UN13A_MOUSE - Protein unc-13 homolog A OS=Mus musculus GN=Unc13a PE=1	0	0	8	0	0	0	Inf	0.3739	8
sp|Q6ZPY2|SMG5_MOUSE - Protein SMG5 OS=Mus musculus GN=Smg5 PE=2 SV=2	0	0	6	0	0	0	Inf	0.3739	6
sp|Q6NZQ4|PAXI1_MOUSE - PAX-interacting protein 1 OS=Mus musculus GN=Paxip1 PE=1	0	0	11	0	0	0	Inf	0.3739	11
sp|Q8R4Y8|RTTN_MOUSE - Rotatin OS=Mus musculus GN=Rttn PE=2 SV=2	0	0	20	0	0	0	Inf	0.3739	20
sp|Q9Z148|EHMT2_MOUSE - Histone-lysine N-methyltransferase EHMT2 OS=Mus musculus	0	0	4	0	0	0	Inf	0.3739	4

sp|Q9JJN2|ZFHX4_MOUSE - Zinc finger homeobox protein 4 OS=Mus musculus GN=Zfhx4	0	0	11	0	0	0	Inf	0.3739	11
sp|Q8CJF7|ELYS_MOUSE - Protein ELYS OS=Mus musculus GN=Ahctf1 PE=1 SV=1	0	0	6	0	0	0	Inf	0.3739	6
sp|P97433|ARG28_MOUSE - Rho guanine nucleotide exchange factor 28 OS=Mus musculu	0	0	12	0	0	0	Inf	0.3739	12
sp|Q9Z1N9|UN13B_MOUSE - Protein unc-13 homolog B OS=Mus musculus GN=Unc13b PE=2	0	0	5	0	0	0	Inf	0.3739	5
sp|Q8CGS6|DPOLQ_MOUSE - DNA polymerase theta OS=Mus musculus GN=Polq PE=1 SV=2	0	0	12	0	0	0	Inf	0.3739	12
sp|Q9D365|SPCS3_MOUSE - Signal peptidase complex subunit 3 OS=Mus musculus GN=Sp	0	0	2	0	0	0	Inf	0.3739	2
sp|Q62190|RON_MOUSE - Macrophage-stimulating protein receptor OS=Mus musculus GN	0	0	4	0	0	0	Inf	0.3739	4
sp|Q9ESP1|SDF2L_MOUSE - Stromal cell-derived factor 2-like protein 1 OS=Mus musc	0	0	4	0	0	0	Inf	0.3739	4
sp|Q3UPL5|CK096_MOUSE - Uncharacterized protein C11orf96 homolog OS=Mus musculus	0	0	4	0	0	0	Inf	0.3739	4
sp|O88448|KLC2_MOUSE - Kinesin light chain 2 OS=Mus musculus GN=Klc2 PE=1 SV=1	0	0	7	0	0	0	Inf	0.3739	7
sp|Q3U3E2|F117B_MOUSE - Protein FAM117B OS=Mus musculus GN=Fam117b PE=1 SV=1	0	0	9	0	0	0	Inf	0.3739	9
sp|Q8VDZ4|ZDHC5_MOUSE - Palmitoyltransferase ZDHHC5 OS=Mus musculus GN=Zdhhc5 PE	0	0	15	0	0	0	Inf	0.3739	15
sp|Q8BGR9|UBCP1_MOUSE - Ubiquitin-like domain-containing CTD phosphatase 1 OS=Mu	0	0	3	0	0	0	Inf	0.3739	3
sp|Q9R1K6|GPR34_MOUSE - Probable G-protein coupled receptor 34 OS=Mus musculus G	0	0	5	0	0	0	Inf	0.3739	5
sp|Q922J9|FACR1_MOUSE - Fatty acyl-CoA reductase 1 OS=Mus musculus GN=Far1 PE=1	0	0	6	0	0	0	Inf	0.3739	6
sp|Q8CB44|GRAM4_MOUSE - GRAM domain-containing protein 4 OS=Mus musculus GN=Gram	0	0	6	0	0	0	Inf	0.3739	6
sp|Q8R4C2|RUFY2_MOUSE - RUN and FYVE domain-containing protein 2 OS=Mus musculus	0	0	2	0	0	0	Inf	0.3739	2
sp|Q61233|PLSL_MOUSE - Plastin-2 OS=Mus musculus GN=Lcp1 PE=1 SV=4	0	0	2	0	0	0	Inf	0.3739	2
sp|Q9CTG6|AT132_MOUSE - Probable cation-transporting ATPase 13A2 OS=Mus musculus	0	0	9	0	0	0	Inf	0.3739	9
sp|O88622|PARG_MOUSE - Poly(ADP-ribose) glycohydrolase OS=Mus musculus GN=Parg P	0	0	3	0	0	0	Inf	0.3739	3
sp|P33174|KIF4_MOUSE - Chromosome-associated kinesin KIF4 OS=Mus musculus GN=Kif	0	0	4	0	0	0	Inf	0.3739	4
sp|Q80TD3|FNIP2_MOUSE - Folliculin-interacting protein 2 OS=Mus musculus GN=Fnip	0	0	11	0	0	0	Inf	0.3739	11
sp|Q8R4U0|STAB2_MOUSE - Stabilin-2 OS=Mus musculus GN=Stab2 PE=1 SV=1	10	25	19	2	0	0	27	0.017	56
sp|P35564|CALX_MOUSE - Calnexin OS=Mus musculus GN=Canx PE=1 SV=1	0	34	0	2	0	0	17	0.4006	36
sp|P56656|CP239_MOUSE - Cytochrome P450 2C39 OS=Mus musculus GN=Cyp2c39 PE=2 SV=	0	21	10	2	0	0	15.5	0.1882	33
sp|Q6PGN3|DCLK2_MOUSE - Serine/threonine-protein kinase DCLK2 OS=Mus musculus GN	0	20	7	0	2	0	13.5	0.2305	29
sp|Q52KB6|C2CD3_MOUSE - C2 domain-containing protein 3 OS=Mus musculus GN=C2cd3	0	2	22	2	0	0	12	0.3573	26
sp|P12791|CP2BA_MOUSE - Cytochrome P450 2B10 OS=Mus musculus GN=Cyp2b10 PE=1 SV=	0	22	0	2	0	0	11	0.4164	24
sp|Q8CCJ4|AMER2_MOUSE - APC membrane recruitment protein 2 OS=Mus musculus GN=Am	0	13	9	0	2	0	11	0.1626	24
sp|Q4U4S6|XIRP2_MOUSE - Xin actin-binding repeat-containing protein 2 OS=Mus mus	0	12	32	4	0	0	11	0.2302	48
sp|P60487|PLPP_MOUSE - Pyridoxal phosphate phosphatase OS=Mus musculus GN=Pdxp P	0	0	31	0	0	3	10.3333	0.4194	34
sp|B2RX12|MRP3_MOUSE - Canalicular multispecific organic anion transporter 2 OS=	0	15	5	0	2	0	10	0.2497	22
sp|Q6GYP7|RGPA1_MOUSE - Ral GTPase-activating protein subunit alpha-1 OS=Mus mus	0	19	0	0	2	0	9.5	0.4238	21
sp|Q9CZV8|FXL20_MOUSE - F-box/LRR-repeat protein 20 OS=Mus musculus GN=Fbxl20 PE	0	20	8	0	3	0	9.3333	0.2305	31
sp|Q80XN0|BDH_MOUSE - D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Mus	0	25	0	0	3	0	8.3333	0.4315	28
sp|Q5FW85|ECM2_MOUSE - Extracellular matrix protein 2 OS=Mus musculus GN=Ecm2 PE	0	2	14	2	0	0	8	0.3508	18
sp|Q6ZPR6|IBTK_MOUSE - Inhibitor of Bruton tyrosine kinase OS=Mus musculus GN=Ib	0	15	0	2	0	0	7.5	0.4387	17
sp|Q9CZ92|CENPP_MOUSE - Centromere protein P OS=Mus musculus GN=Cenpp PE=2 SV=1	2	12	0	2	0	0	7	0.3486	16
sp|Q8BH02|TOR4A_MOUSE - Torsin-4A OS=Mus musculus GN=Tor4a PE=2 SV=1	0	6	15	0	3	0	7	0.2508	24
sp|O08756|HCD2_MOUSE - 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Mus musculus GN	0	8	6	0	2	0	7	0.184	16
sp|O70318|E41L2_MOUSE - Band 4.1-like protein 2 OS=Mus musculus GN=Epb41l2 PE=1	0	0	14	0	2	0	7	0.4439	16

sp|Q9EQJ9|MAGI3_MOUSE - Membrane-associated guanylate kinase, WW and PDZ domain-	0	27	0	0	4	0	6.75	0.4468	31
sp|O35904|PK3CD_MOUSE - Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic	0	12	8	0	3	0	6.6666	0.1971	23
sp|Q3UH06|RREB1_MOUSE - Ras-responsive element-binding protein 1 OS=Mus musculus	4	4	5	2	0	0	6.5	0.0079	15
sp|P17047|LAMP2_MOUSE - Lysosome-associated membrane glycoprotein 2 OS=Mus muscu	0	13	0	0	2	0	6.5	0.45	15
sp|Q71KT5|ERG24_MOUSE - Delta(14)-sterol reductase OS=Mus musculus GN=Tm7sf2 PE=	0	13	0	0	2	0	6.5	0.45	15
sp|Q8BRC6|MAAT1_MOUSE - Protein MAATS1 OS=Mus musculus GN=Maats1 PE=2 SV=3	0	11	15	4	0	0	6.5	0.192	30
sp|P11609|CD1D1_MOUSE - Antigen-presenting glycoprotein CD1d1 OS=Mus musculus GN	0	4	9	0	2	0	6.5	0.2441	15
sp|Q99LX5|MMTA2_MOUSE - Multiple myeloma tumor-associated protein 2 homolog OS=M	2	6	24	0	5	0	6.4	0.266	37
sp|Q8BXJ2|TREF1_MOUSE - Transcriptional-regulating factor 1 OS=Mus musculus GN=T	0	22	2	0	4	0	6	0.4038	28
sp|P52430|PON1_MOUSE - Serum paraoxonase/arylesterase 1 OS=Mus musculus GN=Pon1	0	18	0	0	3	0	6	0.4572	21
sp|Q8BU30|SYIC_MOUSE - Isoleucine--tRNA ligase, cytoplasmic OS=Mus musculus GN=I	0	2	10	0	2	0	6	0.3465	14
sp|Q5F201|CFA52_MOUSE - Cilia- and flagella-associated protein 52 OS=Mus musculu	0	7	11	3	0	0	6	0.2116	21
sp|Q9D8C4|IN35_MOUSE - Interferon-induced 35 kDa protein homolog OS=Mus musculus	0	0	12	0	0	2	6	0.4572	14
sp|Q9CQ56|USE1_MOUSE - Vesicle transport protein USE1 OS=Mus musculus GN=Use1 PE	0	3	8	2	0	0	5.5	0.284	13
sp|Q8R1W8|IMPG1_MOUSE - Interphotoreceptor matrix proteoglycan 1 OS=Mus musculus	0	5	6	2	0	0	5.5	0.2028	13
sp|Q810B6|ANFY1_MOUSE - Rabankyrin-5 OS=Mus musculus GN=Ankfy1 PE=2 SV=2	0	11	0	0	2	0	5.5	0.4659	13
sp|Q9QUJ7|ACSL4_MOUSE - Long-chain-fatty-acid--CoA ligase 4 OS=Mus musculus GN=A	0	16	0	0	3	0	5.3333	0.4692	19
sp|Q8VBX6|MPDZ_MOUSE - Multiple PDZ domain protein OS=Mus musculus GN=Mpdz PE=1	0	5	11	0	3	0	5.3333	0.2634	19
sp|P25444|RS2_MOUSE - 40S ribosomal protein S2 OS=Mus musculus GN=Rps2 PE=2 SV=3	2	18	0	0	4	0	5	0.4135	24
sp|P29788|VTNC_MOUSE - Vitronectin OS=Mus musculus GN=Vtn PE=1 SV=2	4	6	0	0	2	0	5	0.2302	12
sp|Q9Z104|HM20B_MOUSE - SWI/SNF-related matrix-associated actin-dependent regula	2	8	25	2	5	0	5	0.2555	42
sp|Q6PR54|RIF1_MOUSE - Telomere-associated protein RIF1 OS=Mus musculus GN=Rif1	0	30	0	0	6	0	5	0.4766	36
sp|Q80W40|ACSM4_MOUSE - Acyl-coenzyme A synthetase ACSM4, mitochondrial OS=Mus m	0	2	8	0	2	0	5	0.3452	12
sp|O88428|PAPS2_MOUSE - Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synth	0	3	56	0	0	13	4.5384	0.4582	72
sp|Q8BH24|TM9S4_MOUSE - Transmembrane 9 superfamily member 4 OS=Mus musculus GN=	0	9	0	0	2	0	4.5	0.4899	11
sp|Q80XC6|NRDE2_MOUSE - Protein NRDE2 homolog OS=Mus musculus GN=Nrde2 PE=2 SV=3	0	9	0	0	2	0	4.5	0.4899	11
sp|E9Q5K9|YTDC1_MOUSE - YTH domain-containing protein 1 OS=Mus musculus GN=Ythdc	0	9	0	0	2	0	4.5	0.4899	11
sp|Q3UZY0|SFI1_MOUSE - Protein SFI1 homolog OS=Mus musculus GN=Sfi1 PE=2 SV=1	0	9	0	2	0	0	4.5	0.4899	11
sp|P48758|CBR1_MOUSE - Carbonyl reductase [NADPH] 1 OS=Mus musculus GN=Cbr1 PE=1	0	9	0	0	2	0	4.5	0.4899	11
sp|P62915|TF2B_MOUSE - Transcription initiation factor IIB OS=Mus musculus GN=Gt	0	10	8	0	4	0	4.5	0.2341	22
sp|Q6DFV1|CNDG2_MOUSE - Condensin-2 complex subunit G2 OS=Mus musculus GN=Ncapg2	5	4	4	3	0	0	4.3333	0.0341	16
sp|Q61391|NEP_MOUSE - Neprilysin OS=Mus musculus GN=Mme PE=1 SV=3	0	16	10	4	2	0	4.3333	0.2378	32
sp|Q8CIF4|BTD_MOUSE - Biotinidase OS=Mus musculus GN=Btd PE=1 SV=2	0	13	0	0	3	0	4.3333	0.4952	16
sp|Q80TP3|UBR5_MOUSE - E3 ubiquitin-protein ligase UBR5 OS=Mus musculus GN=Ubr5	0	14	3	0	4	0	4.25	0.3862	21
sp|D3YXK2|SAFB1_MOUSE - Scaffold attachment factor B1 OS=Mus musculus GN=Safb PE	6	9	27	2	8	0	4.2	0.2014	52
sp|Q8CDI7|CC150_MOUSE - Coiled-coil domain-containing protein 150 OS=Mus musculu	0	22	41	15	0	0	4.2	0.2813	78
sp|P56593|CP2AC_MOUSE - Cytochrome P450 2A12 OS=Mus musculus GN=Cyp2a12 PE=1 SV=	10	74	4	7	11	3	4.1904	0.3774	109
sp|P15392|CP2A4_MOUSE - Cytochrome P450 2A4 OS=Mus musculus GN=Cyp2a4 PE=2 SV=3	0	47	3	0	8	4	4.1666	0.456	62
sp|Q69Z69|ESCO1_MOUSE - N-acetyltransferase ESCO1 OS=Mus musculus GN=Esco1 PE=2	4	20	42	3	0	13	4.125	0.2272	82
sp|P32261|ANT3_MOUSE - Antithrombin-III OS=Mus musculus GN=Serpinc1 PE=1 SV=1	0	26	19	0	5	6	4.0909	0.2288	56
sp|Q3UUG6|TBC24_MOUSE - TBC1 domain family member 24 OS=Mus musculus GN=Tbc1d24	0	12	0	3	0	0	4	0.5071	15

sp|Q9D3E6|STAG1_MOUSE - Cohesin subunit SA-1 OS=Mus musculus GN=Stag1 PE=2 SV=3	0	12	12	0	6	0	4	0.2508	30
sp|Q692V3|GNN_MOUSE - Tetratricopeptide repeat protein GNN OS=Mus musculus GN=Gn	0	8	4	0	3	0	4	0.2991	15
sp|Q8VDK1|NIT1_MOUSE - Nitrilase homolog 1 OS=Mus musculus GN=Nit1 PE=2 SV=2	0	12	0	0	3	0	4	0.5071	15
sp|O35381|AN32A_MOUSE - Acidic leucine-rich nuclear phosphoprotein 32 family mem	0	8	0	0	2	0	4	0.5071	10
sp|A2AGL3|RYR3_MOUSE - Ryanodine receptor 3 OS=Mus musculus GN=Ryr3 PE=1 SV=1	0	12	0	0	3	0	4	0.5071	15
sp|Q91VY5|KDM4B_MOUSE - Lysine-specific demethylase 4B OS=Mus musculus GN=Kdm4b	0	15	0	0	4	0	3.75	0.5177	19
sp|Q9Z315|SNUT1_MOUSE - U4/U6.U5 tri-snRNP-associated protein 1 OS=Mus musculus	0	26	0	3	4	0	3.7142	0.5092	33
sp|P20852|CP2A5_MOUSE - Cytochrome P450 2A5 OS=Mus musculus GN=Cyp2a5 PE=2 SV=1	9	59	13	0	15	7	3.6818	0.3021	103
sp|Q8BVR6|RSPRY_MOUSE - RING finger and SPRY domain-containing protein 1 OS=Mus	2	9	0	0	3	0	3.6666	0.4107	14
sp|P01872|IGHM_MOUSE - Ig mu chain C region OS=Mus musculus GN=Ighm PE=1 SV=2	0	22	0	2	4	0	3.6666	0.5122	28
sp|Q9WVS7|MP2K5_MOUSE - Dual specificity mitogen-activated protein kinase kinase	0	7	4	0	3	0	3.6666	0.3035	14
sp|Q5DW34|EHMT1_MOUSE - Histone-lysine N-methyltransferase EHMT1 OS=Mus musculus	5	2	0	0	2	0	3.5	0.356	9
sp|Q80TN7|NAV3_MOUSE - Neuron navigator 3 OS=Mus musculus GN=Nav3 PE=1 SV=2	4	17	0	0	6	0	3.5	0.4153	27
sp|P17751|TPIS_MOUSE - Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV	3	11	0	0	4	0	3.5	0.4001	18
sp|Q8K2V1|PP4R1_MOUSE - Serine/threonine-protein phosphatase 4 regulatory subuni	3	18	0	0	6	0	3.5	0.4456	27
sp|Q8C1A3|MTRR_MOUSE - Methionine synthase reductase OS=Mus musculus GN=Mtrr PE=	2	5	0	2	0	0	3.5	0.356	9
sp|Q3V125|CC110_MOUSE - Coiled-coil domain-containing protein 110 OS=Mus musculu	3	4	0	0	2	0	3.5	0.2919	9
sp|Q6ZPI0|JADE1_MOUSE - Protein Jade-1 OS=Mus musculus GN=Jade1 PE=1 SV=2	0	7	0	0	2	0	3.5	0.5299	9
sp|Q5S003|SPG17_MOUSE - Sperm-associated antigen 17 OS=Mus musculus GN=Spag17 PE	0	14	0	0	4	0	3.5	0.5299	18
sp|Q7TQA1|IGSF1_MOUSE - Immunoglobulin superfamily member 1 OS=Mus musculus GN=I	0	7	0	0	2	0	3.5	0.5299	9
sp|Q9CXN7|PBLD2_MOUSE - Phenazine biosynthesis-like domain-containing protein 2	0	7	0	2	0	0	3.5	0.5299	9
sp|Q9R112|SQRD_MOUSE - Sulfide:quinone oxidoreductase, mitochondrial OS=Mus musc	0	14	0	0	4	0	3.5	0.5299	18
sp|Q9D8V0|HM13_MOUSE - Minor histocompatibility antigen H13 OS=Mus musculus GN=H	0	7	0	0	2	0	3.5	0.5299	9
sp|P55144|TYRO3_MOUSE - Tyrosine-protein kinase receptor TYRO3 OS=Mus musculus G	0	7	0	0	2	0	3.5	0.5299	9
sp|Q80X82|SYMPK_MOUSE - Symplekin OS=Mus musculus GN=Sympk PE=1 SV=1	0	2	5	2	0	0	3.5	0.356	9
sp|O88986|KBL_MOUSE - 2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial OS	0	7	0	2	0	0	3.5	0.5299	9
sp|Q91VM9|IPYR2_MOUSE - Inorganic pyrophosphatase 2, mitochondrial OS=Mus muscul	0	7	0	0	2	0	3.5	0.5299	9
sp|P47911|RL6_MOUSE - 60S ribosomal protein L6 OS=Mus musculus GN=Rpl6 PE=1 SV=3	0	7	0	0	2	0	3.5	0.5299	9
sp|Q8VEG4|EXD2_MOUSE - Exonuclease 3'-5' domain-containing protein 2 OS=Mus musc	0	7	0	0	2	0	3.5	0.5299	9
sp|O09158|CP3AP_MOUSE - Cytochrome P450 3A25 OS=Mus musculus GN=Cyp3a25 PE=2 SV=	0	7	0	0	2	0	3.5	0.5299	9
sp|Q99N87|RT05_MOUSE - 28S ribosomal protein S5, mitochondrial OS=Mus musculus G	0	2	5	0	2	0	3.5	0.356	9
sp|Q60591|NFAC2_MOUSE - Nuclear factor of activated T-cells, cytoplasmic 2 OS=Mu	0	0	7	0	2	0	3.5	0.5299	9
sp|Q9DBU3|RIOK3_MOUSE - Serine/threonine-protein kinase RIO3 OS=Mus musculus GN=	0	12	12	2	5	0	3.4285	0.2538	31
sp|Q8BPU7|ELMO1_MOUSE - Engulfment and cell motility protein 1 OS=Mus musculus G	0	9	32	3	0	9	3.4166	0.3836	53
sp|E9PV87|TALD3_MOUSE - Protein TALPID3 OS=Mus musculus GN=Talpid3 PE=2 SV=1	2	15	0	5	0	0	3.4	0.4676	22
sp|Q9JJ28|FLII_MOUSE - Protein flightless-1 homolog OS=Mus musculus GN=Flii PE=1	0	17	0	0	5	0	3.4	0.5354	22
sp|Q8BXZ1|TMX3_MOUSE - Protein disulfide-isomerase TMX3 OS=Mus musculus GN=Tmx3	0	10	0	0	3	0	3.3333	0.5392	13
sp|Q9Z319|CORIN_MOUSE - Atrial natriuretic peptide-converting enzyme OS=Mus musc	0	9	24	0	8	2	3.3	0.3587	43
sp|P11531|DMD_MOUSE - Dystrophin OS=Mus musculus GN=Dmd PE=1 SV=3	4	9	0	0	0	4	3.25	0.363	17
sp|Q8BHG1|NRDC_MOUSE - Nardilysin OS=Mus musculus GN=Nrd1 PE=1 SV=1	0	13	0	2	2	0	3.25	0.5314	17
sp|Q8K2I4|MANBA_MOUSE - Beta-mannosidase OS=Mus musculus GN=Manba PE=2 SV=1	0	18	8	0	8	0	3.25	0.363	34

sp|Q811D2|ANR26_MOUSE - Ankyrin repeat domain-containing protein 26 OS=Mus muscu	0	10	3	4	0	0	3.25	0.408	17
sp|D3Z750|MRO2A_MOUSE - Maestro heat-like repeat-containing protein family membe	0	13	0	0	4	0	3.25	0.5443	17
sp|Q5SX40|MYH1_MOUSE - Myosin-1 OS=Mus musculus GN=Myh1 PE=2 SV=1	0	13	0	4	0	0	3.25	0.5443	17
sp|Q91Z83|MYH7_MOUSE - Myosin-7 OS=Mus musculus GN=Myh7 PE=1 SV=1	0	18	11	0	0	9	3.2222	0.3314	38
sp|P28293|CATG_MOUSE - Cathepsin G OS=Mus musculus GN=Ctsg PE=1 SV=2	0	3	13	0	5	0	3.2	0.4388	21
sp|Q64435|UD16_MOUSE - UDP-glucuronosyltransferase 1-6 OS=Mus musculus GN=Ugt1a6	14	128	0	0	46	0	3.0869	0.5012	188
sp|O70456|1433S_MOUSE - 14-3-3 protein sigma OS=Mus musculus GN=Sfn PE=1 SV=2	2	16	19	3	3	6	3.0833	0.1932	49
sp|O35114|SCRB2_MOUSE - Lysosome membrane protein 2 OS=Mus musculus GN=Scarb2 PE	7	49	13	7	13	3	3	0.3173	92
sp|Q9DCG6|PBLD1_MOUSE - Phenazine biosynthesis-like domain-containing protein 1	2	10	0	4	0	0	3	0.4685	16
sp|P47739|AL3A1_MOUSE - Aldehyde dehydrogenase, dimeric NADP-preferring OS=Mus m	2	11	5	2	4	0	3	0.2381	24
sp|Q9D2G5|SYNJ2_MOUSE - Synaptojanin-2 OS=Mus musculus GN=Synj2 PE=2 SV=2	2	7	0	3	0	0	3	0.4353	12
sp|Q80W21|GSTM7_MOUSE - Glutathione S-transferase Mu 7 OS=Mus musculus GN=Gstm7	2	10	0	0	4	0	3	0.4685	16
sp|Q9DCQ2|ASPD_MOUSE - Putative L-aspartate dehydrogenase OS=Mus musculus GN=Asp	3	9	0	0	4	0	3	0.4189	16
sp|Q8C170|MYO9A_MOUSE - Unconventional myosin-IXa OS=Mus musculus GN=Myo9a PE=2	4	24	5	8	3	0	3	0.3485	44
sp|Q7TNF8|RIMB1_MOUSE - Peripheral-type benzodiazepine receptor-associated prote	2	4	0	0	2	0	3	0.3739	8
sp|Q60590|A1AG1_MOUSE - Alpha-1-acid glycoprotein 1 OS=Mus musculus GN=Orm1 PE=1	0	6	0	0	2	0	3	0.5614	8
sp|Q9D8M4|RL7L_MOUSE - 60S ribosomal protein L7-like 1 OS=Mus musculus GN=Rpl7l1	0	6	0	0	2	0	3	0.5614	8
sp|Q8R0E5|ZRAS1_MOUSE - Putative uncharacterized protein ZNRD1-AS1 homolog OS=Mu	0	3	6	3	0	0	3	0.3739	12
sp|Q99MY0|SPZ1_MOUSE - Spermatogenic leucine zipper protein 1 OS=Mus musculus GN	0	5	10	0	5	0	3	0.3739	20
sp|Q9DC29|ABCB6_MOUSE - ATP-binding cassette sub-family B member 6, mitochondria	0	6	0	0	2	0	3	0.5614	8
sp|D3Z7P3|GLSK_MOUSE - Glutaminase kidney isoform, mitochondrial OS=Mus musculus	0	6	0	0	2	0	3	0.5614	8
sp|Q8BGY3|LUZP2_MOUSE - Leucine zipper protein 2 OS=Mus musculus GN=Luzp2 PE=2 S	0	6	0	0	2	0	3	0.5614	8
sp|Q8VE38|OXND1_MOUSE - Oxidoreductase NAD-binding domain-containing protein 1 O	0	4	2	2	0	0	3	0.3739	8
sp|Q9DC71|RT15_MOUSE - 28S ribosomal protein S15, mitochondrial OS=Mus musculus	0	9	0	0	3	0	3	0.5614	12
sp|Q61982|NOTC3_MOUSE - Neurogenic locus notch homolog protein 3 OS=Mus musculus	0	6	0	2	0	0	3	0.5614	8
sp|Q3UPC7|K0825_MOUSE - Uncharacterized protein KIAA0825 homolog OS=Mus musculus	0	9	0	0	3	0	3	0.5614	12
sp|Q9ESE1|LRBA_MOUSE - Lipopolysaccharide-responsive and beige-like anchor prote	0	6	0	2	0	0	3	0.5614	8
sp|Q8BJU9|RF1ML_MOUSE - Peptide chain release factor 1-like, mitochondrial OS=Mu	0	0	6	0	2	0	3	0.5614	8
sp|O35261|E2F3_MOUSE - Transcription factor E2F3 OS=Mus musculus GN=E2f3 PE=1 SV	0	0	41	0	0	14	2.9285	0.5669	55
sp|Q69ZR2|HECD1_MOUSE - E3 ubiquitin-protein ligase HECTD1 OS=Mus musculus GN=He	4	25	0	10	0	0	2.9	0.4947	39
sp|Q91ZE5|EMR4_MOUSE - EGF-like module-containing mucin-like hormone receptor-li	0	15	14	0	10	0	2.9	0.3419	39
sp|P70691|UD12_MOUSE - UDP-glucuronosyltransferase 1-2 OS=Mus musculus GN=Ugt1a2	7	135	20	26	0	30	2.8928	0.445	218
sp|P11983|TCPA_MOUSE - T-complex protein 1 subunit alpha OS=Mus musculus GN=Tcp1	3	18	28	2	0	15	2.8823	0.2852	66
sp|Q8K411|PREP_MOUSE - Presequence protease, mitochondrial OS=Mus musculus GN=Pi	0	17	0	0	6	0	2.8333	0.5747	23
sp|Q9D786|HAUS5_MOUSE - HAUS augmin-like complex subunit 5 OS=Mus musculus GN=Ha	0	14	0	0	5	0	2.8	0.5775	19
sp|Q922Q8|LRC59_MOUSE - Leucine-rich repeat-containing protein 59 OS=Mus musculu	0	14	0	0	5	0	2.8	0.5775	19
sp|Q6PCL9|PAPOG_MOUSE - Poly(A) polymerase gamma OS=Mus musculus GN=Papolg PE=1	5	39	22	5	19	0	2.75	0.2846	90
sp|Q5YD48|A1CF_MOUSE - APOBEC1 complementation factor OS=Mus musculus GN=A1cf PE	3	8	0	0	4	0	2.75	0.4342	15
sp|O88668|CREG1_MOUSE - Protein CREG1 OS=Mus musculus GN=Creg1 PE=2 SV=1	2	31	0	0	8	4	2.75	0.5332	45
sp|Q9D6J5|NDUB8_MOUSE - NADH dehydrogenase [ubiquinone] 1 beta subcomplex subuni	2	20	0	0	8	0	2.75	0.5357	30
sp|Q2M3X8|PHAR1_MOUSE - Phosphatase and actin regulator 1 OS=Mus musculus GN=Pha	6	19	16	0	13	2	2.7333	0.199	56

sp|Q7SIG6|ASAP2_MOUSE - Arf-GAP with SH3 domain, ANK repeat and PH domain-contai	0	19	0	0	7	0	2.7142	0.5853	26
sp|P11588|MUP1_MOUSE - Major urinary protein 1 OS=Mus musculus GN=Mup1 PE=1 SV=1	6	40	0	4	13	0	2.7058	0.4994	63
sp|Q6IFX3|K1C40_MOUSE - Keratin, type I cytoskeletal 40 OS=Mus musculus GN=Krt40	0	28	15	0	16	0	2.6875	0.4055	59
sp|Q9CU65|ZMYM2_MOUSE - Zinc finger MYM-type protein 2 OS=Mus musculus GN=Zmym2	4	4	0	3	0	0	2.6666	0.3739	11
sp|P62918|RL8_MOUSE - 60S ribosomal protein L8 OS=Mus musculus GN=Rpl8 PE=1 SV=2	3	5	0	0	3	0	2.6666	0.3982	11
sp|Q8BH59|CMC1_MOUSE - Calcium-binding mitochondrial carrier protein Aralar1 OS=	0	22	10	2	10	0	2.6666	0.3982	44
sp|Q9D328|TMM35_MOUSE - Transmembrane protein 35 OS=Mus musculus GN=Tmem35 PE=2	0	8	0	0	3	0	2.6666	0.5898	11
sp|Q8K0C4|CP51A_MOUSE - Lanosterol 14-alpha demethylase OS=Mus musculus GN=Cyp51	0	8	0	0	3	0	2.6666	0.5898	11
sp|A2AWA9|RBGP1_MOUSE - Rab GTPase-activating protein 1 OS=Mus musculus GN=Rabga	0	8	0	3	0	0	2.6666	0.5898	11
sp|Q8C267|SETB2_MOUSE - Histone-lysine N-methyltransferase SETDB2 OS=Mus musculu	0	8	0	0	3	0	2.6666	0.5898	11
sp|O09173|HGD_MOUSE - Homogentisate 1,2-dioxygenase OS=Mus musculus GN=Hgd PE=1	0	8	0	0	3	0	2.6666	0.5898	11
sp|Q9WVJ0|KCNH3_MOUSE - Potassium voltage-gated channel subfamily H member 3 OS=	0	0	8	0	3	0	2.6666	0.5898	11
sp|Q9D5S7|LRGUK_MOUSE - Leucine-rich repeat and guanylate kinase domain-containi	2	12	7	0	6	2	2.625	0.2694	29
sp|Q6ZQM0|RFFL_MOUSE - E3 ubiquitin-protein ligase rififylin OS=Mus musculus GN=	4	2	7	2	3	0	2.6	0.1917	18
sp|Q6P9R2|OXSR1_MOUSE - Serine/threonine-protein kinase OSR1 OS=Mus musculus GN=	2	3	8	3	2	0	2.6	0.2641	18
sp|Q920Q2|REV1_MOUSE - DNA repair protein REV1 OS=Mus musculus GN=Rev1 PE=1 SV=1	0	10	16	8	2	0	2.6	0.367	36
sp|Q9QY76|VAPB_MOUSE - Vesicle-associated membrane protein-associated protein B	0	13	0	0	0	5	2.6	0.5964	18
sp|Q8K301|DDX52_MOUSE - Probable ATP-dependent RNA helicase DDX52 OS=Mus musculu	0	13	10	0	0	9	2.5555	0.3986	32
sp|Q9Z1J3|NFS1_MOUSE - Cysteine desulfurase, mitochondrial OS=Mus musculus GN=Nf	3	2	0	0	2	0	2.5	0.4168	7
sp|Q9Z123|SEM4F_MOUSE - Semaphorin-4F OS=Mus musculus GN=Sema4f PE=2 SV=2	2	8	0	2	2	0	2.5	0.4676	14
sp|Q2PFD7|PSD3_MOUSE - PH and SEC7 domain-containing protein 3 OS=Mus musculus G	0	6	9	0	4	2	2.5	0.3573	21
sp|Q68FD5|CLH1_MOUSE - Clathrin heavy chain 1 OS=Mus musculus GN=Cltc PE=1 SV=3	0	5	0	0	2	0	2.5	0.6071	7
sp|A6H6A9|RBG1L_MOUSE - Rab GTPase-activating protein 1-like OS=Mus musculus GN=	0	5	0	0	2	0	2.5	0.6071	7
sp|P70206|PLXA1_MOUSE - Plexin-A1 OS=Mus musculus GN=Plxna1 PE=1 SV=1	0	5	0	0	2	0	2.5	0.6071	7
sp|P62702|RS4X_MOUSE - 40S ribosomal protein S4, X isoform OS=Mus musculus GN=Rp	0	10	0	0	4	0	2.5	0.6071	14
sp|Q9QZD8|DIC_MOUSE - Mitochondrial dicarboxylate carrier OS=Mus musculus GN=Slc	0	5	0	0	2	0	2.5	0.6071	7
sp|P14148|RL7_MOUSE - 60S ribosomal protein L7 OS=Mus musculus GN=Rpl7 PE=1 SV=2	0	5	0	0	2	0	2.5	0.6071	7
sp|Q9CY27|TECR_MOUSE - Very-long-chain enoyl-CoA reductase OS=Mus musculus GN=Te	0	10	0	0	4	0	2.5	0.6071	14
sp|Q91WC3|ACSL6_MOUSE - Long-chain-fatty-acid--CoA ligase 6 OS=Mus musculus GN=A	0	10	0	0	4	0	2.5	0.6071	14
sp|O54916|REPS1_MOUSE - RalBP1-associated Eps domain-containing protein 1 OS=Mus	0	5	0	0	2	0	2.5	0.6071	7
sp|Q9JLV5|CUL3_MOUSE - Cullin-3 OS=Mus musculus GN=Cul3 PE=1 SV=1	0	12	8	4	4	0	2.5	0.3486	28
sp|Q7TSJ6|LATS2_MOUSE - Serine/threonine-protein kinase LATS2 OS=Mus musculus GN	0	5	0	2	0	0	2.5	0.6071	7
sp|Q60841|RELN_MOUSE - Reelin OS=Mus musculus GN=Reln PE=1 SV=3	0	10	0	0	4	0	2.5	0.6071	14
sp|Q8BKV1|GPC2_MOUSE - Glypican-2 OS=Mus musculus GN=Gpc2 PE=2 SV=1	0	2	3	0	2	0	2.5	0.4168	7
sp|Q5NCP0|RNF43_MOUSE - E3 ubiquitin-protein ligase RNF43 OS=Mus musculus GN=Rnf	0	0	5	0	2	0	2.5	0.6071	7
sp|P59759|MKL2_MOUSE - MKL/myocardin-like protein 2 OS=Mus musculus GN=Mkl2 PE=1	3	31	33	6	0	21	2.4814	0.3116	94
sp|Q9DBG6|RPN2_MOUSE - Dolichyl-diphosphooligosaccharide--protein glycosyltransf	2	28	17	5	7	7	2.4736	0.2848	66
sp|Q62452|UD19_MOUSE - UDP-glucuronosyltransferase 1-9 OS=Mus musculus GN=Ugt1a9	26	208	35	27	50	32	2.4678	0.4216	378
sp|P83741|WNK1_MOUSE - Serine/threonine-protein kinase WNK1 OS=Mus musculus GN=W	0	22	0	0	9	0	2.4444	0.6135	31
sp|Q791T5|MTCH1_MOUSE - Mitochondrial carrier homolog 1 OS=Mus musculus GN=Mtch1	2	15	0	0	7	0	2.4285	0.5599	24
sp|Q64464|CP3AD_MOUSE - Cytochrome P450 3A13 OS=Mus musculus GN=Cyp3a13 PE=2 SV=	8	28	0	5	10	0	2.4	0.4714	51

sp|O88833|CP4AA_MOUSE - Cytochrome P450 4A10 OS=Mus musculus GN=Cyp4a10 PE=2 SV=	4	18	2	0	10	0	2.4	0.4826	34
sp|Q9Z0M5|LICH_MOUSE - Lysosomal acid lipase/cholesteryl ester hydrolase OS=Mus	0	27	9	0	7	8	2.4	0.4478	51
sp|Q6P1Y8|INP4B_MOUSE - Type II inositol 3,4-bisphosphate 4-phosphatase OS=Mus m	0	5	7	0	2	3	2.4	0.3603	17
sp|P97445|CAC1A_MOUSE - Voltage-dependent P/Q-type calcium channel subunit alpha	0	17	19	0	5	10	2.4	0.354	51
sp|Q5NC05|TTF2_MOUSE - Transcription termination factor 2 OS=Mus musculus GN=Ttf	0	12	0	3	2	0	2.4	0.5993	17
sp|Q8R0Y6|AL1L1_MOUSE - Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus	0	12	0	0	5	0	2.4	0.6188	17
sp|E9Q286|ICE1_MOUSE - Little elongation complex subunit 1 OS=Mus musculus GN=Ic	0	4	8	0	0	5	2.4	0.4586	17
sp|Q3UB74|TBRG1_MOUSE - Transforming growth factor beta regulator 1 OS=Mus muscu	0	0	12	0	0	5	2.4	0.6188	17
sp|Q5SS00|ZDBF2_MOUSE - DBF4-type zinc finger-containing protein 2 homolog OS=Mu	0	39	16	4	3	16	2.3913	0.4265	78
sp|O70475|UGDH_MOUSE - UDP-glucose 6-dehydrogenase OS=Mus musculus GN=Ugdh PE=1	0	15	11	0	11	0	2.3636	0.4367	37
sp|P10649|GSTM1_MOUSE - Glutathione S-transferase Mu 1 OS=Mus musculus GN=Gstm1	4	29	0	2	12	0	2.3571	0.5534	47
sp|P56655|CP238_MOUSE - Cytochrome P450 2C38 OS=Mus musculus GN=Cyp2c38 PE=2 SV=	6	31	10	0	13	7	2.35	0.3551	67
sp|A6H690|IQCAL_MOUSE - IQ and AAA domain-containing protein 1-like OS=Mus muscu	12	25	19	4	0	20	2.3333	0.2111	80
sp|Q3U0P1|PALB2_MOUSE - Partner and localizer of BRCA2 OS=Mus musculus GN=Palb2	3	20	47	3	7	20	2.3333	0.3886	100
sp|Q8K031|STAR8_MOUSE - StAR-related lipid transfer protein 8 OS=Mus musculus GN	5	2	0	0	3	0	2.3333	0.4917	10
sp|Q8CC88|VWA8_MOUSE - von Willebrand factor A domain-containing protein 8 OS=Mu	3	30	16	6	15	0	2.3333	0.355	70
sp|Q9D1Q6|ERP44_MOUSE - Endoplasmic reticulum resident protein 44 OS=Mus musculu	2	5	0	0	3	0	2.3333	0.4917	10
sp|Q9DBD0|ICA_MOUSE - Inhibitor of carbonic anhydrase OS=Mus musculus GN=Ica PE=	0	2	5	0	3	0	2.3333	0.4917	10
sp|Q8BSI6|R3HC1_MOUSE - R3H and coiled-coil domain-containing protein 1 OS=Mus m	0	7	0	0	3	0	2.3333	0.6272	10
sp|P59999|ARPC4_MOUSE - Actin-related protein 2/3 complex subunit 4 OS=Mus muscu	0	7	0	0	3	0	2.3333	0.6272	10
sp|Q8BP40|PPA6_MOUSE - Lysophosphatidic acid phosphatase type 6 OS=Mus musculus	2	13	8	2	8	0	2.3	0.3381	33
sp|P00405|COX2_MOUSE - Cytochrome c oxidase subunit 2 OS=Mus musculus GN=Mtco2 P	3	15	5	0	8	2	2.3	0.3826	33
sp|Q9D1H6|NDUF4_MOUSE - NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assem	0	16	16	0	2	12	2.2857	0.408	46
sp|Q6P5E4|UGGG1_MOUSE - UDP-glucose:glycoprotein glucosyltransferase 1 OS=Mus mu	0	11	23	0	4	11	2.2666	0.4391	49
sp|G5E8K5|ANK3_MOUSE - Ankyrin-3 OS=Mus musculus GN=Ank3 PE=1 SV=1	0	21	13	4	2	9	2.2666	0.3826	49
sp|Q8CGY6|UN45B_MOUSE - Protein unc-45 homolog B OS=Mus musculus GN=Unc45b PE=1	5	4	0	2	2	0	2.25	0.3739	13
sp|Q61048|WBP4_MOUSE - WW domain-binding protein 4 OS=Mus musculus GN=Wbp4 PE=1	0	9	0	2	2	0	2.25	0.6164	13
sp|P61164|ACTZ_MOUSE - Alpha-centractin OS=Mus musculus GN=Actr1a PE=2 SV=1	0	9	0	0	4	0	2.25	0.6384	13
sp|Q9WU56|TRUA_MOUSE - tRNA pseudouridine synthase A, mitochondrial OS=Mus muscu	0	9	0	0	4	0	2.25	0.6384	13
sp|Q791V5|MTCH2_MOUSE - Mitochondrial carrier homolog 2 OS=Mus musculus GN=Mtch2	7	22	0	4	9	0	2.2307	0.4881	42
sp|Q8R555|CRAC1_MOUSE - Cartilage acidic protein 1 OS=Mus musculus GN=Crtac1 PE=	3	18	10	2	12	0	2.2142	0.3768	45
sp|P70275|SEM3E_MOUSE - Semaphorin-3E OS=Mus musculus GN=Sema3e PE=1 SV=3	2	21	21	4	3	13	2.2	0.322	64
sp|Q6IMF0|KRT83_MOUSE - Keratin, type II cuticular Hb3 OS=Mus musculus GN=Krt83	0	11	0	0	5	0	2.2	0.6455	16
sp|Q8BND4|DX26B_MOUSE - Protein DDX26B OS=Mus musculus GN=Ddx26b PE=2 SV=1	0	11	0	0	5	0	2.2	0.6455	16
sp|Q99ME9|NOG1_MOUSE - Nucleolar GTP-binding protein 1 OS=Mus musculus GN=Gtpbp4	0	0	22	0	0	10	2.2	0.6455	32
sp|Q8BGH2|SAM50_MOUSE - Sorting and assembly machinery component 50 homolog OS=M	0	24	0	0	11	0	2.1818	0.6482	35
sp|Q9D2H6|SP2_MOUSE - Transcription factor Sp2 OS=Mus musculus GN=Sp2 PE=2 SV=2	2	11	0	4	2	0	2.1666	0.5495	19
sp|Q3V1M1|IGS10_MOUSE - Immunoglobulin superfamily member 10 OS=Mus musculus GN=	0	28	0	6	7	0	2.1538	0.6295	41
sp|Q91ZQ5|RPE65_MOUSE - Retinoid isomerohydrolase OS=Mus musculus GN=Rpe65 PE=1	4	26	0	2	12	0	2.1428	0.581	44
sp|P83503|NYX_MOUSE - Nyctalopin OS=Mus musculus GN=Nyx PE=2 SV=1	0	15	0	0	7	0	2.1428	0.6541	22
sp|Q01237|HMDH_MOUSE - 3-hydroxy-3-methylglutaryl-coenzyme A reductase OS=Mus mu	2	13	2	0	8	0	2.125	0.5443	25

sp|Q8K0D5|EFGM_MOUSE - Elongation factor G, mitochondrial OS=Mus musculus GN=Gfm	0	21	0	0	10	0	2.1	0.6609	31
sp|A4Q9F0|TTLL7_MOUSE - Tubulin polyglutamylase TTLL7 OS=Mus musculus GN=Ttll7 P	0	21	0	4	6	0	2.1	0.6382	31
sp|P07309|TTHY_MOUSE - Transthyretin OS=Mus musculus GN=Ttr PE=1 SV=1	4	19	4	2	9	2	2.0769	0.4453	40
sp|Q91X77|CY250_MOUSE - Cytochrome P450 2C50 OS=Mus musculus GN=Cyp2c50 PE=1 SV=	2	56	3	0	30	0	2.0333	0.6398	91
sp|P50608|FMOD_MOUSE - Fibromodulin OS=Mus musculus GN=Fmod PE=2 SV=1	3	9	0	3	3	0	2	0.5185	18
sp|Q4U2R1|HERC2_MOUSE - E3 ubiquitin-protein ligase HERC2 OS=Mus musculus GN=Her	3	9	0	0	6	0	2	0.579	18
sp|O88696|CLPP_MOUSE - ATP-dependent Clp protease proteolytic subunit, mitochond	2	4	0	0	3	0	2	0.5484	9
sp|Q9CYN2|SPCS2_MOUSE - Signal peptidase complex subunit 2 OS=Mus musculus GN=Sp	4	0	0	0	2	0	2	0.6778	6
sp|Q99LD4|CSN1_MOUSE - COP9 signalosome complex subunit 1 OS=Mus musculus GN=Gps	2	16	0	0	9	0	2	0.6356	27
sp|Q99PT9|KIF19_MOUSE - Kinesin-like protein KIF19 OS=Mus musculus GN=Kif19 PE=1	0	14	0	0	7	0	2	0.6778	21
sp|Q8BI29|SARG_MOUSE - Specifically androgen-regulated gene protein OS=Mus muscu	0	19	33	0	5	21	2	0.4919	78
sp|P35294|RAB19_MOUSE - Ras-related protein Rab-19 OS=Mus musculus GN=Rab19 PE=2	0	4	0	0	2	0	2	0.6778	6
sp|Q9D404|OXSM_MOUSE - 3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial	0	4	0	0	2	0	2	0.6778	6
sp|P00186|CP1A2_MOUSE - Cytochrome P450 1A2 OS=Mus musculus GN=Cyp1a2 PE=1 SV=1	0	4	0	0	2	0	2	0.6778	6
sp|Q62384|ZPR1_MOUSE - Zinc finger protein ZPR1 OS=Mus musculus GN=Zpr1 PE=1 SV=	0	6	0	0	3	0	2	0.6778	9
sp|P18572|BASI_MOUSE - Basigin OS=Mus musculus GN=Bsg PE=1 SV=2	0	8	8	0	3	5	2	0.4294	24
sp|Q80YP0|CDK3_MOUSE - Cyclin-dependent kinase 3 OS=Mus musculus GN=Cdk3 PE=1 SV	0	4	0	0	2	0	2	0.6778	6
sp|Q9NYQ2|HAOX2_MOUSE - Hydroxyacid oxidase 2 OS=Mus musculus GN=Hao2 PE=2 SV=1	0	4	0	0	2	0	2	0.6778	6
sp|Q8VDD5|MYH9_MOUSE - Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4	0	6	0	0	3	0	2	0.6778	9
sp|Q9R0C8|VAV3_MOUSE - Guanine nucleotide exchange factor VAV3 OS=Mus musculus G	0	8	0	0	4	0	2	0.6778	12
sp|Q04519|ASM_MOUSE - Sphingomyelin phosphodiesterase OS=Mus musculus GN=Smpd1 P	0	4	0	2	0	0	2	0.6778	6
sp|A2AWL7|MGAP_MOUSE - MAX gene-associated protein OS=Mus musculus GN=Mga PE=2 S	0	18	0	3	6	0	2	0.656	27
sp|Q80XB4|NRAP_MOUSE - Nebulin-related-anchoring protein OS=Mus musculus GN=Nrap	0	22	0	0	11	0	2	0.6778	33
sp|Q5SX79|SHRM1_MOUSE - Protein Shroom1 OS=Mus musculus GN=Shroom1 PE=1 SV=2	0	10	0	0	5	0	2	0.6778	15
sp|Q80UG2|PLXA4_MOUSE - Plexin-A4 OS=Mus musculus GN=Plxna4 PE=1 SV=3	0	4	0	0	2	0	2	0.6778	6
sp|P16015|CAH3_MOUSE - Carbonic anhydrase 3 OS=Mus musculus GN=Ca3 PE=1 SV=3	0	4	0	0	2	0	2	0.6778	6
sp|O88587|COMT_MOUSE - Catechol O-methyltransferase OS=Mus musculus GN=Comt PE=1	0	8	6	0	7	0	2	0.5244	21
sp|P06330|HVM51_MOUSE - Ig heavy chain V region AC38 205.12 OS=Mus musculus PE=1	0	4	0	0	2	0	2	0.6778	6
sp|Q9Z0J0|NPC2_MOUSE - Epididymal secretory protein E1 OS=Mus musculus GN=Npc2 P	0	16	8	0	12	0	2	0.5484	36
sp|Q8VDG7|PAFA2_MOUSE - Platelet-activating factor acetylhydrolase 2, cytoplasmi	0	6	0	0	3	0	2	0.6778	9
sp|P97351|RS3A_MOUSE - 40S ribosomal protein S3a OS=Mus musculus GN=Rps3a PE=1 S	0	6	0	0	3	0	2	0.6778	9
sp|Q9D8S4|ORN_MOUSE - Oligoribonuclease, mitochondrial OS=Mus musculus GN=Rexo2	0	4	0	0	2	0	2	0.6778	6
sp|P00342|LDHC_MOUSE - L-lactate dehydrogenase C chain OS=Mus musculus GN=Ldhc P	0	8	0	2	2	0	2	0.653	12
sp|Q9CXW2|RT22_MOUSE - 28S ribosomal protein S22, mitochondrial OS=Mus musculus	0	3	7	2	3	0	2	0.4929	15
sp|Q05117|PPA5_MOUSE - Tartrate-resistant acid phosphatase type 5 OS=Mus musculu	0	6	0	0	3	0	2	0.6778	9
sp|Q921S7|RM37_MOUSE - 39S ribosomal protein L37, mitochondrial OS=Mus musculus	0	12	22	0	3	14	2	0.5	51
sp|A4Q9F4|TTL11_MOUSE - Tubulin polyglutamylase TTLL11 OS=Mus musculus GN=Ttll11	0	4	0	2	0	0	2	0.6778	6
sp|Q6AW69|CGNL1_MOUSE - Cingulin-like protein 1 OS=Mus musculus GN=Cgnl1 PE=1 SV	0	3	7	0	0	5	2	0.5599	15
sp|Q3UIL6|PKHA7_MOUSE - Pleckstrin homology domain-containing family A member 7	0	4	0	0	2	0	2	0.6778	6
sp|G3X982|AOXC_MOUSE - Aldehyde oxidase 3 OS=Mus musculus GN=Aox3 PE=1 SV=1	0	12	0	4	2	0	2	0.656	18
sp|Q9DCJ5|NDUA8_MOUSE - NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subun	0	8	0	0	4	0	2	0.6778	12

sp|Q9CQF0|RM11_MOUSE - 39S ribosomal protein L11, mitochondrial OS=Mus musculus	0	6	0	0	3	0	2	0.6778	9
sp|Q9Z185|PADI1_MOUSE - Protein-arginine deiminase type-1 OS=Mus musculus GN=Pad	0	20	0	10	0	0	2	0.6778	30
sp|Q80ZX8|SPAG1_MOUSE - Sperm-associated antigen 1 OS=Mus musculus GN=Spag1 PE=2	0	3	17	0	10	0	2	0.6198	30
sp|P49945|FRIL2_MOUSE - Ferritin light chain 2 OS=Mus musculus GN=Ftl2 PE=3 SV=2	0	6	0	0	3	0	2	0.6778	9
sp|Q9DC70|NDUS7_MOUSE - NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, m	0	4	0	0	2	0	2	0.6778	6
sp|P63011|RAB3A_MOUSE - Ras-related protein Rab-3A OS=Mus musculus GN=Rab3a PE=1	0	4	0	0	2	0	2	0.6778	6
sp|Q8BSQ9|PB1_MOUSE - Protein polybromo-1 OS=Mus musculus GN=Pbrm1 PE=1 SV=4	0	4	0	0	0	2	2	0.6778	6
sp|P82343|RENBP_MOUSE - N-acylglucosamine 2-epimerase OS=Mus musculus GN=Renbp P	0	0	6	0	3	0	2	0.6778	9
sp|Q6V3W6|DRC7_MOUSE - Dynein regulatory complex subunit 7 OS=Mus musculus GN=Dr	20	31	76	12	0	53	1.9538	0.4283	192
sp|Q9JII6|AK1A1_MOUSE - Alcohol dehydrogenase [NADP(+)] OS=Mus musculus GN=Akr1a	11	26	0	7	12	0	1.9473	0.5097	56
sp|Q9R092|H17B6_MOUSE - 17-beta-hydroxysteroid dehydrogenase type 6 OS=Mus muscu	3	29	5	5	14	0	1.9473	0.5541	56
sp|Q09M05|CBPC4_MOUSE - Cytosolic carboxypeptidase 4 OS=Mus musculus GN=Agbl1 PE	0	5	28	8	9	0	1.9411	0.5885	50
sp|O35488|S27A2_MOUSE - Very long-chain acyl-CoA synthetase OS=Mus musculus GN=S	10	54	23	13	26	6	1.9333	0.3831	132
sp|Q6ZPF3|TIAM2_MOUSE - T-lymphoma invasion and metastasis-inducing protein 2 OS	0	25	0	0	13	0	1.923	0.6921	38
sp|Q03172|ZEP1_MOUSE - Zinc finger protein 40 OS=Mus musculus GN=Hivep1 PE=1 SV=	0	13	10	0	12	0	1.9166	0.5488	35
sp|P70403|CASP_MOUSE - Protein CASP OS=Mus musculus GN=Cux1 PE=2 SV=2	4	14	26	3	11	9	1.913	0.3613	67
sp|Q8K4E0|ALMS1_MOUSE - Alstrom syndrome protein 1 homolog OS=Mus musculus GN=Al	0	11	8	0	5	5	1.9	0.4609	29
sp|Q91YT0|NDUV1_MOUSE - NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochon	8	40	5	5	21	2	1.8928	0.5462	81
sp|Q8CG70|P3H3_MOUSE - Prolyl 3-hydroxylase 3 OS=Mus musculus GN=Leprel2 PE=2 SV	0	0	17	0	0	9	1.8888	0.6988	26
sp|Q8C753|K0556_MOUSE - Uncharacterized protein KIAA0556 OS=Mus musculus GN=Kiaa	0	0	17	0	9	0	1.8888	0.6988	26
sp|Q9CQY1|ATG12_MOUSE - Ubiquitin-like protein ATG12 OS=Mus musculus GN=Atg12 PE	5	27	0	17	0	0	1.8823	0.6447	49
sp|P62983|RS27A_MOUSE - Ubiquitin-40S ribosomal protein S27a OS=Mus musculus GN=	0	15	0	0	8	0	1.875	0.7016	23
sp|Q9Z2I8|SUCB2_MOUSE - Succinyl-CoA ligase [GDP-forming] subunit beta, mitochon	0	36	50	6	24	16	1.8695	0.4456	132
sp|Q8CAQ8|MIC60_MOUSE - MICOS complex subunit Mic60 OS=Mus musculus GN=Immt PE=1	21	50	33	3	32	21	1.8571	0.2508	160
sp|Q9WVL0|MAAI_MOUSE - Maleylacetoacetate isomerase OS=Mus musculus GN=Gstz1 PE=	2	11	0	0	5	2	1.8571	0.6158	20
sp|Q6NV83|SR140_MOUSE - U2 snRNP-associated SURP motif-containing protein OS=Mus	3	6	4	5	2	0	1.8571	0.3045	20
sp|Q61897|KT33B_MOUSE - Keratin, type I cuticular Ha3-II OS=Mus musculus GN=Krt3	0	25	14	0	9	12	1.8571	0.4991	60
sp|P05063|ALDOC_MOUSE - Fructose-bisphosphate aldolase C OS=Mus musculus GN=Aldo	0	10	3	7	0	0	1.8571	0.6239	20
sp|P54729|NUB1_MOUSE - NEDD8 ultimate buster 1 OS=Mus musculus GN=Nub1 PE=1 SV=2	0	9	15	4	2	7	1.8461	0.4695	37
sp|P12265|BGLR_MOUSE - Beta-glucuronidase OS=Mus musculus GN=Gusb PE=2 SV=2	13	33	11	11	20	0	1.8387	0.3947	88
sp|Q7TMR0|PCP_MOUSE - Lysosomal Pro-X carboxypeptidase OS=Mus musculus GN=Prcp P	0	11	0	0	6	0	1.8333	0.7102	17
sp|Q60932|VDAC1_MOUSE - Voltage-dependent anion-selective channel protein 1 OS=M	20	112	75	16	35	62	1.8318	0.3534	320
sp|Q3TUF7|YETS2_MOUSE - YEATS domain-containing protein 2 OS=Mus musculus GN=Yea	10	22	50	13	9	23	1.8222	0.3817	127
sp|Q9Z175|LOXL3_MOUSE - Lysyl oxidase homolog 3 OS=Mus musculus GN=Loxl3 PE=2 SV	0	0	20	0	0	11	1.8181	0.7134	31
sp|Q9DBG1|CP27A_MOUSE - Sterol 26-hydroxylase, mitochondrial OS=Mus musculus GN=	2	27	0	3	13	0	1.8125	0.673	45
sp|Q61838|A2M_MOUSE - Alpha-2-macroglobulin OS=Mus musculus GN=A2m PE=1 SV=3	8	34	3	3	22	0	1.8	0.6029	70
sp|P14206|RSSA_MOUSE - 40S ribosomal protein SA OS=Mus musculus GN=Rpsa PE=1 SV=	5	4	0	2	3	0	1.8	0.4917	14
sp|Q6PHN9|RAB35_MOUSE - Ras-related protein Rab-35 OS=Mus musculus GN=Rab35 PE=1	2	7	0	0	5	0	1.8	0.6433	14
sp|P47199|QOR_MOUSE - Quinone oxidoreductase OS=Mus musculus GN=Cryz PE=1 SV=1	3	6	0	2	3	0	1.8	0.5304	14
sp|P27659|RL3_MOUSE - 60S ribosomal protein L3 OS=Mus musculus GN=Rpl3 PE=1 SV=3	3	6	0	3	2	0	1.8	0.5304	14
sp|P11714|CP2D9_MOUSE - Cytochrome P450 2D9 OS=Mus musculus GN=Cyp2d9 PE=2 SV=2	0	7	2	0	3	2	1.8	0.587	14

sp|Q8VCA5|TMPS4_MOUSE - Transmembrane protease serine 4 OS=Mus musculus GN=Tmprs	0	9	0	0	5	0	1.8	0.7174	14
sp|P46978|STT3A_MOUSE - Dolichyl-diphosphooligosaccharide--protein glycosyltrans	0	22	5	0	15	0	1.8	0.656	42
sp|O55047|TLK2_MOUSE - Serine/threonine-protein kinase tousled-like 2 OS=Mus mus	0	9	0	0	5	0	1.8	0.7174	14
sp|Q9DCM2|GSTK1_MOUSE - Glutathione S-transferase kappa 1 OS=Mus musculus GN=Gst	18	106	71	13	47	49	1.7889	0.3656	304
sp|Q3URY6|ARMC2_MOUSE - Armadillo repeat-containing protein 2 OS=Mus musculus GN	0	16	0	4	5	0	1.7777	0.6956	25
sp|P20108|PRDX3_MOUSE - Thioredoxin-dependent peroxide reductase, mitochondrial	12	46	34	9	20	23	1.7692	0.2855	144
sp|Q9JJG0|TACC2_MOUSE - Transforming acidic coiled-coil-containing protein 2 OS=	0	12	34	4	2	20	1.7692	0.5922	72
sp|Q91YW3|DNJC3_MOUSE - DnaJ homolog subfamily C member 3 OS=Mus musculus GN=Dna	0	23	0	5	8	0	1.7692	0.6988	36
sp|P14152|MDHC_MOUSE - Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Mdh1	0	24	6	3	7	7	1.7647	0.5863	47
sp|Q9R0H5|K2C71_MOUSE - Keratin, type II cytoskeletal 71 OS=Mus musculus GN=Krt7	0	48	24	0	26	15	1.756	0.5481	113
sp|C8YR32|LOXH1_MOUSE - Lipoxygenase homology domain-containing protein 1 OS=Mus	6	3	5	0	6	2	1.75	0.3678	22
sp|Q9EQI8|RM46_MOUSE - 39S ribosomal protein L46, mitochondrial OS=Mus musculus	2	5	0	0	4	0	1.75	0.6387	11
sp|Q8CCX5|KT222_MOUSE - Keratin-like protein KRT222 OS=Mus musculus GN=Krt222 PE	0	7	0	0	4	0	1.75	0.7287	11
sp|Q03142|FGFR4_MOUSE - Fibroblast growth factor receptor 4 OS=Mus musculus GN=F	0	21	14	0	8	12	1.75	0.5207	55
sp|Q61316|HSP74_MOUSE - Heat shock 70 kDa protein 4 OS=Mus musculus GN=Hspa4 PE=	0	18	24	5	3	16	1.75	0.5081	66
sp|Q8JZZ0|UD3A2_MOUSE - UDP-glucuronosyltransferase 3A2 OS=Mus musculus GN=Ugt3a	0	7	0	0	4	0	1.75	0.7287	11
sp|Q3ULF4|SPG7_MOUSE - Paraplegin OS=Mus musculus GN=Spg7 PE=1 SV=1	0	7	0	0	4	0	1.75	0.7287	11
sp|Q8C7R7|RFX6_MOUSE - DNA-binding protein RFX6 OS=Mus musculus GN=Rfx6 PE=1 SV=	0	7	0	0	4	0	1.75	0.7287	11
sp|Q3UY96|CFA74_MOUSE - Cilia- and flagella-associated protein 74 OS=Mus musculu	0	26	49	0	13	30	1.7441	0.5556	118
sp|Q8JZR0|ACSL5_MOUSE - Long-chain-fatty-acid--CoA ligase 5 OS=Mus musculus GN=A	22	45	6	11	31	0	1.738	0.5156	115
sp|Q9DCN1|NUD12_MOUSE - Peroxisomal NADH pyrophosphatase NUDT12 OS=Mus musculus	4	22	0	5	10	0	1.7333	0.6443	41
sp|Q3V132|ADT4_MOUSE - ADP/ATP translocase 4 OS=Mus musculus GN=Slc25a31 PE=2 SV	2	19	5	4	11	0	1.7333	0.5829	41
sp|Q8VHN7|GPR98_MOUSE - G-protein coupled receptor 98 OS=Mus musculus GN=Gpr98 P	0	26	0	10	5	0	1.7333	0.7086	41
sp|Q99ME3|SNCAP_MOUSE - Synphilin-1 OS=Mus musculus GN=Sncaip PE=2 SV=2	6	9	4	5	6	0	1.7272	0.3211	30
sp|Q3UJU9|RMD3_MOUSE - Regulator of microtubule dynamics protein 3 OS=Mus muscul	0	16	3	4	5	2	1.7272	0.6213	30
sp|P11679|K2C8_MOUSE - Keratin, type II cytoskeletal 8 OS=Mus musculus GN=Krt8 P	0	66	41	0	62	0	1.7258	0.6233	169
sp|Q9Z320|K1C27_MOUSE - Keratin, type I cytoskeletal 27 OS=Mus musculus GN=Krt27	0	30	20	0	14	15	1.7241	0.5248	79
sp|P16460|ASSY_MOUSE - Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=1 S	12	52	48	9	39	17	1.723	0.371	177
sp|Q62261|SPTB2_MOUSE - Spectrin beta chain, non-erythrocytic 1 OS=Mus musculus	0	14	17	15	0	3	1.7222	0.5673	49
sp|Q6NXH9|K2C73_MOUSE - Keratin, type II cytoskeletal 73 OS=Mus musculus GN=Krt7	0	51	28	2	28	16	1.7173	0.5426	125
sp|Q9WVM8|AADAT_MOUSE - Kynurenine/alpha-aminoadipate aminotransferase, mitochon	13	47	0	11	15	9	1.7142	0.5868	95
sp|Q99M73|KRT84_MOUSE - Keratin, type II cuticular Hb4 OS=Mus musculus GN=Krt84	0	32	16	0	28	0	1.7142	0.6384	76
sp|E9Q612|PTPRO_MOUSE - Receptor-type tyrosine-protein phosphatase O OS=Mus musc	0	6	18	3	2	9	1.7142	0.5916	38
sp|Q64727|VINC_MOUSE - Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4	0	19	5	7	3	4	1.7142	0.5969	38
sp|A2ALU4|SHRM2_MOUSE - Protein Shroom2 OS=Mus musculus GN=Shroom2 PE=1 SV=1	0	5	7	4	0	3	1.7142	0.5262	19
sp|A2AUC9|KLH41_MOUSE - Kelch-like protein 41 OS=Mus musculus GN=Klhl41 PE=1 SV=	5	12	0	3	7	0	1.7	0.5934	27
sp|Q3U3R4|LMF1_MOUSE - Lipase maturation factor 1 OS=Mus musculus GN=Lmf1 PE=1 S	0	17	0	3	7	0	1.7	0.7179	27
sp|P85094|ISC2A_MOUSE - Isochorismatase domain-containing protein 2A, mitochondr	4	13	22	2	7	14	1.6956	0.4418	62
sp|Q64133|AOFA_MOUSE - Amine oxidase [flavin-containing] A OS=Mus musculus GN=Ma	20	39	41	25	17	17	1.6949	0.1306	159
sp|P11352|GPX1_MOUSE - Glutathione peroxidase 1 OS=Mus musculus GN=Gpx1 PE=1 SV=	9	82	22	9	30	28	1.6865	0.5489	180
sp|Q8C165|P20D1_MOUSE - Probable carboxypeptidase PM20D1 OS=Mus musculus GN=Pm20	4	28	0	0	19	0	1.6842	0.7086	51

sp|P60710|ACTB_MOUSE - Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1	3	40	4	0	28	0	1.6785	0.7008	75
sp|Q99K28|ARFG2_MOUSE - ADP-ribosylation factor GTPase-activating protein 2 OS=M	5	0	0	3	0	0	1.6666	0.7488	8
sp|Q6P3A8|ODBB_MOUSE - 2-oxoisovalerate dehydrogenase subunit beta, mitochondria	5	24	21	9	14	7	1.6666	0.3465	80
sp|Q8BW70|UBP38_MOUSE - Ubiquitin carboxyl-terminal hydrolase 38 OS=Mus musculus	2	3	0	0	3	0	1.6666	0.6433	8
sp|P50136|ODBA_MOUSE - 2-oxoisovalerate dehydrogenase subunit alpha, mitochondri	11	29	0	3	21	0	1.6666	0.6442	64
sp|Q99LX0|PARK7_MOUSE - Protein deglycase DJ-1 OS=Mus musculus GN=Park7 PE=1 SV=	2	3	0	0	3	0	1.6666	0.6433	8
sp|Q80TV8|CLAP1_MOUSE - CLIP-associating protein 1 OS=Mus musculus GN=Clasp1 PE=	2	3	0	0	3	0	1.6666	0.6433	8
sp|Q9JHD2|KAT2A_MOUSE - Histone acetyltransferase KAT2A OS=Mus musculus GN=Kat2a	0	10	0	0	0	6	1.6666	0.7488	16
sp|Q14DH7|ACSS3_MOUSE - Acyl-CoA synthetase short-chain family member 3, mitocho	0	30	0	0	15	3	1.6666	0.7345	48
sp|Q9WTP5|CAD22_MOUSE - Cadherin-22 OS=Mus musculus GN=Cdh22 PE=2 SV=2	0	5	0	3	0	0	1.6666	0.7488	8
sp|Q6ZQK0|CNDD3_MOUSE - Condensin-2 complex subunit D3 OS=Mus musculus GN=Ncapd3	0	0	15	0	0	9	1.6666	0.7488	24
sp|Q9JHW2|NIT2_MOUSE - Omega-amidase NIT2 OS=Mus musculus GN=Nit2 PE=1 SV=1	0	10	0	0	6	0	1.6666	0.7488	16
sp|Q8R307|VPS18_MOUSE - Vacuolar protein sorting-associated protein 18 homolog O	0	5	0	0	3	0	1.6666	0.7488	8
sp|Q9D1T0|LIGO1_MOUSE - Leucine-rich repeat and immunoglobulin-like domain-conta	0	5	0	0	3	0	1.6666	0.7488	8
sp|Q99N48|SYTL3_MOUSE - Synaptotagmin-like protein 3 OS=Mus musculus GN=Sytl3 PE	0	5	0	3	0	0	1.6666	0.7488	8
sp|Q8BMF5|GRIK4_MOUSE - Glutamate receptor ionotropic, kainate 4 OS=Mus musculus	0	5	0	0	3	0	1.6666	0.7488	8
sp|P86048|RL10L_MOUSE - 60S ribosomal protein L10-like OS=Mus musculus GN=Rpl10l	0	5	0	0	3	0	1.6666	0.7488	8
sp|B7ZCC9|GP112_MOUSE - Probable G-protein coupled receptor 112 OS=Mus musculus	0	5	0	3	0	0	1.6666	0.7488	8
sp|O35600|ABCA4_MOUSE - Retinal-specific ATP-binding cassette transporter OS=Mus	0	5	0	0	3	0	1.6666	0.7488	8
sp|Q5SUC9|SCO1_MOUSE - Protein SCO1 homolog, mitochondrial OS=Mus musculus GN=Sc	0	2	3	0	3	0	1.6666	0.6433	8
sp|Q5SVR0|TBC9B_MOUSE - TBC1 domain family member 9B OS=Mus musculus GN=Tbc1d9b	0	0	15	3	6	0	1.6666	0.7246	24
sp|O88879|APAF_MOUSE - Apoptotic protease-activating factor 1 OS=Mus musculus GN	0	0	5	0	0	3	1.6666	0.7488	8
sp|P55096|ABCD3_MOUSE - ATP-binding cassette sub-family D member 3 OS=Mus muscul	19	39	0	12	23	0	1.6571	0.589	93
sp|P50172|DHI1_MOUSE - Corticosteroid 11-beta-dehydrogenase isozyme 1 OS=Mus mus	16	51	4	6	32	5	1.6511	0.6048	114
sp|Q6A058|ARMX2_MOUSE - Armadillo repeat-containing X-linked protein 2 OS=Mus mu	0	17	11	0	0	17	1.647	0.6523	45
sp|Q80TG1|KANL1_MOUSE - KAT8 regulatory NSL complex subunit 1 OS=Mus musculus GN	0	15	26	0	8	17	1.64	0.585	66
sp|P29341|PABP1_MOUSE - Polyadenylate-binding protein 1 OS=Mus musculus GN=Pabpc	5	31	0	8	14	0	1.6363	0.6777	58
sp|Q9D0D5|T2EA_MOUSE - General transcription factor IIE subunit 1 OS=Mus musculu	0	12	6	4	2	5	1.6363	0.5495	29
sp|Q91W43|GCSP_MOUSE - Glycine dehydrogenase (decarboxylating), mitochondrial OS	3	46	0	6	24	0	1.6333	0.7208	79
sp|Q91WD5|NDUS2_MOUSE - NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, m	8	36	0	10	17	0	1.6296	0.6607	71
sp|Q9ET01|PYGL_MOUSE - Glycogen phosphorylase, liver form OS=Mus musculus GN=Pyg	9	76	29	15	51	4	1.6285	0.5803	184
sp|Q8CI95|OSB11_MOUSE - Oxysterol-binding protein-related protein 11 OS=Mus musc	0	13	0	0	0	8	1.625	0.7596	21
sp|Q9EPE9|AT131_MOUSE - Manganese-transporting ATPase 13A1 OS=Mus musculus GN=At	0	13	0	3	5	0	1.625	0.7338	21
sp|Q62168|K1H2_MOUSE - Keratin, type I cuticular Ha2 OS=Mus musculus GN=Krt32 PE	3	17	14	3	18	0	1.619	0.5698	55
sp|Q921C3|BRWD1_MOUSE - Bromodomain and WD repeat-containing protein 1 OS=Mus mu	0	15	6	0	6	7	1.6153	0.6135	34
sp|Q64521|GPDM_MOUSE - Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Mus	15	52	10	13	32	3	1.6041	0.5723	125
sp|Q05421|CP2E1_MOUSE - Cytochrome P450 2E1 OS=Mus musculus GN=Cyp2e1 PE=2 SV=1	16	131	31	31	58	22	1.6036	0.5852	289
sp|P23589|CAH5A_MOUSE - Carbonic anhydrase 5A, mitochondrial OS=Mus musculus GN=	9	21	10	6	19	0	1.6	0.5028	65
sp|Q9Z0L8|GGH_MOUSE - Gamma-glutamyl hydrolase OS=Mus musculus GN=Ggh PE=1 SV=2	2	6	0	0	5	0	1.6	0.7014	13
sp|P58252|EF2_MOUSE - Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2	4	38	22	16	17	7	1.6	0.4816	104
sp|P13011|ACOD2_MOUSE - Acyl-CoA desaturase 2 OS=Mus musculus GN=Scd2 PE=2 SV=2	0	8	0	0	5	0	1.6	0.7664	13

sp|Q9EQ06|DHB11_MOUSE - Estradiol 17-beta-dehydrogenase 11 OS=Mus musculus GN=Hs	0	8	0	0	5	0	1.6	0.7664	13
sp|Q9Z0K8|VNN1_MOUSE - Pantetheinase OS=Mus musculus GN=Vnn1 PE=1 SV=3	0	8	0	0	5	0	1.6	0.7664	13
sp|Q9WUZ9|ENTP5_MOUSE - Ectonucleoside triphosphate diphosphohydrolase 5 OS=Mus	0	9	7	2	8	0	1.6	0.6115	26
sp|Q5IR70|CAGE1_MOUSE - Cancer-associated gene 1 protein homolog OS=Mus musculus	0	8	0	0	5	0	1.6	0.7664	13
sp|Q70IV5|SYNEM_MOUSE - Synemin OS=Mus musculus GN=Synm PE=1 SV=2	0	5	3	0	2	3	1.6	0.5879	13
sp|Q8BHN1|TXLNG_MOUSE - Gamma-taxilin OS=Mus musculus GN=Txlng PE=1 SV=1	0	0	8	0	5	0	1.6	0.7664	13
sp|P11499|HS90B_MOUSE - Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90a	5	25	13	7	17	3	1.5925	0.4971	70
sp|Q9D379|HYEP_MOUSE - Epoxide hydrolase 1 OS=Mus musculus GN=Ephx1 PE=1 SV=2	4	71	12	12	39	4	1.5818	0.6751	142
sp|P17717|UDB17_MOUSE - UDP-glucuronosyltransferase 2B17 OS=Mus musculus GN=Ugt2	32	152	23	43	62	26	1.5801	0.5862	338
sp|Q99MN9|PCCB_MOUSE - Propionyl-CoA carboxylase beta chain, mitochondrial OS=Mu	22	95	25	27	41	22	1.5777	0.5186	232
sp|O70348|DXO_MOUSE - Decapping and exoribonuclease protein OS=Mus musculus GN=D	0	11	0	0	7	0	1.5714	0.7743	18
sp|P58022|LOXL2_MOUSE - Lysyl oxidase homolog 2 OS=Mus musculus GN=Loxl2 PE=1 SV	0	7	15	0	4	10	1.5714	0.6362	36
sp|Q8C9B9|DIDO1_MOUSE - Death-inducer obliterator 1 OS=Mus musculus GN=Dido1 PE=	0	45	2	20	10	0	1.5666	0.7375	77
sp|P52431|DPOD1_MOUSE - DNA polymerase delta catalytic subunit OS=Mus musculus G	3	0	47	2	2	28	1.5625	0.7488	82
sp|E2JF22|PIEZ1_MOUSE - Piezo-type mechanosensitive ion channel component 1 OS=M	0	25	50	2	6	40	1.5625	0.6572	123
sp|Q64433|CH10_MOUSE - 10 kDa heat shock protein, mitochondrial OS=Mus musculus	10	54	20	5	31	18	1.5555	0.5487	138
sp|Q9EQH2|ERAP1_MOUSE - Endoplasmic reticulum aminopeptidase 1 OS=Mus musculus G	0	14	0	0	9	0	1.5555	0.7788	23
sp|Q8CFX1|G6PE_MOUSE - GDH/6PGL endoplasmic bifunctional protein OS=Mus musculus	2	29	0	0	20	0	1.55	0.7655	51
sp|Q9CXT8|MPPB_MOUSE - Mitochondrial-processing peptidase subunit beta OS=Mus mu	7	22	19	5	10	16	1.5483	0.3671	79
sp|Q91V24|ABCA7_MOUSE - ATP-binding cassette sub-family A member 7 OS=Mus muscul	0	8	9	0	2	9	1.5454	0.6387	28
sp|Q3UVY5|PCX4_MOUSE - Pecanex-like protein 4 OS=Mus musculus GN=Pcnxl4 PE=2 SV=	2	11	58	6	11	29	1.5434	0.6791	117
sp|P16675|PPGB_MOUSE - Lysosomal protective protein OS=Mus musculus GN=Ctsa PE=1	7	30	17	7	21	7	1.5428	0.4795	89
sp|P08228|SODC_MOUSE - Superoxide dismutase [Cu-Zn] OS=Mus musculus GN=Sod1 PE=1	6	26	5	0	16	8	1.5416	0.6273	61
sp|Q8VE95|CH082_MOUSE - UPF0598 protein C8orf82 homolog OS=Mus musculus PE=2 SV=	0	16	4	4	6	3	1.5384	0.658	33
sp|P28665|MUG1_MOUSE - Murinoglobulin-1 OS=Mus musculus GN=Mug1 PE=1 SV=3	16	43	47	14	33	22	1.5362	0.332	175
sp|Q9JMA7|CP341_MOUSE - Cytochrome P450 3A41 OS=Mus musculus GN=Cyp3a41a PE=2 SV	3	43	0	4	26	0	1.5333	0.7562	76
sp|Q8K440|ABC8B_MOUSE - ATP-binding cassette sub-family A member 8-B OS=Mus musc	0	13	16	0	8	11	1.5263	0.6026	48
sp|Q91Y97|ALDOB_MOUSE - Fructose-bisphosphate aldolase B OS=Mus musculus GN=Aldo	18	52	26	27	27	9	1.5238	0.4072	159
sp|Q5SUA5|MYO1G_MOUSE - Unconventional myosin-Ig OS=Mus musculus GN=Myo1g PE=1 S	0	19	19	2	13	10	1.52	0.5763	63
sp|P07758|A1AT1_MOUSE - Alpha-1-antitrypsin 1-1 OS=Mus musculus GN=Serpina1a PE=	4	40	0	7	22	0	1.5172	0.7438	73
sp|Q9JKR6|HYOU1_MOUSE - Hypoxia up-regulated protein 1 OS=Mus musculus GN=Hyou1	0	37	7	9	17	3	1.5172	0.6995	73
sp|Q6A078|CE290_MOUSE - Centrosomal protein of 290 kDa OS=Mus musculus GN=Cep290	8	54	77	23	32	37	1.5108	0.4911	231
sp|Q9Z2I9|SUCB1_MOUSE - Succinyl-CoA ligase [ADP-forming] subunit beta, mitochon	37	111	107	24	67	78	1.5088	0.3808	424
sp|A2AS89|SPEB_MOUSE - Agmatinase, mitochondrial OS=Mus musculus GN=Agmat PE=1 S	31	56	39	30	30	24	1.5	0.1407	210
sp|P16627|HS71L_MOUSE - Heat shock 70 kDa protein 1-like OS=Mus musculus GN=Hspa	16	45	29	43	17	0	1.5	0.5428	150
sp|Q8K1K9|HINFP_MOUSE - Histone H4 transcription factor OS=Mus musculus GN=Hinfp	3	0	0	2	0	0	1.5	0.7952	5
sp|O08677|KNG1_MOUSE - Kininogen-1 OS=Mus musculus GN=Kng1 PE=1 SV=1	3	0	0	0	2	0	1.5	0.7952	5
sp|Q69Z38|PEAK1_MOUSE - Pseudopodium-enriched atypical kinase 1 OS=Mus musculus	3	0	0	2	0	0	1.5	0.7952	5
sp|Q924S8|SPRE1_MOUSE - Sprouty-related, EVH1 domain-containing protein 1 OS=Mus	3	0	0	0	2	0	1.5	0.7952	5
sp|Q9JI60|LRAT_MOUSE - Lecithin retinol acyltransferase OS=Mus musculus GN=Lrat	2	9	10	0	2	12	1.5	0.6303	35
sp|Q8BU14|SEC62_MOUSE - Translocation protein SEC62 OS=Mus musculus GN=Sec62 PE=	3	0	0	0	2	0	1.5	0.7952	5

sp|P69566|RANB9_MOUSE - Ran-binding protein 9 OS=Mus musculus GN=Ranbp9 PE=1 SV=	3	0	0	0	2	0	1.5	0.7952	5
sp|O09043|NAPSA_MOUSE - Napsin-A OS=Mus musculus GN=Napsa PE=1 SV=1	0	10	5	0	6	4	1.5	0.648	25
sp|Q00898|A1AT5_MOUSE - Alpha-1-antitrypsin 1-5 OS=Mus musculus GN=Serpina1e PE=	0	33	0	3	19	0	1.5	0.7835	55
sp|Q8K1N2|PHLB2_MOUSE - Pleckstrin homology-like domain family B member 2 OS=Mus	0	9	0	0	0	6	1.5	0.7952	15
sp|O88322|NID2_MOUSE - Nidogen-2 OS=Mus musculus GN=Nid2 PE=1 SV=2	0	3	0	0	0	2	1.5	0.7952	5
sp|Q8BFZ9|ERLN2_MOUSE - Erlin-2 OS=Mus musculus GN=Erlin2 PE=1 SV=1	0	3	0	0	2	0	1.5	0.7952	5
sp|P47963|RL13_MOUSE - 60S ribosomal protein L13 OS=Mus musculus GN=Rpl13 PE=2 S	0	9	0	3	3	0	1.5	0.7676	15
sp|Q8CJ70|IL19_MOUSE - Interleukin-19 OS=Mus musculus GN=Il19 PE=2 SV=1	0	3	0	0	2	0	1.5	0.7952	5
sp|Q9Z280|PLD1_MOUSE - Phospholipase D1 OS=Mus musculus GN=Pld1 PE=2 SV=1	0	3	0	0	2	0	1.5	0.7952	5
sp|Q80VQ1|LRRC1_MOUSE - Leucine-rich repeat-containing protein 1 OS=Mus musculus	0	3	0	0	2	0	1.5	0.7952	5
sp|Q8CG64|FKRP_MOUSE - Fukutin-related protein OS=Mus musculus GN=Fkrp PE=1 SV=1	0	3	0	2	0	0	1.5	0.7952	5
sp|Q2MHE5|DOK6_MOUSE - Docking protein 6 OS=Mus musculus GN=Dok6 PE=2 SV=1	0	3	0	0	2	0	1.5	0.7952	5
sp|Q640P4|GL8D2_MOUSE - Glycosyltransferase 8 domain-containing protein 2 OS=Mus	0	3	0	0	2	0	1.5	0.7952	5
sp|Q6DFV8|VWDE_MOUSE - von Willebrand factor D and EGF domain-containing protein	0	9	0	0	0	6	1.5	0.7952	15
sp|Q3TYA6|MPP8_MOUSE - M-phase phosphoprotein 8 OS=Mus musculus GN=Mphosph8 PE=1	0	3	0	2	0	0	1.5	0.7952	5
sp|Q01514|GBP1_MOUSE - Interferon-induced guanylate-binding protein 1 OS=Mus mus	0	3	0	2	0	0	1.5	0.7952	5
sp|Q925J9|MED1_MOUSE - Mediator of RNA polymerase II transcription subunit 1 OS=	0	3	0	0	2	0	1.5	0.7952	5
sp|Q6ZQ73|CAND2_MOUSE - Cullin-associated NEDD8-dissociated protein 2 OS=Mus mus	0	3	0	2	0	0	1.5	0.7952	5
sp|Q60875|ARHG2_MOUSE - Rho guanine nucleotide exchange factor 2 OS=Mus musculus	0	3	0	2	0	0	1.5	0.7952	5
sp|A2AKG8|FOCAD_MOUSE - Focadhesin OS=Mus musculus GN=Focad PE=2 SV=1	0	3	0	0	2	0	1.5	0.7952	5
sp|A7XUY5|SKIT5_MOUSE - Selection and upkeep of intraepithelial T-cells protein	0	6	0	0	4	0	1.5	0.7952	10
sp|Q8K4F5|ABHDB_MOUSE - Alpha/beta hydrolase domain-containing protein 11 OS=Mus	0	8	7	3	7	0	1.5	0.6332	25
sp|Q9CYH2|F213A_MOUSE - Redox-regulatory protein FAM213A OS=Mus musculus GN=Fam2	0	3	0	0	2	0	1.5	0.7952	5
sp|Q91VT4|CBR4_MOUSE - Carbonyl reductase family member 4 OS=Mus musculus GN=Cbr	0	3	0	0	2	0	1.5	0.7952	5
sp|Q9DBH5|LMAN2_MOUSE - Vesicular integral-membrane protein VIP36 OS=Mus musculu	0	3	0	0	2	0	1.5	0.7952	5
sp|Q9EP75|CP4FE_MOUSE - Leukotriene-B4 omega-hydroxylase 3 OS=Mus musculus GN=Cy	0	6	0	0	4	0	1.5	0.7952	10
sp|Q80X95|RRAGA_MOUSE - Ras-related GTP-binding protein A OS=Mus musculus GN=Rra	0	3	0	0	2	0	1.5	0.7952	5
sp|Q6ZWV3|RL10_MOUSE - 60S ribosomal protein L10 OS=Mus musculus GN=Rpl10 PE=1 S	0	6	0	0	4	0	1.5	0.7952	10
sp|Q91WL5|CP4CA_MOUSE - Cytochrome P450 4A12A OS=Mus musculus GN=Cyp4a12a PE=2 S	0	3	0	0	2	0	1.5	0.7952	5
sp|P58467|SETD4_MOUSE - SET domain-containing protein 4 OS=Mus musculus GN=Setd4	0	3	0	0	2	0	1.5	0.7952	5
sp|Q9D7J6|DNSL1_MOUSE - Deoxyribonuclease-1-like 1 OS=Mus musculus GN=Dnase1l1 P	0	3	0	0	2	0	1.5	0.7952	5
sp|Q8BH44|COR2B_MOUSE - Coronin-2B OS=Mus musculus GN=Coro2b PE=2 SV=2	0	3	0	2	0	0	1.5	0.7952	5
sp|Q9EQU3|TLR9_MOUSE - Toll-like receptor 9 OS=Mus musculus GN=Tlr9 PE=1 SV=3	0	3	0	0	2	0	1.5	0.7952	5
sp|Q9QX29|TRPC5_MOUSE - Short transient receptor potential channel 5 OS=Mus musc	0	6	0	2	2	0	1.5	0.7676	10
sp|O70481|UBR1_MOUSE - E3 ubiquitin-protein ligase UBR1 OS=Mus musculus GN=Ubr1	0	6	6	0	8	0	1.5	0.7096	20
sp|P56382|ATP5E_MOUSE - ATP synthase subunit epsilon, mitochondrial OS=Mus muscu	0	6	0	0	4	0	1.5	0.7952	10
sp|Q5FW60|MUP20_MOUSE - Major urinary protein 20 OS=Mus musculus GN=Mup20 PE=1 S	0	3	0	0	2	0	1.5	0.7952	5
sp|Q9CRG1|TM7S3_MOUSE - Transmembrane 7 superfamily member 3 OS=Mus musculus GN=	0	3	0	0	2	0	1.5	0.7952	5
sp|Q5U458|DJC11_MOUSE - DnaJ homolog subfamily C member 11 OS=Mus musculus GN=Dn	0	3	0	0	2	0	1.5	0.7952	5
sp|Q7TSS2|UB2Q1_MOUSE - Ubiquitin-conjugating enzyme E2 Q1 OS=Mus musculus GN=Ub	0	3	0	0	2	0	1.5	0.7952	5
sp|Q61614|EDNRA_MOUSE - Endothelin-1 receptor OS=Mus musculus GN=Ednra PE=2 SV=3	0	3	0	0	2	0	1.5	0.7952	5

sp|Q61626|GRIK5_MOUSE - Glutamate receptor ionotropic, kainate 5 OS=Mus musculus	0	3	0	0	2	0	1.5	0.7952	5
sp|Q8K449|ABCA9_MOUSE - ATP-binding cassette sub-family A member 9 OS=Mus muscul	0	2	4	4	0	0	1.5	0.7246	10
sp|P43274|H14_MOUSE - Histone H1.4 OS=Mus musculus GN=Hist1h1e PE=1 SV=2	0	3	0	0	2	0	1.5	0.7952	5
sp|Q9D1I5|MCEE_MOUSE - Methylmalonyl-CoA epimerase, mitochondrial OS=Mus musculu	0	3	0	0	2	0	1.5	0.7952	5
sp|Q9DD03|RAB13_MOUSE - Ras-related protein Rab-13 OS=Mus musculus GN=Rab13 PE=1	0	3	0	0	2	0	1.5	0.7952	5
sp|P35283|RAB12_MOUSE - Ras-related protein Rab-12 OS=Mus musculus GN=Rab12 PE=1	0	3	0	0	2	0	1.5	0.7952	5
sp|P61290|PSME3_MOUSE - Proteasome activator complex subunit 3 OS=Mus musculus G	0	3	0	0	2	0	1.5	0.7952	5
sp|Q8BGF3|WDR92_MOUSE - WD repeat-containing protein 92 OS=Mus musculus GN=Wdr92	0	3	0	0	2	0	1.5	0.7952	5
sp|P23359|BMP7_MOUSE - Bone morphogenetic protein 7 OS=Mus musculus GN=Bmp7 PE=1	0	3	0	0	2	0	1.5	0.7952	5
sp|Q6PFY8|TRI45_MOUSE - Tripartite motif-containing protein 45 OS=Mus musculus G	0	0	15	0	2	8	1.5	0.7788	25
sp|Q8VC48|PEX12_MOUSE - Peroxisome assembly protein 12 OS=Mus musculus GN=Pex12	0	0	3	0	0	2	1.5	0.7952	5
sp|Q8K4R9|DLGP5_MOUSE - Disks large-associated protein 5 OS=Mus musculus GN=Dlga	0	0	3	0	2	0	1.5	0.7952	5
sp|Q149C2|MIPT3_MOUSE - TRAF3-interacting protein 1 OS=Mus musculus GN=Traf3ip1	0	0	12	0	8	0	1.5	0.7952	20
sp|Q9QY30|ABCBB_MOUSE - Bile salt export pump OS=Mus musculus GN=Abcb11 PE=1 SV=	0	0	3	0	2	0	1.5	0.7952	5
sp|Q61464|ZN638_MOUSE - Zinc finger protein 638 OS=Mus musculus GN=Znf638 PE=1 S	0	42	46	14	8	37	1.4915	0.6033	147
sp|Q00896|A1AT3_MOUSE - Alpha-1-antitrypsin 1-3 OS=Mus musculus GN=Serpina1c PE=	6	46	3	8	29	0	1.4864	0.732	92
sp|Q8BWF0|SSDH_MOUSE - Succinate-semialdehyde dehydrogenase, mitochondrial OS=Mu	27	110	59	31	55	46	1.4848	0.4442	328
sp|P38060|HMGCL_MOUSE - Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Mus mu	33	99	104	32	54	73	1.4842	0.3755	395
sp|Q91WN4|KMO_MOUSE - Kynurenine 3-monooxygenase OS=Mus musculus GN=Kmo PE=2 SV=	10	72	38	20	36	25	1.4814	0.5218	201
sp|Q9WTS4|TEN1_MOUSE - Teneurin-1 OS=Mus musculus GN=Tenm1 PE=1 SV=1	0	27	10	2	13	10	1.48	0.6638	62
sp|Q6PGB8|SMCA1_MOUSE - Probable global transcription activator SNF2L1 OS=Mus mu	0	14	20	0	14	9	1.4782	0.6375	57
sp|A2ASS6|TITIN_MOUSE - Titin OS=Mus musculus GN=Ttn PE=1 SV=1	106	388	174	104	289	59	1.4778	0.5496	1120
sp|Q9QXL2|KI21A_MOUSE - Kinesin-like protein KIF21A OS=Mus musculus GN=Kif21a PE	4	22	5	0	15	6	1.4761	0.6711	52
sp|Q99MW1|STK31_MOUSE - Serine/threonine-protein kinase 31 OS=Mus musculus GN=St	0	18	13	13	8	0	1.4761	0.6384	52
sp|Q64458|CP2CT_MOUSE - Cytochrome P450 2C29 OS=Mus musculus GN=Cyp2c29 PE=1 SV=	17	127	52	26	80	27	1.4736	0.6009	329
sp|Q8K2I9|FBX18_MOUSE - F-box only protein 18 OS=Mus musculus GN=Fbxo18 PE=2 SV=	5	23	0	8	11	0	1.4736	0.7172	47
sp|B1AVH7|TBD2A_MOUSE - TBC1 domain family member 2A OS=Mus musculus GN=Tbc1d2 P	0	14	14	0	13	6	1.4736	0.6428	47
sp|Q99LZ3|SLD5_MOUSE - DNA replication complex GINS protein SLD5 OS=Mus musculus	0	0	28	0	0	19	1.4736	0.8034	47
sp|P63038|CH60_MOUSE - 60 kDa heat shock protein, mitochondrial OS=Mus musculus	26	78	180	25	66	102	1.4715	0.5797	477
sp|Q9DCV7|K2C7_MOUSE - Keratin, type II cytoskeletal 7 OS=Mus musculus GN=Krt7 P	0	37	13	0	31	3	1.4705	0.7344	84
sp|Q64459|CP3AB_MOUSE - Cytochrome P450 3A11 OS=Mus musculus GN=Cyp3a11 PE=1 SV=	9	38	0	5	27	0	1.4687	0.7416	79
sp|P07901|HS90A_MOUSE - Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90	4	14	26	6	8	16	1.4666	0.5444	74
sp|Q04692|SMRCD_MOUSE - SWI/SNF-related matrix-associated actin-dependent regula	0	20	2	4	3	8	1.4666	0.7393	37
sp|Q9CWG8|NDUF7_MOUSE - NADH dehydrogenase [ubiquinone] complex I, assembly fact	0	2	20	4	6	5	1.4666	0.7333	37
sp|Q8VED5|K2C79_MOUSE - Keratin, type II cytoskeletal 79 OS=Mus musculus GN=Krt7	0	45	18	0	37	6	1.4651	0.7209	106
sp|P21614|VTDB_MOUSE - Vitamin D-binding protein OS=Mus musculus GN=Gc PE=1 SV=2	0	19	0	2	11	0	1.4615	0.7944	32
sp|O54988|SLK_MOUSE - STE20-like serine/threonine-protein kinase OS=Mus musculus	0	0	19	13	0	0	1.4615	0.8072	32
sp|Q9DCU9|HOGA1_MOUSE - 4-hydroxy-2-oxoglutarate aldolase, mitochondrial OS=Mus	24	80	58	19	29	63	1.4594	0.4644	273
sp|P49935|CATH_MOUSE - Pro-cathepsin H OS=Mus musculus GN=Ctsh PE=2 SV=2	9	66	84	20	23	66	1.4587	0.5711	268
sp|Q9D4I2|MEII1_MOUSE - Meiosis inhibitor protein 1 OS=Mus musculus GN=Mei1 PE=2	3	31	33	12	24	10	1.4565	0.546	113
sp|Q9D3R9|TAF7L_MOUSE - Transcription initiation factor TFIID subunit 7-like OS=	7	9	0	9	2	0	1.4545	0.688	27

sp|Q91VD9|NDUS1_MOUSE - NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochond	41	126	36	42	66	32	1.45	0.534	343
sp|B1AY13|UBP24_MOUSE - Ubiquitin carboxyl-terminal hydrolase 24 OS=Mus musculus	0	10	19	4	5	11	1.45	0.6382	49
sp|Q921I1|TRFE_MOUSE - Serotransferrin OS=Mus musculus GN=Tf PE=1 SV=1	37	109	64	29	72	44	1.4482	0.4263	355
sp|P04104|K2C1_MOUSE - Keratin, type II cytoskeletal 1 OS=Mus musculus GN=Krt1 P	8	192	163	21	88	142	1.4462	0.607	614
sp|P28843|DPP4_MOUSE - Dipeptidyl peptidase 4 OS=Mus musculus GN=Dpp4 PE=1 SV=3	2	8	3	5	4	0	1.4444	0.6086	22
sp|Q8BIP0|SYDM_MOUSE - Aspartate--tRNA ligase, mitochondrial OS=Mus musculus GN=	2	6	18	0	5	13	1.4444	0.6854	44
sp|Q80TE7|LRRC7_MOUSE - Leucine-rich repeat-containing protein 7 OS=Mus musculus	0	13	0	2	7	0	1.4444	0.7952	22
sp|Q80WE4|KI20B_MOUSE - Kinesin-like protein KIF20B OS=Mus musculus GN=Kif20b PE	25	80	78	32	38	57	1.4409	0.3931	310
sp|Q7TSC1|PRC2A_MOUSE - Protein PRRC2A OS=Mus musculus GN=Prrc2a PE=1 SV=1	10	8	28	4	17	11	1.4375	0.5618	78
sp|Q3UNX5|ACSM3_MOUSE - Acyl-coenzyme A synthetase ACSM3, mitochondrial OS=Mus m	4	19	0	5	11	0	1.4375	0.7415	39
sp|Q99P30|NUDT7_MOUSE - Peroxisomal coenzyme A diphosphatase NUDT7 OS=Mus muscul	0	27	6	0	23	0	1.4347	0.7811	56
sp|O88531|PPT1_MOUSE - Palmitoyl-protein thioesterase 1 OS=Mus musculus GN=Ppt1	9	40	24	12	20	19	1.4313	0.4743	124
sp|P16332|MUTA_MOUSE - Methylmalonyl-CoA mutase, mitochondrial OS=Mus musculus G	7	48	35	11	35	17	1.4285	0.5575	153
sp|Q3UPF5|ZCCHV_MOUSE - Zinc finger CCCH-type antiviral protein 1 OS=Mus musculu	7	3	0	5	2	0	1.4285	0.709	17
sp|Q9Z0H8|CLIP2_MOUSE - CAP-Gly domain-containing linker protein 2 OS=Mus muscul	0	10	20	0	14	7	1.4285	0.6922	51
sp|P52760|UK114_MOUSE - Ribonuclease UK114 OS=Mus musculus GN=Hrsp12 PE=1 SV=3	0	20	0	0	7	7	1.4285	0.7911	34
sp|O55137|ACOT1_MOUSE - Acyl-coenzyme A thioesterase 1 OS=Mus musculus GN=Acot1	15	51	31	17	34	17	1.4264	0.4606	165
sp|Q9D7B6|ACAD8_MOUSE - Isobutyryl-CoA dehydrogenase, mitochondrial OS=Mus muscu	3	20	4	0	16	3	1.421	0.736	46
sp|P59598|ASXL1_MOUSE - Putative Polycomb group protein ASXL1 OS=Mus musculus GN	3	7	7	0	6	6	1.4166	0.5262	29
sp|Q64331|MYO6_MOUSE - Unconventional myosin-VI OS=Mus musculus GN=Myo6 PE=1 SV=	0	13	4	0	8	4	1.4166	0.729	29
sp|Q69ZK0|PREX1_MOUSE - Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac e	0	24	0	5	12	0	1.4117	0.8023	41
sp|Q99LC5|ETFA_MOUSE - Electron transfer flavoprotein subunit alpha, mitochondri	42	210	212	84	99	146	1.4103	0.4905	793
sp|Q6ZQI3|MLEC_MOUSE - Malectin OS=Mus musculus GN=Mlec PE=2 SV=2	2	12	0	0	10	0	1.4	0.8024	24
sp|Q8K3J1|NDUS8_MOUSE - NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, m	2	5	0	0	5	0	1.4	0.778	12
sp|Q05793|PGBM_MOUSE - Basement membrane-specific heparan sulfate proteoglycan c	7	0	0	5	0	0	1.4	0.8275	12
sp|Q8JZK9|HMCS1_MOUSE - Hydroxymethylglutaryl-CoA synthase, cytoplasmic OS=Mus m	0	24	4	3	13	4	1.4	0.7578	48
sp|Q925I1|ATAD3_MOUSE - ATPase family AAA domain-containing protein 3 OS=Mus mus	0	7	0	5	0	0	1.4	0.8275	12
sp|Q80UG5|SEPT9_MOUSE - Septin-9 OS=Mus musculus GN=Sept9 PE=1 SV=1	0	14	0	6	4	0	1.4	0.8024	24
sp|Q8BMD2|DZIP1_MOUSE - Zinc finger protein DZIP1 OS=Mus musculus GN=Dzip1 PE=2	0	7	0	0	5	0	1.4	0.8275	12
sp|D3Z6P0|PDIA2_MOUSE - Protein disulfide-isomerase A2 OS=Mus musculus GN=Pdia2	0	3	4	0	0	5	1.4	0.7618	12
sp|Q9WV55|VAPA_MOUSE - Vesicle-associated membrane protein-associated protein A	0	14	0	0	5	5	1.4	0.8011	24
sp|Q8CG47|SMC4_MOUSE - Structural maintenance of chromosomes protein 4 OS=Mus mu	0	14	0	5	3	2	1.4	0.7928	24
sp|P70665|SIAE_MOUSE - Sialate O-acetylesterase OS=Mus musculus GN=Siae PE=2 SV=	0	7	0	0	5	0	1.4	0.8275	12
sp|Q8BVN4|MTEF4_MOUSE - Transcription termination factor 4, mitochondrial OS=Mus	0	2	5	0	0	5	1.4	0.778	12
sp|P33267|CP2F2_MOUSE - Cytochrome P450 2F2 OS=Mus musculus GN=Cyp2f2 PE=2 SV=1	11	74	28	14	40	27	1.395	0.6263	194
sp|Q6PCZ4|MAGE1_MOUSE - Melanoma-associated antigen E1 OS=Mus musculus GN=Magee1	0	75	10	18	43	0	1.3934	0.7786	146
sp|Q9Z331|K2C6B_MOUSE - Keratin, type II cytoskeletal 6B OS=Mus musculus GN=Krt6	0	161	141	10	100	107	1.3917	0.6588	519
sp|Q91WS4|BHMT2_MOUSE - S-methylmethionine--homocysteine S-methyltransferase BHM	19	71	91	13	36	82	1.3816	0.6026	312
sp|P22315|HEMH_MOUSE - Ferrochelatase, mitochondrial OS=Mus musculus GN=Fech PE=	2	31	0	5	19	0	1.375	0.8073	57
sp|Q9CU24|THMS3_MOUSE - Protein THEMIS3 OS=Mus musculus GN=Themis3 PE=2 SV=1	0	2	9	0	4	4	1.375	0.7584	19
sp|Q9DBL1|ACDSB_MOUSE - Short/branched chain specific acyl-CoA dehydrogenase, mi	0	11	0	0	8	0	1.375	0.8362	19

sp|P08003|PDIA4_MOUSE - Protein disulfide-isomerase A4 OS=Mus musculus GN=Pdia4	35	127	66	36	87	43	1.3734	0.5462	394
sp|Q9DCN2|NB5R3_MOUSE - NADH-cytochrome b5 reductase 3 OS=Mus musculus GN=Cyb5r3	27	137	64	42	81	43	1.3734	0.5842	394
sp|Q8BFZ3|ACTBL_MOUSE - Beta-actin-like protein 2 OS=Mus musculus GN=Actbl2 PE=1	2	22	2	0	17	2	1.3684	0.7986	45
sp|P42925|PXMP2_MOUSE - Peroxisomal membrane protein 2 OS=Mus musculus GN=Pxmp2	6	12	8	0	9	10	1.3684	0.556	45
sp|Q6XVG2|CP254_MOUSE - Cytochrome P450 2C54 OS=Mus musculus GN=Cyp2c54 PE=2 SV=	0	61	10	12	33	7	1.3653	0.7727	123
sp|Q8BK48|EST2E_MOUSE - Pyrethroid hydrolase Ces2e OS=Mus musculus GN=Ces2e PE=1	10	80	0	20	44	2	1.3636	0.7889	156
sp|Q9QXS1|PLEC_MOUSE - Plectin OS=Mus musculus GN=Plec PE=1 SV=3	0	15	0	0	11	0	1.3636	0.8402	26
sp|P50446|K2C6A_MOUSE - Keratin, type II cytoskeletal 6A OS=Mus musculus GN=Krt6	0	161	110	14	107	78	1.3618	0.6844	470
sp|P28666|MUG2_MOUSE - Murinoglobulin-2 OS=Mus musculus GN=Mug2 PE=2 SV=2	9	40	15	15	32	0	1.3617	0.6909	111
sp|O08601|MTP_MOUSE - Microsomal triglyceride transfer protein large subunit OS=	16	102	48	26	61	35	1.3606	0.6183	288
sp|P17439|GLCM_MOUSE - Glucosylceramidase OS=Mus musculus GN=Gba PE=1 SV=1	4	30	0	9	16	0	1.36	0.7889	59
sp|O35728|CP4AE_MOUSE - Cytochrome P450 4A14 OS=Mus musculus GN=Cyp4a14 PE=2 SV=	2	32	0	0	25	0	1.36	0.8324	59
sp|Q91Z53|GRHPR_MOUSE - Glyoxylate reductase/hydroxypyruvate reductase OS=Mus mu	2	17	0	2	12	0	1.3571	0.8109	33
sp|Q9JJW6|ALRF2_MOUSE - Aly/REF export factor 2 OS=Mus musculus GN=Alyref2 PE=1	0	5	14	0	10	4	1.3571	0.7566	33
sp|Q91XE8|TM205_MOUSE - Transmembrane protein 205 OS=Mus musculus GN=Tmem205 PE=	10	34	17	2	24	19	1.3555	0.6135	106
sp|Q64511|TOP2B_MOUSE - DNA topoisomerase 2-beta OS=Mus musculus GN=Top2b PE=1 S	0	40	25	15	12	21	1.3541	0.6604	113
sp|P58064|RT06_MOUSE - 28S ribosomal protein S6, mitochondrial OS=Mus musculus G	0	3	20	0	2	15	1.3529	0.8103	40
sp|P23780|BGAL_MOUSE - Beta-galactosidase OS=Mus musculus GN=Glb1 PE=2 SV=1	0	47	3	0	35	2	1.3513	0.8304	87
sp|Q99LP6|GRPE1_MOUSE - GrpE protein homolog 1, mitochondrial OS=Mus musculus GN	5	42	42	15	16	35	1.3484	0.6117	155
sp|Q6ZQM8|UD17C_MOUSE - UDP-glucuronosyltransferase 1-7C OS=Mus musculus GN=Ugt1	43	199	95	48	122	80	1.348	0.5973	587
sp|P20060|HEXB_MOUSE - Beta-hexosaminidase subunit beta OS=Mus musculus GN=Hexb	9	22	0	9	14	0	1.3478	0.7429	54
sp|Q3URR7|ZSC10_MOUSE - Zinc finger and SCAN domain-containing protein 10 OS=Mus	0	0	39	0	5	24	1.3448	0.8341	68
sp|Q8R4N0|CLYBL_MOUSE - Citrate lyase subunit beta-like protein, mitochondrial O	13	38	35	16	28	20	1.3437	0.4435	150
sp|Q8K0T7|UN13C_MOUSE - Protein unc-13 homolog C OS=Mus musculus GN=Unc13c PE=1	0	22	21	5	6	21	1.3437	0.6997	75
sp|O89023|TPP1_MOUSE - Tripeptidyl-peptidase 1 OS=Mus musculus GN=Tpp1 PE=1 SV=2	11	37	3	18	20	0	1.3421	0.7378	89
sp|P61922|GABT_MOUSE - 4-aminobutyrate aminotransferase, mitochondrial OS=Mus mu	17	125	75	32	46	84	1.3395	0.6267	379
sp|Q9CZU6|CISY_MOUSE - Citrate synthase, mitochondrial OS=Mus musculus GN=Cs PE=	34	114	73	28	78	59	1.3393	0.5318	386
sp|Q91YQ5|RPN1_MOUSE - Dolichyl-diphosphooligosaccharide--protein glycosyltransf	0	51	48	6	37	31	1.3378	0.6844	173
sp|Q9QYR9|ACOT2_MOUSE - Acyl-coenzyme A thioesterase 2, mitochondrial OS=Mus mus	22	43	39	14	27	37	1.3333	0.4023	182
sp|Q9WTP7|KAD3_MOUSE - GTP:AMP phosphotransferase AK3, mitochondrial OS=Mus musc	30	92	38	27	72	21	1.3333	0.6255	280
sp|Q8BKF1|RPOM_MOUSE - DNA-directed RNA polymerase, mitochondrial OS=Mus musculu	2	2	0	3	0	0	1.3333	0.7952	7
sp|Q9DB29|IAH1_MOUSE - Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Mus mus	6	6	0	0	9	0	1.3333	0.7952	21
sp|Q3TC72|FAHD2_MOUSE - Fumarylacetoacetate hydrolase domain-containing protein	6	14	0	8	7	0	1.3333	0.7445	35
sp|P35293|RAB18_MOUSE - Ras-related protein Rab-18 OS=Mus musculus GN=Rab18 PE=2	2	2	0	0	3	0	1.3333	0.7952	7
sp|P56654|CP237_MOUSE - Cytochrome P450 2C37 OS=Mus musculus GN=Cyp2c37 PE=2 SV=	3	33	0	9	18	0	1.3333	0.811	63
sp|P11591|MUP5_MOUSE - Major urinary protein 5 OS=Mus musculus GN=Mup5 PE=2 SV=1	0	16	0	6	2	4	1.3333	0.8189	28
sp|P97823|LYPA1_MOUSE - Acyl-protein thioesterase 1 OS=Mus musculus GN=Lypla1 PE	0	8	0	0	6	0	1.3333	0.8512	14
sp|P62754|RS6_MOUSE - 40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1	0	4	0	0	3	0	1.3333	0.8512	7
sp|P17182|ENOA_MOUSE - Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3	0	8	0	4	2	0	1.3333	0.8298	14
sp|P49429|HPPD_MOUSE - 4-hydroxyphenylpyruvate dioxygenase OS=Mus musculus GN=Hp	0	4	0	0	3	0	1.3333	0.8512	7
sp|Q91VA6|PDIP2_MOUSE - Polymerase delta-interacting protein 2 OS=Mus musculus G	0	8	0	0	6	0	1.3333	0.8512	14

sp|P47791|GSHR_MOUSE - Glutathione reductase, mitochondrial OS=Mus musculus GN=G	0	8	0	3	3	0	1.3333	0.8264	14
sp|Q9JKV7|EXTL1_MOUSE - Exostosin-like 1 OS=Mus musculus GN=Extl1 PE=2 SV=2	0	4	0	3	0	0	1.3333	0.8512	7
sp|Q8CIM1|LRC45_MOUSE - Leucine-rich repeat-containing protein 45 OS=Mus musculu	0	4	0	0	0	3	1.3333	0.8512	7
sp|Q61171|PRDX2_MOUSE - Peroxiredoxin-2 OS=Mus musculus GN=Prdx2 PE=1 SV=3	0	6	2	0	6	0	1.3333	0.8149	14
sp|O35435|PYRD_MOUSE - Dihydroorotate dehydrogenase (quinone), mitochondrial OS=	0	4	0	0	3	0	1.3333	0.8512	7
sp|P55249|LX12E_MOUSE - Arachidonate 12-lipoxygenase, epidermal-type OS=Mus musc	0	4	0	0	3	0	1.3333	0.8512	7
sp|Q5SNZ0|GRDN_MOUSE - Girdin OS=Mus musculus GN=Ccdc88a PE=1 SV=2	0	0	8	0	0	6	1.3333	0.8512	14
sp|Q6QI06|RICTR_MOUSE - Rapamycin-insensitive companion of mTOR OS=Mus musculus	0	0	4	0	0	3	1.3333	0.8512	7
sp|Q61730|IL1AP_MOUSE - Interleukin-1 receptor accessory protein OS=Mus musculus	0	0	4	0	0	3	1.3333	0.8512	7
sp|Q8VCW8|ACSF2_MOUSE - Acyl-CoA synthetase family member 2, mitochondrial OS=Mu	15	82	56	16	49	50	1.3304	0.6031	268
sp|Q63886|UD11_MOUSE - UDP-glucuronosyltransferase 1-1 OS=Mus musculus GN=Ugt1a1	52	242	124	65	154	96	1.3269	0.6048	733
sp|P04938|MUP8_MOUSE - Major urinary proteins 11 and 8 (Fragment) OS=Mus musculu	6	40	15	0	25	21	1.326	0.7157	107
sp|Q8BMS1|ECHA_MOUSE - Trifunctional enzyme subunit alpha, mitochondrial OS=Mus	115	431	282	130	269	228	1.3205	0.5401	1455
sp|Q02357|ANK1_MOUSE - Ankyrin-1 OS=Mus musculus GN=Ank1 PE=1 SV=2	9	22	2	9	16	0	1.32	0.739	58
sp|Q922S8|KIF2C_MOUSE - Kinesin-like protein KIF2C OS=Mus musculus GN=Kif2c PE=1	0	22	11	0	0	25	1.32	0.8116	58
sp|O55125|NIPS1_MOUSE - Protein NipSnap homolog 1 OS=Mus musculus GN=Nipsnap1 PE	15	49	23	10	45	11	1.3181	0.6733	153
sp|Q8VCM7|FIBG_MOUSE - Fibrinogen gamma chain OS=Mus musculus GN=Fgg PE=1 SV=1	4	25	0	4	16	2	1.3181	0.8061	51
sp|Q8CI94|PYGB_MOUSE - Glycogen phosphorylase, brain form OS=Mus musculus GN=Pyg	0	15	14	5	17	0	1.3181	0.7553	51
sp|P54823|DDX6_MOUSE - Probable ATP-dependent RNA helicase DDX6 OS=Mus musculus	2	14	9	6	5	8	1.3157	0.6071	44
sp|Q8BGZ7|K2C75_MOUSE - Keratin, type II cytoskeletal 75 OS=Mus musculus GN=Krt7	0	90	77	6	71	50	1.3149	0.7148	294
sp|Q91VA0|ACSM1_MOUSE - Acyl-coenzyme A synthetase ACSM1, mitochondrial OS=Mus m	44	142	70	38	91	66	1.3128	0.5718	451
sp|Q8C5H1|ANO4_MOUSE - Anoctamin-4 OS=Mus musculus GN=Ano4 PE=2 SV=2	5	5	11	6	10	0	1.3125	0.6612	37
sp|Q9QXX4|CMC2_MOUSE - Calcium-binding mitochondrial carrier protein Aralar2 OS=	0	34	4	7	22	0	1.3103	0.8226	67
sp|Q60931|VDAC3_MOUSE - Voltage-dependent anion-selective channel protein 3 OS=M	4	44	37	8	19	38	1.3076	0.6822	150
sp|P24456|CP2DA_MOUSE - Cytochrome P450 2D10 OS=Mus musculus GN=Cyp2d10 PE=2 SV=	9	60	8	14	37	8	1.305	0.7715	136
sp|Q60597|ODO1_MOUSE - 2-oxoglutarate dehydrogenase, mitochondrial OS=Mus muscul	16	75	51	14	57	38	1.3027	0.6307	251
sp|Q9DBM2|ECHP_MOUSE - Peroxisomal bifunctional enzyme OS=Mus musculus GN=Ehhadh	137	443	191	170	291	131	1.3023	0.6031	1363
sp|Q99PG0|AAAD_MOUSE - Arylacetamide deacetylase OS=Mus musculus GN=Aadac PE=1 S	11	105	52	15	57	57	1.3023	0.6928	297
sp|P47740|AL3A2_MOUSE - Fatty aldehyde dehydrogenase OS=Mus musculus GN=Aldh3a2	31	120	48	36	85	32	1.3006	0.6584	352
sp|Q01339|APOH_MOUSE - Beta-2-glycoprotein 1 OS=Mus musculus GN=Apoh PE=1 SV=1	5	8	0	4	6	0	1.3	0.7496	23
sp|Q4LDG0|S27A5_MOUSE - Bile acyl-CoA synthetase OS=Mus musculus GN=Slc27a5 PE=2	18	46	10	21	36	0	1.2982	0.7265	131
sp|Q9CZ13|QCR1_MOUSE - Cytochrome b-c1 complex subunit 1, mitochondrial OS=Mus m	74	175	105	54	105	114	1.2967	0.4862	627
sp|P70434|IRF7_MOUSE - Interferon regulatory factor 7 OS=Mus musculus GN=Irf7 PE	0	48	27	14	44	0	1.2931	0.7805	133
sp|Q9CQQ7|AT5F1_MOUSE - ATP synthase F(0) complex subunit B1, mitochondrial OS=M	24	97	96	33	72	63	1.2916	0.5763	385
sp|P35700|PRDX1_MOUSE - Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1	6	34	0	10	21	0	1.2903	0.8164	71
sp|P08113|ENPL_MOUSE - Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	51	113	45	47	76	39	1.2901	0.5568	371
sp|P52825|CPT2_MOUSE - Carnitine O-palmitoyltransferase 2, mitochondrial OS=Mus	28	118	23	29	72	30	1.29	0.7281	300
sp|A2AJK6|CHD7_MOUSE - Chromodomain-helicase-DNA-binding protein 7 OS=Mus muscul	0	34	24	4	24	17	1.2888	0.7291	103
sp|Q80U72|SCRIB_MOUSE - Protein scribble homolog OS=Mus musculus GN=Scrib PE=1 S	6	12	0	3	11	0	1.2857	0.7938	32
sp|Q8VEM8|MPCP_MOUSE - Phosphate carrier protein, mitochondrial OS=Mus musculus	11	34	9	3	39	0	1.2857	0.8013	96
sp|Q99MD6|TRXR3_MOUSE - Thioredoxin reductase 3 OS=Mus musculus GN=Txnrd3 PE=1 S	2	7	0	4	3	0	1.2857	0.7952	16

sp|P55937|GOGA3_MOUSE - Golgin subfamily A member 3 OS=Mus musculus GN=Golga3 PE	0	12	6	3	2	9	1.2857	0.7611	32
sp|Q5HZI1|MTUS1_MOUSE - Microtubule-associated tumor suppressor 1 homolog OS=Mus	0	16	20	9	7	12	1.2857	0.6929	64
sp|Q6RT24|CENPE_MOUSE - Centromere-associated protein E OS=Mus musculus GN=Cenpe	0	9	0	3	4	0	1.2857	0.8466	16
sp|Q6DFV5|HELZ_MOUSE - Probable helicase with zinc finger domain OS=Mus musculus	0	18	0	3	11	0	1.2857	0.8549	32
sp|Q9DCV4|RMD1_MOUSE - Regulator of microtubule dynamics protein 1 OS=Mus muscul	0	14	4	0	11	3	1.2857	0.8138	32
sp|P00329|ADH1_MOUSE - Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=2	0	7	2	0	7	0	1.2857	0.8416	16
sp|Q99PW8|KIF17_MOUSE - Kinesin-like protein KIF17 OS=Mus musculus GN=Kif17 PE=1	0	9	0	0	7	0	1.2857	0.8692	16
sp|P56657|CP240_MOUSE - Cytochrome P450 2C40 OS=Mus musculus GN=Cyp2c40 PE=2 SV=	17	75	12	13	44	24	1.2839	0.7468	185
sp|Q8BJ64|CHDH_MOUSE - Choline dehydrogenase, mitochondrial OS=Mus musculus GN=C	24	91	71	30	68	47	1.2827	0.5795	331
sp|Q9CQ62|DECR_MOUSE - 2,4-dienoyl-CoA reductase, mitochondrial OS=Mus musculus	30	144	94	54	78	78	1.2761	0.5994	478
sp|Q64176|EST1E_MOUSE - Carboxylesterase 1E OS=Mus musculus GN=Ces1e PE=1 SV=1	15	64	0	17	39	6	1.2741	0.8062	141
sp|Q9D2G2|ODO2_MOUSE - Dihydrolipoyllysine-residue succinyltransferase component	2	12	0	2	9	0	1.2727	0.8387	25
sp|B2RR83|YTDC2_MOUSE - Probable ATP-dependent RNA helicase YTHDC2 OS=Mus muscul	0	14	0	6	5	0	1.2727	0.8518	25
sp|O55022|PGRC1_MOUSE - Membrane-associated progesterone receptor component 1 OS	67	152	72	75	102	52	1.2707	0.5426	520
sp|Q3UL97|MCAF2_MOUSE - Activating transcription factor 7-interacting protein 2	0	13	20	4	10	12	1.2692	0.7312	59
sp|Q8VCH0|THIKB_MOUSE - 3-ketoacyl-CoA thiolase B, peroxisomal OS=Mus musculus G	22	104	77	35	69	56	1.2687	0.6118	363
sp|Q9CQW2|ARL8B_MOUSE - ADP-ribosylation factor-like protein 8B OS=Mus musculus	4	9	6	3	7	5	1.2666	0.5122	34
sp|Q3URE1|ACSF3_MOUSE - Acyl-CoA synthetase family member 3, mitochondrial OS=Mu	0	19	0	5	10	0	1.2666	0.8574	34
sp|Q3UEG6|AGT2_MOUSE - Alanine--glyoxylate aminotransferase 2, mitochondrial OS=	24	90	24	31	56	22	1.266	0.7103	247
sp|Q8CIM7|CP2DQ_MOUSE - Cytochrome P450 2D26 OS=Mus musculus GN=Cyp2d26 PE=2 SV=	5	43	5	8	28	6	1.2619	0.8126	95
sp|P26443|DHE3_MOUSE - Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus	350	1088	732	490	705	526	1.2608	0.5392	3891
sp|Q921H8|THIKA_MOUSE - 3-ketoacyl-CoA thiolase A, peroxisomal OS=Mus musculus G	16	96	67	17	61	64	1.2605	0.6811	321
sp|Q6ZWR6|SYNE1_MOUSE - Nesprin-1 OS=Mus musculus GN=Syne1 PE=1 SV=2	21	116	125	56	70	82	1.2596	0.6255	470
sp|P06151|LDHA_MOUSE - L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha P	7	21	6	3	10	14	1.2592	0.7086	61
sp|P01027|CO3_MOUSE - Complement C3 OS=Mus musculus GN=C3 PE=1 SV=3	23	130	51	35	78	49	1.2592	0.7052	366
sp|O35490|BHMT1_MOUSE - Betaine--homocysteine S-methyltransferase 1 OS=Mus muscu	61	152	162	54	100	146	1.25	0.581	675
sp|Q8CJH3|PLXB1_MOUSE - Plexin-B1 OS=Mus musculus GN=Plxnb1 PE=1 SV=2	4	11	0	7	5	0	1.25	0.8069	27
sp|Q64512|PTN13_MOUSE - Tyrosine-protein phosphatase non-receptor type 13 OS=Mus	2	21	7	7	15	2	1.25	0.7842	54
sp|Q9CYW4|HDHD3_MOUSE - Haloacid dehalogenase-like hydrolase domain-containing p	4	21	0	6	14	0	1.25	0.8373	45
sp|P70694|DHB5_MOUSE - Estradiol 17 beta-dehydrogenase 5 OS=Mus musculus GN=Akr1	3	7	0	4	4	0	1.25	0.7971	18
sp|Q6ZQ58|LARP1_MOUSE - La-related protein 1 OS=Mus musculus GN=Larp1 PE=1 SV=3	0	5	0	0	4	0	1.25	0.8834	9
sp|Q6PAC3|DCA13_MOUSE - DDB1- and CUL4-associated factor 13 OS=Mus musculus GN=D	0	5	0	0	4	0	1.25	0.8834	9
sp|Q80UC6|GPR62_MOUSE - Probable G-protein coupled receptor 62 OS=Mus musculus G	0	5	0	0	4	0	1.25	0.8834	9
sp|O88544|CSN4_MOUSE - COP9 signalosome complex subunit 4 OS=Mus musculus GN=Cop	0	5	40	2	5	29	1.25	0.8532	81
sp|Q8C152|FA46B_MOUSE - Protein FAM46B OS=Mus musculus GN=Fam46b PE=2 SV=3	0	5	0	2	2	0	1.25	0.8617	9
sp|Q62052|P_MOUSE - P protein OS=Mus musculus GN=Oca2 PE=1 SV=1	0	5	0	0	4	0	1.25	0.8834	9
sp|Q61214|DYR1A_MOUSE - Dual specificity tyrosine-phosphorylation-regulated kina	0	5	0	0	4	0	1.25	0.8834	9
sp|Q8R502|LRC8C_MOUSE - Volume-regulated anion channel subunit LRRC8C OS=Mus mus	0	5	0	4	0	0	1.25	0.8834	9
sp|Q80UM7|MOGS_MOUSE - Mannosyl-oligosaccharide glucosidase OS=Mus musculus GN=M	0	5	0	0	4	0	1.25	0.8834	9
sp|Q9WTL4|INSRR_MOUSE - Insulin receptor-related protein OS=Mus musculus GN=Insr	0	0	5	0	0	4	1.25	0.8834	9
sp|Q3B7Z2|OSBP1_MOUSE - Oxysterol-binding protein 1 OS=Mus musculus GN=Osbp PE=1	0	0	5	0	0	4	1.25	0.8834	9

sp|Q3V3Q4|PYDC3_MOUSE - Pyrin domain-containing protein 3 OS=Mus musculus GN=Pyd	0	0	10	0	0	8	1.25	0.8834	18
sp|Q8VCT4|CES1D_MOUSE - Carboxylesterase 1D OS=Mus musculus GN=Ces1d PE=1 SV=1	78	314	236	110	204	189	1.2485	0.6094	1131
sp|P97872|FMO5_MOUSE - Dimethylaniline monooxygenase [N-oxide-forming] 5 OS=Mus	31	60	5	12	54	11	1.2467	0.7808	173
sp|Q8K2B3|SDHA_MOUSE - Succinate dehydrogenase [ubiquinone] flavoprotein subunit	102	228	227	105	163	180	1.2433	0.4878	1005
sp|P67778|PHB_MOUSE - Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1	23	63	37	27	50	22	1.2424	0.6116	222
sp|P97807|FUMH_MOUSE - Fumarate hydratase, mitochondrial OS=Mus musculus GN=Fh P	52	156	116	53	104	104	1.2413	0.578	585
sp|Q61818|RAI1_MOUSE - Retinoic acid-induced protein 1 OS=Mus musculus GN=Rai1 P	2	24	0	4	17	0	1.238	0.8656	47
sp|Q6NZN1|PPRC1_MOUSE - Peroxisome proliferator-activated receptor gamma coactiv	8	22	7	14	16	0	1.2333	0.7551	67
sp|P07744|K2C4_MOUSE - Keratin, type II cytoskeletal 4 OS=Mus musculus GN=Krt4 P	0	45	3	0	39	0	1.2307	0.8851	87
sp|Q6IFX2|K1C42_MOUSE - Keratin, type I cytoskeletal 42 OS=Mus musculus GN=Krt42	23	67	92	18	52	78	1.2297	0.6921	330
sp|Q8C5H8|NAKD2_MOUSE - NAD kinase 2, mitochondrial OS=Mus musculus GN=Nadk2 PE=	10	61	4	7	51	3	1.2295	0.8537	136
sp|Q9CR56|KBRS2_MOUSE - NF-kappa-B inhibitor-interacting Ras-like protein 2 OS=M	12	3	12	8	0	14	1.2272	0.7576	49
sp|Q6PB66|LPPRC_MOUSE - Leucine-rich PPR motif-containing protein, mitochondrial	2	9	16	2	11	9	1.2272	0.7497	49
sp|P48962|ADT1_MOUSE - ADP/ATP translocase 1 OS=Mus musculus GN=Slc25a4 PE=1 SV=	4	52	15	10	32	16	1.2241	0.7991	129
sp|P06801|MAOX_MOUSE - NADP-dependent malic enzyme OS=Mus musculus GN=Me1 PE=1 S	2	9	0	0	9	0	1.2222	0.8774	20
sp|Q9DCX8|IYD1_MOUSE - Iodotyrosine dehalogenase 1 OS=Mus musculus GN=Iyd PE=1 S	0	11	0	0	6	3	1.2222	0.8774	20
sp|Q99K24|S39A3_MOUSE - Zinc transporter ZIP3 OS=Mus musculus GN=Slc39a3 PE=2 SV	0	6	5	0	9	0	1.2222	0.8593	20
sp|Q8CH09|SUGP2_MOUSE - SURP and G-patch domain-containing protein 2 OS=Mus musc	0	5	17	0	14	4	1.2222	0.8484	40
sp|Q6NZP2|GPBL1_MOUSE - Vasculin-like protein 1 OS=Mus musculus GN=Gpbp1l1 PE=1	0	11	0	2	7	0	1.2222	0.882	20
sp|Q99KI0|ACON_MOUSE - Aconitate hydratase, mitochondrial OS=Mus musculus GN=Aco	94	273	201	112	172	181	1.2215	0.5751	1033
sp|P17156|HSP72_MOUSE - Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=H	16	58	42	27	32	36	1.221	0.6057	211
sp|P34914|HYES_MOUSE - Bifunctional epoxide hydrolase 2 OS=Mus musculus GN=Ephx2	37	166	90	52	94	94	1.2208	0.6813	533
sp|Q60770|STXB3_MOUSE - Syntaxin-binding protein 3 OS=Mus musculus GN=Stxbp3 PE=	0	6	22	0	2	21	1.2173	0.8675	51
sp|Q8BW75|AOFB_MOUSE - Amine oxidase [flavin-containing] B OS=Mus musculus GN=Ma	92	271	177	127	191	126	1.2162	0.5982	984
sp|Q9DCC7|ISC2B_MOUSE - Isochorismatase domain-containing protein 2B, mitochondr	0	6	11	0	3	11	1.2142	0.8375	31
sp|O35129|PHB2_MOUSE - Prohibitin-2 OS=Mus musculus GN=Phb2 PE=1 SV=1	24	53	31	23	44	22	1.2134	0.6051	197
sp|O35448|PPT2_MOUSE - Lysosomal thioesterase PPT2 OS=Mus musculus GN=Ppt2 PE=2	2	11	27	0	8	25	1.2121	0.8331	73
sp|Q78PY7|SND1_MOUSE - Staphylococcal nuclease domain-containing protein 1 OS=Mu	17	77	55	16	49	58	1.2113	0.7098	272
sp|Q9Z2U2|ZN292_MOUSE - Zinc finger protein 292 OS=Mus musculus GN=Zfp292 PE=1 S	12	34	23	17	25	15	1.2105	0.6006	126
sp|O54828|RGS9_MOUSE - Regulator of G-protein signaling 9 OS=Mus musculus GN=Rgs	2	12	9	0	12	7	1.2105	0.785	42
sp|Q6GQW0|BTBDB_MOUSE - Ankyrin repeat and BTB/POZ domain-containing protein BTB	0	4	19	0	7	12	1.2105	0.853	42
sp|P19001|K1C19_MOUSE - Keratin, type I cytoskeletal 19 OS=Mus musculus GN=Krt19	22	86	88	13	71	78	1.2098	0.7239	358
sp|Q00897|A1AT4_MOUSE - Alpha-1-antitrypsin 1-4 OS=Mus musculus GN=Serpina1d PE=	13	39	0	14	29	0	1.2093	0.8429	95
sp|Q9D0F3|LMAN1_MOUSE - Protein ERGIC-53 OS=Mus musculus GN=Lman1 PE=2 SV=1	6	28	18	8	24	11	1.2093	0.7278	95
sp|Q3ULD5|MCCB_MOUSE - Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	9	49	0	13	33	2	1.2083	0.8588	106
sp|Q99L27|GMPR2_MOUSE - GMP reductase 2 OS=Mus musculus GN=Gmpr2 PE=2 SV=2	2	6	21	0	3	21	1.2083	0.8581	53
sp|P24369|PPIB_MOUSE - Peptidyl-prolyl cis-trans isomerase B OS=Mus musculus GN=	0	27	2	0	22	2	1.2083	0.8886	53
sp|Q8BGT5|ALAT2_MOUSE - Alanine aminotransferase 2 OS=Mus musculus GN=Gpt2 PE=1	5	30	0	10	19	0	1.2068	0.8618	64
sp|Q8QZT1|THIL_MOUSE - Acetyl-CoA acetyltransferase, mitochondrial OS=Mus muscul	44	261	147	103	174	98	1.2053	0.7223	827
sp|Q9WVJ3|CBPQ_MOUSE - Carboxypeptidase Q OS=Mus musculus GN=Cpq PE=2 SV=1	9	27	17	11	26	7	1.2045	0.7194	97
sp|P09103|PDIA1_MOUSE - Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1	140	497	378	179	307	358	1.2026	0.6534	1859

sp|O55126|NIPS2_MOUSE - Protein NipSnap homolog 2 OS=Mus musculus GN=Gbas PE=2 S	5	13	0	3	12	0	1.2	0.8576	33
sp|Q91XF0|PNPO_MOUSE - Pyridoxine-5'-phosphate oxidase OS=Mus musculus GN=Pnpo P	2	4	0	0	5	0	1.2	0.8774	11
sp|Q9Z1W9|STK39_MOUSE - STE20/SPS1-related proline-alanine-rich protein kinase O	2	2	20	3	0	17	1.2	0.8751	44
sp|Q8BFR4|GNS_MOUSE - N-acetylglucosamine-6-sulfatase OS=Mus musculus GN=Gns PE=	2	19	3	0	12	8	1.2	0.8484	44
sp|Q80XL6|ACD11_MOUSE - Acyl-CoA dehydrogenase family member 11 OS=Mus musculus	2	10	0	4	6	0	1.2	0.8593	22
sp|Q8CEC5|KBRS1_MOUSE - NF-kappa-B inhibitor-interacting Ras-like protein 1 OS=M	0	0	12	0	10	0	1.2	0.9043	22
sp|Q61087|LAMB3_MOUSE - Laminin subunit beta-3 OS=Mus musculus GN=Lamb3 PE=2 SV=	0	20	16	7	2	21	1.2	0.8224	66
sp|P54103|DNJC2_MOUSE - DnaJ homolog subfamily C member 2 OS=Mus musculus GN=Dna	0	5	7	0	0	10	1.2	0.8735	22
sp|P62984|RL40_MOUSE - Ubiquitin-60S ribosomal protein L40 OS=Mus musculus GN=Ub	0	6	0	0	5	0	1.2	0.9043	11
sp|P05064|ALDOA_MOUSE - Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldo	0	6	0	3	2	0	1.2	0.8861	11
sp|Q8VDJ3|VIGLN_MOUSE - Vigilin OS=Mus musculus GN=Hdlbp PE=1 SV=1	0	18	30	4	13	23	1.2	0.8085	88
sp|Q6P5D4|CP135_MOUSE - Centrosomal protein of 135 kDa OS=Mus musculus GN=Cep135	0	6	0	0	5	0	1.2	0.9043	11
sp|Q9D5R3|CEP83_MOUSE - Centrosomal protein of 83 kDa OS=Mus musculus GN=Cep83 P	0	2	16	0	0	15	1.2	0.8947	33
sp|Q0VGY8|TANC1_MOUSE - Protein TANC1 OS=Mus musculus GN=Tanc1 PE=2 SV=2	0	0	12	0	0	10	1.2	0.9043	22
sp|Q91VR2|ATPG_MOUSE - ATP synthase subunit gamma, mitochondrial OS=Mus musculus	24	138	62	39	89	59	1.1978	0.7526	411
sp|Q9DBT9|M2GD_MOUSE - Dimethylglycine dehydrogenase, mitochondrial OS=Mus muscu	106	423	175	117	310	162	1.1952	0.7505	1293
sp|P23953|EST1C_MOUSE - Carboxylesterase 1C OS=Mus musculus GN=Ces1c PE=1 SV=4	9	57	58	18	39	47	1.1923	0.7345	228
sp|Q9DC50|OCTC_MOUSE - Peroxisomal carnitine O-octanoyltransferase OS=Mus muscul	17	79	67	22	56	59	1.1897	0.7183	300
sp|Q9JLC8|SACS_MOUSE - Sacsin OS=Mus musculus GN=Sacs PE=1 SV=2	4	36	4	27	10	0	1.1891	0.8689	81
sp|Q08EC4|CASS4_MOUSE - Cas scaffolding protein family member 4 OS=Mus musculus	4	7	8	6	6	4	1.1875	0.5071	35
sp|Q9D312|K1C20_MOUSE - Keratin, type I cytoskeletal 20 OS=Mus musculus GN=Krt20	0	19	0	0	16	0	1.1875	0.9097	35
sp|P63017|HSP7C_MOUSE - Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hsp	31	100	73	46	72	54	1.186	0.6457	376
sp|P24270|CATA_MOUSE - Catalase OS=Mus musculus GN=Cat PE=1 SV=4	231	884	606	322	584	546	1.1852	0.6859	3173
sp|Q921G7|ETFD_MOUSE - Electron transfer flavoprotein-ubiquinone oxidoreductase,	55	164	162	48	111	163	1.1832	0.7087	703
sp|B2RQC6|PYR1_MOUSE - CAD protein OS=Mus musculus GN=Cad PE=2 SV=1	39	96	60	43	75	47	1.1818	0.6342	360
sp|P62737|ACTA_MOUSE - Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1	0	26	0	0	22	0	1.1818	0.9121	48
sp|P26039|TLN1_MOUSE - Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=2	0	13	0	0	5	6	1.1818	0.8943	24
sp|Q9D0M3|CY1_MOUSE - Cytochrome c1, heme protein, mitochondrial OS=Mus musculus	15	80	3	36	47	0	1.1807	0.866	181
sp|E9Q557|DESP_MOUSE - Desmoplakin OS=Mus musculus GN=Dsp PE=1 SV=1	5	64	23	10	52	16	1.1794	0.8412	170
sp|Q9QXE0|HACL1_MOUSE - 2-hydroxyacyl-CoA lyase 1 OS=Mus musculus GN=Hacl1 PE=1	40	133	44	47	84	53	1.1793	0.7516	401
sp|Q9Z2Z6|MCAT_MOUSE - Mitochondrial carnitine/acylcarnitine carrier protein OS=	4	25	18	3	18	19	1.175	0.7864	87
sp|Q6IFZ6|K2C1B_MOUSE - Keratin, type II cytoskeletal 1b OS=Mus musculus GN=Krt7	0	97	11	8	77	7	1.1739	0.8963	200
sp|Q99KB8|GLO2_MOUSE - Hydroxyacylglutathione hydrolase, mitochondrial OS=Mus mu	0	24	10	7	14	8	1.1724	0.8305	63
sp|A6BLY7|K1C28_MOUSE - Keratin, type I cytoskeletal 28 OS=Mus musculus GN=Krt28	7	29	47	8	32	31	1.169	0.7888	154
sp|P51174|ACADL_MOUSE - Long-chain specific acyl-CoA dehydrogenase, mitochondria	84	267	245	104	177	229	1.1686	0.6955	1106
sp|Q07417|ACADS_MOUSE - Short-chain specific acyl-CoA dehydrogenase, mitochondri	39	129	131	55	86	115	1.1679	0.7026	555
sp|Q9CQY5|MAGT1_MOUSE - Magnesium transporter protein 1 OS=Mus musculus GN=Magt1	2	5	0	0	6	0	1.1666	0.8992	13
sp|Q0VET5|LMTD2_MOUSE - Lamin tail domain-containing protein 2 OS=Mus musculus G	0	13	8	5	10	3	1.1666	0.8283	39
sp|Q9D7N9|APMAP_MOUSE - Adipocyte plasma membrane-associated protein OS=Mus musc	0	7	0	0	6	0	1.1666	0.9188	13
sp|O09159|MA2B1_MOUSE - Lysosomal alpha-mannosidase OS=Mus musculus GN=Man2b1 PE	17	58	17	26	44	9	1.1645	0.8113	171
sp|P38647|GRP75_MOUSE - Stress-70 protein, mitochondrial OS=Mus musculus GN=Hspa	159	461	263	219	292	248	1.1633	0.6735	1642

sp|P52196|THTR_MOUSE - Thiosulfate sulfurtransferase OS=Mus musculus GN=Tst PE=1	69	245	164	107	159	146	1.1601	0.7004	890
sp|P70248|MYO1F_MOUSE - Unconventional myosin-If OS=Mus musculus GN=Myo1f PE=1 S	0	27	24	0	22	22	1.159	0.8459	95
sp|Q9DB77|QCR2_MOUSE - Cytochrome b-c1 complex subunit 2, mitochondrial OS=Mus m	51	143	40	66	99	37	1.1584	0.7888	436
sp|Q9JLT4|TRXR2_MOUSE - Thioredoxin reductase 2, mitochondrial OS=Mus musculus G	10	21	13	2	22	14	1.1578	0.7793	82
sp|O08749|DLDH_MOUSE - Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus musculu	33	115	102	52	71	93	1.1574	0.707	466
sp|Q922J3|CLIP1_MOUSE - CAP-Gly domain-containing linker protein 1 OS=Mus muscul	0	12	69	0	14	56	1.1571	0.899	151
sp|Q9CQA3|SDHB_MOUSE - Succinate dehydrogenase [ubiquinone] iron-sulfur subunit,	22	79	54	15	63	56	1.1567	0.769	289
sp|P20029|GRP78_MOUSE - 78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa	114	423	284	192	296	223	1.1547	0.7178	1532
sp|P62932|FBX40_MOUSE - F-box only protein 40 OS=Mus musculus GN=Fbxo40 PE=2 SV=	0	0	15	0	0	13	1.1538	0.9246	28
sp|Q9JLJ2|AL9A1_MOUSE - 4-trimethylaminobutyraldehyde dehydrogenase OS=Mus muscu	30	86	28	37	61	27	1.152	0.7831	269
sp|P36552|HEM6_MOUSE - Oxygen-dependent coproporphyrinogen-III oxidase, mitochon	6	32	0	11	22	0	1.1515	0.8935	71
sp|Q924C1|XPO5_MOUSE - Exportin-5 OS=Mus musculus GN=Xpo5 PE=2 SV=1	0	13	10	3	0	17	1.15	0.886	43
sp|Q62148|AL1A2_MOUSE - Retinal dehydrogenase 2 OS=Mus musculus GN=Aldh1a2 PE=2	11	41	41	8	25	48	1.1481	0.8067	174
sp|P97821|CATC_MOUSE - Dipeptidyl peptidase 1 OS=Mus musculus GN=Ctsc PE=2 SV=1	2	23	14	7	10	17	1.147	0.8175	73
sp|Q9R0G8|NRK_MOUSE - Nik-related protein kinase OS=Mus musculus GN=Nrk PE=1 SV=	78	249	381	112	168	339	1.1437	0.8027	1327
sp|P97461|RS5_MOUSE - 40S ribosomal protein S5 OS=Mus musculus GN=Rps5 PE=1 SV=3	4	4	0	2	5	0	1.1428	0.8739	15
sp|P15508|SPTB1_MOUSE - Spectrin beta chain, erythrocytic OS=Mus musculus GN=Spt	3	17	4	0	16	5	1.1428	0.8857	45
sp|Q69ZQ1|K1161_MOUSE - Uncharacterized family 31 glucosidase KIAA1161 OS=Mus mu	0	8	0	0	7	0	1.1428	0.9295	15
sp|Q9Z247|FKBP9_MOUSE - Peptidyl-prolyl cis-trans isomerase FKBP9 OS=Mus musculu	0	0	8	0	0	7	1.1428	0.9295	15
sp|Q60930|VDAC2_MOUSE - Voltage-dependent anion-selective channel protein 2 OS=M	15	33	41	9	23	46	1.141	0.7956	167
sp|Q05920|PYC_MOUSE - Pyruvate carboxylase, mitochondrial OS=Mus musculus GN=Pc	168	432	330	218	352	247	1.1383	0.6873	1747
sp|Q9D845|TEX9_MOUSE - Testis-expressed sequence 9 protein OS=Mus musculus GN=Te	0	6	27	7	0	22	1.1379	0.9045	62
sp|P45952|ACADM_MOUSE - Medium-chain specific acyl-CoA dehydrogenase, mitochondr	81	195	231	102	199	145	1.1367	0.7218	953
sp|Q91ZU6|DYST_MOUSE - Dystonin OS=Mus musculus GN=Dst PE=1 SV=2	30	68	103	41	78	58	1.1355	0.752	378
sp|Q9R087|GPC6_MOUSE - Glypican-6 OS=Mus musculus GN=Gpc6 PE=1 SV=1	8	19	7	3	14	13	1.1333	0.8105	64
sp|Q8BWT1|THIM_MOUSE - 3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN	80	526	184	174	319	206	1.1301	0.8409	1489
sp|Q60759|GCDH_MOUSE - Glutaryl-CoA dehydrogenase, mitochondrial OS=Mus musculus	27	97	76	41	71	65	1.1299	0.7522	377
sp|Q9JHI5|IVD_MOUSE - Isovaleryl-CoA dehydrogenase, mitochondrial OS=Mus musculu	48	144	135	53	87	150	1.1275	0.7824	617
sp|P29758|OAT_MOUSE - Ornithine aminotransferase, mitochondrial OS=Mus musculus	64	204	95	80	154	88	1.1273	0.792	685
sp|Q99JY0|ECHB_MOUSE - Trifunctional enzyme subunit beta, mitochondrial OS=Mus m	66	194	121	59	175	104	1.1272	0.7892	719
sp|Q61578|ADRO_MOUSE - NADPH:adrenodoxin oxidoreductase, mitochondrial OS=Mus mu	10	40	13	12	34	10	1.125	0.8582	119
sp|Q9D3S3|SNX29_MOUSE - Sorting nexin-29 OS=Mus musculus GN=Snx29 PE=1 SV=2	3	6	0	4	4	0	1.125	0.8861	17
sp|Q3UTB7|FOXR1_MOUSE - Forkhead box protein R1 OS=Mus musculus GN=Foxr1 PE=2 SV	2	7	0	4	4	0	1.125	0.8992	17
sp|Q62087|PON3_MOUSE - Serum paraoxonase/lactonase 3 OS=Mus musculus GN=Pon3 PE=	2	11	5	0	12	4	1.125	0.8871	34
sp|Q9CZ42|NNRD_MOUSE - ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Mus musc	0	9	0	3	5	0	1.125	0.9251	17
sp|O55143|AT2A2_MOUSE - Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=M	0	9	0	0	8	0	1.125	0.9378	17
sp|A2CG63|ARI4B_MOUSE - AT-rich interactive domain-containing protein 4B OS=Mus	0	9	0	2	0	6	1.125	0.9283	17
sp|Q61102|ABCB7_MOUSE - ATP-binding cassette sub-family B member 7, mitochondria	0	9	0	2	6	0	1.125	0.9283	17
sp|O08638|MYH11_MOUSE - Myosin-11 OS=Mus musculus GN=Myh11 PE=1 SV=1	0	9	0	0	8	0	1.125	0.9378	17
sp|Q3U1N2|SRBP2_MOUSE - Sterol regulatory element-binding protein 2 OS=Mus muscu	0	4	5	0	0	8	1.125	0.9188	17
sp|P29391|FRIL1_MOUSE - Ferritin light chain 1 OS=Mus musculus GN=Ftl1 PE=1 SV=2	0	9	0	2	6	0	1.125	0.9283	17

sp|P47738|ALDH2_MOUSE - Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN	186	559	356	260	387	333	1.1234	0.7411	2081
sp|Q9D826|SOX_MOUSE - Peroxisomal sarcosine oxidase OS=Mus musculus GN=Pipox PE=	10	82	55	23	58	50	1.1221	0.8317	278
sp|Q9ET22|DPP2_MOUSE - Dipeptidyl peptidase 2 OS=Mus musculus GN=Dpp7 PE=2 SV=2	15	22	0	6	21	6	1.1212	0.8786	70
sp|Q8VCU1|EST3B_MOUSE - Carboxylesterase 3B OS=Mus musculus GN=Ces3b PE=2 SV=2	2	26	0	2	23	0	1.12	0.9327	53
sp|Q60603|KCNH1_MOUSE - Potassium voltage-gated channel subfamily H member 1 OS=	2	30	24	3	21	26	1.12	0.8646	106
sp|Q8R086|SUOX_MOUSE - Sulfite oxidase, mitochondrial OS=Mus musculus GN=Suox PE	25	83	25	33	72	14	1.1176	0.8652	252
sp|Q8VCC2|EST1_MOUSE - Liver carboxylesterase 1 OS=Mus musculus GN=Ces1 PE=2 SV=	40	140	134	52	98	131	1.1174	0.7952	595
sp|P07724|ALBU_MOUSE - Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3	338	1240	980	515	863	919	1.1136	0.7836	4855
sp|P08730|K1C13_MOUSE - Keratin, type I cytoskeletal 13 OS=Mus musculus GN=Krt13	32	126	90	45	100	78	1.1121	0.8056	471
sp|Q9CPW4|ARPC5_MOUSE - Actin-related protein 2/3 complex subunit 5 OS=Mus muscu	4	6	0	5	4	0	1.1111	0.8933	19
sp|Q5FWI3|TMEM2_MOUSE - Transmembrane protein 2 OS=Mus musculus GN=Tmem2 PE=1 SV	0	10	0	2	2	5	1.1111	0.9283	19
sp|Q60648|SAP3_MOUSE - Ganglioside GM2 activator OS=Mus musculus GN=Gm2a PE=1 SV	0	10	0	2	7	0	1.1111	0.9364	19
sp|Q99NB9|SF3B1_MOUSE - Splicing factor 3B subunit 1 OS=Mus musculus GN=Sf3b1 PE	0	3	7	7	2	0	1.1111	0.9142	19
sp|A2ARZ3|FSIP2_MOUSE - Fibrous sheath-interacting protein 2 OS=Mus musculus GN=	33	88	84	57	61	67	1.1081	0.729	390
sp|Q9QWL7|K1C17_MOUSE - Keratin, type I cytoskeletal 17 OS=Mus musculus GN=Krt17	17	109	100	30	86	88	1.1078	0.8438	430
sp|Q9EQ20|MMSA_MOUSE - Methylmalonate-semialdehyde dehydrogenase [acylating], mi	66	275	144	92	185	161	1.1073	0.8267	923
sp|Q8C196|CPSM_MOUSE - Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=	1102	3059	2312	1790	2405	1651	1.1072	0.7512	12319
sp|Q6PCM1|KDM3A_MOUSE - Lysine-specific demethylase 3A OS=Mus musculus GN=Kdm3a	0	14	28	5	9	24	1.1052	0.8997	80
sp|Q7TMY8|HUWE1_MOUSE - E3 ubiquitin-protein ligase HUWE1 OS=Mus musculus GN=Huw	0	0	21	7	0	12	1.1052	0.9361	40
sp|Q63880|EST3A_MOUSE - Carboxylesterase 3A OS=Mus musculus GN=Ces3a PE=1 SV=2	13	52	34	13	41	36	1.1	0.8428	189
sp|Q91W64|CP270_MOUSE - Cytochrome P450 2C70 OS=Mus musculus GN=Cyp2c70 PE=2 SV=	2	20	0	7	13	0	1.1	0.9324	42
sp|Q9Z0W3|NU160_MOUSE - Nuclear pore complex protein Nup160 OS=Mus musculus GN=N	0	11	0	2	8	0	1.1	0.943	21
sp|Q8VCZ9|PROD2_MOUSE - Probable proline dehydrogenase 2 OS=Mus musculus GN=Prod	11	61	30	25	45	23	1.0967	0.8619	195
sp|Q8K370|ACD10_MOUSE - Acyl-CoA dehydrogenase family member 10 OS=Mus musculus	0	19	4	3	15	3	1.0952	0.929	44
sp|Q03265|ATPA_MOUSE - ATP synthase subunit alpha, mitochondrial OS=Mus musculus	260	726	494	386	561	405	1.0946	0.7839	2832
sp|Q8BHN3|GANAB_MOUSE - Neutral alpha-glucosidase AB OS=Mus musculus GN=Ganab PE	23	56	3	15	54	6	1.0933	0.9182	157
sp|Q91ZA3|PCCA_MOUSE - Propionyl-CoA carboxylase alpha chain, mitochondrial OS=M	47	117	49	54	80	61	1.0923	0.817	408
sp|Q99MZ7|PECR_MOUSE - Peroxisomal trans-2-enoyl-CoA reductase OS=Mus musculus G	13	37	10	11	24	20	1.0909	0.8674	115
sp|Q3TUA9|SG196_MOUSE - Protein O-mannose kinase OS=Mus musculus GN=Pomk PE=2 SV	0	0	12	0	0	11	1.0909	0.9539	23
sp|Q9DCM0|ETHE1_MOUSE - Persulfide dioxygenase ETHE1, mitochondrial OS=Mus muscu	15	39	20	20	24	24	1.0882	0.8011	142
sp|Q922U2|K2C5_MOUSE - Keratin, type II cytoskeletal 5 OS=Mus musculus GN=Krt5 P	0	108	55	6	116	28	1.0866	0.9292	313
sp|Q9WV54|ASAH1_MOUSE - Acid ceramidase OS=Mus musculus GN=Asah1 PE=1 SV=1	2	18	6	4	10	10	1.0833	0.9043	50
sp|A6H6A4|LRIQ4_MOUSE - Leucine-rich repeat and IQ domain-containing protein 4 O	2	11	0	8	4	0	1.0833	0.939	25
sp|Q9DA08|SGF29_MOUSE - SAGA-associated factor 29 homolog OS=Mus musculus GN=Ccd	0	16	23	4	9	23	1.0833	0.9156	75
sp|Q99104|MYO5A_MOUSE - Unconventional myosin-Va OS=Mus musculus GN=Myo5a PE=1 S	0	16	23	0	14	22	1.0833	0.92	75
sp|Q8BIJ6|SYIM_MOUSE - Isoleucine--tRNA ligase, mitochondrial OS=Mus musculus GN	0	13	0	0	12	0	1.0833	0.9576	25
sp|P16406|AMPE_MOUSE - Glutamyl aminopeptidase OS=Mus musculus GN=Enpep PE=1 SV=	0	13	0	3	9	0	1.0833	0.9508	25
sp|O09174|AMACR_MOUSE - Alpha-methylacyl-CoA racemase OS=Mus musculus GN=Amacr P	34	95	54	48	72	49	1.0828	0.8234	352
sp|Q61781|K1C14_MOUSE - Keratin, type I cytoskeletal 14 OS=Mus musculus GN=Krt14	13	99	114	19	103	87	1.0813	0.8959	435
sp|P16858|G3P_MOUSE - Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus G	0	27	0	0	25	0	1.08	0.9592	52
sp|Q8R164|BPHL_MOUSE - Valacyclovir hydrolase OS=Mus musculus GN=Bphl PE=1 SV=1	22	125	44	29	108	40	1.079	0.9125	368

sp|Q6Q2Z6|ACOT5_MOUSE - Acyl-coenzyme A thioesterase 5 OS=Mus musculus GN=Acot5	12	44	40	23	40	26	1.0786	0.8471	185
sp|Q99KR7|PPIF_MOUSE - Peptidyl-prolyl cis-trans isomerase F, mitochondrial OS=M	0	8	6	0	10	3	1.0769	0.9345	27
sp|P50544|ACADV_MOUSE - Very long-chain specific acyl-CoA dehydrogenase, mitocho	20	97	10	24	87	7	1.0762	0.9388	245
sp|O88451|RDH7_MOUSE - Retinol dehydrogenase 7 OS=Mus musculus GN=Rdh7 PE=2 SV=1	19	59	7	22	41	16	1.0759	0.9141	164
sp|Q8BGA8|ACSM5_MOUSE - Acyl-coenzyme A synthetase ACSM5, mitochondrial OS=Mus m	2	35	6	8	30	2	1.075	0.9442	83
sp|Q5SSH7|ZZEF1_MOUSE - Zinc finger ZZ-type and EF-hand domain-containing protei	6	23	0	10	4	13	1.074	0.9323	56
sp|Q9QWR8|NAGAB_MOUSE - Alpha-N-acetylgalactosaminidase OS=Mus musculus GN=Naga	3	21	5	6	17	4	1.074	0.9285	56
sp|Q91X34|BAAT_MOUSE - Bile acid-CoA:amino acid N-acyltransferase OS=Mus musculu	12	42	20	17	35	17	1.0724	0.8847	143
sp|Q7TMF3|NDUAC_MOUSE - NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subun	0	15	0	0	14	0	1.0714	0.9634	29
sp|Q61414|K1C15_MOUSE - Keratin, type I cytoskeletal 15 OS=Mus musculus GN=Krt15	14	132	130	22	124	112	1.0697	0.9112	534
sp|Q9R0H0|ACOX1_MOUSE - Peroxisomal acyl-coenzyme A oxidase 1 OS=Mus musculus GN	104	448	323	126	347	347	1.067	0.8901	1695
sp|Q61646|HPT_MOUSE - Haptoglobin OS=Mus musculus GN=Hp PE=1 SV=1	7	17	8	6	17	7	1.0666	0.8949	62
sp|P15105|GLNA_MOUSE - Glutamine synthetase OS=Mus musculus GN=Glul PE=1 SV=6	10	22	0	2	28	0	1.0666	0.9547	62
sp|P54869|HMCS2_MOUSE - Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Mus	69	298	170	91	223	190	1.0654	0.8936	1041
sp|Q9D172|ES1_MOUSE - ES1 protein homolog, mitochondrial OS=Mus musculus GN=D10J	11	39	82	22	34	68	1.0645	0.9196	256
sp|B2RY04|DOCK5_MOUSE - Dedicator of cytokinesis protein 5 OS=Mus musculus GN=Do	0	3	30	3	9	19	1.0645	0.9529	64
sp|Q99MR8|MCCA_MOUSE - Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondr	26	56	37	29	58	25	1.0625	0.872	231
sp|A2AUM9|CE152_MOUSE - Centrosomal protein of 152 kDa OS=Mus musculus GN=Cep152	0	17	18	0	18	15	1.0606	0.9381	68
sp|Q922R8|PDIA6_MOUSE - Protein disulfide-isomerase A6 OS=Mus musculus GN=Pdia6	16	49	23	30	43	10	1.0602	0.9102	171
sp|Q80X89|UD2A1_MOUSE - UDP-glucuronosyltransferase 2A1 OS=Mus musculus GN=Ugt2a	0	18	0	0	17	0	1.0588	0.9697	35
sp|Q8R0N6|HOT_MOUSE - Hydroxyacid-oxoacid transhydrogenase, mitochondrial OS=Mus	0	16	2	5	10	2	1.0588	0.9549	35
sp|E9PZQ0|RYR1_MOUSE - Ryanodine receptor 1 OS=Mus musculus GN=Ryr1 PE=1 SV=1	0	18	0	0	17	0	1.0588	0.9697	35
sp|O08573|LEG9_MOUSE - Galectin-9 OS=Mus musculus GN=Lgals9 PE=1 SV=1	0	18	0	0	8	9	1.0588	0.9623	35
sp|P02535|K1C10_MOUSE - Keratin, type I cytoskeletal 10 OS=Mus musculus GN=Krt10	47	240	183	62	213	169	1.0585	0.9108	914
sp|P41216|ACSL1_MOUSE - Long-chain-fatty-acid--CoA ligase 1 OS=Mus musculus GN=A	47	133	64	44	107	80	1.0562	0.8988	475
sp|Q9JLZ3|AUHM_MOUSE - Methylglutaconyl-CoA hydratase, mitochondrial OS=Mus musc	10	38	50	18	31	44	1.0537	0.9111	191
sp|Q8VHE6|DYH5_MOUSE - Dynein heavy chain 5, axonemal OS=Mus musculus GN=Dnah5 P	0	20	0	6	13	0	1.0526	0.9673	39
sp|Q811M1|RHG15_MOUSE - Rho GTPase-activating protein 15 OS=Mus musculus GN=Arhg	11	56	119	21	51	105	1.0508	0.9435	363
sp|Q9CQX2|CYB5B_MOUSE - Cytochrome b5 type B OS=Mus musculus GN=Cyb5b PE=1 SV=1	21	66	43	14	59	51	1.0483	0.9212	254
sp|Q571F8|GLSL_MOUSE - Glutaminase liver isoform, mitochondrial OS=Mus musculus	2	19	2	5	17	0	1.0454	0.967	45
sp|Q9QZZ4|MYO15_MOUSE - Unconventional myosin-XV OS=Mus musculus GN=Myo15a PE=1	0	14	9	0	9	13	1.0454	0.9555	45
sp|Q9DBF1|AL7A1_MOUSE - Alpha-aminoadipic semialdehyde dehydrogenase OS=Mus musc	54	138	112	64	122	105	1.0446	0.8928	595
sp|Q9WUB3|PYGM_MOUSE - Glycogen phosphorylase, muscle form OS=Mus musculus GN=Py	0	14	11	3	17	4	1.0416	0.9597	49
sp|Q8CHT0|AL4A1_MOUSE - Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochond	79	263	259	109	215	253	1.0415	0.9195	1178
sp|P14211|CALR_MOUSE - Calreticulin OS=Mus musculus GN=Calr PE=1 SV=1	20	61	20	21	49	27	1.0412	0.9379	198
sp|Q8QZR3|EST2A_MOUSE - Pyrethroid hydrolase Ces2a OS=Mus musculus GN=Ces2a PE=1	26	83	45	35	66	47	1.0405	0.9213	302
sp|P27773|PDIA3_MOUSE - Protein disulfide-isomerase A3 OS=Mus musculus GN=Pdia3	50	153	87	56	124	99	1.0394	0.9239	569
sp|O35711|LIPB2_MOUSE - Liprin-beta-2 OS=Mus musculus GN=Ppfibp2 PE=1 SV=3	6	47	0	10	41	0	1.0392	0.974	104
sp|P08249|MDHM_MOUSE - Malate dehydrogenase, mitochondrial OS=Mus musculus GN=Md	62	215	156	105	179	133	1.0383	0.9193	850
sp|Q99LB7|SARDH_MOUSE - Sarcosine dehydrogenase, mitochondrial OS=Mus musculus G	249	604	499	303	493	507	1.0376	0.9016	2655
sp|Q497I4|KRT35_MOUSE - Keratin, type I cuticular Ha5 OS=Mus musculus GN=Krt35 P	7	36	14	5	35	15	1.0363	0.9597	112

sp|Q91WG0|EST2C_MOUSE - Acylcarnitine hydrolase OS=Mus musculus GN=Ces2c PE=1 SV	5	25	0	12	17	0	1.0344	0.9727	59
sp|Q9DB20|ATPO_MOUSE - ATP synthase subunit O, mitochondrial OS=Mus musculus GN=	44	109	31	52	92	34	1.0337	0.9493	362
sp|P47708|RP3A_MOUSE - Rabphilin-3A OS=Mus musculus GN=Rph3a PE=1 SV=2	24	59	135	21	60	130	1.0331	0.9617	429
sp|P54071|IDHP_MOUSE - Isocitrate dehydrogenase [NADP], mitochondrial OS=Mus mus	40	129	80	36	106	99	1.0331	0.9413	490
sp|Q61425|HCDH_MOUSE - Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Mu	50	212	145	92	134	169	1.0303	0.9423	802
sp|P05202|AATM_MOUSE - Aspartate aminotransferase, mitochondrial OS=Mus musculus	174	475	351	235	396	340	1.0298	0.9271	1971
sp|Q9D6Y7|MSRA_MOUSE - Mitochondrial peptide methionine sulfoxide reductase OS=M	5	24	6	6	23	5	1.0294	0.9706	69
sp|Q8CFA2|GCST_MOUSE - Aminomethyltransferase, mitochondrial OS=Mus musculus GN=	6	17	12	0	20	14	1.0294	0.9628	69
sp|A6PWD2|FHAD1_MOUSE - Forkhead-associated domain-containing protein 1 OS=Mus m	0	19	18	15	17	4	1.0277	0.9661	73
sp|P18242|CATD_MOUSE - Cathepsin D OS=Mus musculus GN=Ctsd PE=1 SV=1	16	48	22	20	35	29	1.0238	0.9535	170
sp|P05784|K1C18_MOUSE - Keratin, type I cytoskeletal 18 OS=Mus musculus GN=Krt18	7	36	45	9	32	45	1.0232	0.9678	174
sp|Q9QXD1|ACOX2_MOUSE - Peroxisomal acyl-coenzyme A oxidase 2 OS=Mus musculus GN	19	118	48	34	100	47	1.022	0.9719	366
sp|Q9CZS1|AL1B1_MOUSE - Aldehyde dehydrogenase X, mitochondrial OS=Mus musculus	32	95	59	28	79	75	1.0219	0.9592	368
sp|B5X0G2|MUP17_MOUSE - Major urinary protein 17 OS=Mus musculus GN=Mup17 PE=2 S	5	26	19	4	12	33	1.0204	0.9764	99
sp|P22599|A1AT2_MOUSE - Alpha-1-antitrypsin 1-2 OS=Mus musculus GN=Serpina1b PE=	7	46	0	13	39	0	1.0192	0.9863	105
sp|Q8BWN8|ACOT4_MOUSE - Acyl-coenzyme A thioesterase 4 OS=Mus musculus GN=Acot4	32	66	41	24	67	49	0.9928	0.9844	279
sp|P58710|GGLO_MOUSE - L-gulonolactone oxidase OS=Mus musculus GN=Gulo PE=1 SV=3	24	53	37	37	44	34	0.9913	0.9719	229
sp|Q99NH2|PARD3_MOUSE - Partitioning defective 3 homolog OS=Mus musculus GN=Pard	8	20	30	6	22	31	0.983	0.9742	117
sp|P56480|ATPB_MOUSE - ATP synthase subunit beta, mitochondrial OS=Mus musculus	252	714	336	461	561	303	0.9826	0.9642	2627
sp|P97501|FMO3_MOUSE - Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Mus	6	34	4	4	33	8	0.9777	0.9811	89
sp|Q61543|GSLG1_MOUSE - Golgi apparatus protein 1 OS=Mus musculus GN=Glg1 PE=1 S	4	33	6	16	28	0	0.9772	0.9798	87
sp|Q99LB2|DHRS4_MOUSE - Dehydrogenase/reductase SDR family member 4 OS=Mus muscu	21	44	15	25	47	10	0.9756	0.964	162
sp|Q8BWQ1|UD2A3_MOUSE - UDP-glucuronosyltransferase 2A3 OS=Mus musculus GN=Ugt2a	4	59	13	15	57	6	0.9743	0.9784	154
sp|P57016|LAD1_MOUSE - Ladinin-1 OS=Mus musculus GN=Lad1 PE=2 SV=1	0	15	61	0	22	56	0.9743	0.9796	154
sp|Q6ZQ06|CE162_MOUSE - Centrosomal protein of 162 kDa OS=Mus musculus GN=Cep162	33	121	47	68	91	48	0.971	0.95	408
sp|Q8QZS1|HIBCH_MOUSE - 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Mus	5	35	23	10	28	27	0.9692	0.9524	128
sp|Q922Q1|MARC2_MOUSE - Mitochondrial amidoxime reducing component 2 OS=Mus musc	28	66	54	20	74	59	0.9673	0.9363	301
sp|Q3UV17|K22O_MOUSE - Keratin, type II cytoskeletal 2 oral OS=Mus musculus GN=K	3	57	29	4	51	37	0.9673	0.9641	181
sp|O08807|PRDX4_MOUSE - Peroxiredoxin-4 OS=Mus musculus GN=Prdx4 PE=1 SV=1	0	27	0	12	16	0	0.9642	0.9755	55
sp|Q9Z2K1|K1C16_MOUSE - Keratin, type I cytoskeletal 16 OS=Mus musculus GN=Krt16	10	80	96	10	93	90	0.9637	0.9538	379
sp|P11930|NUD19_MOUSE - Nucleoside diphosphate-linked moiety X motif 19, mitocho	4	21	0	6	20	0	0.9615	0.9714	51
sp|Q8C9S4|CC186_MOUSE - Coiled-coil domain-containing protein 186 OS=Mus musculu	0	5	43	4	12	34	0.96	0.9692	98
sp|P50429|ARSB_MOUSE - Arylsulfatase B OS=Mus musculus GN=Arsb PE=2 SV=3	5	17	0	4	19	0	0.9565	0.9674	45
sp|Q9WU19|HAOX1_MOUSE - Hydroxyacid oxidase 1 OS=Mus musculus GN=Hao1 PE=1 SV=1	8	12	0	10	11	0	0.9523	0.9498	41
sp|P48410|ABCD1_MOUSE - ATP-binding cassette sub-family D member 1 OS=Mus muscul	2	17	0	4	16	0	0.95	0.9653	39
sp|O88844|IDHC_MOUSE - Isocitrate dehydrogenase [NADP] cytoplasmic OS=Mus muscul	7	56	21	8	45	36	0.9438	0.9319	173
sp|A2A6A1|GPTC8_MOUSE - G patch domain-containing protein 8 OS=Mus musculus GN=G	0	13	3	3	6	8	0.9411	0.9404	33
sp|Q80U49|C170B_MOUSE - Centrosomal protein of 170 kDa protein B OS=Mus musculus	0	0	16	0	9	8	0.9411	0.9586	33
sp|Q71RI9|KAT3_MOUSE - Kynurenine--oxoglutarate transaminase 3 OS=Mus musculus G	5	25	0	10	20	2	0.9375	0.9459	62
sp|P46460|NSF_MOUSE - Vesicle-fusing ATPase OS=Mus musculus GN=Nsf PE=1 SV=2	0	5	10	0	6	10	0.9375	0.939	31
sp|P97464|EXT1_MOUSE - Exostosin-1 OS=Mus musculus GN=Ext1 PE=1 SV=1	0	5	10	3	13	0	0.9375	0.9487	31

sp|Q91ZB0|ALPK2_MOUSE - Alpha-protein kinase 2 OS=Mus musculus GN=Alpk2 PE=2 SV=	0	2	13	0	16	0	0.9375	0.9626	31
sp|A3KFM7|CHD6_MOUSE - Chromodomain-helicase-DNA-binding protein 6 OS=Mus muscul	10	42	20	21	37	19	0.935	0.8872	149
sp|B9EJR8|DAAF5_MOUSE - Dynein assembly factor 5, axonemal OS=Mus musculus GN=Dn	3	11	0	0	15	0	0.9333	0.9582	29
sp|Q9EST3|4ET_MOUSE - Eukaryotic translation initiation factor 4E transporter OS	0	14	0	6	2	7	0.9333	0.9491	29
sp|Q7TMS5|ABCG2_MOUSE - ATP-binding cassette sub-family G member 2 OS=Mus muscul	3	10	0	6	8	0	0.9285	0.9345	27
sp|P02762|MUP6_MOUSE - Major urinary protein 6 OS=Mus musculus GN=Mup6 PE=1 SV=2	8	45	24	5	43	35	0.9277	0.9051	160
sp|Q3TLP5|ECHD2_MOUSE - Enoyl-CoA hydratase domain-containing protein 2, mitocho	0	25	0	6	21	0	0.9259	0.952	52
sp|Q8BX17|GEMI5_MOUSE - Gem-associated protein 5 OS=Mus musculus GN=Gemin5 PE=2	35	109	14	81	74	16	0.9239	0.9085	329
sp|Q6PDK2|KMT2D_MOUSE - Histone-lysine N-methyltransferase 2D OS=Mus musculus GN	0	24	0	5	21	0	0.923	0.951	50
sp|Q8BLG0|PHF20_MOUSE - PHD finger protein 20 OS=Mus musculus GN=Phf20 PE=1 SV=2	0	0	12	0	0	13	0.923	0.9576	25
sp|P42125|ECI1_MOUSE - Enoyl-CoA delta isomerase 1, mitochondrial OS=Mus musculu	15	72	17	25	63	25	0.9203	0.9006	217
sp|Q32Q92|ACOT6_MOUSE - Acyl-coenzyme A thioesterase 6 OS=Mus musculus GN=Acot6	11	34	23	22	32	20	0.9189	0.8056	142
sp|Q9QYX7|PCLO_MOUSE - Protein piccolo OS=Mus musculus GN=Pclo PE=1 SV=4	34	75	60	65	81	38	0.9184	0.7874	353
sp|Q3TTY5|K22E_MOUSE - Keratin, type II cytoskeletal 2 epidermal OS=Mus musculus	0	101	0	3	103	4	0.9181	0.9524	211
sp|Q9QUQ5|TRPC4_MOUSE - Short transient receptor potential channel 4 OS=Mus musc	6	5	0	4	8	0	0.9166	0.9158	23
sp|P10126|EF1A1_MOUSE - Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE	4	7	0	0	12	0	0.9166	0.9443	23
sp|O89019|INVS_MOUSE - Inversin OS=Mus musculus GN=Invs PE=1 SV=2	0	11	0	2	10	0	0.9166	0.9476	23
sp|Q3THK3|T2FA_MOUSE - General transcription factor IIF subunit 1 OS=Mus musculu	0	3	8	0	6	6	0.9166	0.9188	23
sp|P11725|OTC_MOUSE - Ornithine carbamoyltransferase, mitochondrial OS=Mus muscu	198	397	284	291	388	280	0.9165	0.7112	1838
sp|Q9DCW4|ETFB_MOUSE - Electron transfer flavoprotein subunit beta OS=Mus muscul	140	316	345	262	270	343	0.9154	0.7389	1676
sp|Q99J39|DCMC_MOUSE - Malonyl-CoA decarboxylase, mitochondrial OS=Mus musculus	7	34	13	12	33	14	0.9152	0.8823	113
sp|Q99K67|AASS_MOUSE - Alpha-aminoadipic semialdehyde synthase, mitochondrial OS	21	77	15	25	75	24	0.9112	0.8944	237
sp|Q6IME9|K2C72_MOUSE - Keratin, type II cytoskeletal 72 OS=Mus musculus GN=Krt7	0	20	0	0	22	0	0.909	0.9496	42
sp|Q80UU9|PGRC2_MOUSE - Membrane-associated progesterone receptor component 2 OS	0	10	0	0	11	0	0.909	0.9496	21
sp|Q9CR68|UCRI_MOUSE - Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=	13	45	21	9	43	35	0.908	0.8588	166
sp|E9Q634|MYO1E_MOUSE - Unconventional myosin-Ie OS=Mus musculus GN=Myo1e PE=1 S	0	6	23	0	12	20	0.9062	0.917	61
sp|Q8BMF4|ODP2_MOUSE - Dihydrolipoyllysine-residue acetyltransferase component o	0	19	0	0	10	11	0.9047	0.931	40
sp|P53762|ARNT_MOUSE - Aryl hydrocarbon receptor nuclear translocator OS=Mus mus	2	7	0	4	6	0	0.9	0.9086	19
sp|P39054|DYN2_MOUSE - Dynamin-2 OS=Mus musculus GN=Dnm2 PE=1 SV=2	5	4	0	4	6	0	0.9	0.8933	19
sp|P20357|MTAP2_MOUSE - Microtubule-associated protein 2 OS=Mus musculus GN=Map2	0	4	5	2	8	0	0.9	0.9124	19
sp|Q9WTP6|KAD2_MOUSE - Adenylate kinase 2, mitochondrial OS=Mus musculus GN=Ak2	50	128	79	77	112	97	0.8986	0.7178	543
sp|P24549|AL1A1_MOUSE - Retinal dehydrogenase 1 OS=Mus musculus GN=Aldh1a1 PE=1	2	16	15	15	22	0	0.8918	0.8742	70
sp|A1L317|K1C24_MOUSE - Keratin, type I cytoskeletal 24 OS=Mus musculus GN=Krt24	5	36	40	10	37	44	0.8901	0.8367	172
sp|P17879|HS71B_MOUSE - Heat shock 70 kDa protein 1B OS=Mus musculus GN=Hspa1b P	11	39	22	23	20	38	0.8888	0.7762	153
sp|Q673U1|HS3S2_MOUSE - Heparan sulfate glucosamine 3-O-sulfotransferase 2 OS=Mu	2	6	0	0	9	0	0.8888	0.9283	17
sp|Q8BX70|VP13C_MOUSE - Vacuolar protein sorting-associated protein 13C OS=Mus m	6	18	0	10	17	0	0.8888	0.8967	51
sp|Q61329|ZFHX3_MOUSE - Zinc finger homeobox protein 3 OS=Mus musculus GN=Zfhx3	3	5	0	0	9	0	0.8888	0.9251	17
sp|P27046|MA2A1_MOUSE - Alpha-mannosidase 2 OS=Mus musculus GN=Man2a1 PE=1 SV=2	0	8	0	2	7	0	0.8888	0.9262	17
sp|Q04207|TF65_MOUSE - Transcription factor p65 OS=Mus musculus GN=Rela PE=1 SV=	0	16	0	2	16	0	0.8888	0.9319	34
sp|Q920B0|FRM4B_MOUSE - FERM domain-containing protein 4B OS=Mus musculus GN=Frm	0	18	5	0	16	10	0.8846	0.8949	49
sp|P62196|PRS8_MOUSE - 26S protease regulatory subunit 8 OS=Mus musculus GN=Psmc	0	12	11	3	12	11	0.8846	0.8446	49

sp|Q8R4B8|NALP3_MOUSE - NACHT, LRR and PYD domains-containing protein 3 OS=Mus m	0	12	11	3	16	7	0.8846	0.863	49
sp|P11589|MUP2_MOUSE - Major urinary protein 2 OS=Mus musculus GN=Mup2 PE=1 SV=1	0	62	29	4	56	43	0.8834	0.8745	194
sp|Q8JZS7|HMGC2_MOUSE - 3-hydroxymethyl-3-methylglutaryl-CoA lyase, cytoplasmic	3	2	10	3	8	6	0.8823	0.8298	32
sp|Q9D6J6|NDUV2_MOUSE - NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochon	3	12	0	3	14	0	0.8823	0.9106	32
sp|Q8C0V0|TLK1_MOUSE - Serine/threonine-protein kinase tousled-like 1 OS=Mus mus	0	15	0	0	8	9	0.8823	0.9133	32
sp|Q3TCN2|PLBL2_MOUSE - Putative phospholipase B-like 2 OS=Mus musculus GN=Plbd2	8	14	0	2	21	2	0.88	0.9006	47
sp|Q14BI7|TDRD9_MOUSE - Putative ATP-dependent RNA helicase TDRD9 OS=Mus musculu	0	9	13	0	5	20	0.88	0.8953	47
sp|Q6ZWQ0|SYNE2_MOUSE - Nesprin-2 OS=Mus musculus GN=Syne2 PE=1 SV=2	0	53	20	24	37	22	0.8795	0.8465	156
sp|Q9JHW9|AL1A3_MOUSE - Aldehyde dehydrogenase family 1 member A3 OS=Mus musculu	4	23	29	8	17	39	0.875	0.8336	120
sp|Q67E05|BPI_MOUSE - Bactericidal permeability-increasing protein OS=Mus muscul	5	2	0	0	8	0	0.875	0.9178	15
sp|O35405|PLD3_MOUSE - Phospholipase D3 OS=Mus musculus GN=Pld3 PE=2 SV=1	0	7	0	2	6	0	0.875	0.9147	15
sp|O88685|PRS6A_MOUSE - 26S protease regulatory subunit 6A OS=Mus musculus GN=Ps	0	7	0	0	4	4	0.875	0.9072	15
sp|P09671|SODM_MOUSE - Superoxide dismutase [Mn], mitochondrial OS=Mus musculus	5	59	56	13	53	72	0.8695	0.8199	258
sp|P50285|FMO1_MOUSE - Dimethylaniline monooxygenase [N-oxide-forming] 1 OS=Mus	15	59	12	15	53	31	0.8686	0.8287	185
sp|P25688|URIC_MOUSE - Uricase OS=Mus musculus GN=Uox PE=1 SV=2	4	65	3	16	56	11	0.8674	0.8903	155
sp|P19253|RL13A_MOUSE - 60S ribosomal protein L13a OS=Mus musculus GN=Rpl13a PE=	2	11	0	4	11	0	0.8666	0.8933	28
sp|P70699|LYAG_MOUSE - Lysosomal alpha-glucosidase OS=Mus musculus GN=Gaa PE=1 S	2	37	0	7	25	13	0.8666	0.8862	84
sp|Q8C6E0|CFA36_MOUSE - Cilia- and flagella-associated protein 36 OS=Mus musculu	0	30	22	5	19	36	0.8666	0.8437	112
sp|Q8CDN1|CC020_MOUSE - Uncharacterized protein C3orf20 homolog OS=Mus musculus	0	4	9	0	0	15	0.8666	0.9115	28
sp|Q9WUR2|ECI2_MOUSE - Enoyl-CoA delta isomerase 2, mitochondrial OS=Mus musculu	6	36	3	10	37	5	0.8653	0.8798	97
sp|Q920A5|RISC_MOUSE - Retinoid-inducible serine carboxypeptidase OS=Mus musculu	0	16	22	0	19	25	0.8636	0.8511	82
sp|Q61176|ARGI1_MOUSE - Arginase-1 OS=Mus musculus GN=Arg1 PE=1 SV=1	9	44	39	18	41	48	0.8598	0.7424	199
sp|Q9CWU6|UQCC1_MOUSE - Ubiquinol-cytochrome-c reductase complex assembly factor	2	2	2	5	2	0	0.8571	0.8298	13
sp|Q9CPV4|GLOD4_MOUSE - Glyoxalase domain-containing protein 4 OS=Mus musculus G	2	10	0	3	9	2	0.8571	0.8677	26
sp|P25962|ADRB3_MOUSE - Beta-3 adrenergic receptor OS=Mus musculus GN=Adrb3 PE=2	3	3	0	0	7	0	0.8571	0.9018	13
sp|Q9CXJ4|ABCB8_MOUSE - ATP-binding cassette sub-family B member 8, mitochondria	0	6	0	0	7	0	0.8571	0.9188	13
sp|Q99M28|RNPS1_MOUSE - RNA-binding protein with serine-rich domain 1 OS=Mus mus	0	6	0	0	3	4	0.8571	0.8933	13
sp|Q9QZ05|E2AK4_MOUSE - Eukaryotic translation initiation factor 2-alpha kinase	0	6	0	0	2	5	0.8571	0.8992	13
sp|Q8BZ21|KAT6A_MOUSE - Histone acetyltransferase KAT6A OS=Mus musculus GN=Kat6a	0	12	0	4	10	0	0.8571	0.8992	26
sp|Q2TPA8|HSDL2_MOUSE - Hydroxysteroid dehydrogenase-like protein 2 OS=Mus muscu	0	6	0	2	3	2	0.8571	0.8774	13
sp|O70628|PDE9A_MOUSE - High affinity cGMP-specific 3',5'-cyclic phosphodiestera	0	6	0	0	0	7	0.8571	0.9188	13
sp|Q32KI9|ARSI_MOUSE - Arylsulfatase I OS=Mus musculus GN=Arsi PE=2 SV=1	0	14	15	3	19	12	0.8529	0.8158	63
sp|P35505|FAAA_MOUSE - Fumarylacetoacetase OS=Mus musculus GN=Fah PE=1 SV=2	3	20	0	7	16	4	0.8518	0.862	50
sp|P51881|ADT2_MOUSE - ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=	9	89	22	23	74	44	0.851	0.8203	261
sp|Q5F226|FAT2_MOUSE - Protocadherin Fat 2 OS=Mus musculus GN=Fat2 PE=2 SV=1	0	24	16	2	3	42	0.851	0.8834	87
sp|Q3U155|CC174_MOUSE - Coiled-coil domain-containing protein 174 OS=Mus musculu	13	32	0	28	23	2	0.849	0.8381	98
sp|Q9WUM5|SUCA_MOUSE - Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mito	10	34	12	7	28	31	0.8484	0.7725	122
sp|A2AGT5|CKAP5_MOUSE - Cytoskeleton-associated protein 5 OS=Mus musculus GN=Cka	0	21	7	8	14	11	0.8484	0.8077	61
sp|Q9DC69|NDUA9_MOUSE - NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subun	5	30	4	14	23	9	0.8478	0.8169	85
sp|P24457|CP2DB_MOUSE - Cytochrome P450 2D11 OS=Mus musculus GN=Cyp2d11 PE=2 SV=	5	17	0	7	19	0	0.8461	0.8675	48
sp|Q8CGK3|LONM_MOUSE - Lon protease homolog, mitochondrial OS=Mus musculus GN=Lo	11	16	6	13	22	4	0.8461	0.7534	72

sp|P26041|MOES_MOUSE - Moesin OS=Mus musculus GN=Msn PE=1 SV=3	0	11	0	0	13	0	0.8461	0.9121	24
sp|P37040|NCPR_MOUSE - NADPH--cytochrome P450 reductase OS=Mus musculus GN=Por P	15	75	5	31	72	10	0.8407	0.8432	208
sp|Q99PL5|RRBP1_MOUSE - Ribosome-binding protein 1 OS=Mus musculus GN=Rrbp1 PE=1	6	58	15	40	41	13	0.8404	0.8001	173
sp|Q9CPY7|AMPL_MOUSE - Cytosol aminopeptidase OS=Mus musculus GN=Lap3 PE=1 SV=3	3	20	8	7	23	7	0.8378	0.7987	68
sp|Q62448|IF4G2_MOUSE - Eukaryotic translation initiation factor 4 gamma 2 OS=Mu	2	3	0	0	6	0	0.8333	0.8861	11
sp|Q99P88|NU155_MOUSE - Nuclear pore complex protein Nup155 OS=Mus musculus GN=N	2	8	0	0	12	0	0.8333	0.8933	22
sp|Q9DCT2|NDUS3_MOUSE - NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, m	0	10	0	2	8	2	0.8333	0.8721	22
sp|Q9WV68|DECR2_MOUSE - Peroxisomal 2,4-dienoyl-CoA reductase OS=Mus musculus GN	0	10	0	4	8	0	0.8333	0.8774	22
sp|O88809|DCX_MOUSE - Neuronal migration protein doublecortin OS=Mus musculus GN	0	5	0	0	6	0	0.8333	0.9043	11
sp|Q3U0J8|TBD2B_MOUSE - TBC1 domain family member 2B OS=Mus musculus GN=Tbc1d2b	0	5	0	4	2	0	0.8333	0.8774	11
sp|Q64291|K1C12_MOUSE - Keratin, type I cytoskeletal 12 OS=Mus musculus GN=Krt12	0	3	7	0	3	9	0.8333	0.8512	22
sp|P30730|LSHR_MOUSE - Lutropin-choriogonadotropic hormone receptor OS=Mus muscu	0	0	10	0	2	10	0.8333	0.8899	22
sp|Q80TT2|BAIP3_MOUSE - BAI1-associated protein 3 OS=Mus musculus GN=Baiap3 PE=3	0	0	5	0	0	6	0.8333	0.9043	11
sp|A2A3V1|AK17B_MOUSE - A-kinase anchor protein 17B OS=Mus musculus GN=Akap17b P	0	0	5	4	2	0	0.8333	0.8774	11
sp|Q3V0Q1|DYH12_MOUSE - Dynein heavy chain 12, axonemal OS=Mus musculus GN=Dnah1	0	25	4	4	26	5	0.8285	0.859	64
sp|Q09XV5|CHD8_MOUSE - Chromodomain-helicase-DNA-binding protein 8 OS=Mus muscul	0	24	0	15	14	0	0.8275	0.8672	53
sp|Q91XQ0|DYH8_MOUSE - Dynein heavy chain 8, axonemal OS=Mus musculus GN=Dnah8 P	0	19	0	5	13	5	0.826	0.8556	42
sp|P35396|PPARD_MOUSE - Peroxisome proliferator-activated receptor delta OS=Mus	3	0	11	0	0	17	0.8235	0.886	31
sp|Q8BX02|KANK2_MOUSE - KN motif and ankyrin repeat domain-containing protein 2	2	2	10	3	7	7	0.8235	0.7541	31
sp|Q01853|TERA_MOUSE - Transitional endoplasmic reticulum ATPase OS=Mus musculus	0	14	0	0	17	0	0.8235	0.8982	31
sp|Q9Z2G1|FM1AA_MOUSE - Protein fem-1 homolog A-A OS=Mus musculus GN=Fem1aa PE=2	0	3	11	3	6	8	0.8235	0.7944	31
sp|Q62504|MINT_MOUSE - Msx2-interacting protein OS=Mus musculus GN=Spen PE=1 SV=	0	18	0	0	17	5	0.8181	0.8732	40
sp|P46735|MYO1B_MOUSE - Unconventional myosin-Ib OS=Mus musculus GN=Myo1b PE=2 S	0	5	4	0	7	4	0.8181	0.8058	20
sp|Q76I79|SSH1_MOUSE - Protein phosphatase Slingshot homolog 1 OS=Mus musculus G	0	0	9	0	0	11	0.8181	0.8949	20
sp|Q6PCN7|HLTF_MOUSE - Helicase-like transcription factor OS=Mus musculus GN=Hlt	0	9	4	3	8	5	0.8125	0.7541	29
sp|Q91V92|ACLY_MOUSE - ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1	0	21	5	4	28	0	0.8125	0.862	58
sp|P02104|HBE_MOUSE - Hemoglobin subunit epsilon-Y2 OS=Mus musculus GN=Hbb-y PE=	0	13	0	0	16	0	0.8125	0.8913	29
sp|P51660|DHB4_MOUSE - Peroxisomal multifunctional enzyme type 2 OS=Mus musculus	35	127	73	39	127	126	0.8047	0.6559	527
sp|Q8VCR2|DHB13_MOUSE - 17-beta-hydroxysteroid dehydrogenase 13 OS=Mus musculus	2	6	0	0	8	2	0.8	0.834	18
sp|Q5SV80|MYO19_MOUSE - Unconventional myosin-XIX OS=Mus musculus GN=Myo19 PE=2	2	2	0	0	5	0	0.8	0.8617	9
sp|Q9DD20|MET7B_MOUSE - Methyltransferase-like protein 7B OS=Mus musculus GN=Met	0	8	0	0	10	0	0.8	0.8834	18
sp|P16330|CN37_MOUSE - 2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Mus muscu	0	4	0	0	0	5	0.8	0.8834	9
sp|Q8JZM7|CDC73_MOUSE - Parafibromin OS=Mus musculus GN=Cdc73 PE=2 SV=1	0	8	0	3	5	2	0.8	0.824	18
sp|Q9Z160|COG1_MOUSE - Conserved oligomeric Golgi complex subunit 1 OS=Mus muscu	0	4	0	2	3	0	0.8	0.845	9
sp|Q99NG0|ARIP4_MOUSE - Helicase ARIP4 OS=Mus musculus GN=Rad54l2 PE=1 SV=1	0	8	0	2	8	0	0.8	0.8617	18
sp|Q9DCU6|RM04_MOUSE - 39S ribosomal protein L4, mitochondrial OS=Mus musculus G	0	4	0	0	5	0	0.8	0.8834	9
sp|Q3UGF1|WDR19_MOUSE - WD repeat-containing protein 19 OS=Mus musculus GN=Wdr19	0	4	0	2	3	0	0.8	0.845	9
sp|C3VPR6|NLRC5_MOUSE - Protein NLRC5 OS=Mus musculus GN=Nlrc5 PE=1 SV=2	0	4	0	0	5	0	0.8	0.8834	9
sp|Q9Z0F3|B2L10_MOUSE - Bcl-2-like protein 10 OS=Mus musculus GN=Bcl2l10 PE=1 SV	0	4	0	0	0	5	0.8	0.8834	9
sp|Q14C59|TM11B_MOUSE - Transmembrane protease serine 11B-like protein OS=Mus mu	0	4	0	0	0	5	0.8	0.8834	9
sp|O08689|GDF8_MOUSE - Growth/differentiation factor 8 OS=Mus musculus GN=Mstn P	0	2	10	0	0	15	0.8	0.8727	27

sp|P56135|ATPK_MOUSE - ATP synthase subunit f, mitochondrial OS=Mus musculus GN=	0	4	0	0	5	0	0.8	0.8834	9
sp|P97742|CPT1A_MOUSE - Carnitine O-palmitoyltransferase 1, liver isoform OS=Mus	0	4	0	0	5	0	0.8	0.8834	9
sp|Q8K2G4|BBS7_MOUSE - Bardet-Biedl syndrome 7 protein homolog OS=Mus musculus G	0	0	4	0	0	5	0.8	0.8834	9
sp|Q9JMH9|MY18A_MOUSE - Unconventional myosin-XVIIIa OS=Mus musculus GN=Myo18a P	0	0	8	0	0	10	0.8	0.8834	18
sp|Q8BYR5|CAPS2_MOUSE - Calcium-dependent secretion activator 2 OS=Mus musculus	0	0	4	0	0	5	0.8	0.8834	9
sp|Q8BGN6|TMG4_MOUSE - Transmembrane gamma-carboxyglutamic acid protein 4 OS=Mus	0	0	4	0	0	5	0.8	0.8834	9
sp|A2ARI4|LGR4_MOUSE - Leucine-rich repeat-containing G-protein coupled receptor	0	0	4	0	0	5	0.8	0.8834	9
sp|Q9DCX2|ATP5H_MOUSE - ATP synthase subunit d, mitochondrial OS=Mus musculus GN	5	26	8	5	36	8	0.7959	0.7924	88
sp|Q91YP0|L2HDH_MOUSE - L-2-hydroxyglutarate dehydrogenase, mitochondrial OS=Mus	0	35	0	10	34	0	0.7954	0.8552	79
sp|P53395|ODB2_MOUSE - Lipoamide acyltransferase component of branched-chain alp	2	17	0	0	24	0	0.7916	0.871	43
sp|Q9CXB8|ALPK1_MOUSE - Alpha-protein kinase 1 OS=Mus musculus GN=Alpk1 PE=2 SV=	0	11	8	11	8	5	0.7916	0.6766	43
sp|Q80VW7|AKNA_MOUSE - AT-hook-containing transcription factor OS=Mus musculus G	8	18	0	12	17	4	0.7878	0.7353	59
sp|Q6PDI5|ECM29_MOUSE - Proteasome-associated protein ECM29 homolog OS=Mus muscu	0	16	10	0	13	20	0.7878	0.7709	59
sp|Q6EJB6|UT14B_MOUSE - U3 small nucleolar RNA-associated protein 14 homolog B O	6	5	0	14	0	0	0.7857	0.8518	25
sp|Q8K0E8|FIBB_MOUSE - Fibrinogen beta chain OS=Mus musculus GN=Fgb PE=2 SV=1	0	11	0	3	11	0	0.7857	0.8489	25
sp|P10605|CATB_MOUSE - Cathepsin B OS=Mus musculus GN=Ctsb PE=1 SV=2	9	48	15	7	49	36	0.7826	0.7203	164
sp|Q80SY4|MIB1_MOUSE - E3 ubiquitin-protein ligase MIB1 OS=Mus musculus GN=Mib1	13	5	0	10	13	0	0.7826	0.7752	41
sp|Q5HZG4|TAF3_MOUSE - Transcription initiation factor TFIID subunit 3 OS=Mus mu	0	10	8	7	7	9	0.7826	0.6222	41
sp|Q6PFC5|LRIT2_MOUSE - Leucine-rich repeat, immunoglobulin-like domain and tran	8	6	0	5	13	0	0.7777	0.781	32
sp|Q9CYR0|SSBP_MOUSE - Single-stranded DNA-binding protein, mitochondrial OS=Mus	4	3	0	2	7	0	0.7777	0.7952	16
sp|Q8BVY0|RL1D1_MOUSE - Ribosomal L1 domain-containing protein 1 OS=Mus musculus	5	2	0	5	4	0	0.7777	0.7676	16
sp|Q5SSE9|ABCAD_MOUSE - ATP-binding cassette sub-family A member 13 OS=Mus muscu	4	14	10	9	20	7	0.7777	0.6205	64
sp|Q8BYJ6|TBCD4_MOUSE - TBC1 domain family member 4 OS=Mus musculus GN=Tbc1d4 PE	4	3	0	0	9	0	0.7777	0.8466	16
sp|Q7TN60|TMC6_MOUSE - Transmembrane channel-like protein 6 OS=Mus musculus GN=T	0	7	0	0	9	0	0.7777	0.8692	16
sp|Q9Z210|PX11B_MOUSE - Peroxisomal membrane protein 11B OS=Mus musculus GN=Pex1	0	7	0	4	5	0	0.7777	0.8228	16
sp|Q9D6S7|RRFM_MOUSE - Ribosome-recycling factor, mitochondrial OS=Mus musculus	0	3	4	3	3	3	0.7777	0.6086	16
sp|Q9CXZ1|NDUS4_MOUSE - NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, m	0	7	0	0	9	0	0.7777	0.8692	16
sp|Q5SYL1|SG494_MOUSE - Uncharacterized serine/threonine-protein kinase SgK494 O	4	17	10	6	5	29	0.775	0.7473	71
sp|Q8CJ27|ASPM_MOUSE - Abnormal spindle-like microcephaly-associated protein hom	8	54	0	26	44	10	0.775	0.7734	142
sp|P97329|KI20A_MOUSE - Kinesin-like protein KIF20A OS=Mus musculus GN=Kif20a PE	4	5	25	7	10	27	0.7727	0.7368	78
sp|Q99J99|THTM_MOUSE - 3-mercaptopyruvate sulfurtransferase OS=Mus musculus GN=M	8	19	40	12	29	46	0.7701	0.6492	154
sp|Q8BLR5|PSD4_MOUSE - PH and SEC7 domain-containing protein 4 OS=Mus musculus G	0	4	6	3	5	5	0.7692	0.6239	23
sp|Q5D525|SYC1L_MOUSE - Synaptonemal complex central element protein 1-like OS=M	0	9	11	0	10	16	0.7692	0.746	46
sp|Q8R1N0|ZN830_MOUSE - Zinc finger protein 830 OS=Mus musculus GN=Znf830 PE=1 S	3	8	2	9	2	6	0.7647	0.653	30
sp|Q8VCW2|K1C25_MOUSE - Keratin, type I cytoskeletal 25 OS=Mus musculus GN=Krt25	0	34	18	0	57	11	0.7647	0.8032	120
sp|Q8K561|OTOAN_MOUSE - Otoancorin OS=Mus musculus GN=Otoa PE=2 SV=1	0	0	13	0	10	7	0.7647	0.812	30
sp|Q9DC37|MFSD1_MOUSE - Major facilitator superfamily domain-containing protein	8	8	0	2	19	0	0.7619	0.8128	37
sp|Q9QYR7|ACOT3_MOUSE - Acyl-coenzyme A thioesterase 3 OS=Mus musculus GN=Acot3	16	48	24	26	46	44	0.7586	0.4635	204
sp|Q6NS59|F135A_MOUSE - Protein FAM135A OS=Mus musculus GN=Fam135a PE=2 SV=2	6	19	0	10	23	0	0.7575	0.7746	58
sp|Q8K1Z0|COQ9_MOUSE - Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Mu	4	24	0	6	26	5	0.7567	0.7811	65
sp|Q9Z268|RASL1_MOUSE - RasGAP-activating-like protein 1 OS=Mus musculus GN=Rasa	3	3	0	0	8	0	0.75	0.8264	14

sp|Q6PCN3|TTBK1_MOUSE - Tau-tubulin kinase 1 OS=Mus musculus GN=Ttbk1 PE=2 SV=3	6	0	0	8	0	0	0.75	0.8512	14
sp|O35295|PURB_MOUSE - Transcriptional activator protein Pur-beta OS=Mus musculu	0	3	0	0	0	4	0.75	0.8512	7
sp|Q3UVG3|F91A1_MOUSE - Protein FAM91A1 OS=Mus musculus GN=Fam91a1 PE=2 SV=1	0	3	0	4	0	0	0.75	0.8512	7
sp|Q61153|IOD1_MOUSE - Type I iodothyronine deiodinase OS=Mus musculus GN=Dio1 P	0	6	0	4	4	0	0.75	0.7952	14
sp|Q9Z2W0|DNPEP_MOUSE - Aspartyl aminopeptidase OS=Mus musculus GN=Dnpep PE=2 SV	0	3	0	4	0	0	0.75	0.8512	7
sp|Q9Z2A0|PDPK1_MOUSE - 3-phosphoinositide-dependent protein kinase 1 OS=Mus mus	0	3	0	0	4	0	0.75	0.8512	7
sp|Q6S5J6|KRIT1_MOUSE - Krev interaction trapped protein 1 OS=Mus musculus GN=Kr	0	3	0	0	4	0	0.75	0.8512	7
sp|Q924X6|LRP8_MOUSE - Low-density lipoprotein receptor-related protein 8 OS=Mus	0	3	0	0	4	0	0.75	0.8512	7
sp|Q9EPU4|CPSF1_MOUSE - Cleavage and polyadenylation specificity factor subunit	0	3	0	0	4	0	0.75	0.8512	7
sp|O54782|MA2B2_MOUSE - Epididymis-specific alpha-mannosidase OS=Mus musculus GN	0	12	0	6	8	2	0.75	0.7755	28
sp|B2RXS4|PLXB2_MOUSE - Plexin-B2 OS=Mus musculus GN=Plxnb2 PE=1 SV=1	0	10	11	6	14	8	0.75	0.6126	49
sp|P04939|MUP3_MOUSE - Major urinary protein 3 OS=Mus musculus GN=Mup3 PE=1 SV=1	0	3	0	0	4	0	0.75	0.8512	7
sp|Q8C080|SNX16_MOUSE - Sorting nexin-16 OS=Mus musculus GN=Snx16 PE=1 SV=2	0	3	0	2	2	0	0.75	0.7952	7
sp|Q8BKZ9|ODPX_MOUSE - Pyruvate dehydrogenase protein X component, mitochondrial	0	3	0	0	4	0	0.75	0.8512	7
sp|Q8BH86|CN159_MOUSE - UPF0317 protein C14orf159 homolog, mitochondrial OS=Mus	0	3	0	0	4	0	0.75	0.8512	7
sp|P09411|PGK1_MOUSE - Phosphoglycerate kinase 1 OS=Mus musculus GN=Pgk1 PE=1 SV	0	3	0	0	4	0	0.75	0.8512	7
sp|A2CE44|ZXDB_MOUSE - Zinc finger X-linked protein ZXDB OS=Mus musculus GN=Zxdb	0	3	0	0	4	0	0.75	0.8512	7
sp|Q6PB44|PTN23_MOUSE - Tyrosine-protein phosphatase non-receptor type 23 OS=Mus	0	3	0	0	4	0	0.75	0.8512	7
sp|Q8BXV2|BRI3B_MOUSE - BRI3-binding protein OS=Mus musculus GN=Bri3bp PE=2 SV=1	0	6	0	3	5	0	0.75	0.8007	14
sp|Q69ZH9|RHG23_MOUSE - Rho GTPase-activating protein 23 OS=Mus musculus GN=Arhg	0	2	4	4	4	0	0.75	0.7246	14
sp|P55258|RAB8A_MOUSE - Ras-related protein Rab-8A OS=Mus musculus GN=Rab8a PE=1	0	6	0	0	8	0	0.75	0.8512	14
sp|P14131|RS16_MOUSE - 40S ribosomal protein S16 OS=Mus musculus GN=Rps16 PE=2 S	0	3	0	0	4	0	0.75	0.8512	7
sp|P39053|DYN1_MOUSE - Dynamin-1 OS=Mus musculus GN=Dnm1 PE=1 SV=2	0	3	0	2	2	0	0.75	0.7952	7
sp|Q6KAQ7|ZZZ3_MOUSE - ZZ-type zinc finger-containing protein 3 OS=Mus musculus	0	0	3	0	0	4	0.75	0.8512	7
sp|Q02566|MYH6_MOUSE - Myosin-6 OS=Mus musculus GN=Myh6 PE=1 SV=2	0	0	6	0	0	8	0.75	0.8512	14
sp|Q60864|STIP1_MOUSE - Stress-induced-phosphoprotein 1 OS=Mus musculus GN=Stip1	0	4	22	2	7	26	0.7428	0.7782	61
sp|A2AAJ9|OBSCN_MOUSE - Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2	3	22	9	16	30	0	0.7391	0.7181	80
sp|Q4VGL6|RC3H1_MOUSE - Roquin-1 OS=Mus musculus GN=Rc3h1 PE=1 SV=1	2	9	0	2	13	0	0.7333	0.798	26
sp|A2ARV4|LRP2_MOUSE - Low-density lipoprotein receptor-related protein 2 OS=Mus	9	15	0	13	20	0	0.7272	0.7022	57
sp|Q9WU79|PROD_MOUSE - Proline dehydrogenase 1, mitochondrial OS=Mus musculus GN	0	8	0	0	11	0	0.7272	0.8362	19
sp|Q99LC3|NDUAA_MOUSE - NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subun	7	6	0	3	15	0	0.7222	0.7591	31
sp|P97412|LYST_MOUSE - Lysosomal-trafficking regulator OS=Mus musculus GN=Lyst P	0	13	0	7	11	0	0.7222	0.7728	31
sp|Q8BH00|AL8A1_MOUSE - Aldehyde dehydrogenase family 8 member A1 OS=Mus musculu	5	19	43	5	28	60	0.7204	0.6786	160
sp|Q9QUK4|BIR1B_MOUSE - Baculoviral IAP repeat-containing protein 1b OS=Mus musc	3	25	0	14	25	0	0.7179	0.749	67
sp|O54734|OST48_MOUSE - Dolichyl-diphosphooligosaccharide--protein glycosyltrans	3	17	0	9	19	0	0.7142	0.7429	48
sp|Q9JHU4|DYHC1_MOUSE - Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dy	0	10	0	4	10	0	0.7142	0.778	24
sp|Q9QYC0|ADDA_MOUSE - Alpha-adducin OS=Mus musculus GN=Add1 PE=1 SV=2	0	5	0	0	7	0	0.7142	0.8275	12
sp|Q811W2|CP26B_MOUSE - Cytochrome P450 26B1 OS=Mus musculus GN=Cyp26b1 PE=1 SV=	0	5	0	4	3	0	0.7142	0.7618	12
sp|Q69ZI1|SH3R1_MOUSE - E3 ubiquitin-protein ligase SH3RF1 OS=Mus musculus GN=Sh	0	5	0	5	0	2	0.7142	0.778	12
sp|Q61043|NIN_MOUSE - Ninein OS=Mus musculus GN=Nin PE=2 SV=3	0	0	5	0	7	0	0.7142	0.8275	12
sp|P35486|ODPA_MOUSE - Pyruvate dehydrogenase E1 component subunit alpha, somati	2	23	7	2	30	13	0.7111	0.696	77

sp|Q80VU4|NTF4_MOUSE - Neurotrophin-4 OS=Mus musculus GN=Ntf4 PE=2 SV=1	0	0	12	0	7	10	0.7058	0.7545	29
sp|Q91WT4|DJC17_MOUSE - DnaJ homolog subfamily C member 17 OS=Mus musculus GN=Dn	0	7	0	0	0	10	0.7	0.8179	17
sp|Q9D6R2|IDH3A_MOUSE - Isocitrate dehydrogenase [NAD] subunit alpha, mitochondr	0	23	5	3	20	17	0.7	0.6706	68
sp|P47934|CACP_MOUSE - Carnitine O-acetyltransferase OS=Mus musculus GN=Crat PE=	0	7	0	0	10	0	0.7	0.8179	17
sp|O35182|SMAD6_MOUSE - Mothers against decapentaplegic homolog 6 OS=Mus musculu	0	2	5	0	4	6	0.7	0.6842	17
sp|Q5DTM8|BRE1A_MOUSE - E3 ubiquitin-protein ligase BRE1A OS=Mus musculus GN=Rnf	0	0	7	0	0	10	0.7	0.8179	17
sp|Q9QYC1|PCX1_MOUSE - Pecanex-like protein 1 OS=Mus musculus GN=Pcnx PE=2 SV=3	2	11	3	0	18	5	0.6956	0.7204	39
sp|Q70FJ1|AKAP9_MOUSE - A-kinase anchor protein 9 OS=Mus musculus GN=Akap9 PE=2	34	60	54	44	46	123	0.6948	0.4698	361
sp|Q922D8|C1TC_MOUSE - C-1-tetrahydrofolate synthase, cytoplasmic OS=Mus musculu	0	18	0	0	26	0	0.6923	0.8127	44
sp|Q99LM2|CK5P3_MOUSE - CDK5 regulatory subunit-associated protein 3 OS=Mus musc	2	26	10	6	3	46	0.6909	0.734	93
sp|P61407|TDRD6_MOUSE - Tudor domain-containing protein 6 OS=Mus musculus GN=Tdr	2	5	24	13	10	22	0.6888	0.5807	76
sp|Q99MY8|ASH1L_MOUSE - Histone-lysine N-methyltransferase ASH1L OS=Mus musculus	0	11	0	0	16	0	0.6875	0.8094	27
sp|Q4FZC9|SYNE3_MOUSE - Nesprin-3 OS=Mus musculus GN=Syne3 PE=1 SV=1	3	15	8	10	7	21	0.6842	0.5071	64
sp|Q8CG76|ARK72_MOUSE - Aflatoxin B1 aldehyde reductase member 2 OS=Mus musculus	0	17	0	4	21	0	0.68	0.7713	42
sp|P97302|BACH1_MOUSE - Transcription regulator protein BACH1 OS=Mus musculus GN	2	0	0	0	3	0	0.6666	0.7952	5
sp|Q3UMY5|EMAL4_MOUSE - Echinoderm microtubule-associated protein-like 4 OS=Mus	4	14	0	6	13	8	0.6666	0.5543	45
sp|Q9D773|RM02_MOUSE - 39S ribosomal protein L2, mitochondrial OS=Mus musculus G	2	2	0	0	6	0	0.6666	0.7676	10
sp|P56400|GP1BB_MOUSE - Platelet glycoprotein Ib beta chain OS=Mus musculus GN=G	3	3	0	2	7	0	0.6666	0.6873	15
sp|Q9DCS9|NDUBA_MOUSE - NADH dehydrogenase [ubiquinone] 1 beta subcomplex subuni	2	0	0	0	3	0	0.6666	0.7952	5
sp|Q8BZ98|DYN3_MOUSE - Dynamin-3 OS=Mus musculus GN=Dnm3 PE=1 SV=1	3	5	0	3	9	0	0.6666	0.6815	20
sp|Q80Y50|CMTA2_MOUSE - Calmodulin-binding transcription activator 2 OS=Mus musc	0	2	0	0	3	0	0.6666	0.7952	5
sp|Q0QWG9|GRD2I_MOUSE - Delphilin OS=Mus musculus GN=Grid2ip PE=1 SV=1	0	2	0	0	3	0	0.6666	0.7952	5
sp|Q8CFE2|CD027_MOUSE - UPF0609 protein C4orf27 homolog OS=Mus musculus PE=1 SV=	0	4	0	3	3	0	0.6666	0.7096	10
sp|O88983|STX8_MOUSE - Syntaxin-8 OS=Mus musculus GN=Stx8 PE=1 SV=1	0	6	0	2	3	4	0.6666	0.656	15
sp|Q80ST9|LCA5_MOUSE - Lebercilin OS=Mus musculus GN=Lca5 PE=2 SV=1	0	8	0	0	12	0	0.6666	0.7952	20
sp|Q07797|LG3BP_MOUSE - Galectin-3-binding protein OS=Mus musculus GN=Lgals3bp P	0	6	0	2	7	0	0.6666	0.7464	15
sp|Q9D2D7|ZN687_MOUSE - Zinc finger protein 687 OS=Mus musculus GN=Znf687 PE=1 S	0	12	0	0	6	12	0.6666	0.7246	30
sp|Q8CIV8|TBCE_MOUSE - Tubulin-specific chaperone E OS=Mus musculus GN=Tbce PE=1	0	2	0	0	3	0	0.6666	0.7952	5
sp|Q80XM3|KCNG4_MOUSE - Potassium voltage-gated channel subfamily G member 4 OS=	0	8	0	9	3	0	0.6666	0.7405	20
sp|Q3USJ8|FCSD2_MOUSE - F-BAR and double SH3 domains protein 2 OS=Mus musculus G	0	2	0	0	0	3	0.6666	0.7952	5
sp|P18826|KPB1_MOUSE - Phosphorylase b kinase regulatory subunit alpha, skeletal	0	2	0	0	3	0	0.6666	0.7952	5
sp|Q6P5B0|RRP12_MOUSE - RRP12-like protein OS=Mus musculus GN=Rrp12 PE=1 SV=1	0	2	0	3	0	0	0.6666	0.7952	5
sp|Q9QXH4|ITAX_MOUSE - Integrin alpha-X OS=Mus musculus GN=Itgax PE=2 SV=1	0	2	0	0	3	0	0.6666	0.7952	5
sp|Q8BL99|DOP1_MOUSE - Protein dopey-1 OS=Mus musculus GN=Dopey1 PE=2 SV=2	0	2	0	0	3	0	0.6666	0.7952	5
sp|Q9DCS3|MECR_MOUSE - Trans-2-enoyl-CoA reductase, mitochondrial OS=Mus musculu	0	10	2	12	6	0	0.6666	0.6873	30
sp|P13707|GPDA_MOUSE - Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	0	8	0	0	12	0	0.6666	0.7952	20
sp|Q80W54|FACE1_MOUSE - CAAX prenyl protease 1 homolog OS=Mus musculus GN=Zmpste	0	4	4	3	7	2	0.6666	0.5467	20
sp|Q8BGG9|ACNT2_MOUSE - Acyl-coenzyme A amino acid N-acyltransferase 2 OS=Mus mu	0	2	0	0	3	0	0.6666	0.7952	5
sp|Q6NTA4|RRAGB_MOUSE - Ras-related GTP-binding protein B OS=Mus musculus GN=Rra	0	2	0	0	3	0	0.6666	0.7952	5
sp|Q3UHN9|NDST1_MOUSE - Bifunctional heparan sulfate N-deacetylase/N-sulfotransf	0	2	0	0	0	3	0.6666	0.7952	5
sp|P29621|SPA3C_MOUSE - Serine protease inhibitor A3C OS=Mus musculus GN=Serpina	0	2	0	3	0	0	0.6666	0.7952	5

sp|Q91WK5|GCSH_MOUSE - Glycine cleavage system H protein, mitochondrial OS=Mus m	0	2	0	0	0	3	0.6666	0.7952	5
sp|P62267|RS23_MOUSE - 40S ribosomal protein S23 OS=Mus musculus GN=Rps23 PE=1 S	0	2	0	0	3	0	0.6666	0.7952	5
sp|Q9R0P6|SC11A_MOUSE - Signal peptidase complex catalytic subunit SEC11A OS=Mus	0	4	0	0	6	0	0.6666	0.7952	10
sp|Q9CXV1|DHSD_MOUSE - Succinate dehydrogenase [ubiquinone] cytochrome b small s	0	2	0	0	3	0	0.6666	0.7952	5
sp|Q61011|GBB3_MOUSE - Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit	0	2	0	0	3	0	0.6666	0.7952	5
sp|P50427|STS_MOUSE - Steryl-sulfatase OS=Mus musculus GN=Sts PE=2 SV=1	0	2	0	0	3	0	0.6666	0.7952	5
sp|Q8R3H7|HS2ST_MOUSE - Heparan sulfate 2-O-sulfotransferase 1 OS=Mus musculus G	0	2	0	3	0	0	0.6666	0.7952	5
sp|Q5DTT2|PSD1_MOUSE - PH and SEC7 domain-containing protein 1 OS=Mus musculus G	0	2	0	0	3	0	0.6666	0.7952	5
sp|A2AHJ4|BRWD3_MOUSE - Bromodomain and WD repeat-containing protein 3 OS=Mus mu	0	2	0	0	3	0	0.6666	0.7952	5
sp|Q80YV3|TRRAP_MOUSE - Transformation/transcription domain-associated protein O	0	2	0	0	3	0	0.6666	0.7952	5
sp|Q9D853|MET10_MOUSE - Protein-lysine N-methyltransferase Mettl10 OS=Mus muscul	0	0	2	0	3	0	0.6666	0.7952	5
sp|Q9Z2B9|KS6A4_MOUSE - Ribosomal protein S6 kinase alpha-4 OS=Mus musculus GN=R	0	0	4	0	2	4	0.6666	0.7246	10
sp|Q9CQN1|TRAP1_MOUSE - Heat shock protein 75 kDa, mitochondrial OS=Mus musculus	2	11	12	10	11	17	0.6578	0.3242	63
sp|Q6P5D8|SMHD1_MOUSE - Structural maintenance of chromosomes flexible hinge dom	2	21	0	8	23	4	0.6571	0.6745	58
sp|Q8K1A6|C2D1A_MOUSE - Coiled-coil and C2 domain-containing protein 1A OS=Mus m	4	3	8	10	13	0	0.6521	0.5614	38
sp|O55201|SPT5H_MOUSE - Transcription elongation factor SPT5 OS=Mus musculus GN=	3	12	0	14	9	0	0.6521	0.6506	38
sp|P80313|TCPH_MOUSE - T-complex protein 1 subunit eta OS=Mus musculus GN=Cct7 P	7	8	0	2	21	0	0.6521	0.728	38
sp|Q80T11|USH1G_MOUSE - Usher syndrome type-1G protein homolog OS=Mus musculus G	0	11	0	10	7	0	0.647	0.6932	28
sp|Q6R891|NEB2_MOUSE - Neurabin-2 OS=Mus musculus GN=Ppp1r9b PE=1 SV=1	6	3	0	5	9	0	0.6428	0.6222	23
sp|Q64374|RGN_MOUSE - Regucalcin OS=Mus musculus GN=Rgn PE=1 SV=1	0	9	0	4	6	4	0.6428	0.6164	23
sp|Q8VCI0|PLBL1_MOUSE - Phospholipase B-like 1 OS=Mus musculus GN=Plbd1 PE=1 SV=	0	9	0	4	8	2	0.6428	0.657	23
sp|Q6PE87|CF165_MOUSE - UPF0704 protein C6orf165 homolog OS=Mus musculus PE=2 SV	6	17	9	11	9	30	0.64	0.4659	82
sp|Q7M732|RTL1_MOUSE - Retrotransposon-like protein 1 OS=Mus musculus GN=Rtl1 PE	7	9	0	8	17	0	0.64	0.6216	41
sp|O35423|SPYA_MOUSE - Serine--pyruvate aminotransferase, mitochondrial OS=Mus m	4	38	0	7	50	9	0.6363	0.6874	108
sp|Q9JIH2|NUP50_MOUSE - Nuclear pore complex protein Nup50 OS=Mus musculus GN=Nu	0	7	0	0	6	5	0.6363	0.6778	18
sp|Q91XE0|GLYAT_MOUSE - Glycine N-acyltransferase OS=Mus musculus GN=Glyat PE=1	2	56	27	18	60	56	0.6343	0.4713	219
sp|Q9CQE1|NPS3B_MOUSE - Protein NipSnap homolog 3B OS=Mus musculus GN=Nipsnap3b	0	22	0	0	35	0	0.6285	0.7688	57
sp|P84099|RL19_MOUSE - 60S ribosomal protein L19 OS=Mus musculus GN=Rpl19 PE=1 S	0	5	0	3	5	0	0.625	0.6745	13
sp|Q91YI0|ARLY_MOUSE - Argininosuccinate lyase OS=Mus musculus GN=Asl PE=1 SV=1	0	5	0	2	6	0	0.625	0.7014	13
sp|P62631|EF1A2_MOUSE - Elongation factor 1-alpha 2 OS=Mus musculus GN=Eef1a2 PE	0	5	0	0	8	0	0.625	0.7664	13
sp|P01029|CO4B_MOUSE - Complement C4-B OS=Mus musculus GN=C4b PE=1 SV=3	0	5	0	0	8	0	0.625	0.7664	13
sp|P35436|NMDE1_MOUSE - Glutamate receptor ionotropic, NMDA 2A OS=Mus musculus G	0	5	0	0	8	0	0.625	0.7664	13
sp|Q9ES52|SHIP1_MOUSE - Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1	0	5	0	0	8	0	0.625	0.7664	13
sp|P61028|RAB8B_MOUSE - Ras-related protein Rab-8B OS=Mus musculus GN=Rab8b PE=1	0	5	0	0	8	0	0.625	0.7664	13
sp|Q9WTI7|MYO1C_MOUSE - Unconventional myosin-Ic OS=Mus musculus GN=Myo1c PE=1 S	0	7	6	0	7	14	0.619	0.5927	34
sp|Q5FWK3|RHG01_MOUSE - Rho GTPase-activating protein 1 OS=Mus musculus GN=Arhga	2	14	0	3	23	0	0.6153	0.713	42
sp|Q8BNA6|FAT3_MOUSE - Protocadherin Fat 3 OS=Mus musculus GN=Fat3 PE=1 SV=2	0	8	0	0	0	13	0.6153	0.7596	21
sp|Q70KF4|CMYA5_MOUSE - Cardiomyopathy-associated protein 5 OS=Mus musculus GN=C	0	0	8	0	0	13	0.6153	0.7596	21
sp|Q8C0S1|DI3L1_MOUSE - DIS3-like exonuclease 1 OS=Mus musculus GN=Dis3l PE=2 SV	0	11	0	0	18	0	0.6111	0.7566	29
sp|P59672|ANS1A_MOUSE - Ankyrin repeat and SAM domain-containing protein 1A OS=M	0	5	6	4	7	7	0.6111	0.3304	29
sp|O88329|MYO1A_MOUSE - Unconventional myosin-Ia OS=Mus musculus GN=Myo1a PE=2 S	0	0	11	0	7	11	0.6111	0.6572	29

sp|Q60592|MAST2_MOUSE - Microtubule-associated serine/threonine-protein kinase 2	6	12	13	15	10	26	0.6078	0.2696	82
sp|Q8JZN5|ACAD9_MOUSE - Acyl-CoA dehydrogenase family member 9, mitochondrial OS	3	21	5	2	26	20	0.6041	0.5286	77
sp|Q8C3R1|BRAT1_MOUSE - BRCA1-associated ATM activator 1 OS=Mus musculus GN=Brat	3	0	0	0	5	0	0.6	0.7488	8
sp|Q9Z0N1|IF2G_MOUSE - Eukaryotic translation initiation factor 2 subunit 3, X-l	0	6	0	2	5	3	0.6	0.5748	16
sp|Q61207|SAP_MOUSE - Prosaposin OS=Mus musculus GN=Psap PE=1 SV=2	0	6	0	0	4	6	0.6	0.6433	16
sp|Q3U3N6|AP4AT_MOUSE - AP-4 complex accessory subunit tepsin OS=Mus musculus GN	0	6	0	0	10	0	0.6	0.7488	16
sp|Q3V3R1|C1TM_MOUSE - Monofunctional C1-tetrahydrofolate synthase, mitochondria	0	6	0	0	10	0	0.6	0.7488	16
sp|P09470|ACE_MOUSE - Angiotensin-converting enzyme OS=Mus musculus GN=Ace PE=1	0	6	0	0	2	8	0.6	0.6917	16
sp|P43277|H13_MOUSE - Histone H1.3 OS=Mus musculus GN=Hist1h1d PE=1 SV=2	0	3	0	0	5	0	0.6	0.7488	8
sp|Q8K386|RAB15_MOUSE - Ras-related protein Rab-15 OS=Mus musculus GN=Rab15 PE=1	0	3	0	0	5	0	0.6	0.7488	8
sp|Q8R1S0|COQ6_MOUSE - Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial	0	3	0	0	5	0	0.6	0.7488	8
sp|Q9EPL9|ACOX3_MOUSE - Peroxisomal acyl-coenzyme A oxidase 3 OS=Mus musculus GN	0	3	0	0	5	0	0.6	0.7488	8
sp|Q99NB1|ACS2L_MOUSE - Acetyl-coenzyme A synthetase 2-like, mitochondrial OS=Mu	0	3	0	0	5	0	0.6	0.7488	8
sp|Q8VC57|KCTD5_MOUSE - BTB/POZ domain-containing protein KCTD5 OS=Mus musculus	0	0	6	2	2	6	0.6	0.6086	16
sp|Q3UHQ6|DOP2_MOUSE - Protein dopey-2 OS=Mus musculus GN=Dopey2 PE=1 SV=3	2	8	0	0	17	0	0.5882	0.7239	27
sp|Q8BH95|ECHM_MOUSE - Enoyl-CoA hydratase, mitochondrial OS=Mus musculus GN=Ech	17	57	26	22	70	78	0.5882	0.3343	270
sp|Q9CPQ1|COX6C_MOUSE - Cytochrome c oxidase subunit 6C OS=Mus musculus GN=Cox6c	2	15	0	0	20	9	0.5862	0.6199	46
sp|P26040|EZRI_MOUSE - Ezrin OS=Mus musculus GN=Ezr PE=1 SV=3	0	7	0	0	12	0	0.5833	0.7371	19
sp|Q80YX1|TENA_MOUSE - Tenascin OS=Mus musculus GN=Tnc PE=1 SV=1	0	0	14	3	16	5	0.5833	0.6178	38
sp|Q80Y44|DDX10_MOUSE - Probable ATP-dependent RNA helicase DDX10 OS=Mus musculu	0	4	7	6	5	8	0.5789	0.2942	30
sp|Q149T7|PPM1J_MOUSE - Protein phosphatase 1J OS=Mus musculus GN=Ppm1j PE=1 SV=	0	4	4	7	7	0	0.5714	0.4981	22
sp|Q5SYD0|MYO1D_MOUSE - Unconventional myosin-Id OS=Mus musculus GN=Myo1d PE=1 S	0	4	0	0	7	0	0.5714	0.7287	11
sp|Q60953|PML_MOUSE - Protein PML OS=Mus musculus GN=Pml PE=1 SV=3	0	4	0	0	7	0	0.5714	0.7287	11
sp|Q9D1G1|RAB1B_MOUSE - Ras-related protein Rab-1B OS=Mus musculus GN=Rab1b PE=1	0	4	0	0	7	0	0.5714	0.7287	11
sp|Q3TTL0|CC038_MOUSE - Uncharacterized protein C3orf38 homolog OS=Mus musculus	0	4	0	0	7	0	0.5714	0.7287	11
sp|Q6P549|SHIP2_MOUSE - Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2	0	21	0	2	19	16	0.5675	0.5748	58
sp|O35459|ECH1_MOUSE - Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondria	18	38	0	23	61	15	0.5656	0.469	155
sp|Q9CUL5|IQCA1_MOUSE - IQ and AAA domain-containing protein 1 OS=Mus musculus G	0	0	13	7	3	13	0.5652	0.5576	36
sp|Q61765|K1H1_MOUSE - Keratin, type I cuticular Ha1 OS=Mus musculus GN=Krt31 PE	3	21	3	0	19	29	0.5625	0.5381	75
sp|Q9D952|EVPL_MOUSE - Envoplakin OS=Mus musculus GN=Evpl PE=2 SV=3	0	9	0	0	16	0	0.5625	0.7223	25
sp|Q80UV9|TAF1_MOUSE - Transcription initiation factor TFIID subunit 1 OS=Mus mu	0	17	16	3	28	28	0.5593	0.4345	92
sp|Q8CAK1|CAF17_MOUSE - Putative transferase CAF17 homolog, mitochondrial OS=Mus	0	5	0	4	3	2	0.5555	0.4917	14
sp|Q91YP2|NEUL_MOUSE - Neurolysin, mitochondrial OS=Mus musculus GN=Nln PE=2 SV=	0	10	0	4	7	7	0.5555	0.4862	28
sp|Q8R3P2|DTX2_MOUSE - Probable E3 ubiquitin-protein ligase DTX2 OS=Mus musculus	0	5	0	6	3	0	0.5555	0.6086	14
sp|Q9CRB3|HIUH_MOUSE - 5-hydroxyisourate hydrolase OS=Mus musculus GN=Urah PE=1	0	5	0	0	7	2	0.5555	0.6433	14
sp|P26043|RADI_MOUSE - Radixin OS=Mus musculus GN=Rdx PE=1 SV=3	0	10	0	4	14	0	0.5555	0.6433	28
sp|Q9QY40|PLXB3_MOUSE - Plexin-B3 OS=Mus musculus GN=Plxnb3 PE=1 SV=2	0	5	0	5	4	0	0.5555	0.587	14
sp|A1L3T7|FA65C_MOUSE - Protein FAM65C OS=Mus musculus GN=Fam65c PE=2 SV=1	0	5	0	0	9	0	0.5555	0.7174	14
sp|P30115|GSTA3_MOUSE - Glutathione S-transferase A3 OS=Mus musculus GN=Gsta3 PE	0	16	0	0	26	3	0.5517	0.6809	45
sp|Q99KR3|LACB2_MOUSE - Beta-lactamase-like protein 2 OS=Mus musculus GN=Lactb2	5	14	9	6	24	21	0.549	0.2803	79
sp|Q9D5Y1|CCD39_MOUSE - Coiled-coil domain-containing protein 39 OS=Mus musculus	0	6	0	0	0	11	0.5454	0.7102	17

sp|Q8R310|TMCC3_MOUSE - Transmembrane and coiled-coil domains protein 3 OS=Mus m	0	6	0	3	8	0	0.5454	0.6164	17
sp|Q91YR7|PRP6_MOUSE - Pre-mRNA-processing factor 6 OS=Mus musculus GN=Prpf6 PE=	0	6	0	3	8	0	0.5454	0.6164	17
sp|Q9CQ69|QCR8_MOUSE - Cytochrome b-c1 complex subunit 8 OS=Mus musculus GN=Uqcr	0	6	0	0	11	0	0.5454	0.7102	17
sp|Q9JI39|ABCBA_MOUSE - ATP-binding cassette sub-family B member 10, mitochondri	0	0	6	7	0	4	0.5454	0.5898	17
sp|Q6UQ17|AT8B3_MOUSE - Phospholipid-transporting ATPase IK OS=Mus musculus GN=A	0	0	6	0	6	5	0.5454	0.5743	17
sp|Q9DBU6|RSRC1_MOUSE - Serine/Arginine-related protein 53 OS=Mus musculus GN=Rs	4	6	9	9	19	7	0.5428	0.2519	54
sp|Q80W93|HYDIN_MOUSE - Hydrocephalus-inducing protein OS=Mus musculus GN=Hydin	5	28	7	33	41	0	0.5405	0.4794	114
sp|Q8K482|EMIL2_MOUSE - EMILIN-2 OS=Mus musculus GN=Emilin2 PE=1 SV=1	0	7	0	5	8	0	0.5384	0.5771	20
sp|P12787|COX5A_MOUSE - Cytochrome c oxidase subunit 5A, mitochondrial OS=Mus mu	12	49	15	46	50	46	0.5352	0.1391	218
sp|Q8BKX6|SMG1_MOUSE - Serine/threonine-protein kinase SMG1 OS=Mus musculus GN=S	2	6	0	5	10	0	0.5333	0.5283	23
sp|Q8R5G7|ARAP3_MOUSE - Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-co	0	8	0	5	10	0	0.5333	0.5846	23
sp|P17742|PPIA_MOUSE - Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=	3	6	0	0	12	5	0.5294	0.5304	26
sp|Q99NH0|ANR17_MOUSE - Ankyrin repeat domain-containing protein 17 OS=Mus muscu	0	9	12	3	28	9	0.525	0.4905	61
sp|Q99L13|3HIDH_MOUSE - 3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Mus	8	55	4	19	64	46	0.5193	0.3798	196
sp|P99029|PRDX5_MOUSE - Peroxiredoxin-5, mitochondrial OS=Mus musculus GN=Prdx5	5	20	3	13	29	12	0.5185	0.3226	82
sp|Q99MB1|TLR3_MOUSE - Toll-like receptor 3 OS=Mus musculus GN=Tlr3 PE=1 SV=2	0	3	11	6	11	10	0.5185	0.2974	41
sp|Q3U214|MAST3_MOUSE - Microtubule-associated serine/threonine-protein kinase 3	0	15	0	11	5	13	0.5172	0.4476	44
sp|Q811L6|MAST4_MOUSE - Microtubule-associated serine/threonine-protein kinase 4	5	20	10	14	22	32	0.5147	0.1822	103
sp|P08032|SPTA1_MOUSE - Spectrin alpha chain, erythrocytic 1 OS=Mus musculus GN=	0	23	11	24	43	0	0.5074	0.4789	101
sp|Q9QUG2|POLK_MOUSE - DNA polymerase kappa OS=Mus musculus GN=Polk PE=1 SV=1	0	3	0	3	3	0	0.5	0.5185	9
sp|Q9CT10|RANB3_MOUSE - Ran-binding protein 3 OS=Mus musculus GN=Ranbp3 PE=1 SV=	2	0	0	0	4	0	0.5	0.6778	6
sp|Q62077|PLCG1_MOUSE - 1-phosphatidylinositol 4,5-bisphosphate phosphodiesteras	3	11	0	2	21	5	0.5	0.5273	42
sp|Q00PI9|HNRL2_MOUSE - Heterogeneous nuclear ribonucleoprotein U-like protein 2	2	0	0	2	2	0	0.5	0.5185	6
sp|Q9WUF3|C8AP2_MOUSE - CASP8-associated protein 2 OS=Mus musculus GN=Casp8ap2 P	3	5	0	7	9	0	0.5	0.4369	24
sp|Q9DBT5|AMPD2_MOUSE - AMP deaminase 2 OS=Mus musculus GN=Ampd2 PE=1 SV=1	0	2	0	0	4	0	0.5	0.6778	6
sp|Q64445|COX8A_MOUSE - Cytochrome c oxidase subunit 8A, mitochondrial OS=Mus mu	0	2	0	0	4	0	0.5	0.6778	6
sp|Q02257|PLAK_MOUSE - Junction plakoglobin OS=Mus musculus GN=Jup PE=1 SV=3	0	3	0	0	6	0	0.5	0.6778	9
sp|Q9D5V6|SYAP1_MOUSE - Synapse-associated protein 1 OS=Mus musculus GN=Syap1 PE	0	2	0	4	0	0	0.5	0.6778	6
sp|Q5GFD5|HS3S6_MOUSE - Heparan sulfate glucosamine 3-O-sulfotransferase 6 OS=Mu	0	6	0	2	10	0	0.5	0.613	18
sp|Q9CZX2|CEP89_MOUSE - Centrosomal protein of 89 kDa OS=Mus musculus GN=Cep89 P	0	5	0	6	4	0	0.5	0.5299	15
sp|Q99MV7|RNF17_MOUSE - RING finger protein 17 OS=Mus musculus GN=Rnf17 PE=1 SV=	0	7	0	10	4	0	0.5	0.5652	21
sp|A2ALS5|RPGP1_MOUSE - Rap1 GTPase-activating protein 1 OS=Mus musculus GN=Rap1	0	2	0	2	2	0	0.5	0.5185	6
sp|Q61066|NR0B1_MOUSE - Nuclear receptor subfamily 0 group B member 1 OS=Mus mus	0	2	0	0	4	0	0.5	0.6778	6
sp|O35134|RPA1_MOUSE - DNA-directed RNA polymerase I subunit RPA1 OS=Mus musculu	0	4	0	0	5	3	0.5	0.536	12
sp|Q91X05|PODO_MOUSE - Podocin OS=Mus musculus GN=Nphs2 PE=1 SV=2	0	2	0	0	4	0	0.5	0.6778	6
sp|Q91WT8|RBM47_MOUSE - RNA-binding protein 47 OS=Mus musculus GN=Rbm47 PE=2 SV=	0	2	0	0	4	0	0.5	0.6778	6
sp|Q6VVW5|ANPRB_MOUSE - Atrial natriuretic peptide receptor 2 OS=Mus musculus GN	0	3	0	3	3	0	0.5	0.5185	9
sp|E1U8D0|SOGA1_MOUSE - Protein SOGA1 OS=Mus musculus GN=Soga1 PE=1 SV=3	0	7	0	2	12	0	0.5	0.6227	21
sp|Q8R420|ABCA3_MOUSE - ATP-binding cassette sub-family A member 3 OS=Mus muscul	0	2	0	0	4	0	0.5	0.6778	6
sp|Q9JLB4|CUBN_MOUSE - Cubilin OS=Mus musculus GN=Cubn PE=1 SV=3	0	3	0	3	3	0	0.5	0.5185	9
sp|Q9DC23|DJC10_MOUSE - DnaJ homolog subfamily C member 10 OS=Mus musculus GN=Dn	0	2	0	0	0	4	0.5	0.6778	6

sp|P42703|LIFR_MOUSE - Leukemia inhibitory factor receptor OS=Mus musculus GN=Li	0	2	0	0	4	0	0.5	0.6778	6
sp|Q3UBX0|TM109_MOUSE - Transmembrane protein 109 OS=Mus musculus GN=Tmem109 PE=	0	2	0	0	4	0	0.5	0.6778	6
sp|O35857|TIM44_MOUSE - Mitochondrial import inner membrane translocase subunit	0	5	0	0	6	4	0.5	0.5299	15
sp|Q9R013|CATF_MOUSE - Cathepsin F OS=Mus musculus GN=Ctsf PE=2 SV=1	0	2	0	0	4	0	0.5	0.6778	6
sp|Q8C2E4|PTCD1_MOUSE - Pentatricopeptide repeat-containing protein 1, mitochond	0	4	0	0	2	6	0.5	0.579	12
sp|Q8K4P0|WDR33_MOUSE - pre-mRNA 3' end processing protein WDR33 OS=Mus musculus	0	2	0	0	4	0	0.5	0.6778	6
sp|Q62120|JAK2_MOUSE - Tyrosine-protein kinase JAK2 OS=Mus musculus GN=Jak2 PE=1	0	2	0	0	2	2	0.5	0.5185	6
sp|O70343|PRGC1_MOUSE - Peroxisome proliferator-activated receptor gamma coactiv	0	0	3	0	3	3	0.5	0.5185	9
sp|A2AQ19|RTF1_MOUSE - RNA polymerase-associated protein RTF1 homolog OS=Mus mus	0	0	12	0	0	24	0.5	0.6778	36
sp|Q3UHX0|NOL8_MOUSE - Nucleolar protein 8 OS=Mus musculus GN=Nol8 PE=1 SV=2	0	0	5	0	0	10	0.5	0.6778	15
sp|Q059U7|INTU_MOUSE - Protein inturned OS=Mus musculus GN=Intu PE=1 SV=1	0	0	4	0	0	8	0.5	0.6778	12
sp|Q61025|IFT20_MOUSE - Intraflagellar transport protein 20 homolog OS=Mus muscu	0	0	3	0	0	6	0.5	0.6778	9
sp|Q5FW57|GLYAL_MOUSE - Glycine N-acyltransferase-like protein OS=Mus musculus G	6	28	9	14	44	30	0.4886	0.2469	131
sp|P02088|HBB1_MOUSE - Hemoglobin subunit beta-1 OS=Mus musculus GN=Hbb-b1 PE=1	0	18	0	0	26	11	0.4864	0.5467	55
sp|P02089|HBB2_MOUSE - Hemoglobin subunit beta-2 OS=Mus musculus GN=Hbb-b2 PE=1	0	17	0	0	24	11	0.4857	0.5396	52
sp|Q9CW42|MARC1_MOUSE - Mitochondrial amidoxime-reducing component 1 OS=Mus musc	2	11	0	3	15	9	0.4814	0.3897	40
sp|Q64467|G3PT_MOUSE - Glyceraldehyde-3-phosphate dehydrogenase, testis-specific	0	10	0	4	17	0	0.4761	0.5813	31
sp|P13745|GSTA1_MOUSE - Glutathione S-transferase A1 OS=Mus musculus GN=Gsta1 PE	0	8	0	0	15	2	0.4705	0.6084	25
sp|P32020|NLTP_MOUSE - Non-specific lipid-transfer protein OS=Mus musculus GN=Sc	7	48	16	20	84	48	0.4671	0.2928	223
sp|A2AQ25|SKT_MOUSE - Sickle tail protein OS=Mus musculus GN=Skt PE=1 SV=1	0	4	13	12	18	7	0.4594	0.2524	54
sp|P49025|CTRO_MOUSE - Citron Rho-interacting kinase OS=Mus musculus GN=Cit PE=1	0	11	0	5	12	7	0.4583	0.3621	35
sp|P63328|PP2BA_MOUSE - Serine/threonine-protein phosphatase 2B catalytic subuni	0	13	0	0	10	19	0.4482	0.4881	42
sp|Q7TNH6|NPHP3_MOUSE - Nephrocystin-3 OS=Mus musculus GN=Nphp3 PE=1 SV=2	0	13	0	13	16	0	0.4482	0.4611	42
sp|P11276|FINC_MOUSE - Fibronectin OS=Mus musculus GN=Fn1 PE=1 SV=4	4	0	0	0	7	2	0.4444	0.5371	13
sp|P01864|GCAB_MOUSE - Ig gamma-2A chain C region secreted form OS=Mus musculus	0	4	0	0	2	7	0.4444	0.5371	13
sp|Q8C1F5|TTC16_MOUSE - Tetratricopeptide repeat protein 16 OS=Mus musculus GN=T	0	4	0	0	9	0	0.4444	0.6384	13
sp|P21271|MYO5B_MOUSE - Unconventional myosin-Vb OS=Mus musculus GN=Myo5b PE=2 S	0	3	4	0	7	9	0.4375	0.3712	23
sp|Q3TYL0|YH010_MOUSE - Putative IQ motif and ankyrin repeat domain-containing p	0	0	10	6	9	8	0.4347	0.2772	33
sp|P48725|PCNT_MOUSE - Pericentrin OS=Mus musculus GN=Pcnt PE=1 SV=2	5	8	0	11	11	8	0.4333	0.0893	43
sp|Q9D7J9|ECHD3_MOUSE - Enoyl-CoA hydratase domain-containing protein 3, mitocho	9	18	10	16	30	40	0.4302	0.0956	123
sp|Q9JLN9|MTOR_MOUSE - Serine/threonine-protein kinase mTOR OS=Mus musculus GN=M	0	3	0	4	3	0	0.4285	0.4418	10
sp|E9QMW4|CP096_MOUSE - Uncharacterized protein C16orf96 homolog OS=Mus musculus	0	3	0	0	7	0	0.4285	0.6272	10
sp|O70372|TERT_MOUSE - Telomerase reverse transcriptase OS=Mus musculus GN=Tert	0	3	0	0	7	0	0.4285	0.6272	10
sp|Q3UIU2|NDUB6_MOUSE - NADH dehydrogenase [ubiquinone] 1 beta subcomplex subuni	0	3	0	0	7	0	0.4285	0.6272	10
sp|Q5SYL3|K0100_MOUSE - Protein KIAA0100 OS=Mus musculus GN=Kiaa0100 PE=2 SV=1	0	0	3	0	7	0	0.4285	0.6272	10
sp|Q9Z329|ITPR2_MOUSE - Inositol 1,4,5-trisphosphate receptor type 2 OS=Mus musc	0	16	0	20	18	0	0.421	0.4268	54
sp|Q69ZT1|FAN1_MOUSE - Fanconi-associated nuclease 1 OS=Mus musculus GN=Fan1 PE=	2	3	0	0	8	4	0.4166	0.3986	17
sp|Q9DC61|MPPA_MOUSE - Mitochondrial-processing peptidase subunit alpha OS=Mus m	3	2	0	0	10	2	0.4166	0.5037	17
sp|Q4ACU6|SHAN3_MOUSE - SH3 and multiple ankyrin repeat domains protein 3 OS=Mus	3	7	0	5	19	0	0.4166	0.4826	34
sp|Q80U19|DAAM2_MOUSE - Disheveled-associated activator of morphogenesis 2 OS=Mu	0	5	0	0	12	0	0.4166	0.6188	17
sp|Q6PDH0|PHLB1_MOUSE - Pleckstrin homology-like domain family B member 1 OS=Mus	0	9	5	6	6	22	0.4117	0.3241	48

sp|Q7M6Y6|MRO2B_MOUSE - Maestro heat-like repeat-containing protein family membe	0	9	0	0	7	15	0.409	0.4571	31
sp|P70268|PKN1_MOUSE - Serine/threonine-protein kinase N1 OS=Mus musculus GN=Pkn	2	6	0	5	7	8	0.4	0.1124	28
sp|Q9R1L5|MAST1_MOUSE - Microtubule-associated serine/threonine-protein kinase 1	4	8	0	11	8	11	0.4	0.0756	42
sp|Q8BXR5|NALCN_MOUSE - Sodium leak channel non-selective protein OS=Mus musculu	2	0	0	2	3	0	0.4	0.4168	7
sp|P40630|TFAM_MOUSE - Transcription factor A, mitochondrial OS=Mus musculus GN=	0	2	0	0	5	0	0.4	0.6071	7
sp|Q8R092|CA043_MOUSE - Uncharacterized protein C1orf43 homolog OS=Mus musculus	0	6	0	0	2	13	0.4	0.5422	21
sp|Q9CZG9|PDZ11_MOUSE - PDZ domain-containing protein 11 OS=Mus musculus GN=Pdzd	0	2	0	3	2	0	0.4	0.4168	7
sp|Q7TMK9|HNRPQ_MOUSE - Heterogeneous nuclear ribonucleoprotein Q OS=Mus musculu	0	2	0	0	5	0	0.4	0.6071	7
sp|Q8BGZ4|CDC23_MOUSE - Cell division cycle protein 23 homolog OS=Mus musculus G	0	4	0	5	5	0	0.4	0.4017	14
sp|Q99KJ8|DCTN2_MOUSE - Dynactin subunit 2 OS=Mus musculus GN=Dctn2 PE=1 SV=3	0	2	0	5	0	0	0.4	0.6071	7
sp|Q6P1E1|ZMIZ1_MOUSE - Zinc finger MIZ domain-containing protein 1 OS=Mus muscu	0	2	0	3	2	0	0.4	0.4168	7
sp|Q5SSM3|RHG44_MOUSE - Rho GTPase-activating protein 44 OS=Mus musculus GN=Arhg	0	2	0	0	0	5	0.4	0.6071	7
sp|P39039|MBL1_MOUSE - Mannose-binding protein A OS=Mus musculus GN=Mbl1 PE=2 SV	0	2	0	0	5	0	0.4	0.6071	7
sp|Q99K48|NONO_MOUSE - Non-POU domain-containing octamer-binding protein OS=Mus	0	2	0	0	5	0	0.4	0.6071	7
sp|Q5SVQ0|KAT7_MOUSE - Histone acetyltransferase KAT7 OS=Mus musculus GN=Kat7 PE	0	4	0	4	6	0	0.4	0.4168	14
sp|Q3TL44|NLRX1_MOUSE - NLR family member X1 OS=Mus musculus GN=Nlrx1 PE=2 SV=1	0	6	0	4	11	0	0.4	0.4724	21
sp|Q9DBV3|DHX34_MOUSE - Probable ATP-dependent RNA helicase DHX34 OS=Mus musculu	0	2	0	0	5	0	0.4	0.6071	7
sp|Q9ERS2|NDUAD_MOUSE - NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subun	5	8	0	12	17	4	0.3939	0.2082	46
sp|Q8BFR5|EFTU_MOUSE - Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tu	0	7	4	0	19	9	0.3928	0.3875	39
sp|Q8CGB6|TNS2_MOUSE - Tensin-2 OS=Mus musculus GN=Tns2 PE=1 SV=1	0	0	5	0	11	2	0.3846	0.5185	18
sp|Q00612|G6PD1_MOUSE - Glucose-6-phosphate 1-dehydrogenase X OS=Mus musculus GN	0	3	0	0	8	0	0.375	0.5898	11
sp|Q8C9H6|STRP2_MOUSE - Striatin-interacting proteins 2 OS=Mus musculus GN=Strip	0	6	0	0	5	11	0.375	0.425	22
sp|O70311|NMT2_MOUSE - Glycylpeptide N-tetradecanoyltransferase 2 OS=Mus musculu	0	3	0	5	3	0	0.375	0.3982	11
sp|Q4VA61|DSCL1_MOUSE - Down syndrome cell adhesion molecule-like protein 1 homo	0	3	0	0	8	0	0.375	0.5898	11
sp|Q9D0S9|HINT2_MOUSE - Histidine triad nucleotide-binding protein 2, mitochondr	0	3	0	0	8	0	0.375	0.5898	11
sp|Q7TMY7|IPO8_MOUSE - Importin-8 OS=Mus musculus GN=Ipo8 PE=1 SV=3	0	0	3	5	3	0	0.375	0.3982	11
sp|Q9D3D9|ATPD_MOUSE - ATP synthase subunit delta, mitochondrial OS=Mus musculus	0	6	4	0	11	16	0.3703	0.3241	37
sp|Q9ER60|SCN4A_MOUSE - Sodium channel protein type 4 subunit alpha OS=Mus muscu	0	7	0	10	9	0	0.3684	0.3678	26
sp|Q9CPP6|NDUA5_MOUSE - NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subun	2	2	0	4	7	0	0.3636	0.3357	15
sp|Q8BPM0|DAAM1_MOUSE - Disheveled-associated activator of morphogenesis 1 OS=Mu	0	0	4	8	3	0	0.3636	0.4342	15
sp|A2AEY4|MA7D3_MOUSE - MAP7 domain-containing protein 3 OS=Mus musculus GN=Map7	0	5	0	0	4	10	0.3571	0.4211	19
sp|Q14AT2|TEX11_MOUSE - Testis-expressed sequence 11 protein OS=Mus musculus GN=	0	0	7	6	0	14	0.35	0.4067	27
sp|Q91VS7|MGST1_MOUSE - Microsomal glutathione S-transferase 1 OS=Mus musculus G	15	42	20	20	145	57	0.3468	0.2722	299
sp|B1AQ75|KRT36_MOUSE - Keratin, type I cuticular Ha6 OS=Mus musculus GN=Krt36 P	4	6	0	3	14	12	0.3448	0.1722	39
sp|O88735|MAP7_MOUSE - Ensconsin OS=Mus musculus GN=Map7 PE=1 SV=1	2	0	0	0	6	0	0.3333	0.5614	8
sp|Q8R1B4|EIF3C_MOUSE - Eukaryotic translation initiation factor 3 subunit C OS=	3	0	0	0	9	0	0.3333	0.5614	12
sp|O08599|STXB1_MOUSE - Syntaxin-binding protein 1 OS=Mus musculus GN=Stxbp1 PE=	3	0	0	5	4	0	0.3333	0.3348	12
sp|P29416|HEXA_MOUSE - Beta-hexosaminidase subunit alpha OS=Mus musculus GN=Hexa	0	5	0	5	10	0	0.3333	0.3739	20
sp|P61982|1433G_MOUSE - 14-3-3 protein gamma OS=Mus musculus GN=Ywhag PE=1 SV=2	0	2	0	0	6	0	0.3333	0.5614	8
sp|P70352|NAR5_MOUSE - Ecto-ADP-ribosyltransferase 5 OS=Mus musculus GN=Art5 PE=	0	2	0	0	6	0	0.3333	0.5614	8
sp|Q9Z2T6|KRT85_MOUSE - Keratin, type II cuticular Hb5 OS=Mus musculus GN=Krt85	0	2	0	0	6	0	0.3333	0.5614	8

sp|Q3UQ22|NET5_MOUSE - Netrin-5 OS=Mus musculus GN=Ntn5 PE=2 SV=2	0	2	0	2	4	0	0.3333	0.3739	8
sp|Q3UPI1|F198B_MOUSE - Protein FAM198B OS=Mus musculus GN=Fam198b PE=2 SV=1	0	5	0	3	12	0	0.3333	0.4486	20
sp|O88967|YMEL1_MOUSE - ATP-dependent zinc metalloprotease YME1L1 OS=Mus musculu	0	4	0	0	8	4	0.3333	0.3739	16
sp|Q61879|MYH10_MOUSE - Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2	0	2	0	0	6	0	0.3333	0.5614	8
sp|Q9ERI6|RDH14_MOUSE - Retinol dehydrogenase 14 OS=Mus musculus GN=Rdh14 PE=2 S	0	2	0	3	3	0	0.3333	0.3294	8
sp|Q571E4|GALNS_MOUSE - N-acetylgalactosamine-6-sulfatase OS=Mus musculus GN=Gal	0	2	0	0	6	0	0.3333	0.5614	8
sp|O55230|RA51D_MOUSE - DNA repair protein RAD51 homolog 4 OS=Mus musculus GN=Ra	0	2	0	0	6	0	0.3333	0.5614	8
sp|Q8BZ25|ANKK1_MOUSE - Ankyrin repeat and protein kinase domain-containing prot	0	2	0	0	6	0	0.3333	0.5614	8
sp|Q9R0M0|CELR2_MOUSE - Cadherin EGF LAG seven-pass G-type receptor 2 OS=Mus mus	0	2	0	0	4	2	0.3333	0.3739	8
sp|Q01768|NDKB_MOUSE - Nucleoside diphosphate kinase B OS=Mus musculus GN=Nme2 P	0	3	0	0	9	0	0.3333	0.5614	12
sp|P08226|APOE_MOUSE - Apolipoprotein E OS=Mus musculus GN=Apoe PE=1 SV=2	0	4	0	0	6	6	0.3333	0.3294	16
sp|Q9CQV8|1433B_MOUSE - 14-3-3 protein beta/alpha OS=Mus musculus GN=Ywhab PE=1	0	2	0	0	6	0	0.3333	0.5614	8
sp|P54116|STOM_MOUSE - Erythrocyte band 7 integral membrane protein OS=Mus muscu	0	2	0	0	6	0	0.3333	0.5614	8
sp|Q8CJF8|AGO4_MOUSE - Protein argonaute-4 OS=Mus musculus GN=Ago4 PE=2 SV=2	0	2	0	0	6	0	0.3333	0.5614	8
sp|Q6PDD0|UD2A2_MOUSE - UDP-glucuronosyltransferase 2A2 OS=Mus musculus GN=Ugt2a	0	8	0	0	26	0	0.3076	0.5443	34
sp|Q9CQC7|NDUB4_MOUSE - NADH dehydrogenase [ubiquinone] 1 beta subcomplex subuni	2	5	0	0	14	9	0.3043	0.287	30
sp|P52592|S1PR2_MOUSE - Sphingosine 1-phosphate receptor 2 OS=Mus musculus GN=S1	2	0	0	0	7	0	0.2857	0.5299	9
sp|Q61292|LAMB2_MOUSE - Laminin subunit beta-2 OS=Mus musculus GN=Lamb2 PE=2 SV=	0	2	0	0	2	5	0.2857	0.356	9
sp|Q8VDM4|PSMD2_MOUSE - 26S proteasome non-ATPase regulatory subunit 2 OS=Mus mu	0	2	0	0	7	0	0.2857	0.5299	9
sp|Q921R7|S35A5_MOUSE - Probable UDP-sugar transporter protein SLC35A5 OS=Mus mu	0	6	0	10	11	0	0.2857	0.2836	27
sp|Q61493|DPOLZ_MOUSE - DNA polymerase zeta catalytic subunit OS=Mus musculus GN	0	2	0	0	0	7	0.2857	0.5299	9
sp|P19246|NFH_MOUSE - Neurofilament heavy polypeptide OS=Mus musculus GN=Nefh PE	0	0	4	0	4	10	0.2857	0.356	18
sp|A7XUZ6|SKIT6_MOUSE - Selection and upkeep of intraepithelial T-cells protein	0	5	0	8	10	0	0.2777	0.281	23
sp|O70362|PHLD_MOUSE - Phosphatidylinositol-glycan-specific phospholipase D OS=M	0	3	0	2	9	0	0.2727	0.4107	14
sp|P01942|HBA_MOUSE - Hemoglobin subunit alpha OS=Mus musculus GN=Hba PE=1 SV=2	5	11	3	10	37	27	0.2567	0.0901	93
sp|Q9CQJ8|NDUB9_MOUSE - NADH dehydrogenase [ubiquinone] 1 beta subcomplex subuni	2	0	0	2	6	0	0.25	0.3486	10
sp|Q99N64|GMCLL_MOUSE - Putative germ cell-less protein-like 1-like OS=Mus muscu	2	0	0	2	6	0	0.25	0.3486	10
sp|Q8BIH0|SP130_MOUSE - Histone deacetylase complex subunit SAP130 OS=Mus muscul	0	2	0	0	8	0	0.25	0.5071	10
sp|B8ZXI1|QTRD1_MOUSE - Queuine tRNA-ribosyltransferase subunit QTRTD1 OS=Mus mu	0	2	0	0	2	6	0.25	0.3486	10
sp|Q8R1Q0|STX19_MOUSE - Syntaxin-19 OS=Mus musculus GN=Stx19 PE=2 SV=1	0	2	0	0	0	8	0.25	0.5071	10
sp|P62334|PRS10_MOUSE - 26S protease regulatory subunit 10B OS=Mus musculus GN=P	0	2	0	0	2	6	0.25	0.3486	10
sp|Q8VDN2|AT1A1_MOUSE - Sodium/potassium-transporting ATPase subunit alpha-1 OS=	0	2	0	3	5	0	0.25	0.279	10
sp|Q8C3J5|DOCK2_MOUSE - Dedicator of cytokinesis protein 2 OS=Mus musculus GN=Do	0	2	0	0	8	0	0.25	0.5071	10
sp|O88799|ZAN_MOUSE - Zonadhesin OS=Mus musculus GN=Zan PE=2 SV=1	0	3	0	3	5	4	0.25	0.0601	15
sp|Q91YD4|TRPM2_MOUSE - Transient receptor potential cation channel subfamily M	0	2	0	8	0	0	0.25	0.5071	10
sp|Q9CR98|F136A_MOUSE - Protein FAM136A OS=Mus musculus GN=Fam136a PE=2 SV=1	0	5	0	3	10	7	0.25	0.1294	25
sp|Q4KKZ1|CA158_MOUSE - Uncharacterized protein C1orf158 homolog OS=Mus musculus	2	0	0	0	9	0	0.2222	0.4899	11
sp|Q8QZY6|TSN14_MOUSE - Tetraspanin-14 OS=Mus musculus GN=Tspan14 PE=1 SV=1	0	6	0	10	3	14	0.2222	0.1381	33
sp|Q5PR69|K1211_MOUSE - Uncharacterized protein KIAA1211 OS=Mus musculus GN=Kiaa	0	2	0	5	4	0	0.2222	0.2341	11
sp|Q9Z1Z0|USO1_MOUSE - General vesicular transport factor p115 OS=Mus musculus G	0	2	0	3	3	3	0.2222	0.0248	11
sp|O88196|TTC3_MOUSE - E3 ubiquitin-protein ligase TTC3 OS=Mus musculus GN=Ttc3	0	2	0	0	4	5	0.2222	0.2341	11

sp|P30677|GNA14_MOUSE - Guanine nucleotide-binding protein subunit alpha-14 OS=M	0	2	0	4	5	0	0.2222	0.2341	11
sp|Q8BU40|NAL4A_MOUSE - NACHT, LRR and PYD domains-containing protein 4A OS=Mus	0	2	0	4	5	0	0.2222	0.2341	11
sp|P24472|GSTA4_MOUSE - Glutathione S-transferase A4 OS=Mus musculus GN=Gsta4 PE	0	2	0	0	9	0	0.2222	0.4899	11
sp|Q8BWS5|GRIN3_MOUSE - G protein-regulated inducer of neurite outgrowth 3 OS=Mu	0	2	0	6	3	0	0.2222	0.277	11
sp|Q5DU14|MYO16_MOUSE - Unconventional myosin-XVI OS=Mus musculus GN=Myo16 PE=1	0	3	0	0	14	0	0.2142	0.4851	17
sp|P29699|FETUA_MOUSE - Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=	0	3	0	5	0	10	0.2	0.2605	18
sp|P35546|RET_MOUSE - Proto-oncogene tyrosine-protein kinase receptor Ret OS=Mus	0	2	0	5	5	0	0.2	0.2115	12
sp|Q8R1G2|CMBL_MOUSE - Carboxymethylenebutenolidase homolog OS=Mus musculus GN=C	0	2	0	2	4	4	0.2	0.0474	12
sp|O08550|KMT2B_MOUSE - Histone-lysine N-methyltransferase 2B OS=Mus musculus GN	0	2	0	0	10	0	0.2	0.4766	12
sp|Q06185|ATP5I_MOUSE - ATP synthase subunit e, mitochondrial OS=Mus musculus GN	0	3	0	0	7	8	0.2	0.2137	18
sp|Q60952|CP250_MOUSE - Centrosome-associated protein CEP250 OS=Mus musculus GN=	0	3	0	0	13	3	0.1875	0.3454	19
sp|P42859|HD_MOUSE - Huntingtin OS=Mus musculus GN=Htt PE=1 SV=2	0	4	0	9	13	0	0.1818	0.2143	26
sp|Q9Z2Q6|SEPT5_MOUSE - Septin-5 OS=Mus musculus GN=Sept5 PE=1 SV=2	0	5	0	14	14	0	0.1785	0.1967	33
sp|P19783|COX41_MOUSE - Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	12	19	0	37	74	66	0.1751	0.0178	208
sp|Q9CQR4|ACO13_MOUSE - Acyl-coenzyme A thioesterase 13 OS=Mus musculus GN=Acot1	0	4	0	2	10	11	0.1739	0.1142	27
sp|Q8BYR2|LATS1_MOUSE - Serine/threonine-protein kinase LATS1 OS=Mus musculus GN	0	2	0	0	3	9	0.1666	0.2889	14
sp|P56395|CYB5_MOUSE - Cytochrome b5 OS=Mus musculus GN=Cyb5a PE=1 SV=2	6	18	0	39	49	67	0.1548	0.011	179
sp|Q8VHI5|VITRN_MOUSE - Vitrin OS=Mus musculus GN=Vit PE=1 SV=2	0	3	0	13	7	0	0.15	0.2186	23
sp|P70404|IDHG1_MOUSE - Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochon	2	0	0	4	10	0	0.1428	0.2508	16
sp|P12710|FABPL_MOUSE - Fatty acid-binding protein, liver OS=Mus musculus GN=Fab	0	3	0	0	13	8	0.1428	0.2002	24
sp|Q9ES34|UBE3B_MOUSE - Ubiquitin-protein ligase E3B OS=Mus musculus GN=Ube3b PE	0	3	0	11	10	0	0.1428	0.1756	24
sp|P00015|CYC2_MOUSE - Cytochrome c, testis-specific OS=Mus musculus GN=Cyct PE=	0	2	0	0	6	9	0.1333	0.1874	17
sp|Q8K4S1|PLCE1_MOUSE - 1-phosphatidylinositol 4,5-bisphosphate phosphodiesteras	0	2	0	4	13	0	0.1176	0.2692	19
sp|Q9D855|QCR7_MOUSE - Cytochrome b-c1 complex subunit 7 OS=Mus musculus GN=Uqcr	0	3	0	0	24	4	0.1071	0.3282	31
sp|P19536|COX5B_MOUSE - Cytochrome c oxidase subunit 5B, mitochondrial OS=Mus mu	0	6	0	7	25	24	0.1071	0.0541	62
sp|P13705|MSH3_MOUSE - DNA mismatch repair protein Msh3 OS=Mus musculus GN=Msh3	0	2	0	4	16	0	0.1	0.284	22
sp|Q6VH22|IF172_MOUSE - Intraflagellar transport protein 172 homolog OS=Mus musc	0	4	0	6	11	25	0.0952	0.0959	46
sp|P60469|LIPA3_MOUSE - Liprin-alpha-3 OS=Mus musculus GN=Ppfia3 PE=1 SV=1	0	2	0	0	8	13	0.0952	0.1747	23
sp|F7A4A7|OTOGL_MOUSE - Otogelin-like protein OS=Mus musculus GN=Otogl PE=1 SV=1	0	2	0	9	12	0	0.0952	0.1591	23
sp|Q8K0L3|ACSM2_MOUSE - Acyl-coenzyme A synthetase ACSM2, mitochondrial OS=Mus m	0	0	0	0	7	0	0	0.3739	7
sp|Q60893|OL151_MOUSE - Olfactory receptor 151 OS=Mus musculus GN=Olfr151 PE=2 S	0	0	0	7	3	0	0	0.1755	10
sp|Q9R0N3|SYT11_MOUSE - Synaptotagmin-11 OS=Mus musculus GN=Syt11 PE=1 SV=2	0	0	0	17	13	0	0	0.1231	30
sp|Q8CHK4|KAT5_MOUSE - Histone acetyltransferase KAT5 OS=Mus musculus GN=Kat5 PE	0	0	0	0	3	0	0	0.3739	3
sp|Q8C0Z1|ITFG3_MOUSE - Protein ITFG3 OS=Mus musculus GN=Itfg3 PE=1 SV=1	0	0	0	2	2	10	0	0.155	14
sp|Q8R1Q3|ANGL7_MOUSE - Angiopoietin-related protein 7 OS=Mus musculus GN=Angptl	0	0	0	0	0	2	0	0.3739	2
sp|Q91WC0|SETD3_MOUSE - Histone-lysine N-methyltransferase setd3 OS=Mus musculus	0	0	0	0	0	14	0	0.3739	14
sp|Q0VG85|CC162_MOUSE - Coiled-coil domain-containing protein 162 OS=Mus musculu	0	0	0	0	0	3	0	0.3739	3
sp|O08915|AIP_MOUSE - AH receptor-interacting protein OS=Mus musculus GN=Aip PE=	0	0	0	0	0	12	0	0.3739	12
sp|Q8JZQ5|AOC1_MOUSE - Amiloride-sensitive amine oxidase [copper-containing] OS=	0	0	0	3	0	0	0	0.3739	3
sp|Q497V5|SRBD1_MOUSE - S1 RNA-binding domain-containing protein 1 OS=Mus muscul	0	0	0	3	0	0	0	0.3739	3
sp|Q9CR09|UFC1_MOUSE - Ubiquitin-fold modifier-conjugating enzyme 1 OS=Mus muscu	0	0	0	2	3	0	0	0.1317	5

sp|Q64279|HAND1_MOUSE - Heart- and neural crest derivatives-expressed protein 1	0	0	0	3	0	0	0	0.3739	3
sp|Q03734|SPA3M_MOUSE - Serine protease inhibitor A3M OS=Mus musculus GN=Serpina	0	0	0	8	0	0	0	0.3739	8
sp|Q91YQ1|RAB7L_MOUSE - Ras-related protein Rab-7L1 OS=Mus musculus GN=Rab29 PE=	0	0	0	4	0	0	0	0.3739	4
sp|Q99J64|RBM43_MOUSE - RNA-binding protein 43 OS=Mus musculus GN=Rbm43 PE=2 SV=	0	0	0	3	0	0	0	0.3739	3
sp|Q8CHS4|PLCX1_MOUSE - PI-PLC X domain-containing protein 1 OS=Mus musculus GN=	0	0	0	3	2	0	0	0.1317	5
sp|P06325|TVC4_MOUSE - T-cell receptor gamma chain V region 5/10-13 OS=Mus muscu	0	0	0	3	0	0	0	0.3739	3
sp|Q5I2A0|SPA3G_MOUSE - Serine protease inhibitor A3G OS=Mus musculus GN=Serpina	0	0	0	3	0	0	0	0.3739	3
sp|Q80V26|IMPA3_MOUSE - Inositol monophosphatase 3 OS=Mus musculus GN=Impad1 PE=	0	0	0	4	2	0	0	0.1583	6
sp|Q9CZX5|PINX1_MOUSE - PIN2/TERF1-interacting telomerase inhibitor 1 OS=Mus mus	0	0	0	3	0	0	0	0.3739	3
sp|Q3UBG2|PCLI1_MOUSE - PTB-containing, cubilin and LRP1-interacting protein OS=	0	0	0	2	0	0	0	0.3739	2
sp|Q8VCK5|KLH20_MOUSE - Kelch-like protein 20 OS=Mus musculus GN=Klhl20 PE=2 SV=	0	0	0	3	0	0	0	0.3739	3
sp|P07759|SPA3K_MOUSE - Serine protease inhibitor A3K OS=Mus musculus GN=Serpina	0	0	0	2	0	0	0	0.3739	2
sp|P54369|OAZ1_MOUSE - Ornithine decarboxylase antizyme 1 OS=Mus musculus GN=Oaz	0	0	0	2	0	0	0	0.3739	2
sp|Q9ES83|POPD1_MOUSE - Blood vessel epicardial substance OS=Mus musculus GN=Bve	0	0	0	2	0	0	0	0.3739	2
sp|Q9CY64|BIEA_MOUSE - Biliverdin reductase A OS=Mus musculus GN=Blvra PE=2 SV=1	0	0	0	32	0	0	0	0.3739	32
sp|Q91WP6|SPA3N_MOUSE - Serine protease inhibitor A3N OS=Mus musculus GN=Serpina	0	0	0	3	0	0	0	0.3739	3
sp|Q62420|SH3G2_MOUSE - Endophilin-A1 OS=Mus musculus GN=Sh3gl2 PE=1 SV=2	0	0	0	3	0	0	0	0.3739	3
sp|Q9R0Y8|GBRG1_MOUSE - Gamma-aminobutyric acid receptor subunit gamma-1 OS=Mus	0	0	0	2	0	0	0	0.3739	2
sp|Q8VDF3|DAPK2_MOUSE - Death-associated protein kinase 2 OS=Mus musculus GN=Dap	0	0	0	3	4	0	0	0.1241	7
sp|Q8BYL4|SYYM_MOUSE - Tyrosine--tRNA ligase, mitochondrial OS=Mus musculus GN=Y	0	0	0	3	0	0	0	0.3739	3
sp|Q9CU62|SMC1A_MOUSE - Structural maintenance of chromosomes protein 1A OS=Mus	0	0	0	6	17	0	0	0.1983	23
sp|P17125|TGFB3_MOUSE - Transforming growth factor beta-3 OS=Mus musculus GN=Tgf	0	0	0	2	0	3	0	0.1317	5
sp|Q8BP92|RCN2_MOUSE - Reticulocalbin-2 OS=Mus musculus GN=Rcn2 PE=2 SV=1	0	0	0	5	0	0	0	0.3739	5
sp|Q8BTZ4|APC5_MOUSE - Anaphase-promoting complex subunit 5 OS=Mus musculus GN=A	0	0	0	6	0	21	0	0.2229	27
sp|Q9CQG2|MET16_MOUSE - Methyltransferase-like protein 16 OS=Mus musculus GN=Met	0	0	0	5	0	0	0	0.3739	5
sp|P26369|U2AF2_MOUSE - Splicing factor U2AF 65 kDa subunit OS=Mus musculus GN=U	0	0	0	6	0	0	0	0.3739	6
sp|Q8K2F8|LS14A_MOUSE - Protein LSM14 homolog A OS=Mus musculus GN=Lsm14a PE=1 S	0	0	0	2	2	0	0	0.1161	4
sp|P28271|ACOC_MOUSE - Cytoplasmic aconitate hydratase OS=Mus musculus GN=Aco1 P	0	0	0	4	2	0	0	0.1583	6
sp|P81122|IRS2_MOUSE - Insulin receptor substrate 2 OS=Mus musculus GN=Irs2 PE=1	0	0	0	3	0	0	0	0.3739	3
sp|Q3UA37|QRIC1_MOUSE - Glutamine-rich protein 1 OS=Mus musculus GN=Qrich1 PE=2	0	0	0	3	0	0	0	0.3739	3
sp|Q99MU3|DSRAD_MOUSE - Double-stranded RNA-specific adenosine deaminase OS=Mus	0	0	0	8	0	0	0	0.3739	8
sp|Q3UG61|MRGB1_MOUSE - Mas-related G-protein coupled receptor member B1 OS=Mus	0	0	0	2	0	0	0	0.3739	2
sp|O08739|AMPD3_MOUSE - AMP deaminase 3 OS=Mus musculus GN=Ampd3 PE=2 SV=2	0	0	0	3	0	0	0	0.3739	3
sp|Q8K1N4|SPAS2_MOUSE - Spermatogenesis-associated serine-rich protein 2 OS=Mus	0	0	0	2	0	0	0	0.3739	2
sp|P31750|AKT1_MOUSE - RAC-alpha serine/threonine-protein kinase OS=Mus musculus	0	0	0	2	2	7	0	0.0926	11
sp|Q8VHR5|P66B_MOUSE - Transcriptional repressor p66-beta OS=Mus musculus GN=Gat	0	0	0	2	0	0	0	0.3739	2
sp|P23249|MOV10_MOUSE - Putative helicase MOV-10 OS=Mus musculus GN=Mov10 PE=1 S	0	0	0	8	5	0	0	0.1368	13
sp|Q91V93|RHBT2_MOUSE - Rho-related BTB domain-containing protein 2 OS=Mus muscu	0	0	0	2	0	0	0	0.3739	2
sp|P97384|ANX11_MOUSE - Annexin A11 OS=Mus musculus GN=Anxa11 PE=2 SV=2	0	0	0	2	0	0	0	0.3739	2
sp|Q05860|FMN1_MOUSE - Formin-1 OS=Mus musculus GN=Fmn1 PE=1 SV=2	0	0	0	5	12	0	0	0.1787	17
sp|A2AGB2|CA087_MOUSE - Uncharacterized protein C1orf87 homolog OS=Mus musculus	0	0	0	3	0	0	0	0.3739	3

sp|Q3TYD4|ARSG_MOUSE - Arylsulfatase G OS=Mus musculus GN=Arsg PE=2 SV=1	0	0	0	8	0	0	0	0.3739	8
sp|Q3TEI4|CO039_MOUSE - Uncharacterized protein C15orf39 homolog OS=Mus musculus	0	0	0	6	0	0	0	0.3739	6
sp|Q80YT5|SPT20_MOUSE - Spermatogenesis-associated protein 20 OS=Mus musculus GN	0	0	0	9	0	0	0	0.3739	9
sp|Q14DL3|LRIQ3_MOUSE - Leucine-rich repeat and IQ domain-containing protein 3 O	0	0	0	3	0	0	0	0.3739	3
sp|D0QMC3|MNDAL_MOUSE - Myeloid cell nuclear differentiation antigen-like protei	0	0	0	3	0	0	0	0.3739	3
sp|Q9DA75|NLS1_MOUSE - Sodium-dependent lysophosphatidylcholine symporter 1 OS=M	0	0	0	2	0	0	0	0.3739	2
sp|Q7TMX5|SHQ1_MOUSE - Protein SHQ1 homolog OS=Mus musculus GN=Shq1 PE=2 SV=2	0	0	0	2	0	0	0	0.3739	2
sp|Q8BZW2|SWAHB_MOUSE - Ankyrin repeat domain-containing protein SOWAHB OS=Mus m	0	0	0	2	0	0	0	0.3739	2
sp|Q8CIW5|PEO1_MOUSE - Twinkle protein, mitochondrial OS=Mus musculus GN=Peo1 PE	0	0	0	2	0	0	0	0.3739	2
sp|Q8C0Q4|NEK11_MOUSE - Serine/threonine-protein kinase Nek11 OS=Mus musculus GN	0	0	0	2	0	0	0	0.3739	2
sp|Q9Z0Y7|IRS4_MOUSE - Insulin receptor substrate 4 OS=Mus musculus GN=Irs4 PE=1	0	0	0	5	5	0	0	0.1161	10
sp|Q62036|CP131_MOUSE - Centrosomal protein of 131 kDa OS=Mus musculus GN=Cep131	0	0	0	3	0	0	0	0.3739	3
sp|Q8BGD7|NPAS4_MOUSE - Neuronal PAS domain-containing protein 4 OS=Mus musculus	0	0	0	3	0	0	0	0.3739	3
sp|Q99KC8|VMA5A_MOUSE - von Willebrand factor A domain-containing protein 5A OS=	0	0	0	4	0	0	0	0.3739	4
sp|Q5XG71|UTP20_MOUSE - Small subunit processome component 20 homolog OS=Mus mus	0	0	0	13	14	0	0	0.1166	27
sp|P35601|RFC1_MOUSE - Replication factor C subunit 1 OS=Mus musculus GN=Rfc1 PE	0	0	0	6	0	0	0	0.3739	6
sp|Q5DU56|NLRC3_MOUSE - Protein NLRC3 OS=Mus musculus GN=Nlrc3 PE=2 SV=2	0	0	0	3	4	0	0	0.1241	7
sp|Q9JJ59|ABCB9_MOUSE - ATP-binding cassette sub-family B member 9 OS=Mus muscul	0	0	0	2	0	0	0	0.3739	2
sp|Q8BVL9|JKIP1_MOUSE - Janus kinase and microtubule-interacting protein 1 OS=Mu	0	0	0	6	0	0	0	0.3739	6
sp|Q3UZB0|ARMX5_MOUSE - Armadillo repeat-containing X-linked protein 5 OS=Mus mu	0	0	0	2	2	0	0	0.1161	4
sp|Q8BLF2|CDKL3_MOUSE - Cyclin-dependent kinase-like 3 OS=Mus musculus GN=Cdkl3	0	0	0	2	0	5	0	0.1835	7
sp|Q60996|2A5G_MOUSE - Serine/threonine-protein phosphatase 2A 56 kDa regulatory	0	0	0	5	4	0	0	0.121	9
sp|Q76K27|SIAT2_MOUSE - Beta-galactoside alpha-2,6-sialyltransferase 2 OS=Mus mu	0	0	0	2	3	0	0	0.1317	5
sp|O35945|AL1A7_MOUSE - Aldehyde dehydrogenase, cytosolic 1 OS=Mus musculus GN=A	0	0	0	2	6	10	0	0.0601	18
sp|Q8BW94|DYH3_MOUSE - Dynein heavy chain 3, axonemal OS=Mus musculus GN=Dnah3 P	0	0	0	8	9	0	0	0.1174	17
sp|Q6ZQ29|TAOK2_MOUSE - Serine/threonine-protein kinase TAO2 OS=Mus musculus GN=	0	0	0	3	0	0	0	0.3739	3
sp|Q8CIF6|SIDT2_MOUSE - SID1 transmembrane family member 2 OS=Mus musculus GN=Si	0	0	0	2	0	0	0	0.3739	2
sp|Q5SSW2|PSME4_MOUSE - Proteasome activator complex subunit 4 OS=Mus musculus G	0	0	0	3	0	0	0	0.3739	3
sp|Q6R6I7|RXFP1_MOUSE - Relaxin receptor 1 OS=Mus musculus GN=Rxfp1 PE=2 SV=1	0	0	0	2	0	0	0	0.3739	2
sp|Q8CIW6|S26A6_MOUSE - Solute carrier family 26 member 6 OS=Mus musculus GN=Slc	0	0	0	2	0	0	0	0.3739	2
sp|Q6NXI6|RPRD2_MOUSE - Regulation of nuclear pre-mRNA domain-containing protein	0	0	0	4	0	0	0	0.3739	4
sp|Q62245|SOS1_MOUSE - Son of sevenless homolog 1 OS=Mus musculus GN=Sos1 PE=1 S	0	0	0	10	0	26	0	0.1881	36
sp|Q5F2E8|TAOK1_MOUSE - Serine/threonine-protein kinase TAO1 OS=Mus musculus GN=	0	0	0	4	0	0	0	0.3739	4
sp|Q2TV84|TRPM1_MOUSE - Transient receptor potential cation channel subfamily M	0	0	0	3	0	0	0	0.3739	3
sp|Q32MD9|CDON_MOUSE - Cell adhesion molecule-related/down-regulated by oncogene	0	0	0	3	4	0	0	0.1241	7
sp|Q5DTH5|TSH1_MOUSE - Teashirt homolog 1 OS=Mus musculus GN=Tshz1 PE=1 SV=2	0	0	0	2	0	0	0	0.3739	2
sp|Q3UJD6|UBP19_MOUSE - Ubiquitin carboxyl-terminal hydrolase 19 OS=Mus musculus	0	0	0	3	0	0	0	0.3739	3
sp|Q1EG27|MYO3B_MOUSE - Myosin-IIIb OS=Mus musculus GN=Myo3b PE=2 SV=2	0	0	0	5	0	0	0	0.3739	5
sp|Q65Z40|WAPL_MOUSE - Wings apart-like protein homolog OS=Mus musculus GN=Wapal	0	0	0	3	0	0	0	0.3739	3
sp|Q8VDP3|MICA1_MOUSE - Protein-methionine sulfoxide oxidase MICAL1 OS=Mus muscu	0	0	0	2	0	0	0	0.3739	2
sp|Q32NZ6|TMC5_MOUSE - Transmembrane channel-like protein 5 OS=Mus musculus GN=T	0	0	0	2	0	0	0	0.3739	2

sp|Q3TDN0|DISP1_MOUSE - Protein dispatched homolog 1 OS=Mus musculus GN=Disp1 PE	0	0	0	2	0	0	0	0.3739	2
sp|Q6GQT6|SCAP_MOUSE - Sterol regulatory element-binding protein cleavage-activa	0	0	0	3	0	0	0	0.3739	3
sp|Q3UVX5|GRM5_MOUSE - Metabotropic glutamate receptor 5 OS=Mus musculus GN=Grm5	0	0	0	3	0	0	0	0.3739	3
sp|Q8CBX0|CSC1_MOUSE - Calcium permeable stress-gated cation channel 1 OS=Mus mu	0	0	0	2	0	0	0	0.3739	2
sp|Q80YV4|PANK4_MOUSE - Pantothenate kinase 4 OS=Mus musculus GN=Pank4 PE=1 SV=2	0	0	0	2	0	0	0	0.3739	2
sp|Q99JT1|GATB_MOUSE - Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondr	0	0	0	2	0	0	0	0.3739	2
sp|Q6DFV3|RHG21_MOUSE - Rho GTPase-activating protein 21 OS=Mus musculus GN=Arhg	0	0	0	4	6	2	0	0.0257	12
sp|Q80VA5|S3TC2_MOUSE - SH3 domain and tetratricopeptide repeat-containing prote	0	0	0	2	0	0	0	0.3739	2
sp|Q8C0R0|UBP37_MOUSE - Ubiquitin carboxyl-terminal hydrolase 37 OS=Mus musculus	0	0	0	2	0	0	0	0.3739	2
sp|Q9QXZ0|MACF1_MOUSE - Microtubule-actin cross-linking factor 1 OS=Mus musculus	0	0	0	10	22	32	0	0.0284	64
sp|Q61555|FBN2_MOUSE - Fibrillin-2 OS=Mus musculus GN=Fbn2 PE=1 SV=2	0	0	0	6	2	0	0	0.2051	8
sp|Q8BTM8|FLNA_MOUSE - Filamin-A OS=Mus musculus GN=Flna PE=1 SV=5	0	0	0	2	0	0	0	0.3739	2
sp|Q9ERU9|RBP2_MOUSE - E3 SUMO-protein ligase RanBP2 OS=Mus musculus GN=Ranbp2 P	0	0	0	4	8	9	0	0.0101	21
sp|O88466|ZN106_MOUSE - Zinc finger protein 106 OS=Mus musculus GN=Znf106 PE=1 S	0	0	0	4	0	0	0	0.3739	4
sp|Q3V129|ULK4_MOUSE - Serine/threonine-protein kinase ULK4 OS=Mus musculus GN=U	0	0	0	2	0	0	0	0.3739	2
sp|B1AZP2|DLGP4_MOUSE - Disks large-associated protein 4 OS=Mus musculus GN=Dlga	0	0	0	5	0	0	0	0.3739	5
sp|Q6P5H2|NEST_MOUSE - Nestin OS=Mus musculus GN=Nes PE=1 SV=1	0	0	0	2	6	0	0	0.2051	8
sp|Q04592|PCSK5_MOUSE - Proprotein convertase subtilisin/kexin type 5 OS=Mus mus	0	0	0	4	0	0	0	0.3739	4
sp|Q6PZE0|MUC19_MOUSE - Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2	0	0	0	2	0	0	0	0.3739	2
sp|O70166|STMN3_MOUSE - Stathmin-3 OS=Mus musculus GN=Stmn3 PE=1 SV=1	0	0	0	3	0	0	0	0.3739	3
sp|Q9D1J3|SARNP_MOUSE - SAP domain-containing ribonucleoprotein OS=Mus musculus	0	0	0	2	0	0	0	0.3739	2
sp|Q9JHR9|NRIP2_MOUSE - Nuclear receptor-interacting protein 2 OS=Mus musculus G	0	0	0	2	0	0	0	0.3739	2
sp|O09131|GSTO1_MOUSE - Glutathione S-transferase omega-1 OS=Mus musculus GN=Gst	0	0	0	2	0	0	0	0.3739	2
sp|Q6GQV0|CP059_MOUSE - Uncharacterized protein C16orf59 homolog OS=Mus musculus	0	0	0	3	0	0	0	0.3739	3
sp|Q91YI4|ARRB2_MOUSE - Beta-arrestin-2 OS=Mus musculus GN=Arrb2 PE=1 SV=1	0	0	0	2	0	0	0	0.3739	2
sp|Q8C3W1|CA198_MOUSE - Uncharacterized protein C1orf198 homolog OS=Mus musculus	0	0	0	2	0	0	0	0.3739	2
sp|Q8R1G1|TASP1_MOUSE - Threonine aspartase 1 OS=Mus musculus GN=Tasp1 PE=2 SV=1	0	0	0	2	2	0	0	0.1161	4
sp|Q5RJG7|ISPD_MOUSE - Isoprenoid synthase domain-containing protein OS=Mus musc	0	0	0	2	0	0	0	0.3739	2
sp|P39098|MA1A2_MOUSE - Mannosyl-oligosaccharide 1,2-alpha-mannosidase IB OS=Mus	0	0	0	2	0	0	0	0.3739	2
sp|Q8CDE2|CALI_MOUSE - Calicin OS=Mus musculus GN=Ccin PE=2 SV=1	0	0	0	4	0	0	0	0.3739	4
sp|Q8CHP0|ZC3H3_MOUSE - Zinc finger CCCH domain-containing protein 3 OS=Mus musc	0	0	0	5	0	0	0	0.3739	5
sp|Q8BMK0|CEP85_MOUSE - Centrosomal protein of 85 kDa OS=Mus musculus GN=Cep85 P	0	0	0	5	0	0	0	0.3739	5
sp|Q3TLD5|RMP_MOUSE - Unconventional prefoldin RPB5 interactor OS=Mus musculus G	0	0	0	3	0	0	0	0.3739	3
sp|Q8BMD7|MORC4_MOUSE - MORC family CW-type zinc finger protein 4 OS=Mus musculu	0	0	0	9	0	0	0	0.3739	9
sp|Q8BU03|PWP2_MOUSE - Periodic tryptophan protein 2 homolog OS=Mus musculus GN=	0	0	0	4	0	0	0	0.3739	4
sp|O35066|KIF3C_MOUSE - Kinesin-like protein KIF3C OS=Mus musculus GN=Kif3c PE=1	0	0	0	6	9	0	0	0.1317	15
sp|Q6NZF1|ZC11A_MOUSE - Zinc finger CCCH domain-containing protein 11A OS=Mus mu	0	0	0	7	0	0	0	0.3739	7
sp|Q8CFG8|CS1B_MOUSE - Complement C1s-B subcomponent OS=Mus musculus GN=C1sb PE=	0	0	0	4	0	0	0	0.3739	4
sp|Q8BX09|RBBP5_MOUSE - Retinoblastoma-binding protein 5 OS=Mus musculus GN=Rbbp	0	0	0	5	0	0	0	0.3739	5
sp|P28661|SEPT4_MOUSE - Septin-4 OS=Mus musculus GN=Sept4 PE=1 SV=1	0	0	0	2	0	0	0	0.3739	2
sp|Q8CF89|TAB1_MOUSE - TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	0	0	0	2	0	0	0	0.3739	2

sp|Q9QZR0|RNF25_MOUSE - E3 ubiquitin-protein ligase RNF25 OS=Mus musculus GN=Rnf	0	0	0	2	2	0	0	0.1161	4
sp|Q3TVW5|TCHP_MOUSE - Trichoplein keratin filament-binding protein OS=Mus muscu	0	0	0	3	3	8	0	0.0488	14
sp|Q9DA73|CCD89_MOUSE - Coiled-coil domain-containing protein 89 OS=Mus musculus	0	0	0	2	3	0	0	0.1317	5
sp|Q8C3P7|MTA70_MOUSE - N6-adenosine-methyltransferase subunit METTL3 OS=Mus mus	0	0	0	3	3	0	0	0.1161	6
sp|Q8C1B2|PARPT_MOUSE - TCDD-inducible poly [ADP-ribose] polymerase OS=Mus muscu	0	0	0	3	0	0	0	0.3739	3
sp|G5E8Z2|TAF4B_MOUSE - Transcription initiation factor TFIID subunit 4B OS=Mus	0	0	0	2	0	0	0	0.3739	2
sp|Q91ZJ9|HYAL1_MOUSE - Hyaluronidase-1 OS=Mus musculus GN=Hyal1 PE=1 SV=3	0	0	0	2	0	10	0	0.2605	12
sp|Q8CFY5|COX10_MOUSE - Protoheme IX farnesyltransferase, mitochondrial OS=Mus m	0	0	0	2	0	0	0	0.3739	2
sp|Q922Q9|CHID1_MOUSE - Chitinase domain-containing protein 1 OS=Mus musculus GN	0	0	0	2	0	0	0	0.3739	2
sp|Q9Z1M7|LARGE_MOUSE - Glycosyltransferase-like protein LARGE1 OS=Mus musculus	0	0	0	2	0	0	0	0.3739	2
sp|Q8CAA7|PGM2L_MOUSE - Glucose 1,6-bisphosphate synthase OS=Mus musculus GN=Pgm	0	0	0	2	0	0	0	0.3739	2
sp|Q9R0L1|HSF4_MOUSE - Heat shock factor protein 4 OS=Mus musculus GN=Hsf4 PE=1	0	0	0	2	0	0	0	0.3739	2
sp|A2ACP1|TT39A_MOUSE - Tetratricopeptide repeat protein 39A OS=Mus musculus GN=	0	0	0	2	0	0	0	0.3739	2
sp|Q8R313|EXOC6_MOUSE - Exocyst complex component 6 OS=Mus musculus GN=Exoc6 PE=	0	0	0	3	0	0	0	0.3739	3
sp|Q8BQC3|IGDC3_MOUSE - Immunoglobulin superfamily DCC subclass member 3 OS=Mus	0	0	0	2	2	0	0	0.1161	4
sp|Q3UHU5|MTCL1_MOUSE - Microtubule cross-linking factor 1 OS=Mus musculus GN=Mt	0	0	0	7	3	0	0	0.1755	10
sp|Q6PIC6|AT1A3_MOUSE - Sodium/potassium-transporting ATPase subunit alpha-3 OS=	0	0	0	3	0	0	0	0.3739	3
sp|Q8C863|ITCH_MOUSE - E3 ubiquitin-protein ligase Itchy OS=Mus musculus GN=Itch	0	0	0	2	0	0	0	0.3739	2
sp|A2AKB4|FRPD1_MOUSE - FERM and PDZ domain-containing protein 1 OS=Mus musculus	0	0	0	2	0	0	0	0.3739	2
sp|P15975|UBP53_MOUSE - Inactive ubiquitin carboxyl-terminal hydrolase 53 OS=Mus	0	0	0	3	0	0	0	0.3739	3
sp|Q9D6A1|MYO1H_MOUSE - Unconventional myosin-Ih OS=Mus musculus GN=Myo1h PE=2 S	0	0	0	4	0	0	0	0.3739	4
sp|Q8C7U7|GALT6_MOUSE - Polypeptide N-acetylgalactosaminyltransferase 6 OS=Mus m	0	0	0	2	0	0	0	0.3739	2
sp|Q6A070|F179B_MOUSE - Protein FAM179B OS=Mus musculus GN=Fam179b PE=3 SV=3	0	0	0	3	0	0	0	0.3739	3
sp|Q8R516|MIB2_MOUSE - E3 ubiquitin-protein ligase MIB2 OS=Mus musculus GN=Mib2	0	0	0	2	0	0	0	0.3739	2
sp|Q04690|NF1_MOUSE - Neurofibromin OS=Mus musculus GN=Nf1 PE=1 SV=1	0	0	0	4	0	0	0	0.3739	4
sp|Q3V0C3|NT806_MOUSE - NUT family member Gm806 OS=Mus musculus GN=Gm806 PE=2 SV	0	0	0	2	0	0	0	0.3739	2
sp|Q8BYH8|CHD9_MOUSE - Chromodomain-helicase-DNA-binding protein 9 OS=Mus muscul	0	0	0	6	17	0	0	0.1983	23
sp|Q6P9R4|ARHGI_MOUSE - Rho guanine nucleotide exchange factor 18 OS=Mus musculu	0	0	0	2	9	0	0	0.2501	11
sp|G5E870|TRIPC_MOUSE - E3 ubiquitin-protein ligase TRIP12 OS=Mus musculus GN=Tr	0	0	0	3	4	0	0	0.1241	7
sp|Q5SX39|MYH4_MOUSE - Myosin-4 OS=Mus musculus GN=Myh4 PE=2 SV=1	0	0	0	4	0	0	0	0.3739	4
sp|Q9WU60|ATRN_MOUSE - Attractin OS=Mus musculus GN=Atrn PE=2 SV=3	0	0	0	3	0	0	0	0.3739	3
sp|Q80XI3|IF4G3_MOUSE - Eukaryotic translation initiation factor 4 gamma 3 OS=Mu	0	0	0	4	6	0	0	0.1317	10
sp|P16882|GHR_MOUSE - Growth hormone receptor OS=Mus musculus GN=Ghr PE=1 SV=1	0	0	0	4	0	0	0	0.3739	4
sp|P13808|B3A2_MOUSE - Anion exchange protein 2 OS=Mus musculus GN=Slc4a2 PE=1 S	0	0	0	2	0	0	0	0.3739	2
sp|Q8BMG7|RBGPR_MOUSE - Rab3 GTPase-activating protein non-catalytic subunit OS=	0	0	0	2	3	0	0	0.1317	5
sp|Q7TMB8|CYFP1_MOUSE - Cytoplasmic FMR1-interacting protein 1 OS=Mus musculus G	0	0	0	2	0	0	0	0.3739	2
sp|Q8BQ48|CE295_MOUSE - Centrosomal protein of 295 kDa OS=Mus musculus GN=Cep295	0	0	0	4	6	0	0	0.1317	10
sp|Q6PFD5|DLGP3_MOUSE - Disks large-associated protein 3 OS=Mus musculus GN=Dlga	0	0	0	2	0	0	0	0.3739	2
sp|D3YVE8|S35G2_MOUSE - Solute carrier family 35 member G2 OS=Mus musculus GN=Sl	0	0	0	2	0	0	0	0.3739	2
sp|D3Z3C6|ZFAN4_MOUSE - AN1-type zinc finger protein 4 OS=Mus musculus GN=Zfand4	0	0	0	8	0	0	0	0.3739	8
sp|Q8K2J0|PLCD3_MOUSE - 1-phosphatidylinositol 4,5-bisphosphate phosphodiesteras	0	0	0	2	2	0	0	0.1161	4

sp|Q9JM62|REEP6_MOUSE - Receptor expression-enhancing protein 6 OS=Mus musculus	0	0	0	4	3	12	0	0.0902	19
sp|Q8BGC4|ZADH2_MOUSE - Zinc-binding alcohol dehydrogenase domain-containing pro	0	0	0	6	0	0	0	0.3739	6
sp|Q3TVP5|F105A_MOUSE - Inactive ubiquitin thioesterase FAM105A OS=Mus musculus	0	0	0	7	6	0	0	0.1184	13
sp|Q9D4B2|TTC25_MOUSE - Tetratricopeptide repeat protein 25 OS=Mus musculus GN=T	0	0	0	4	5	0	0	0.121	9
sp|Q8C398|PIGW_MOUSE - Phosphatidylinositol-glycan biosynthesis class W protein	0	0	0	2	0	0	0	0.3739	2
sp|Q8VCD3|LMA1L_MOUSE - Protein ERGIC-53-like OS=Mus musculus GN=Lman1l PE=2 SV=	0	0	0	2	0	0	0	0.3739	2
sp|O88335|KCNJ1_MOUSE - ATP-sensitive inward rectifier potassium channel 1 OS=Mu	0	0	0	2	0	0	0	0.3739	2
sp|Q3U1D0|LINES_MOUSE - Protein Lines homolog OS=Mus musculus GN=Lins PE=2 SV=2	0	0	0	3	0	0	0	0.3739	3
sp|Q69ZK7|F214A_MOUSE - Protein FAM214A OS=Mus musculus GN=Fam214a PE=2 SV=3	0	0	0	7	8	0	0	0.1178	15
sp|Q7TT79|MCPH1_MOUSE - Microcephalin OS=Mus musculus GN=Mcph1 PE=2 SV=1	0	0	0	2	0	0	0	0.3739	2
sp|Q8CHY6|P66A_MOUSE - Transcriptional repressor p66 alpha OS=Mus musculus GN=Ga	0	0	0	2	0	0	0	0.3739	2
sp|Q505F5|LRC47_MOUSE - Leucine-rich repeat-containing protein 47 OS=Mus musculu	0	0	0	2	2	0	0	0.1161	4
sp|Q8VE18|SMG8_MOUSE - Protein SMG8 OS=Mus musculus GN=Smg8 PE=2 SV=1	0	0	0	5	0	0	0	0.3739	5
sp|P51830|ADCY9_MOUSE - Adenylate cyclase type 9 OS=Mus musculus GN=Adcy9 PE=1 S	0	0	0	4	3	0	0	0.1241	7
sp|Q61194|P3C2A_MOUSE - Phosphatidylinositol 4-phosphate 3-kinase C2 domain-cont	0	0	0	4	0	0	0	0.3739	4
sp|Q9EPX2|PPN_MOUSE - Papilin OS=Mus musculus GN=Papln PE=2 SV=2	0	0	0	2	0	0	0	0.3739	2
sp|Q8CIE6|COPA_MOUSE - Coatomer subunit alpha OS=Mus musculus GN=Copa PE=1 SV=2	0	0	0	3	0	0	0	0.3739	3
sp|Q0HA38|TT21B_MOUSE - Tetratricopeptide repeat protein 21B OS=Mus musculus GN=	0	0	0	2	0	0	0	0.3739	2
sp|Q6PIX5|RHDF1_MOUSE - Inactive rhomboid protein 1 OS=Mus musculus GN=Rhbdf1 PE	0	0	0	2	2	0	0	0.1161	4
sp|A8C756|THADA_MOUSE - Thyroid adenoma-associated protein homolog OS=Mus muscul	0	0	0	2	0	0	0	0.3739	2
sp|Q5H8B9|FREM3_MOUSE - FRAS1-related extracellular matrix protein 3 OS=Mus musc	0	0	0	7	4	0	0	0.1448	11
sp|Q80T14|FRAS1_MOUSE - Extracellular matrix protein FRAS1 OS=Mus musculus GN=Fr	0	0	0	2	0	0	0	0.3739	2
sp|Q64324|STXB2_MOUSE - Syntaxin-binding protein 2 OS=Mus musculus GN=Stxbp2 PE=	0	0	0	0	14	0	0	0.3739	14
sp|Q3U4G3|XXLT1_MOUSE - Xyloside xylosyltransferase 1 OS=Mus musculus GN=Xxylt1	0	0	0	0	9	0	0	0.3739	9
sp|Q9JMD3|PCTL_MOUSE - PCTP-like protein OS=Mus musculus GN=Stard10 PE=1 SV=1	0	0	0	0	2	0	0	0.3739	2
sp|Q9CQI7|RU2B_MOUSE - U2 small nuclear ribonucleoprotein B'' OS=Mus musculus GN	0	0	0	0	2	0	0	0.3739	2
sp|Q9JHK5|PLEK_MOUSE - Pleckstrin OS=Mus musculus GN=Plek PE=1 SV=1	0	0	0	0	6	0	0	0.3739	6
sp|Q8JZL2|MCHR1_MOUSE - Melanin-concentrating hormone receptor 1 OS=Mus musculus	0	0	0	0	2	0	0	0.3739	2
sp|Q8CII2|CD123_MOUSE - Cell division cycle protein 123 homolog OS=Mus musculus	0	0	0	0	5	0	0	0.3739	5
sp|Q91ZK0|AP2D_MOUSE - Transcription factor AP-2-delta OS=Mus musculus GN=Tfap2d	0	0	0	0	5	0	0	0.3739	5
sp|Q64687|SIA8A_MOUSE - Alpha-N-acetylneuraminide alpha-2,8-sialyltransferase OS	0	0	0	0	3	0	0	0.3739	3
sp|Q6P6M7|SPCS_MOUSE - O-phosphoseryl-tRNA(Sec) selenium transferase OS=Mus musc	0	0	0	0	16	0	0	0.3739	16
sp|Q8BVW3|TRI14_MOUSE - Tripartite motif-containing protein 14 OS=Mus musculus G	0	0	0	0	2	0	0	0.3739	2
sp|Q8VC66|ADIP_MOUSE - Afadin- and alpha-actinin-binding protein OS=Mus musculus	0	0	0	0	8	0	0	0.3739	8
sp|Q80YS6|AFAP1_MOUSE - Actin filament-associated protein 1 OS=Mus musculus GN=A	0	0	0	0	6	0	0	0.3739	6
sp|Q4VBE8|WDR18_MOUSE - WD repeat-containing protein 18 OS=Mus musculus GN=Wdr18	0	0	0	0	2	0	0	0.3739	2
sp|P00520|ABL1_MOUSE - Tyrosine-protein kinase ABL1 OS=Mus musculus GN=Abl1 PE=1	0	0	0	0	10	0	0	0.3739	10
sp|Q80UK0|SESD1_MOUSE - SEC14 domain and spectrin repeat-containing protein 1 OS	0	0	0	0	8	0	0	0.3739	8
sp|Q8CDJ3|BAKOR_MOUSE - Beclin 1-associated autophagy-related key regulator OS=M	0	0	0	0	3	5	0	0.1403	8
sp|Q8CC35|SYNPO_MOUSE - Synaptopodin OS=Mus musculus GN=Synpo PE=1 SV=2	0	0	0	0	3	0	0	0.3739	3
sp|Q3TJM4|CENPT_MOUSE - Centromere protein T OS=Mus musculus GN=Cenpt PE=2 SV=2	0	0	0	0	12	0	0	0.3739	12

sp|Q8VID5|RECQ5_MOUSE - ATP-dependent DNA helicase Q5 OS=Mus musculus GN=Recql5	0	0	0	0	3	0	0	0.3739	3
sp|Q9WTM3|SEM6C_MOUSE - Semaphorin-6C OS=Mus musculus GN=Sema6c PE=2 SV=1	0	0	0	0	5	0	0	0.3739	5
sp|Q9JLG4|PK2L2_MOUSE - Polycystic kidney disease 2-like 2 protein OS=Mus muscul	0	0	0	0	6	0	0	0.3739	6
sp|Q8C2B3|HDAC7_MOUSE - Histone deacetylase 7 OS=Mus musculus GN=Hdac7 PE=1 SV=2	0	0	0	0	17	0	0	0.3739	17
sp|P98192|GNPAT_MOUSE - Dihydroxyacetone phosphate acyltransferase OS=Mus muscul	0	0	0	0	3	0	0	0.3739	3
sp|Q9JI33|NET4_MOUSE - Netrin-4 OS=Mus musculus GN=Ntn4 PE=2 SV=2	0	0	0	0	2	0	0	0.3739	2
sp|Q99K01|PDXD1_MOUSE - Pyridoxal-dependent decarboxylase domain-containing prot	0	0	0	0	7	5	0	0.127	12
sp|Q9ESN6|TRIM2_MOUSE - Tripartite motif-containing protein 2 OS=Mus musculus GN	0	0	0	0	4	15	0	0.2307	19
sp|Q8VDT1|SC5A9_MOUSE - Sodium/glucose cotransporter 4 OS=Mus musculus GN=Slc5a9	0	0	0	0	6	0	0	0.3739	6
sp|Q8BZH4|POGZ_MOUSE - Pogo transposable element with ZNF domain OS=Mus musculus	0	0	0	0	7	0	0	0.3739	7
sp|Q0KL02|TRIO_MOUSE - Triple functional domain protein OS=Mus musculus GN=Trio	0	0	0	0	10	0	0	0.3739	10
sp|Q9WTR2|M3K6_MOUSE - Mitogen-activated protein kinase kinase kinase 6 OS=Mus m	0	0	0	0	5	0	0	0.3739	5
sp|P18654|KS6A3_MOUSE - Ribosomal protein S6 kinase alpha-3 OS=Mus musculus GN=R	0	0	0	0	7	0	0	0.3739	7
sp|Q9WV76|AP4B1_MOUSE - AP-4 complex subunit beta-1 OS=Mus musculus GN=Ap4b1 PE=	0	0	0	0	2	0	0	0.3739	2
sp|Q91YE5|BAZ2A_MOUSE - Bromodomain adjacent to zinc finger domain protein 2A OS	0	0	0	0	3	2	0	0.1317	5
sp|Q0P5X1|LRIQ1_MOUSE - Leucine-rich repeat and IQ domain-containing protein 1 O	0	0	0	0	7	0	0	0.3739	7
sp|Q9Z2E3|ERN2_MOUSE - Serine/threonine-protein kinase/endoribonuclease IRE2 OS=	0	0	0	0	2	0	0	0.3739	2
sp|Q99PJ1|PCD15_MOUSE - Protocadherin-15 OS=Mus musculus GN=Pcdh15 PE=1 SV=3	0	0	0	0	7	0	0	0.3739	7
sp|Q9JJF3|NO66_MOUSE - Bifunctional lysine-specific demethylase and histidyl-hyd	0	0	0	0	2	0	0	0.3739	2
sp|Q2EMV9|PAR14_MOUSE - Poly [ADP-ribose] polymerase 14 OS=Mus musculus GN=Parp1	0	0	0	0	3	0	0	0.3739	3
sp|Q6P9K9|NRX3A_MOUSE - Neurexin-3 OS=Mus musculus GN=Nrxn3 PE=1 SV=2	0	0	0	0	3	8	0	0.1911	11
sp|Q9Z1L5|CA2D3_MOUSE - Voltage-dependent calcium channel subunit alpha-2/delta-	0	0	0	0	7	0	0	0.3739	7
sp|Q78DX7|ROS1_MOUSE - Proto-oncogene tyrosine-protein kinase ROS OS=Mus musculu	0	0	0	0	4	0	0	0.3739	4
sp|Q6ZPE2|MTMR5_MOUSE - Myotubularin-related protein 5 OS=Mus musculus GN=Sbf1 P	0	0	0	0	3	0	0	0.3739	3
sp|Q6ZPG2|WDR90_MOUSE - WD repeat-containing protein 90 OS=Mus musculus GN=Wdr90	0	0	0	0	17	0	0	0.3739	17
sp|Q7TN88|PK1L2_MOUSE - Polycystic kidney disease protein 1-like 2 OS=Mus muscul	0	0	0	0	9	0	0	0.3739	9
sp|P63300|SELW_MOUSE - Selenoprotein W OS=Mus musculus GN=Sepw1 PE=1 SV=3	0	0	0	0	3	0	0	0.3739	3
sp|P70445|4EBP2_MOUSE - Eukaryotic translation initiation factor 4E-binding prot	0	0	0	0	4	0	0	0.3739	4
sp|Q5PR73|DIRA2_MOUSE - GTP-binding protein Di-Ras2 OS=Mus musculus GN=Diras2 PE	0	0	0	0	2	0	0	0.3739	2
sp|P62259|1433E_MOUSE - 14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=	0	0	0	0	6	0	0	0.3739	6
sp|Q9D110|MTHFS_MOUSE - 5-formyltetrahydrofolate cyclo-ligase OS=Mus musculus GN	0	0	0	0	4	0	0	0.3739	4
sp|Q60664|LRMP_MOUSE - Lymphoid-restricted membrane protein OS=Mus musculus GN=L	0	0	0	0	8	0	0	0.3739	8
sp|Q99KP3|CRYL1_MOUSE - Lambda-crystallin homolog OS=Mus musculus GN=Cryl1 PE=2	0	0	0	0	3	0	0	0.3739	3
sp|Q80VV3|4EBP3_MOUSE - Eukaryotic translation initiation factor 4E-binding prot	0	0	0	0	2	0	0	0.3739	2
sp|Q3TRJ4|K1C26_MOUSE - Keratin, type I cytoskeletal 26 OS=Mus musculus GN=Krt26	0	0	0	0	4	0	0	0.3739	4
sp|O54784|DAPK3_MOUSE - Death-associated protein kinase 3 OS=Mus musculus GN=Dap	0	0	0	0	5	0	0	0.3739	5
sp|Q8CCH2|NHLC3_MOUSE - NHL repeat-containing protein 3 OS=Mus musculus GN=Nhlrc	0	0	0	0	7	0	0	0.3739	7
sp|P23198|CBX3_MOUSE - Chromobox protein homolog 3 OS=Mus musculus GN=Cbx3 PE=1	0	0	0	0	2	0	0	0.3739	2
sp|Q6NSR8|PEPL1_MOUSE - Probable aminopeptidase NPEPL1 OS=Mus musculus GN=Npepl1	0	0	0	0	3	0	0	0.3739	3
sp|Q8QZX0|SBK1_MOUSE - Serine/threonine-protein kinase SBK1 OS=Mus musculus GN=S	0	0	0	0	7	0	0	0.3739	7
sp|O09161|CASQ2_MOUSE - Calsequestrin-2 OS=Mus musculus GN=Casq2 PE=1 SV=3	0	0	0	0	5	0	0	0.3739	5

sp|D3KU66|ASMT_MOUSE - Acetylserotonin O-methyltransferase OS=Mus musculus GN=As	0	0	0	0	3	6	0	0.1583	9
sp|Q9WV86|KTNA1_MOUSE - Katanin p60 ATPase-containing subunit A1 OS=Mus musculus	0	0	0	0	2	0	0	0.3739	2
sp|P31313|HXC11_MOUSE - Homeobox protein Hox-C11 OS=Mus musculus GN=Hoxc11 PE=2	0	0	0	0	4	0	0	0.3739	4
sp|Q5PR68|CE112_MOUSE - Centrosomal protein of 112 kDa OS=Mus musculus GN=Cep112	0	0	0	0	10	0	0	0.3739	10
sp|Q80UK7|SAS6_MOUSE - Spindle assembly abnormal protein 6 homolog OS=Mus muscul	0	0	0	0	6	0	0	0.3739	6
sp|Q32MW3|ACO10_MOUSE - Acyl-coenzyme A thioesterase 10, mitochondrial OS=Mus mu	0	0	0	0	3	0	0	0.3739	3
sp|Q91VY6|CYTIP_MOUSE - Cytohesin-interacting protein OS=Mus musculus GN=Cytip P	0	0	0	0	4	0	0	0.3739	4
sp|Q9WVL5|MORC1_MOUSE - MORC family CW-type zinc finger protein 1 OS=Mus musculu	0	0	0	0	9	0	0	0.3739	9
sp|Q6P5F9|XPO1_MOUSE - Exportin-1 OS=Mus musculus GN=Xpo1 PE=1 SV=1	0	0	0	0	5	0	0	0.3739	5
sp|Q2TB54|FCAMR_MOUSE - High affinity immunoglobulin alpha and immunoglobulin mu	0	0	0	0	4	0	0	0.3739	4
sp|P37238|PPARG_MOUSE - Peroxisome proliferator-activated receptor gamma OS=Mus	0	0	0	0	2	0	0	0.3739	2
sp|Q6P5G3|MBTD1_MOUSE - MBT domain-containing protein 1 OS=Mus musculus GN=Mbtd1	0	0	0	0	3	0	0	0.3739	3
sp|Q8BYK5|PHAR3_MOUSE - Phosphatase and actin regulator 3 OS=Mus musculus GN=Pha	0	0	0	0	2	0	0	0.3739	2
sp|O55134|PCD12_MOUSE - Protocadherin-12 OS=Mus musculus GN=Pcdh12 PE=2 SV=2	0	0	0	0	5	0	0	0.3739	5
sp|Q9JLI8|SART3_MOUSE - Squamous cell carcinoma antigen recognized by T-cells 3	0	0	0	0	5	0	0	0.3739	5
sp|O35594|IFT81_MOUSE - Intraflagellar transport protein 81 homolog OS=Mus muscu	0	0	0	0	6	0	0	0.3739	6
sp|Q80VM4|ZN579_MOUSE - Zinc finger protein 579 OS=Mus musculus GN=Znf579 PE=1 S	0	0	0	0	9	0	0	0.3739	9
sp|Q6PDC8|MFSD4_MOUSE - Major facilitator superfamily domain-containing protein	0	0	0	0	3	0	0	0.3739	3
sp|Q6DID5|MUM1_MOUSE - PWWP domain-containing protein MUM1 OS=Mus musculus GN=Mu	0	0	0	0	5	0	0	0.3739	5
sp|Q9JMC2|INSM2_MOUSE - Insulinoma-associated protein 2 OS=Mus musculus GN=Insm2	0	0	0	0	2	0	0	0.3739	2
sp|Q3TKT4|SMCA4_MOUSE - Transcription activator BRG1 OS=Mus musculus GN=Smarca4	0	0	0	0	5	0	0	0.3739	5
sp|Q3UTH8|ARHG9_MOUSE - Rho guanine nucleotide exchange factor 9 OS=Mus musculus	0	0	0	0	2	0	0	0.3739	2
sp|Q91ZD4|VANG2_MOUSE - Vang-like protein 2 OS=Mus musculus GN=Vangl2 PE=1 SV=3	0	0	0	0	2	0	0	0.3739	2
sp|Q9CS72|FLIP1_MOUSE - Filamin-A-interacting protein 1 OS=Mus musculus GN=Filip	0	0	0	0	6	0	0	0.3739	6
sp|Q9DBG3|AP2B1_MOUSE - AP-2 complex subunit beta OS=Mus musculus GN=Ap2b1 PE=1	0	0	0	0	2	0	0	0.3739	2
sp|Q99KK7|DPP3_MOUSE - Dipeptidyl peptidase 3 OS=Mus musculus GN=Dpp3 PE=2 SV=2	0	0	0	0	3	0	0	0.3739	3
sp|Q6DIC0|SMCA2_MOUSE - Probable global transcription activator SNF2L2 OS=Mus mu	0	0	0	0	5	0	0	0.3739	5
sp|Q8C0Y0|PP4R4_MOUSE - Serine/threonine-protein phosphatase 4 regulatory subuni	0	0	0	0	2	0	0	0.3739	2
sp|Q00547|HMMR_MOUSE - Hyaluronan mediated motility receptor OS=Mus musculus GN=	0	0	0	0	4	0	0	0.3739	4
sp|O70496|CLCN7_MOUSE - H(+)/Cl(-) exchange transporter 7 OS=Mus musculus GN=Clc	0	0	0	0	2	0	0	0.3739	2
sp|Q6P5G0|MK04_MOUSE - Mitogen-activated protein kinase 4 OS=Mus musculus GN=Map	0	0	0	0	2	0	0	0.3739	2
sp|Q80Z96|VANG1_MOUSE - Vang-like protein 1 OS=Mus musculus GN=Vangl1 PE=1 SV=2	0	0	0	0	2	0	0	0.3739	2
sp|E9QAF0|SPT31_MOUSE - Spermatogenesis-associated protein 31 OS=Mus musculus GN	0	0	0	0	3	0	0	0.3739	3
sp|Q5SPL2|PHF12_MOUSE - PHD finger protein 12 OS=Mus musculus GN=Phf12 PE=1 SV=1	0	0	0	0	3	0	0	0.3739	3
sp|Q80TN5|ZDH17_MOUSE - Palmitoyltransferase ZDHHC17 OS=Mus musculus GN=Zdhhc17	0	0	0	0	3	35	0	0.3213	38
sp|Q9Z2R9|E2AK1_MOUSE - Eukaryotic translation initiation factor 2-alpha kinase	0	0	0	0	6	0	0	0.3739	6
sp|Q4FZD7|PLK5_MOUSE - Inactive serine/threonine-protein kinase PLK5 OS=Mus musc	0	0	0	0	2	5	0	0.1835	7
sp|Q3THK7|GUAA_MOUSE - GMP synthase [glutamine-hydrolyzing] OS=Mus musculus GN=G	0	0	0	0	2	0	0	0.3739	2
sp|Q8BW41|PMGT2_MOUSE - Protein O-linked-mannose beta-1,4-N-acetylglucosaminyltr	0	0	0	0	3	0	0	0.3739	3
sp|Q99KW3|TARA_MOUSE - TRIO and F-actin-binding protein OS=Mus musculus GN=Triob	0	0	0	0	4	0	0	0.3739	4
sp|Q6T3U4|NPCL1_MOUSE - Niemann-Pick C1-like protein 1 OS=Mus musculus GN=Npc1l1	0	0	0	0	3	0	0	0.3739	3

sp|Q6QNU9|TLR12_MOUSE - Toll-like receptor 12 OS=Mus musculus GN=Tlr12 PE=2 SV=1	0	0	0	0	2	0	0	0.3739	2
sp|Q8K4F6|NSUN5_MOUSE - Probable 28S rRNA (cytosine-C(5))-methyltransferase OS=M	0	0	0	0	2	0	0	0.3739	2
sp|Q5DU28|PCX2_MOUSE - Pecanex-like protein 2 OS=Mus musculus GN=Pcnxl2 PE=2 SV=	0	0	0	0	7	0	0	0.3739	7
sp|Q6ZPR4|KCNT1_MOUSE - Potassium channel subfamily T member 1 OS=Mus musculus G	0	0	0	0	4	0	0	0.3739	4
sp|Q9ER65|CSTN2_MOUSE - Calsyntenin-2 OS=Mus musculus GN=Clstn2 PE=1 SV=2	0	0	0	0	2	0	0	0.3739	2
sp|Q810B7|SLIK5_MOUSE - SLIT and NTRK-like protein 5 OS=Mus musculus GN=Slitrk5	0	0	0	0	2	0	0	0.3739	2
sp|Q5GIG6|TNI3K_MOUSE - Serine/threonine-protein kinase TNNI3K OS=Mus musculus G	0	0	0	0	3	11	0	0.2282	14
sp|Q9JJZ9|CNGB3_MOUSE - Cyclic nucleotide-gated cation channel beta-3 OS=Mus mus	0	0	0	0	4	0	0	0.3739	4
sp|Q3U2I3|F16A2_MOUSE - FTS and Hook-interacting protein OS=Mus musculus GN=Fam1	0	0	0	0	2	0	0	0.3739	2
sp|Q8BYI9|TENR_MOUSE - Tenascin-R OS=Mus musculus GN=Tnr PE=1 SV=2	0	0	0	0	3	0	0	0.3739	3
sp|P46062|SIPA1_MOUSE - Signal-induced proliferation-associated protein 1 OS=Mus	0	0	0	0	2	0	0	0.3739	2
sp|Q8BUE1|SL9A4_MOUSE - Sodium/hydrogen exchanger 4 OS=Mus musculus GN=Slc9a4 PE	0	0	0	0	2	0	0	0.3739	2
sp|Q07113|MPRI_MOUSE - Cation-independent mannose-6-phosphate receptor OS=Mus mu	0	0	0	0	2	0	0	0.3739	2
sp|Q921M4|GOGA2_MOUSE - Golgin subfamily A member 2 OS=Mus musculus GN=Golga2 PE	0	0	0	0	2	0	0	0.3739	2
sp|Q8C6S9|CFA54_MOUSE - Cilia- and flagella-associated protein 54 OS=Mus musculu	0	0	0	0	3	0	0	0.3739	3
sp|Q8CJ19|MICA3_MOUSE - Protein-methionine sulfoxide oxidase MICAL3 OS=Mus muscu	0	0	0	0	15	6	0	0.1835	21
sp|Q8BUR4|DOCK1_MOUSE - Dedicator of cytokinesis protein 1 OS=Mus musculus GN=Do	0	0	0	0	2	0	0	0.3739	2
sp|Q7TPD0|INT3_MOUSE - Integrator complex subunit 3 OS=Mus musculus GN=Ints3 PE=	0	0	0	0	3	0	0	0.3739	3
sp|Q0VAV2|EXPH5_MOUSE - Exophilin-5 OS=Mus musculus GN=Exph5 PE=1 SV=1	0	0	0	0	5	0	0	0.3739	5
sp|P62821|RAB1A_MOUSE - Ras-related protein Rab-1A OS=Mus musculus GN=Rab1A PE=1	0	0	0	0	7	0	0	0.3739	7
sp|P03985|TCC2_MOUSE - T-cell receptor gamma chain C region C7.5 OS=Mus musculus	0	0	0	0	3	0	0	0.3739	3
sp|P62897|CYC_MOUSE - Cytochrome c, somatic OS=Mus musculus GN=Cycs PE=1 SV=2	0	0	0	0	20	12	0	0.1403	32
sp|Q8C551|R51A1_MOUSE - RAD51-associated protein 1 OS=Mus musculus GN=Rad51ap1 P	0	0	0	0	6	0	0	0.3739	6
sp|P06334|TCC3_MOUSE - T-cell receptor gamma chain C region DFL12 OS=Mus musculu	0	0	0	0	2	0	0	0.3739	2
sp|Q6ZWV7|RL35_MOUSE - 60S ribosomal protein L35 OS=Mus musculus GN=Rpl35 PE=2 S	0	0	0	0	4	0	0	0.3739	4
sp|Q8VCM4|LIPT_MOUSE - Lipoyltransferase 1, mitochondrial OS=Mus musculus GN=Lip	0	0	0	0	4	0	0	0.3739	4
sp|Q9JIK9|RT34_MOUSE - 28S ribosomal protein S34, mitochondrial OS=Mus musculus	0	0	0	0	6	0	0	0.3739	6
sp|Q9CQ01|RNT2_MOUSE - Ribonuclease T2 OS=Mus musculus GN=Rnaset2 PE=2 SV=1	0	0	0	0	3	0	0	0.3739	3
sp|Q8R104|SIR3_MOUSE - NAD-dependent protein deacetylase sirtuin-3 OS=Mus muscul	0	0	0	0	3	0	0	0.3739	3
sp|Q64105|SPRE_MOUSE - Sepiapterin reductase OS=Mus musculus GN=Spr PE=1 SV=1	0	0	0	0	2	0	0	0.3739	2
sp|Q9R022|DJC12_MOUSE - DnaJ homolog subfamily C member 12 OS=Mus musculus GN=Dn	0	0	0	0	3	0	0	0.3739	3
sp|P62082|RS7_MOUSE - 40S ribosomal protein S7 OS=Mus musculus GN=Rps7 PE=2 SV=1	0	0	0	0	2	0	0	0.3739	2
sp|Q50H32|GRCR1_MOUSE - Glutaredoxin domain-containing cysteine-rich protein 1 O	0	0	0	0	4	2	0	0.1583	6
sp|Q925N0|SFXN5_MOUSE - Sideroflexin-5 OS=Mus musculus GN=Sfxn5 PE=1 SV=2	0	0	0	0	5	0	0	0.3739	5
sp|P12246|SAMP_MOUSE - Serum amyloid P-component OS=Mus musculus GN=Apcs PE=1 SV	0	0	0	0	4	0	0	0.3739	4
sp|Q8BYK4|RDH12_MOUSE - Retinol dehydrogenase 12 OS=Mus musculus GN=Rdh12 PE=2 S	0	0	0	0	3	0	0	0.3739	3
sp|Q9Z2Q5|RM40_MOUSE - 39S ribosomal protein L40, mitochondrial OS=Mus musculus	0	0	0	0	2	0	0	0.3739	2
sp|Q9DBN5|LONP2_MOUSE - Lon protease homolog 2, peroxisomal OS=Mus musculus GN=L	0	0	0	0	6	0	0	0.3739	6
sp|P46412|GPX3_MOUSE - Glutathione peroxidase 3 OS=Mus musculus GN=Gpx3 PE=2 SV=	0	0	0	0	2	0	0	0.3739	2
sp|Q9JKF7|RM39_MOUSE - 39S ribosomal protein L39, mitochondrial OS=Mus musculus	0	0	0	0	2	0	0	0.3739	2
sp|Q7TNG8|LDHD_MOUSE - Probable D-lactate dehydrogenase, mitochondrial OS=Mus mu	0	0	0	0	3	0	0	0.3739	3

sp|P54846|NRL_MOUSE - Neural retina-specific leucine zipper protein OS=Mus muscu	0	0	0	0	2	0	0	0.3739	2
sp|Q9CY16|RT28_MOUSE - 28S ribosomal protein S28, mitochondrial OS=Mus musculus	0	0	0	0	4	0	0	0.3739	4
sp|Q9D2Y5|SNX20_MOUSE - Sorting nexin-20 OS=Mus musculus GN=Snx20 PE=2 SV=2	0	0	0	0	4	0	0	0.3739	4
sp|Q9EQC1|3BHS7_MOUSE - 3 beta-hydroxysteroid dehydrogenase type 7 OS=Mus muscul	0	0	0	0	2	0	0	0.3739	2
sp|Q6P6J9|TXD15_MOUSE - Thioredoxin domain-containing protein 15 OS=Mus musculus	0	0	0	0	2	0	0	0.3739	2
sp|Q8BIG7|CMTD1_MOUSE - Catechol O-methyltransferase domain-containing protein 1	0	0	0	0	2	0	0	0.3739	2
sp|Q8R1N4|NUDC3_MOUSE - NudC domain-containing protein 3 OS=Mus musculus GN=Nudc	0	0	0	0	3	0	0	0.3739	3
sp|Q9QZM8|FBX17_MOUSE - F-box only protein 17 OS=Mus musculus GN=Fbxo17 PE=2 SV=	0	0	0	0	6	0	0	0.3739	6
sp|Q9WV32|ARC1B_MOUSE - Actin-related protein 2/3 complex subunit 1B OS=Mus musc	0	0	0	0	2	0	0	0.3739	2
sp|O55131|SEPT7_MOUSE - Septin-7 OS=Mus musculus GN=Sept7 PE=1 SV=1	0	0	0	0	3	0	0	0.3739	3
sp|Q5DTY9|KCD16_MOUSE - BTB/POZ domain-containing protein KCTD16 OS=Mus musculus	0	0	0	0	2	0	0	0.3739	2
sp|Q4VBD2|TAPT1_MOUSE - Transmembrane anterior posterior transformation protein	0	0	0	0	2	0	0	0.3739	2
sp|Q6TCG2|PAQR9_MOUSE - Progestin and adipoQ receptor family member 9 OS=Mus mus	0	0	0	0	3	0	0	0.3739	3
sp|Q91W90|TXND5_MOUSE - Thioredoxin domain-containing protein 5 OS=Mus musculus	0	0	0	0	3	0	0	0.3739	3
sp|P0CG49|UBB_MOUSE - Polyubiquitin-B OS=Mus musculus GN=Ubb PE=2 SV=1	0	0	0	0	2	0	0	0.3739	2
sp|Q64FW2|RETST_MOUSE - All-trans-retinol 13,14-reductase OS=Mus musculus GN=Ret	0	0	0	0	2	0	0	0.3739	2
sp|Q9WV71|ASB4_MOUSE - Ankyrin repeat and SOCS box protein 4 OS=Mus musculus GN=	0	0	0	0	2	0	0	0.3739	2
sp|E9Q6X9|RHG40_MOUSE - Rho GTPase-activating protein 40 OS=Mus musculus GN=Arhg	0	0	0	0	14	0	0	0.3739	14
sp|Q91ZX6|SENP2_MOUSE - Sentrin-specific protease 2 OS=Mus musculus GN=Senp2 PE=	0	0	0	0	3	0	0	0.3739	3
sp|Q62073|M3K7_MOUSE - Mitogen-activated protein kinase kinase kinase 7 OS=Mus m	0	0	0	0	2	0	0	0.3739	2
sp|Q9DA97|SEP14_MOUSE - Septin-14 OS=Mus musculus GN=Sept14 PE=2 SV=3	0	0	0	0	3	0	0	0.3739	3
sp|Q3V124|EID3_MOUSE - EP300-interacting inhibitor of differentiation 3 OS=Mus m	0	0	0	0	7	0	0	0.3739	7
sp|Q14CH0|F171B_MOUSE - Protein FAM171B OS=Mus musculus GN=Fam171b PE=1 SV=2	0	0	0	0	3	0	0	0.3739	3
sp|Q8BYY4|TT39B_MOUSE - Tetratricopeptide repeat protein 39B OS=Mus musculus GN=	0	0	0	0	3	0	0	0.3739	3
sp|Q91ZE0|TMLH_MOUSE - Trimethyllysine dioxygenase, mitochondrial OS=Mus musculu	0	0	0	0	2	0	0	0.3739	2
sp|Q9CRC8|LRC40_MOUSE - Leucine-rich repeat-containing protein 40 OS=Mus musculu	0	0	0	0	2	0	0	0.3739	2
sp|Q149B8|PERM1_MOUSE - PGC-1 and ERR-induced regulator in muscle protein 1 OS=M	0	0	0	0	2	0	0	0.3739	2
sp|Q03141|MARK3_MOUSE - MAP/microtubule affinity-regulating kinase 3 OS=Mus musc	0	0	0	0	5	0	0	0.3739	5
sp|Q68FG3|SPT2_MOUSE - Protein SPT2 homolog OS=Mus musculus GN=Spty2d1 PE=2 SV=1	0	0	0	0	4	0	0	0.3739	4
sp|Q8VD46|ASZ1_MOUSE - Ankyrin repeat, SAM and basic leucine zipper domain-conta	0	0	0	0	2	0	0	0.3739	2
sp|Q8CGC7|SYEP_MOUSE - Bifunctional glutamate/proline--tRNA ligase OS=Mus muscul	0	0	0	0	7	7	0	0.1161	14
sp|Q8BPM2|M4K5_MOUSE - Mitogen-activated protein kinase kinase kinase kinase 5 O	0	0	0	0	6	0	0	0.3739	6
sp|Q8CI12|SMTL2_MOUSE - Smoothelin-like protein 2 OS=Mus musculus GN=Smtnl2 PE=1	0	0	0	0	4	0	0	0.3739	4
sp|Q80X53|CC116_MOUSE - Coiled-coil domain-containing protein 116 OS=Mus musculu	0	0	0	0	5	0	0	0.3739	5
sp|Q80YT7|MYOME_MOUSE - Myomegalin OS=Mus musculus GN=Pde4dip PE=2 SV=2	0	0	0	0	8	0	0	0.3739	8
sp|Q9WUH7|SEM4G_MOUSE - Semaphorin-4G OS=Mus musculus GN=Sema4g PE=1 SV=1	0	0	0	0	4	0	0	0.3739	4
sp|Q8BU25|PAMR1_MOUSE - Inactive serine protease PAMR1 OS=Mus musculus GN=Pamr1	0	0	0	0	4	0	0	0.3739	4
sp|Q8R3I3|COG6_MOUSE - Conserved oligomeric Golgi complex subunit 6 OS=Mus muscu	0	0	0	0	2	0	0	0.3739	2
sp|B2RPU2|PLHD1_MOUSE - Pleckstrin homology domain-containing family D member 1	0	0	0	0	2	0	0	0.3739	2
sp|Q3UP24|NLRC4_MOUSE - NLR family CARD domain-containing protein 4 OS=Mus muscu	0	0	0	0	5	0	0	0.3739	5
sp|D3YYU8|OBSL1_MOUSE - Obscurin-like protein 1 OS=Mus musculus GN=Obsl1 PE=2 SV	0	0	0	0	9	0	0	0.3739	9

sp|P25799|NFKB1_MOUSE - Nuclear factor NF-kappa-B p105 subunit OS=Mus musculus G	0	0	0	0	4	0	0	0.3739	4
sp|Q499E4|DZI1L_MOUSE - Zinc finger protein DZIP1L OS=Mus musculus GN=Dzip1l PE=	0	0	0	0	3	0	0	0.3739	3
sp|P16054|KPCE_MOUSE - Protein kinase C epsilon type OS=Mus musculus GN=Prkce PE	0	0	0	0	3	0	0	0.3739	3
sp|Q91X88|PMGT1_MOUSE - Protein O-linked-mannose beta-1,2-N-acetylglucosaminyltr	0	0	0	0	2	0	0	0.3739	2
sp|Q9JI78|NGLY1_MOUSE - Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amid	0	0	0	0	2	0	0	0.3739	2
sp|Q8K4Z5|SF3A1_MOUSE - Splicing factor 3A subunit 1 OS=Mus musculus GN=Sf3a1 PE	0	0	0	0	2	0	0	0.3739	2
sp|Q61967|ZFP90_MOUSE - Zinc finger protein 90 OS=Mus musculus GN=Zfp90 PE=2 SV=	0	0	0	0	3	0	0	0.3739	3
sp|Q8BXN9|TM87A_MOUSE - Transmembrane protein 87A OS=Mus musculus GN=Tmem87a PE=	0	0	0	0	2	0	0	0.3739	2
sp|O88444|ADCY1_MOUSE - Adenylate cyclase type 1 OS=Mus musculus GN=Adcy1 PE=2 S	0	0	0	0	2	0	0	0.3739	2
sp|Q8C3S2|TNG6_MOUSE - Transport and Golgi organization protein 6 homolog OS=Mus	0	0	0	0	3	0	0	0.3739	3
sp|Q9Z1P7|KANK3_MOUSE - KN motif and ankyrin repeat domain-containing protein 3	0	0	0	0	2	0	0	0.3739	2
sp|Q8BJL1|FBX30_MOUSE - F-box only protein 30 OS=Mus musculus GN=Fbxo30 PE=1 SV=	0	0	0	0	2	0	0	0.3739	2
sp|Q499M4|TIGD5_MOUSE - Tigger transposable element derived 5 OS=Mus musculus GN	0	0	0	0	4	0	0	0.3739	4
sp|Q66X22|NAL9B_MOUSE - NACHT, LRR and PYD domains-containing protein 9B OS=Mus	0	0	0	0	3	2	0	0.1317	5
sp|Q8VIJ6|SFPQ_MOUSE - Splicing factor, proline- and glutamine-rich OS=Mus muscu	0	0	0	0	2	0	0	0.3739	2
sp|Q3V3R4|ITA1_MOUSE - Integrin alpha-1 OS=Mus musculus GN=Itga1 PE=1 SV=2	0	0	0	0	2	0	0	0.3739	2
sp|Q8CJ78|ZN628_MOUSE - Zinc finger protein 628 OS=Mus musculus GN=Znf628 PE=2 S	0	0	0	0	2	0	0	0.3739	2
sp|Q6VNS1|NTRK3_MOUSE - NT-3 growth factor receptor OS=Mus musculus GN=Ntrk3 PE=	0	0	0	0	2	0	0	0.3739	2
sp|Q80TE0|RPAP1_MOUSE - RNA polymerase II-associated protein 1 OS=Mus musculus G	0	0	0	0	2	0	0	0.3739	2
sp|P70261|PALD_MOUSE - Paladin OS=Mus musculus GN=Pald1 PE=1 SV=1	0	0	0	0	2	0	0	0.3739	2
sp|B1AXH1|NHSL2_MOUSE - NHS-like protein 2 OS=Mus musculus GN=Nhsl2 PE=2 SV=1	0	0	0	0	3	0	0	0.3739	3
sp|Q91WD2|TRPV6_MOUSE - Transient receptor potential cation channel subfamily V	0	0	0	0	4	3	0	0.1241	7
sp|P08122|CO4A2_MOUSE - Collagen alpha-2(IV) chain OS=Mus musculus GN=Col4a2 PE=	0	0	0	0	3	0	0	0.3739	3
sp|Q91VB4|HPS3_MOUSE - Hermansky-Pudlak syndrome 3 protein homolog OS=Mus muscul	0	0	0	0	2	0	0	0.3739	2
sp|Q3TRM8|HXK3_MOUSE - Hexokinase-3 OS=Mus musculus GN=Hk3 PE=2 SV=2	0	0	0	0	2	0	0	0.3739	2
sp|Q3KNY0|IGFN1_MOUSE - Immunoglobulin-like and fibronectin type III domain-cont	0	0	0	0	4	0	0	0.3739	4
sp|Q91ZX7|LRP1_MOUSE - Prolow-density lipoprotein receptor-related protein 1 OS=	0	0	0	0	9	0	0	0.3739	9
sp|B2RU80|PTPRB_MOUSE - Receptor-type tyrosine-protein phosphatase beta OS=Mus m	0	0	0	0	3	0	0	0.3739	3
sp|Q61137|ASTN1_MOUSE - Astrotactin-1 OS=Mus musculus GN=Astn1 PE=2 SV=4	0	0	0	0	2	0	0	0.3739	2
sp|Q91W89|MA2C1_MOUSE - Alpha-mannosidase 2C1 OS=Mus musculus GN=Man2c1 PE=2 SV=	0	0	0	0	2	2	0	0.1161	4
sp|Q8BWZ3|NAA25_MOUSE - N-alpha-acetyltransferase 25, NatB auxiliary subunit OS=	0	0	0	0	2	0	0	0.3739	2
sp|Q8VDR9|DOCK6_MOUSE - Dedicator of cytokinesis protein 6 OS=Mus musculus GN=Do	0	0	0	0	3	0	0	0.3739	3
sp|Q63ZW7|INADL_MOUSE - InaD-like protein OS=Mus musculus GN=Inadl PE=1 SV=2	0	0	0	0	3	0	0	0.3739	3
sp|Q6NZJ6|IF4G1_MOUSE - Eukaryotic translation initiation factor 4 gamma 1 OS=Mu	0	0	0	0	2	0	0	0.3739	2
sp|Q05909|PTPRG_MOUSE - Receptor-type tyrosine-protein phosphatase gamma OS=Mus	0	0	0	0	2	0	0	0.3739	2
sp|Q62388|ATM_MOUSE - Serine-protein kinase ATM OS=Mus musculus GN=Atm PE=1 SV=2	0	0	0	0	7	12	0	0.1428	19
sp|A3KGS3|RGPA2_MOUSE - Ral GTPase-activating protein subunit alpha-2 OS=Mus mus	0	0	0	0	6	0	0	0.3739	6
sp|Q5SWW4|MED13_MOUSE - Mediator of RNA polymerase II transcription subunit 13 O	0	0	0	0	2	0	0	0.3739	2
sp|Q91YM2|RHG35_MOUSE - Rho GTPase-activating protein 35 OS=Mus musculus GN=Arhg	0	0	0	0	5	0	0	0.3739	5
sp|O08852|PKD1_MOUSE - Polycystin-1 OS=Mus musculus GN=Pkd1 PE=1 SV=2	0	0	0	0	12	7	0	0.1428	19
sp|Q91WS0|CISD1_MOUSE - CDGSH iron-sulfur domain-containing protein 1 OS=Mus mus	0	0	0	0	7	2	0	0.2229	9

sp|Q9CQ54|NDUC2_MOUSE - NADH dehydrogenase [ubiquinone] 1 subunit C2 OS=Mus musc	0	0	0	0	6	0	0	0.3739	6
sp|Q9CR61|NDUB7_MOUSE - NADH dehydrogenase [ubiquinone] 1 beta subcomplex subuni	0	0	0	0	19	0	0	0.3739	19
sp|O55142|RL35A_MOUSE - 60S ribosomal protein L35a OS=Mus musculus GN=Rpl35a PE=	0	0	0	0	3	0	0	0.3739	3
sp|Q99N89|RM43_MOUSE - 39S ribosomal protein L43, mitochondrial OS=Mus musculus	0	0	0	0	3	0	0	0.3739	3
sp|P62823|RAB3C_MOUSE - Ras-related protein Rab-3C OS=Mus musculus GN=Rab3c PE=1	0	0	0	0	4	0	0	0.3739	4
sp|Q9CPT4|MYDGF_MOUSE - Myeloid-derived growth factor OS=Mus musculus GN=Mydgf P	0	0	0	0	7	0	0	0.3739	7
sp|Q8BHD0|RB39A_MOUSE - Ras-related protein Rab-39A OS=Mus musculus GN=Rab39a PE	0	0	0	0	2	0	0	0.3739	2
sp|P01837|IGKC_MOUSE - Ig kappa chain C region OS=Mus musculus PE=1 SV=1	0	0	0	0	2	0	0	0.3739	2
sp|Q0VBK2|K2C80_MOUSE - Keratin, type II cytoskeletal 80 OS=Mus musculus GN=Krt8	0	0	0	0	5	0	0	0.3739	5
sp|Q6P6M5|PX11C_MOUSE - Peroxisomal membrane protein 11C OS=Mus musculus GN=Pex1	0	0	0	0	2	0	0	0.3739	2
sp|O55208|FIGLA_MOUSE - Factor in the germline alpha OS=Mus musculus GN=Figla PE	0	0	0	0	2	0	0	0.3739	2
sp|Q9CR59|G45IP_MOUSE - Growth arrest and DNA damage-inducible proteins-interact	0	0	0	0	2	0	0	0.3739	2
sp|P11672|NGAL_MOUSE - Neutrophil gelatinase-associated lipocalin OS=Mus musculu	0	0	0	0	2	0	0	0.3739	2
sp|Q9D8N0|EF1G_MOUSE - Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 S	0	0	0	0	2	0	0	0.3739	2
sp|Q9CYC3|TM39A_MOUSE - Transmembrane protein 39A OS=Mus musculus GN=Tmem39a PE=	0	0	0	0	2	0	0	0.3739	2
sp|O35310|HS3S1_MOUSE - Heparan sulfate glucosamine 3-O-sulfotransferase 1 OS=Mu	0	0	0	0	2	0	0	0.3739	2
sp|P14429|HA17_MOUSE - H-2 class I histocompatibility antigen, Q7 alpha chain OS	0	0	0	0	2	0	0	0.3739	2
sp|P83093|STIM2_MOUSE - Stromal interaction molecule 2 OS=Mus musculus GN=Stim2	0	0	0	0	3	0	0	0.3739	3
sp|P50580|PA2G4_MOUSE - Proliferation-associated protein 2G4 OS=Mus musculus GN=	0	0	0	0	2	0	0	0.3739	2
sp|Q99M87|DNJA3_MOUSE - DnaJ homolog subfamily A member 3, mitochondrial OS=Mus	0	0	0	0	2	0	0	0.3739	2
sp|Q9CXG3|PPIL4_MOUSE - Peptidyl-prolyl cis-trans isomerase-like 4 OS=Mus muscul	0	0	0	0	4	0	0	0.3739	4
sp|Q922R5|P4R3B_MOUSE - Serine/threonine-protein phosphatase 4 regulatory subuni	0	0	0	0	3	0	0	0.3739	3
sp|Q8BH34|SEM3D_MOUSE - Semaphorin-3D OS=Mus musculus GN=Sema3d PE=1 SV=1	0	0	0	0	2	0	0	0.3739	2
sp|Q80UN9|MOD5_MOUSE - tRNA dimethylallyltransferase, mitochondrial OS=Mus muscu	0	0	0	0	6	0	0	0.3739	6
sp|Q9Z307|KCJ16_MOUSE - Inward rectifier potassium channel 16 OS=Mus musculus GN	0	0	0	0	2	0	0	0.3739	2
sp|O35738|KLF12_MOUSE - Krueppel-like factor 12 OS=Mus musculus GN=Klf12 PE=2 SV	0	0	0	0	3	0	0	0.3739	3
sp|Q7TSC3|NEK5_MOUSE - Serine/threonine-protein kinase Nek5 OS=Mus musculus GN=N	0	0	0	0	2	0	0	0.3739	2
sp|Q4QRL3|CC88B_MOUSE - Coiled-coil domain-containing protein 88B OS=Mus musculu	0	0	0	0	4	0	0	0.3739	4
sp|Q0VGM9|RTEL1_MOUSE - Regulator of telomere elongation helicase 1 OS=Mus muscu	0	0	0	0	6	0	0	0.3739	6
sp|Q8R3N1|NOP14_MOUSE - Nucleolar protein 14 OS=Mus musculus GN=Nop14 PE=1 SV=2	0	0	0	0	2	0	0	0.3739	2
sp|Q6P2K6|P4R3A_MOUSE - Serine/threonine-protein phosphatase 4 regulatory subuni	0	0	0	0	2	0	0	0.3739	2
sp|P49135|ERCC3_MOUSE - TFIIH basal transcription factor complex helicase XPB su	0	0	0	0	2	0	0	0.3739	2
sp|Q9Z0H1|WDR46_MOUSE - WD repeat-containing protein 46 OS=Mus musculus GN=Wdr46	0	0	0	0	6	0	0	0.3739	6
sp|Q0P5V2|SOBP_MOUSE - Sine oculis-binding protein homolog OS=Mus musculus GN=So	0	0	0	0	2	0	0	0.3739	2
sp|P56476|GBRR2_MOUSE - Gamma-aminobutyric acid receptor subunit rho-2 OS=Mus mu	0	0	0	0	2	0	0	0.3739	2
sp|Q6P4S8|INT1_MOUSE - Integrator complex subunit 1 OS=Mus musculus GN=Ints1 PE=	0	0	0	0	5	0	0	0.3739	5
sp|Q8CDN9|LRRC9_MOUSE - Leucine-rich repeat-containing protein 9 OS=Mus musculus	0	0	0	0	3	0	0	0.3739	3
sp|Q3V0Y1|SMEK3_MOUSE - Putative SMEK homolog 3 OS=Mus musculus GN=Smek3p PE=5 S	0	0	0	0	2	0	0	0.3739	2
sp|B8JK39|ITA9_MOUSE - Integrin alpha-9 OS=Mus musculus GN=Itga9 PE=1 SV=1	0	0	0	0	2	0	0	0.3739	2
sp|Q9JJH7|TRPM5_MOUSE - Transient receptor potential cation channel subfamily M	0	0	0	0	2	0	0	0.3739	2
sp|P59328|WDHD1_MOUSE - WD repeat and HMG-box DNA-binding protein 1 OS=Mus muscu	0	0	0	0	2	0	0	0.3739	2

sp|E9Q555|RN213_MOUSE - E3 ubiquitin-protein ligase RNF213 OS=Mus musculus GN=Rn	0	0	0	0	4	0	0	0.3739	4
sp|Q9JI18|LRP1B_MOUSE - Low-density lipoprotein receptor-related protein 1B OS=M	0	0	0	0	5	0	0	0.3739	5
sp|Q8R0W0|EPIPL_MOUSE - Epiplakin OS=Mus musculus GN=Eppk1 PE=1 SV=2	0	0	0	0	6	0	0	0.3739	6
sp|Q9CPQ8|ATP5L_MOUSE - ATP synthase subunit g, mitochondrial OS=Mus musculus GN	0	0	0	0	2	0	0	0.3739	2
sp|Q9CQZ6|NDUB3_MOUSE - NADH dehydrogenase [ubiquinone] 1 beta subcomplex subuni	0	0	0	0	5	0	0	0.3739	5
sp|P52503|NDUS6_MOUSE - NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, m	0	0	0	0	2	0	0	0.3739	2
sp|O70404|VAMP8_MOUSE - Vesicle-associated membrane protein 8 OS=Mus musculus GN	0	0	0	0	2	0	0	0.3739	2
sp|P60867|RS20_MOUSE - 40S ribosomal protein S20 OS=Mus musculus GN=Rps20 PE=1 S	0	0	0	0	2	0	0	0.3739	2
sp|Q3UFF7|LYPL1_MOUSE - Lysophospholipase-like protein 1 OS=Mus musculus GN=Lypl	0	0	0	0	5	0	0	0.3739	5
sp|Q8VCR7|ABHEB_MOUSE - Alpha/beta hydrolase domain-containing protein 14B OS=Mu	0	0	0	0	3	0	0	0.3739	3
sp|P63030|MPC1_MOUSE - Mitochondrial pyruvate carrier 1 OS=Mus musculus GN=Mpc1	0	0	0	0	2	0	0	0.3739	2
sp|P01887|B2MG_MOUSE - Beta-2-microglobulin OS=Mus musculus GN=B2m PE=1 SV=2	0	0	0	0	2	0	0	0.3739	2
sp|Q91WM2|CECR5_MOUSE - Cat eye syndrome critical region protein 5 homolog OS=Mu	0	0	0	0	5	0	0	0.3739	5
sp|Q64524|H2B2E_MOUSE - Histone H2B type 2-E OS=Mus musculus GN=Hist2h2be PE=1 S	0	0	0	0	2	0	0	0.3739	2
sp|Q07133|H1T_MOUSE - Histone H1t OS=Mus musculus GN=Hist1h1t PE=1 SV=4	0	0	0	0	2	0	0	0.3739	2
sp|P62889|RL30_MOUSE - 60S ribosomal protein L30 OS=Mus musculus GN=Rpl30 PE=3 S	0	0	0	0	2	0	0	0.3739	2
sp|Q9D7Q0|LYG1_MOUSE - Lysozyme g-like protein 1 OS=Mus musculus GN=Lyg1 PE=2 SV	0	0	0	0	3	0	0	0.3739	3
sp|Q9CQV5|RT24_MOUSE - 28S ribosomal protein S24, mitochondrial OS=Mus musculus	0	0	0	0	3	0	0	0.3739	3
sp|Q9CQB5|CISD2_MOUSE - CDGSH iron-sulfur domain-containing protein 2 OS=Mus mus	0	0	0	0	2	0	0	0.3739	2
sp|P97350|PKP1_MOUSE - Plakophilin-1 OS=Mus musculus GN=Pkp1 PE=2 SV=1	0	0	0	0	8	0	0	0.3739	8
sp|P45878|FKBP2_MOUSE - Peptidyl-prolyl cis-trans isomerase FKBP2 OS=Mus musculu	0	0	0	0	2	0	0	0.3739	2
sp|Q9CQZ5|NDUA6_MOUSE - NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subun	0	0	0	0	3	0	0	0.3739	3
sp|Q9CY25|MIS12_MOUSE - Protein MIS12 homolog OS=Mus musculus GN=Mis12 PE=2 SV=1	0	0	0	0	3	0	0	0.3739	3
sp|Q8R2Z0|ADIPL_MOUSE - Adipolin OS=Mus musculus GN=Fam132a PE=1 SV=2	0	0	0	0	4	0	0	0.3739	4
sp|Q9D1D4|TMEDA_MOUSE - Transmembrane emp24 domain-containing protein 10 OS=Mus	0	0	0	0	2	0	0	0.3739	2
sp|P12970|RL7A_MOUSE - 60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=1 S	0	0	0	0	2	0	0	0.3739	2
sp|Q9DCT1|AKCL2_MOUSE - 1,5-anhydro-D-fructose reductase OS=Mus musculus GN=Akr1	0	0	0	0	2	0	0	0.3739	2
sp|Q8R5F3|OARD1_MOUSE - O-acetyl-ADP-ribose deacetylase 1 OS=Mus musculus GN=Oar	0	0	0	0	4	0	0	0.3739	4
sp|Q99N84|RT18B_MOUSE - 28S ribosomal protein S18b, mitochondrial OS=Mus musculu	0	0	0	0	2	0	0	0.3739	2
sp|O35465|FKBP8_MOUSE - Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Mus musculu	0	0	0	0	5	0	0	0.3739	5
sp|Q8R0F8|FAHD1_MOUSE - Acylpyruvase FAHD1, mitochondrial OS=Mus musculus GN=Fah	0	0	0	0	3	4	0	0.1241	7
sp|Q6ZWY3|RS27L_MOUSE - 40S ribosomal protein S27-like OS=Mus musculus GN=Rps27l	0	0	0	0	2	0	0	0.3739	2
sp|Q9DCY0|KEG1_MOUSE - Glycine N-acyltransferase-like protein Keg1 OS=Mus muscul	0	0	0	0	2	0	0	0.3739	2
sp|P07356|ANXA2_MOUSE - Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2	0	0	0	0	2	0	0	0.3739	2
sp|Q3UHX9|CI114_MOUSE - Putative methyltransferase C9orf114 homolog OS=Mus muscu	0	0	0	0	2	0	0	0.3739	2
sp|Q8BKT6|TSN12_MOUSE - Tetraspanin-12 OS=Mus musculus GN=Tspan12 PE=1 SV=1	0	0	0	0	5	12	0	0.1787	17
sp|Q8C4Q6|AIDA_MOUSE - Axin interactor, dorsalization-associated protein OS=Mus	0	0	0	0	3	0	0	0.3739	3
sp|Q0VBM2|FA83B_MOUSE - Protein FAM83B OS=Mus musculus GN=Fam83b PE=2 SV=1	0	0	0	0	5	0	0	0.3739	5
sp|Q9CXE0|PRDM5_MOUSE - PR domain zinc finger protein 5 OS=Mus musculus GN=Prdm5	0	0	0	0	3	0	0	0.3739	3
sp|Q5DTT4|RGAG4_MOUSE - Retrotransposon gag domain-containing protein 4 OS=Mus m	0	0	0	0	4	0	0	0.3739	4
sp|P03966|MYCN_MOUSE - N-myc proto-oncogene protein OS=Mus musculus GN=Mycn PE=2	0	0	0	0	3	0	0	0.3739	3

sp|P01740|TVC1_MOUSE - T-cell receptor gamma chain V region V108A OS=Mus musculu	0	0	0	0	2	0	0	0.3739	2
sp|Q5Y4Y6|GSDA3_MOUSE - Gasdermin-A3 OS=Mus musculus GN=Gsdma3 PE=1 SV=1	0	0	0	0	2	0	0	0.3739	2
sp|Q6NXY9|RPC7_MOUSE - DNA-directed RNA polymerase III subunit RPC7 OS=Mus muscu	0	0	0	0	9	0	0	0.3739	9
sp|Q9D1A4|ASB5_MOUSE - Ankyrin repeat and SOCS box protein 5 OS=Mus musculus GN=	0	0	0	0	2	0	0	0.3739	2
sp|Q9JLB9|PVRL3_MOUSE - Nectin-3 OS=Mus musculus GN=Pvrl3 PE=1 SV=1	0	0	0	0	3	0	0	0.3739	3
sp|Q3TPE9|ANKY2_MOUSE - Ankyrin repeat and MYND domain-containing protein 2 OS=M	0	0	0	0	2	0	0	0.3739	2
sp|Q6P9S0|MTSSL_MOUSE - MTSS1-like protein OS=Mus musculus GN=Mtss1l PE=1 SV=1	0	0	0	0	2	0	0	0.3739	2
sp|Q9Z108|STAU1_MOUSE - Double-stranded RNA-binding protein Staufen homolog 1 OS	0	0	0	0	2	0	0	0.3739	2
sp|Q8R1S4|MTSS1_MOUSE - Metastasis suppressor protein 1 OS=Mus musculus GN=Mtss1	0	0	0	0	2	0	0	0.3739	2
sp|Q69ZK5|KLH14_MOUSE - Kelch-like protein 14 OS=Mus musculus GN=Klhl14 PE=1 SV=	0	0	0	0	4	0	0	0.3739	4
sp|O08832|GALT4_MOUSE - Polypeptide N-acetylgalactosaminyltransferase 4 OS=Mus m	0	0	0	0	2	0	0	0.3739	2
sp|Q6PGC1|DHX29_MOUSE - ATP-dependent RNA helicase Dhx29 OS=Mus musculus GN=Dhx2	0	0	0	0	4	0	0	0.3739	4
sp|Q9ERK4|XPO2_MOUSE - Exportin-2 OS=Mus musculus GN=Cse1l PE=2 SV=1	0	0	0	0	2	0	0	0.3739	2
sp|Q14B46|RTKN2_MOUSE - Rhotekin-2 OS=Mus musculus GN=Rtkn2 PE=2 SV=2	0	0	0	0	2	0	0	0.3739	2
sp|Q3U0D9|HACE1_MOUSE - E3 ubiquitin-protein ligase HACE1 OS=Mus musculus GN=Hac	0	0	0	0	2	0	0	0.3739	2
sp|P18911|RARG_MOUSE - Retinoic acid receptor gamma OS=Mus musculus GN=Rarg PE=1	0	0	0	0	2	0	0	0.3739	2
sp|Q8K2Z2|PRP39_MOUSE - Pre-mRNA-processing factor 39 OS=Mus musculus GN=Prpf39	0	0	0	0	2	0	0	0.3739	2
sp|Q69ZW3|EHBP1_MOUSE - EH domain-binding protein 1 OS=Mus musculus GN=Ehbp1 PE=	0	0	0	0	3	0	0	0.3739	3
sp|Q8K1G2|LBN_MOUSE - Limbin OS=Mus musculus GN=Evc2 PE=1 SV=1	0	0	0	0	3	0	0	0.3739	3
sp|Q8BV57|SRCRL_MOUSE - Soluble scavenger receptor cysteine-rich domain-containi	0	0	0	0	2	0	0	0.3739	2
sp|Q6A000|K0753_MOUSE - Uncharacterized protein KIAA0753 OS=Mus musculus GN=Kiaa	0	0	0	0	2	0	0	0.3739	2
sp|Q8BNW9|KBTBB_MOUSE - Kelch repeat and BTB domain-containing protein 11 OS=Mus	0	0	0	0	2	0	0	0.3739	2
sp|Q8CHR6|DPYD_MOUSE - Dihydropyrimidine dehydrogenase [NADP(+)] OS=Mus musculus	0	0	0	0	2	0	0	0.3739	2
sp|Q8R2N2|CIR1A_MOUSE - Cirhin OS=Mus musculus GN=Cirh1a PE=2 SV=3	0	0	0	0	2	0	0	0.3739	2
sp|Q6KCD5|NIPBL_MOUSE - Nipped-B-like protein OS=Mus musculus GN=Nipbl PE=1 SV=1	0	0	0	0	4	0	0	0.3739	4
sp|B2RX88|CSPP1_MOUSE - Centrosome and spindle pole associated protein 1 OS=Mus	0	0	0	0	2	0	0	0.3739	2
sp|Q8BZZ3|WWP1_MOUSE - NEDD4-like E3 ubiquitin-protein ligase WWP1 OS=Mus muscul	0	0	0	0	2	0	0	0.3739	2
sp|Q3TAP4|AP5B1_MOUSE - AP-5 complex subunit beta-1 OS=Mus musculus GN=Ap5b1 PE=	0	0	0	0	3	0	0	0.3739	3
sp|Q1PSW8|LIN41_MOUSE - E3 ubiquitin-protein ligase TRIM71 OS=Mus musculus GN=Tr	0	0	0	0	2	0	0	0.3739	2
sp|Q8BXX2|ZBT49_MOUSE - Zinc finger and BTB domain-containing protein 49 OS=Mus	0	0	0	0	3	0	0	0.3739	3
sp|O70492|SNX3_MOUSE - Sorting nexin-3 OS=Mus musculus GN=Snx3 PE=1 SV=3	0	0	0	0	0	6	0	0.3739	6
sp|Q9JHX2|SP5_MOUSE - Transcription factor Sp5 OS=Mus musculus GN=Sp5 PE=2 SV=1	0	0	0	0	0	3	0	0.3739	3
sp|Q8VBX4|CLC4K_MOUSE - C-type lectin domain family 4 member K OS=Mus musculus G	0	0	0	0	0	2	0	0.3739	2
sp|Q61884|MNS1_MOUSE - Meiosis-specific nuclear structural protein 1 OS=Mus musc	0	0	0	0	0	2	0	0.3739	2
sp|P70169|DOC2B_MOUSE - Double C2-like domain-containing protein beta OS=Mus mus	0	0	0	0	0	6	0	0.3739	6
sp|P05201|AATC_MOUSE - Aspartate aminotransferase, cytoplasmic OS=Mus musculus G	0	0	0	0	0	2	0	0.3739	2
sp|Q8R4U7|LUZP1_MOUSE - Leucine zipper protein 1 OS=Mus musculus GN=Luzp1 PE=1 S	0	0	0	0	0	7	0	0.3739	7
sp|Q56A08|GPKOW_MOUSE - G patch domain and KOW motifs-containing protein OS=Mus	0	0	0	0	0	6	0	0.3739	6
sp|O54749|CP2J5_MOUSE - Cytochrome P450 2J5 OS=Mus musculus GN=Cyp2j5 PE=2 SV=1	0	0	0	0	0	6	0	0.3739	6
sp|Q8CGW4|SOX30_MOUSE - Transcription factor SOX-30 OS=Mus musculus GN=Sox30 PE=	0	0	0	0	0	2	0	0.3739	2
sp|Q8C754|VPS52_MOUSE - Vacuolar protein sorting-associated protein 52 homolog O	0	0	0	0	0	10	0	0.3739	10

sp|Q8R5H1|UBP15_MOUSE - Ubiquitin carboxyl-terminal hydrolase 15 OS=Mus musculus	0	0	0	0	0	9	0	0.3739	9
sp|Q3UPP8|CEP63_MOUSE - Centrosomal protein of 63 kDa OS=Mus musculus GN=Cep63 P	0	0	0	0	0	6	0	0.3739	6
sp|Q571C7|BDP1_MOUSE - Transcription factor TFIIIB component B'' homolog OS=Mus	0	0	0	0	0	3	0	0.3739	3
sp|Q9ERC8|DSCAM_MOUSE - Down syndrome cell adhesion molecule homolog OS=Mus musc	0	0	0	0	0	9	0	0.3739	9
sp|P55200|KMT2A_MOUSE - Histone-lysine N-methyltransferase 2A OS=Mus musculus GN	0	0	0	0	0	7	0	0.3739	7
sp|Q8C547|HTR5B_MOUSE - HEAT repeat-containing protein 5B OS=Mus musculus GN=Hea	0	0	0	0	0	5	0	0.3739	5
sp|Q8R216|SIR4_MOUSE - NAD-dependent protein deacetylase sirtuin-4 OS=Mus muscul	0	0	0	0	0	6	0	0.3739	6
sp|Q8BSF4|PISD_MOUSE - Phosphatidylserine decarboxylase proenzyme OS=Mus musculu	0	0	0	0	0	3	0	0.3739	3
sp|Q9D8E6|RL4_MOUSE - 60S ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=3	0	0	0	0	0	4	0	0.3739	4
sp|Q3T9Z9|ZUFSP_MOUSE - Zinc finger with UFM1-specific peptidase domain protein	0	0	0	0	0	7	0	0.3739	7
sp|Q5NCC9|TRI58_MOUSE - E3 ubiquitin-protein ligase TRIM58 OS=Mus musculus GN=Tr	0	0	0	0	0	4	0	0.3739	4
sp|Q9CQ07|LRC18_MOUSE - Leucine-rich repeat-containing protein 18 OS=Mus musculu	0	0	0	0	0	2	0	0.3739	2
sp|Q61146|OCLN_MOUSE - Occludin OS=Mus musculus GN=Ocln PE=1 SV=1	0	0	0	0	0	2	0	0.3739	2
sp|Q9WV89|STXB4_MOUSE - Syntaxin-binding protein 4 OS=Mus musculus GN=Stxbp4 PE=	0	0	0	0	0	2	0	0.3739	2
sp|Q9D668|ARRD2_MOUSE - Arrestin domain-containing protein 2 OS=Mus musculus GN=	0	0	0	0	0	2	0	0.3739	2
sp|O54774|AP3D1_MOUSE - AP-3 complex subunit delta-1 OS=Mus musculus GN=Ap3d1 PE	0	0	0	0	0	7	0	0.3739	7
sp|A2AJ15|MA1B1_MOUSE - Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha	0	0	0	0	0	7	0	0.3739	7
sp|Q8R3B7|BRD8_MOUSE - Bromodomain-containing protein 8 OS=Mus musculus GN=Brd8	0	0	0	0	0	2	0	0.3739	2
sp|Q80W68|KIRR1_MOUSE - Kin of IRRE-like protein 1 OS=Mus musculus GN=Kirrel PE=	0	0	0	0	0	4	0	0.3739	4
sp|Q3V3Q7|PACS2_MOUSE - Phosphofurin acidic cluster sorting protein 2 OS=Mus mus	0	0	0	0	0	4	0	0.3739	4
sp|B2RX14|TUT4_MOUSE - Terminal uridylyltransferase 4 OS=Mus musculus GN=Zcchc11	0	0	0	0	0	3	0	0.3739	3
sp|Q9QWF0|CAF1A_MOUSE - Chromatin assembly factor 1 subunit A OS=Mus musculus GN	0	0	0	0	0	2	0	0.3739	2
sp|O88572|LRP6_MOUSE - Low-density lipoprotein receptor-related protein 6 OS=Mus	0	0	0	0	0	3	0	0.3739	3
sp|O89032|SPD2A_MOUSE - SH3 and PX domain-containing protein 2A OS=Mus musculus	0	0	0	0	0	2	0	0.3739	2
sp|Q8BHZ4|ZN592_MOUSE - Zinc finger protein 592 OS=Mus musculus GN=Znf592 PE=2 S	0	0	0	0	0	3	0	0.3739	3
sp|Q8K368|FANCI_MOUSE - Fanconi anemia group I protein homolog OS=Mus musculus G	0	0	0	0	0	2	0	0.3739	2
sp|Q91YU3|MSD4_MOUSE - Myb/SANT-like DNA-binding domain-containing protein 4 OS=	0	0	0	0	0	4	0	0.3739	4
sp|Q99J95|CDK9_MOUSE - Cyclin-dependent kinase 9 OS=Mus musculus GN=Cdk9 PE=1 SV	0	0	0	0	0	11	0	0.3739	11
sp|Q3U1G5|I20L2_MOUSE - Interferon-stimulated 20 kDa exonuclease-like 2 OS=Mus m	0	0	0	0	0	8	0	0.3739	8
sp|P21803|FGFR2_MOUSE - Fibroblast growth factor receptor 2 OS=Mus musculus GN=F	0	0	0	0	0	2	0	0.3739	2
sp|P59222|SREC2_MOUSE - Scavenger receptor class F member 2 OS=Mus musculus GN=S	0	0	0	0	0	5	0	0.3739	5
sp|Q8CCP0|NEMF_MOUSE - Nuclear export mediator factor Nemf OS=Mus musculus GN=Ne	0	0	0	0	0	2	0	0.3739	2
sp|P31650|S6A11_MOUSE - Sodium- and chloride-dependent GABA transporter 3 OS=Mus	0	0	0	0	0	4	0	0.3739	4
sp|O08789|MNT_MOUSE - Max-binding protein MNT OS=Mus musculus GN=Mnt PE=2 SV=2	0	0	0	0	0	6	0	0.3739	6
sp|Q80VH0|BANK1_MOUSE - B-cell scaffold protein with ankyrin repeats OS=Mus musc	0	0	0	0	0	5	0	0.3739	5
sp|Q6PDJ1|CAHD1_MOUSE - VWFA and cache domain-containing protein 1 OS=Mus muscul	0	0	0	0	0	2	0	0.3739	2
sp|Q8CGV9|TSH3_MOUSE - Teashirt homolog 3 OS=Mus musculus GN=Tshz3 PE=1 SV=2	0	0	0	0	0	11	0	0.3739	11
sp|P97313|PRKDC_MOUSE - DNA-dependent protein kinase catalytic subunit OS=Mus mu	0	0	0	0	0	8	0	0.3739	8
sp|Q7M6U3|TEX14_MOUSE - Inactive serine/threonine-protein kinase TEX14 OS=Mus mu	0	0	0	0	0	6	0	0.3739	6
sp|Q80TF6|STAR9_MOUSE - StAR-related lipid transfer protein 9 OS=Mus musculus GN	0	0	0	0	0	6	0	0.3739	6
sp|P53808|PPCT_MOUSE - Phosphatidylcholine transfer protein OS=Mus musculus GN=P	0	0	0	0	0	2	0	0.3739	2

sp|Q3UA16|SPC25_MOUSE - Kinetochore protein Spc25 OS=Mus musculus GN=Spc25 PE=2	0	0	0	0	0	14	0	0.3739	14
sp|Q3UMM4|CDK10_MOUSE - Cyclin-dependent kinase 10 OS=Mus musculus GN=Cdk10 PE=2	0	0	0	0	0	2	0	0.3739	2
sp|Q9D2E2|TOE1_MOUSE - Target of EGR1 protein 1 OS=Mus musculus GN=Toe1 PE=1 SV=	0	0	0	0	0	2	0	0.3739	2
sp|Q8BR65|SDS3_MOUSE - Sin3 histone deacetylase corepressor complex component SD	0	0	0	0	0	2	0	0.3739	2
sp|Q62443|NPTX1_MOUSE - Neuronal pentraxin-1 OS=Mus musculus GN=Nptx1 PE=2 SV=1	0	0	0	0	0	3	0	0.3739	3
sp|P80317|TCPZ_MOUSE - T-complex protein 1 subunit zeta OS=Mus musculus GN=Cct6a	0	0	0	0	0	11	0	0.3739	11
sp|Q3TXX4|VGLU1_MOUSE - Vesicular glutamate transporter 1 OS=Mus musculus GN=Slc	0	0	0	0	0	4	0	0.3739	4
sp|Q80UE6|WNK4_MOUSE - Serine/threonine-protein kinase WNK4 OS=Mus musculus GN=W	0	0	0	0	0	6	0	0.3739	6
sp|Q9JMA9|S6A14_MOUSE - Sodium- and chloride-dependent neutral and basic amino a	0	0	0	0	0	2	0	0.3739	2
sp|Q9CZX0|ELP3_MOUSE - Elongator complex protein 3 OS=Mus musculus GN=Elp3 PE=1	0	0	0	0	0	6	0	0.3739	6
sp|Q3V0K9|PLSI_MOUSE - Plastin-1 OS=Mus musculus GN=Pls1 PE=2 SV=1	0	0	0	0	0	2	0	0.3739	2
sp|Q62108|DLG4_MOUSE - Disks large homolog 4 OS=Mus musculus GN=Dlg4 PE=1 SV=1	0	0	0	0	0	7	0	0.3739	7
sp|Q99K51|PLST_MOUSE - Plastin-3 OS=Mus musculus GN=Pls3 PE=1 SV=3	0	0	0	0	0	4	0	0.3739	4
sp|Q8BLI0|ATL1_MOUSE - ADAMTS-like protein 1 OS=Mus musculus GN=Adamtsl1 PE=2 SV	0	0	0	0	0	8	0	0.3739	8
sp|Q569L8|CENPJ_MOUSE - Centromere protein J OS=Mus musculus GN=Cenpj PE=2 SV=2	0	0	0	0	0	5	0	0.3739	5
sp|P97772|GRM1_MOUSE - Metabotropic glutamate receptor 1 OS=Mus musculus GN=Grm1	0	0	0	0	0	5	0	0.3739	5
sp|D3Z4R1|HFM1_MOUSE - Probable ATP-dependent DNA helicase HFM1 OS=Mus musculus	0	0	0	0	0	4	0	0.3739	4
sp|Q4PJX1|ODR4_MOUSE - Protein odr-4 homolog OS=Mus musculus GN=Odr4 PE=2 SV=2	0	0	0	0	0	7	0	0.3739	7
sp|Q0VF94|NKPD1_MOUSE - NTPase KAP family P-loop domain-containing protein 1 OS=	0	0	0	0	0	6	0	0.3739	6
sp|P70402|MYBPH_MOUSE - Myosin-binding protein H OS=Mus musculus GN=Mybph PE=2 S	0	0	0	0	0	5	0	0.3739	5
sp|Q9DBG7|SRPR_MOUSE - Signal recognition particle receptor subunit alpha OS=Mus	0	0	0	0	0	3	0	0.3739	3
sp|Q01065|PDE1B_MOUSE - Calcium/calmodulin-dependent 3',5'-cyclic nucleotide pho	0	0	0	0	0	2	0	0.3739	2
sp|P13020|GELS_MOUSE - Gelsolin OS=Mus musculus GN=Gsn PE=1 SV=3	0	0	0	0	0	17	0	0.3739	17
sp|P51655|GPC4_MOUSE - Glypican-4 OS=Mus musculus GN=Gpc4 PE=2 SV=2	0	0	0	0	0	4	0	0.3739	4
sp|A2RT91|ANKAR_MOUSE - Ankyrin and armadillo repeat-containing protein OS=Mus m	0	0	0	0	0	5	0	0.3739	5

Chapter 3

α-KB improves healthspan and lifespan by functioning through mitochondrial network homeostasis and AMPK downstream components

Abstract

α-ketobutyrate (α-KB), an endogenous short-chain α-keto acid, increases the lifespan of adult *C. elegans* and mice [1]. α-KB regulates longevity through activating AMPK, which promotes healthspan and lifespan when activated throughout adulthood [1-3]. CREB-regulated transcriptional coactivators (CRTCs) are a family of cofactors involved in genetic regulations for diverse physiological processes, and AMPK increases longevity though inhibiting CRTC-1 nuclear localization [4, 5]. PPARα ortholog, NHR-49, shares overlapping metabolic targets with CRTC-1/CREB and they antagonistically regulate the downstream genes for longevity [5]. By orchestrating the activity of opposing transcriptional effectors, CRTC-1 and NHR-49, AMPK maintains mitochondrial morphology and mediates longevity in *C. elegans* [5, 6]. Here, we examine the beneficial effects of α-KB on healthspan of the nematodes and found that α-KB improves the locomotion levels during aging. We also investigated the roles of CRTC-1 and NHR-49 in α-KB-induced longevity, and discovered that both of them are

required for α-KB to regulate aging. Together, these findings further support the model of AMPK activation by α-KB for healthspan and lifespan.

Introduction

We have previously demonstrated that metabolite α-ketobutyrate promotes longevity *in C. elegans* and in mice [1]. We identified MACF1/VAB-10 protein as the target of α-KB by Gelfree DARTS-MS[1]. By binding to VAB-10, α-KB upregulates the phosphorylation of *aak-2*/AMPK and therefore influences the rate of aging of the treated animals [1].

AMPK (adenosine monophosphate-activated protein kinase) regulates various metabolic processes to extend lifespan and healthspan across different species [2, 3, 7, 8]. Under the conditions of low energy or stress, AMPK becomes activated and phosphorylates CREB-regulated transcriptional coactivator CRTC-1 [4, 9]. AMPK directly targets at serines 76 and 179 on CRTC-1, which also reside within 14-3-3-binding motifs [9]. Subsequently, 14-3-3 proteins sequester CRTC-1 in the cytosol, suppressing CRTC-1 activity [4]. This translocation prevents CRTC-1 from interacting with the CREB homologue-1 (CRH-1) transcription factor in the nucleus, thereby affecting the expression of their target genes [4, 9].

The nuclear hormone receptor NHR-49 serves as a functional PPARα ortholog in *C. elegans* [9]. The function of NHR-49 is crucial for AMPK/calcineurin-mediated longevity, as constitutively active AMPK fails to extend the lifespan of *nhr-49* mutants [9]. Neuronal

CRTC-1/CREB and NHR-49 antagonistically regulate the shared metabolic and aging-related gene expressions [9].

Our previous study suggests that α-KB influences aging process by promoting mitochondrial network homeostasis, similar to how AMPK regulate mitochondrial morphology and content during aging [9]. Treatment with α-KB or activation of AMPK maintains a youthful mitochondrial network, characterized by increased mitochondrial content and connectivity [1, 5]. Neuronal CRTC-1 regulates mitochondrial dynamics and lifespan through a cell-nonautonomous catecholamine signal, with NHR-49 downstream of it [9]. Loss of *nhr-49* and upregulation of CRTC-1 both lead to mitochondrial fragmentation in early adulthood compared to wildtype [5]. Preservation of mitochondrial network homeostasis is a unique feature of AMPK activation and dietary restrictions, as fission and fusion are not required for lifespan extension in *daf-2* mutation [10].

Mutations on mitochondrial electron transport chain (ETC) components extend lifespan in multiple species [11-16]. *aak-2*/AMPK mutation significantly reduces the extended lifespan in *clk-1* (a ubiquinone hydroxylase) and *isp-1* (iron-sulfur protein 1 in the mitochondrial complex III) mutants, suggesting AMPK involvement in the downstream longevity pathways of mitochondrial ETC inhibition [17, 18]. Mitochondrial ETC mutants were found to exhibit elevated mitochondrial ROS levels, which may increase the phosphorylation of AMPK [17, 19, 20]. Inhibition of ETC components was also reported to affect ATP synthesis, and potentially influencing AMPK activity indirectly by reducing cellular energy status [18, 21].

In this chapter, we investigate the roles of the AMPK downstream components CRTC-1 and NHR-49 in the mechanism through which α-KB upregulates longevity. Additionally, this study explores whether α-KB affects the lifespan of mitochondrial ETC mutants. We also examine if the mitochondrial fusion is critical for α-KB to regulate lifespan, with worms carrying mutated FZO-1, a protein that plays a crucial role in mitochondrial fusion [22].

Materials and Methods

Nematode strains. The following strains were used (strain, genotype): Bristol N2, wild type; AM44, *rmIs190 [F25B3.3p::Q67::CFP]*; MQ887, *isp-1(qm150) IV*; MQ1333, *nuo-6(qm200) I*; RB1716, *nhr-49(ok2165) I*; AGD466, *uthEx222 [crtc-1p::crtc-1 cDNA (S76A, S179A)::tdTomato::unc-54 3'UTR + rol-6(su1006)]*; CU5991, *fzo-1(tm1133) II*. All strains were obtained from the Caenorhabditis Genetics Center (CGC).

Lifespan analysis. *C. elegans* lifespan assays were conducted as described [23] at 20-25 ^{o}C on solid nematode growth media (NGM) using standard protocols and were replicated in at least two independent experiments. All lifespan data are available in Supplementary Table 1. The sample size was chosen on the basis of standards done in the field in published manuscripts. No statistical method was used to predetermine the sample size. Animals were assigned randomly to the experimental groups. Worms that ruptured, bagged (that is, exhibited internal progeny hatching), or crawled off the plates

were censored. Lifespan data were analyzed using GraphPad Prism; *P* values were calculated using the log-rank (Mantel–Cox) test.

Killed-OP50 Treatment. 10 cm NGM plates were seeded with OP50 and allowed to dry over for 2 days. To kill the bacteria with Ultraviolet (UV) light, the OP50 bacteria lawn were exposed to UV light from Ultraviolet Transilluminator (Fisher Scientific, FB-TIV-614A, 312nm UV) with intensity of 8000μw/cm^2 for 15 minutes. Colonies of UV-Killed OP50 were incubated in LB liquid culture overnight and no bacteria growth was observed. To kill the bacteria with antibiotics, 120 μl of 10 mg/ml ampicillin solution or carbenicillin solution was added onto the top of the bacteria lawns. The drugs were then added onto the plates at least one day later.

***C. elegans* healthspan assessment.** Worms were treated with vehicle or α-KB starting from adult day 1. On adult day 4 and adult day 10, treated worms were monitored for their locomotion levels, evaluated by the number of body bends in M9 buffer. During the locomotion test, worms were picked up with a platinum wire from the vehicle or α-KB agar plates and placed in 20 μl of M9 buffer. The subjects were allowed to stay in M9 buffer for 30 seconds, and then the body bends were counted during the next 30 seconds, following the protocol from previous studies with adaptions [24, 25]. Sony Handycam Video camera recorder (Sony HDR-PJ430V) was also used to film the swimming activity. Only living worms were evaluated with activity levels; worms that were found dead upon inspection were excluded (rather than assigned a body bend number of 0). Activity levels data was analyzed using GraphPad Prism.

Results

We have reported the longevity effects in the published article [1], and besides the extended lifespan, we also observed that the α-KB treated worms had greater healthspan during aging, including better motility. To objectively examine the observation, we recorded the activity level of worms during swimming in M9 buffer (Fig. 1a-b). α-KB did not affect the number of body bends during swimming of young worms (Fig. 1a), but α-KB-treated aged worms maintained greater mobility compared to vehicle-treated worms (Fig.1b).

To test if bacterial metabolism is required for α-KB to prolong lifespan, we used ultraviolet (UV) radiation and antibiotics (ampicillin and carbenicillin) to kill the bacteria on agar plates before α-KB was applied on top of the killed bacteria. We found that α-KB can still significantly extend the lifespan without bacterial metabolism (Fig. 2a). We did observe the magnitude of the lifespan extension was usually smaller compared to alive bacteria. This result suggests that α-KB itself does not need to be converted to another compound by bacterial metabolism to prolong lifespan, however some of the α-KB-induced longevity effects we observed from the previous lifespan analysis with alive OP50 might be enhanced by α-KB-converted compounds.

Different longevity pathways were reported to function through different stages of age to influence lifespan. Young adult stage was reported to be essential for DAF-2 to affect longevity [26]. Development-only DAF-2 knockdown does not affect lifespan [26], and

the longevity effects are largely decreased if the DAF-2 knockdown only occurs after young adult stage [26]. Another major longevity pathway, dietary restriction, was reported to be effective across different stages of lifespan [27]. Here we examine the longevity effects of α-KB treatment starting from hatching and late-life. α-KB from development did not have greater lifespan compared to α-KB from adulthood (Fig. 2b). α-KB from late-life can still extend the lifespan, if the treatment was not starting within 5 days from the mean lifespan or with higher concentration (Fig. 2c). However, the lifespan extension is significantly smaller compared to the worms treated from adult day1, suggesting that it may be beneficial to start the treatment as early as possible after reaching adulthood.

Inhibition of mitochondrial respiration chain increases lifespan in different species [28]. In the long-lived mitochondrial mutants, the AMP:ATP ratio is higher than wildtype worms, and this phenomenon may further trigger the activation of AMPK [18]. In another proposed mechanism, phosphorylation of AMPK is induced by elevated mitochondrial ROS (mtROS) from inhibition of respiratory chain [17, 19]. Our results from lifespan analysis showed that α-KB could not extend the lifespan of long-lived *isp-1* and *nuo-6* mitochondrial mutants (Fig. 3a-b). These findings suggest that α-KB and ETC mutations share similar downstream pathways to regulate longevity, potentially through AMPK activation.

AMPK activation leads to nuclear exclusion of transcriptional regulator CRTC-1 (CREB-regulated transcriptional coactivator-1) by the phosphorylation of CRTC-1 [4]. When

CRTC-1 is “on” without the phosphorylation, it collaborates with CREB homologue-1 (CRH-1), the cAMP response element-binding protein CREB in *C. elegans* to regulate their common targets [4, 9]. Since CRTC-1 is out of the nucleus when AMPK is activated, it cannot interact with the CRH-1 transcription factor and coregulate the expression of the downstream genes [4]. Mutations of on CRTC-1 (S76A, S179A) rendered it constitutively nuclear and made it resistant to AMPK activation [4]. In this study, we applied α-KB treatment to CRTC-1 (S76A, S179A) mutants, and α-KB did not extend the lifespan (Fig 4a). This result further verifies that α-KB activates AMPK to promote longevity.

Previous studies showed that PPARα ortholog *nhr-49* responses to low energy status and is essential for AMPK-induced lifespan extension [4, 29]. NHR-49 acts antagonistically to CRTC-1/CREB for the expression of the shared target genes, and the *nhr-49*(nr2041) deletion allele inhibits the longevity effects of AMPK activation [4]. α-KB treatment on NHR-49 mutant worms caused no changes in the longevity (Fig. 4b). This finding indicates that similar to AMPK activation, α-KB treatment requires NHR-49 to increase longevity.

Aged worms have increased mitochondrial fragmentation compared to young worms, in addition to the loss of mitochondrial content during aging [10]. AMPK has been shown to keep youthful mitochondrial morphology in aged worms and regulate longevity via promoting mitochondrial network homeostasis [10]. In contrast, CRTC-1 mutations (S76A,S179A) and *nhr-49*(nr2041) deletion allele can both induce fragmentation of the

mitochondrial network in *C. elegans* [9]. FZO-1 is an ortholog of human MFN2 (mitofusin 2) in *C. elegans.* FZO-1 mediates outer mitochondrial membrane fusion, and the mutants therefore have highly fragmented mitochondrial networks even from adult day1 [10]. We has reported that α-KB treatment maintains the mitochondrial morphology and content in aged worms [1]. To examine if mitochondrial network homeostasis plays a crucial role in α-KB-induced longevity, worms carrying mutation *fzo-1*(tm1133) were treated with α-KB from adult day1 in this study. α-KB only slightly increased the lifespan of the *fzo-1* mutants, suggesting α-KB promotes longevity through preserving mitochondrial network homeostasis (Fig. 4c).

Discussion

We have shown that α-ketobutyrate regulates aging by activating AMPK in the previous chapter. In this chapter, we first show that α-KB promotes the locomotion of worms during aging, suggesting that in addition to lifespan, α-KB also extends the healthspan in *C. elegans*. In addition, we also found that bacterial metabolism is not required for α-KB to increase lifespan, while upregulation of other metabolites by α-KB may further enhance the longevity effects. This study investigates the timing requirements for α-KB to prolong lifespan, and while development stage is not crucial for α-KB-induced longevity, late-life only α-KB treatment can still extend lifespan in *C. elegans*, similar to the results previously observed in mice [1].

AMPK is an important downstream component in the longevity pathways of mitochondrial ETC inhibition [17, 18]. Here we show that α-KB cannot increase the lifespan of worms carrying *isp-1* and *nuo-6* mutations, implying that α-KB shares longevity pathways similar to inhibition of respiratory chain, and AMPK is the potential common target of them.

Nuclear exclusion of CRTC-1 is required for AMPK to promote longevity [4, 5]. In this study, we show that α-KB treatment fails to influence the longevity of worms overexpressing CRTC-1 with mutations to the conserved AMPK target sites. Since the mutated CRTC-1 does not react to AMPK phosphorylation from α-KB treatment, no lifespan extension was observed.

Last, we demonstrate that similar to AMPK, α-KB requires fusion to maintain mitochondrial network homeostasis and thereby prolong lifespan. These findings further validate the connection between α-KB and AMPK activation. This study expands the knowledge on the downstream pathways of α-KB, and its effects on healthspan. From the results, we provided more evidence indicating α-KB can be an ideal strategy to pharmacologically trigger AMPK activation in order to promote healthspan and lifespan.

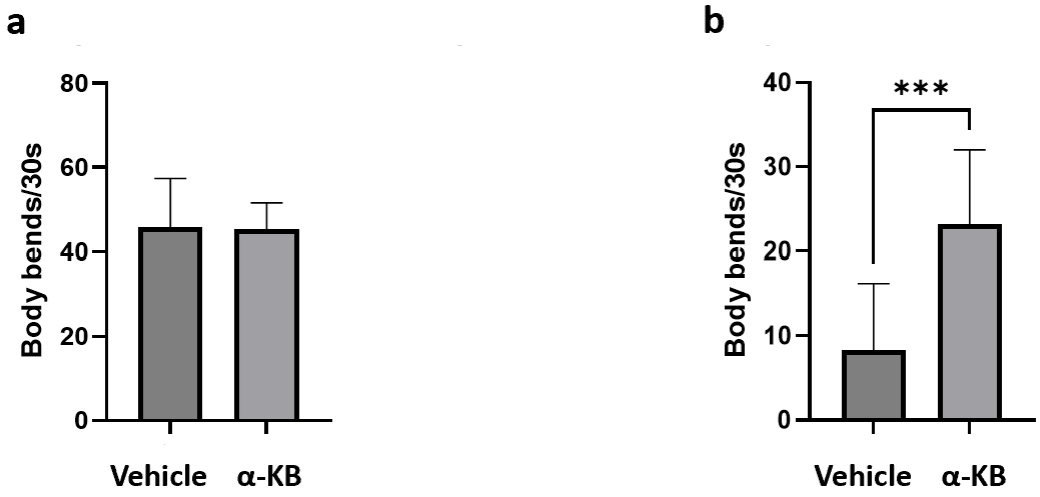
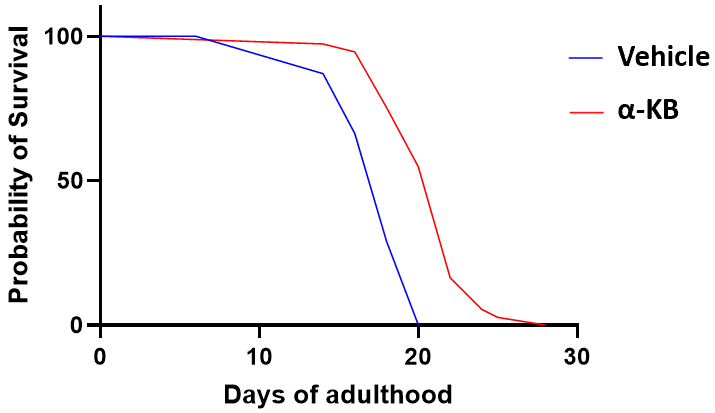
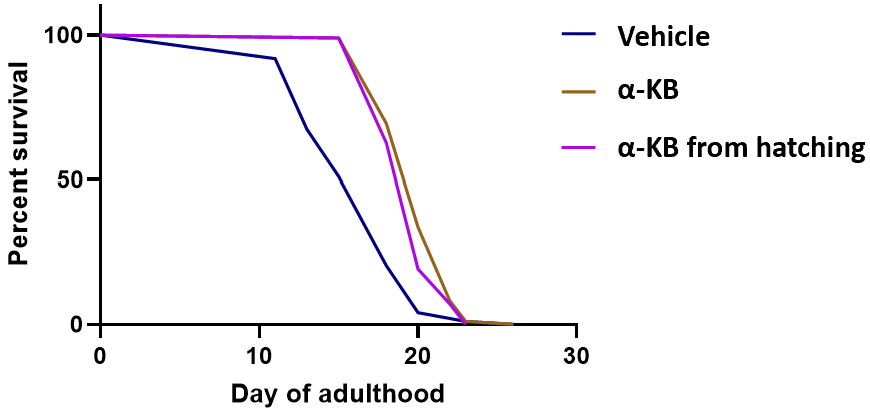


Fig. 1. α-KB increases the healthspan of *C. elegans*. a, α-KB did not change the motility of young adult worms, mean body bends per 30 seconds of adult day 4 worms with vehicle treatment (m_{veh}) = 45.75 (n = 8 animals tested), $m_{\alpha\text{-KB}}$ = 45.25 (n = 8), P < 0.9162. **b**, α-KB increased the healthspan of old adult worms, mean body bends per 30 seconds of adult day 10 worms with vehicle treatment (m_{veh}) = 8.3 (n = 10 animals tested), $m_{\alpha\text{-KB}}$ = 23.2 (n = 10), P < 0.0009.

a


Probability of Survival
100
50
0
0
10
20
30
Days of adulthood
Vehicle
α-KB

b


Percent survival
100
50
0
0
10
20
30
Day of adulthood
Vehicle
α-KB
α-KB from hatching

c

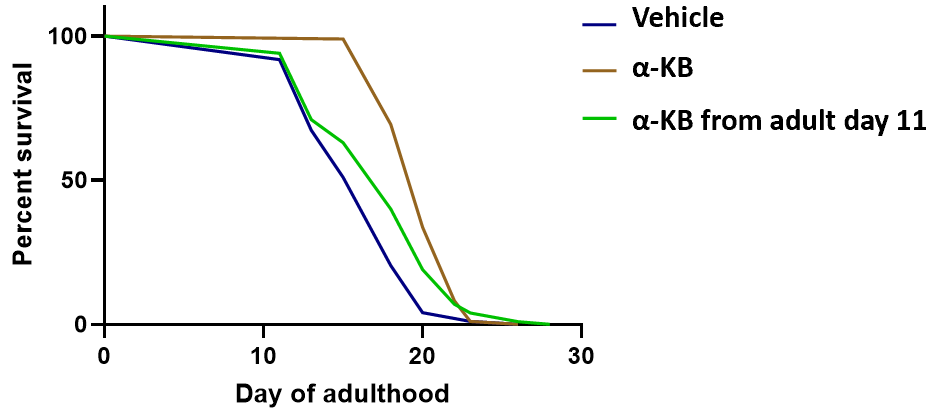

Percent survival
100
50
0
0
10
20
30
Day of adulthood
Vehicle
α-KB
α-KB from adult day 11

Fig. 2. α-KB treatment from different stages of age in *C. elegans*. a, α-KB does not require bacteria metabolism to extend lifespan, mean lifespan (days of adulthood) with vehicle treatment (m_{veh}) = 17.6 (n = 49 animals tested), $m_{\alpha\text{-KB}}$ = 20.9 (n = 73), P < 0.0001. **b**, α-KB treatment from hatching does not further extend the lifespan compared to adulthood only treatment, mean lifespan (days of adulthood) with vehicle treatment (m_{veh}) = 16.3 (n = 98 animals tested), $m_{\alpha\text{-KB adult only}}$ = 20.1 (n = 98), P < 0.0001. $m_{\alpha\text{-KB from hatching}}$ = 19.7 (n = 99), P = 0.0851 ($m_{\alpha\text{-KB adult only}}$ vs $m_{\alpha\text{-KB from hatching}}$) **c**, α-KB treatment on aged worms still extend the lifespan, mean lifespan (days of adulthood) with vehicle treatment (m_{veh}) = 16.3 (n = 98 animals tested), $m_{\alpha\text{-KB}}$ = 20.1 (n = 98), P < 0.0001. $m_{\alpha\text{-KB from old}}$ = 17.6 (n = 100), P = 0.0019 (m_{veh} vs $m_{\alpha\text{-KB from hatching}}$). P values were determined by the log-rank test.

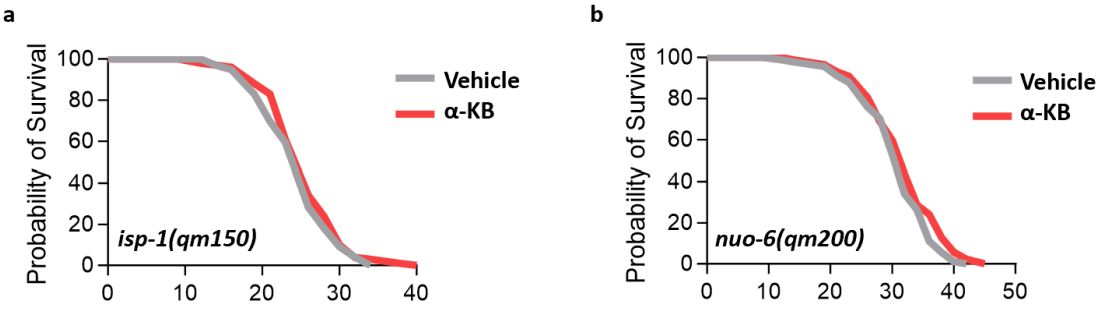


Fig. 3. α-KB fails to promote the lifespan of long-lived mitochondrial mutants in *C. elegans*. a, α-KB fails to extend the lifespan of *isp-1* mutants, mean lifespan (days of adulthood) with vehicle treatment (m_{veh}) = 24.8 (n = 99 animals tested), $m_{\alpha\text{-KB}}$ = 25.6 (n = 100), P = 0.2685. **b**, α-KB fails to extend the lifespan of *nuo-6* mutants, mean lifespan (days of adulthood) with vehicle treatment (m_{veh}) = 30.8 (n = 91 animals tested), $m_{\alpha\text{-KB}}$ = 32.0 (n = 87), P = 0.0730. Experiments done by Brett Lomenick and Randall M. Chin.

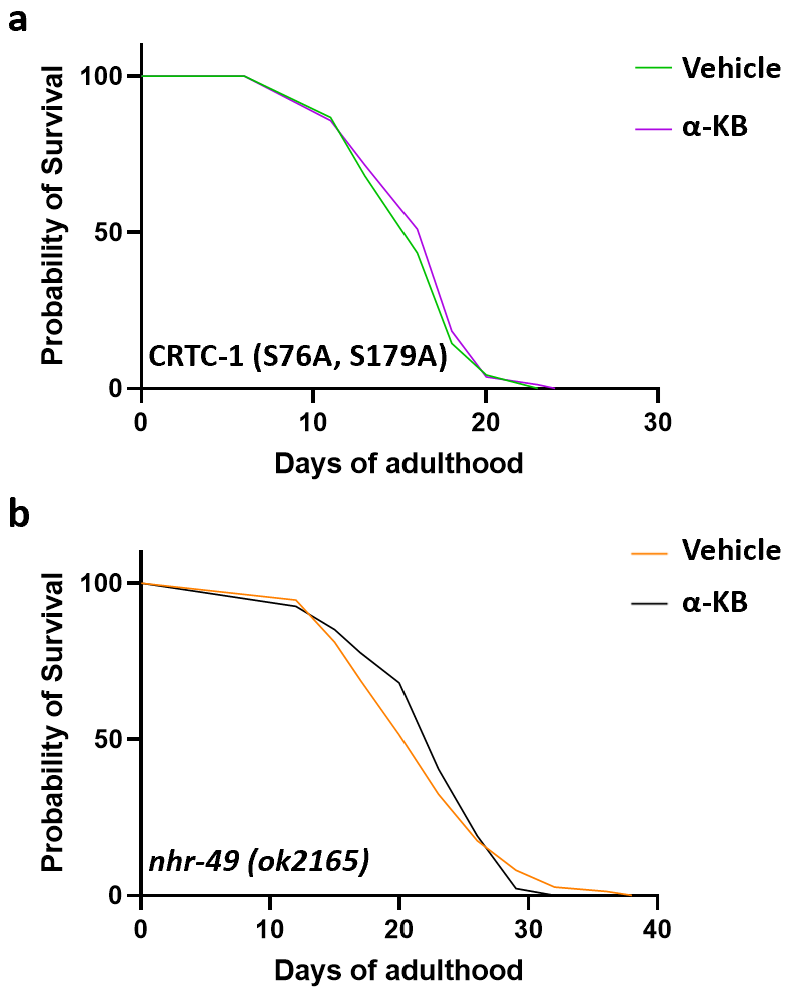


Fig. 4. α-KB fails to affect the lifespan of AMPK downstream mutants in *C. elegans*. a, α-KB fails to extend the lifespan of worms overexpressing CRTC-1 with mutations to the conserved AMPK target sites, mean lifespan (days of adulthood) with vehicle treatment (m_{veh}) = 15.8 (n = 73 animals tested), $m_{\alpha\text{-KB}}$ = 16.2 (n = 95), P = 0.4304. **b**, α-KB fails to extend the lifespan of *nhr-49* mutants, mean lifespan (days of adulthood) with vehicle treatment (m_{veh}) = 21.9 (n = 74 animals tested), $m_{\alpha\text{-KB}}$ = 22.6 (n = 93), P = 0.5883.

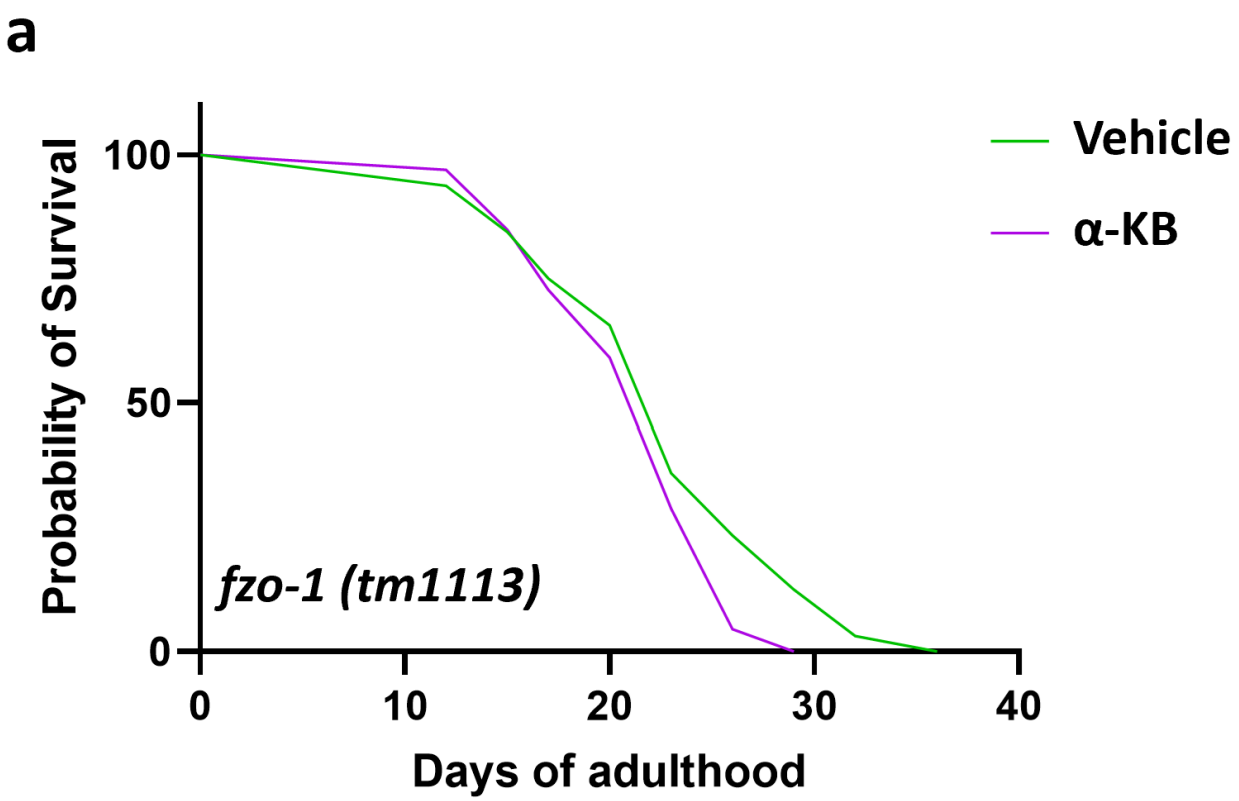


Fig. 5. Mitochondrial fusion is crucial for α-KB to extend lifespan in *C. elegans*.

a, *fzo-1* mutation significantly suppressed the lifespan extension from α-KB, mean lifespan (days of adulthood) with vehicle treatment (m_{veh}) = 23.0 (n = 64 animals tested), $m_{\alpha\text{-KB}}$ = 21.6 (n = 66), P = 0.0254.

Extended Data Table 1. Summary of lifespan data

Strain	*m* (mean lifespan, days)		% difference	*p*-value	*n* (number of animals)		
	vehicle	α-KB			vehicle	α-KB	
N2	18.2	20.9	14.8	0.0013	54	56	
isp-1(qm150)	24.8	25.6	3.3	0.2689	99	100	
nuo-6(qm200)	30.8	32.0	4.0	0.0729	91	87	
N2	15.4	17.7	15.3	< 0.0001	75	75	
AGD466	15.8	16.2	2.8	0.4304	73	95	
N2	13.4	19.1	42.5	< 0.0001	75	75	
AGD466	14.5	17.7	22.4	< 0.0001	74	72	
N2	15.8	21.7	37.0	< 0.0001	107	89	
RB1716	21.9	22.6	3.1	0.5883	74	93	
fzo-1(tm1113)	23.0	21.6	-6.3	0.0254	64	66	
N2	15.6	24.4	56.5	< 0.0001	91	96	
fzo-1(tm1113)	19.7	22.1	12.6	0.0046	80	86	

Strain	*m*		% difference	*p*-value	*n*		Note
	vehicle	α-KB			vehicle	α-KB	
N2	17.6	20.9	18.8	< 0.0001	49	73	UV Killed OP50
N2	18.4	21.3	15.6	< 0.0001	92	73	UV Killed OP51
N2	21.6	23.8	10.2	< 0.0001	104	111	CB-killed OP50
N2	22.4	24.7	10.3	< 0.0001	94	60	CB-killed OP50
N2	18.1	20.4	12.7	0.0012	77	48	AMP-killed OP50
N2	16.3	20.1	23.3	< 0.0001	98	98	From adult day1
N2	16.3	19.7	21.2	< 0.0001	98	99	From hatching
N2	16.3	17.6	8.2	0.0019	98	100	From adult day11
N2	13.9	20.9	50.4	< 0.0001	72	65	From adult day1
N2	13.9	14.6	5.0	0.4054	71	74	From adult day11
N2	15.8	20.3	29.0	< 0.0001	100	100	From adult day1
N2	15.8	15.8	0.3	0.6376	100	74	From adult day12
N2	15.8	16.7	5.7	0.414	100	70	From adult day12,16mMKB

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Chapter 4

Conclusions

This dissertation delves into the mechanisms by which the metabolite α-ketobutyrate (α-KB) promotes longevity in nematodes and mammals. Given the limited knowledge linking α-KB to longevity, we employed drug affinity responsive target stability (DARTS), a label-free and unbiased biochemical approach, to identify potential target proteins of α-KB [1]. In our experimental design, we treated mouse liver mitochondrial lysates with DMSO and α-KB, followed by pronase digestion and analysis using liquid chromatography-mass spectrometry (LC-MS). Proteins resistant to proteolysis in the presence of α-KB were identified as potential binding targets, since the interactions between α-KB and target proteins should stabilize the protein structures [1]. DARTS revealed that microtubule-actin cross-linking factor 1 (MACF1), a cytoskeletal linker protein belonging to the spectraplakin family [2], is a direct target of α-KB. However, the relationship between MACF1 and longevity regulation remained unclear at the time.

In *C. elegans*, the ortholog of mammalian MACF1 is VAB-10 [3]. Lifespan analyses underscored the critical role of VAB-10 in α-KB-induced longevity, as mutations in VAB-10 abolished the lifespan extension effect. To further elucidate the pathways through

which α-KB affects aging, we tested α-KB treatment on worms carrying mutations in major genes known for regulating longevity. Our findings revealed that AAK-2/AMPK is indispensable for α-KB-mediated lifespan extension. Given that plectin, another plakin family member, has been shown to regulate AMPK activity in myofibers [4], we investigated the interaction between VAB-10 and AMPK. Our results demonstrated that both VAB-10 RNA interference and α-KB treatment increased AMPK phosphorylation levels.

Previous studies have highlighted VAB-10's role in mitochondrial maintenance, and research on MACF1 and plectin-deficient mice has shown increased mitochondrial fusion and biogenesis [5-8]. Our investigations in aged worms confirmed that α-KB is able to preserve mitochondrial network homeostasis, with mitochondrial fusion being essential for α-KB to extend lifespan. Furthermore, our study revealed that α-KB acts through AMPK downstream effectors CRTC-1 and NHR-49 to regulate longevity [9], presenting a model wherein α-KB promotes longevity by modulating VAB-10/MACF1 to activate AMPK and the downstream longevity pathways.

Another research group reported that α-KB extends lifespan in *C. elegans* through peroxisomal pathways [10]. Their study indicated that *aak-2* was not required for α-KB-induced lifespan extension, and they observed no change in AMPK phosphorylation with α-KB treatment [10]. Furthermore, α-KB was shown to have no effect on mitochondrial content during aging in the same study [10]. The difference between these results and our findings is intriguing, but it can be explained by the nuance in

methodology. First, in our study, we found that the optimal concentration of α-KB is 4 mM for lifespan extension and this concentration was used in most of our experiments throughout the research, whereas the Nature Communications publication applied a concentration of 500 μM [10, 11]. The lower concentration may have masked the effects of α-KB on mitochondrial content and AMPK phosphorylation. Additionally, in the mitochondrial experiments, the authors used adult day 5 worms to represent the aged group [10]. However, at this stage, the reduction in mitochondrial content is not as pronounced as it is in day 11 adults. Last, the study used RNA interference (RNAi) to knockdown *aak-2* in order to verify the significance of AMPK in α-KB-induced longevity [10]. While feeding RNAi is a powerful tool in research using *C. elegans* as a model, it is important to note that neuronal cells are resistant to the genetic knockdown through this method due to the absence of dsRNA transport channel [12-16]. Previous studies have highlighted the crucial role of cell-nonautonomous regulation by neurons in the longevity mechanisms associated with AMPK activation [9, 17, 18]. In a recent study, it is reported that *aak-2* RNAi did not suppress lifespan extension resulting from glucose restriction (GR)-induced AMPK activation, whereas the longevity effects were completely abolished by the *aak-2(ok524)* mutation [18]. These data suggest that, unlike genetic mutations, feeding RNAi knockdown is insufficient to block AMPK activation in neurons and the subsequent non-cell autonomous regulation of longevity [18]. These results provide a plausible explanation for the observation that α-KB-induced lifespan extension remains unaffected in worms fed bacteria expressing *aak-2* RNAi. Given the connections between AMPK and peroxisomes [19], the reported upregulation of peroxisome functions may be a consequence of AMPK activation induced by α-KB.

We demonstrate in this dissertation that α-KB's longevity effects are conserved across species. Treatment with α-KB late in life extended the lifespan of aged male mice and preserved the health conditions of both male and female aged mice. Intriguingly, late-life α-KB treatment did not extend the lifespan of female mice. The lifespan curves of the control and α-KB-treated groups intersect, with α-KB-treated female mice showing a higher death rate initially but achieving a longer maximum lifespan. Results from the Log-rank (Mantel-Cox) test indicate that there are no significant effects of α-KB on the lifespan curves of treated female mice, regardless of whether the analysis starts from birth or from the inception of the treatment. However, the Gehan-Breslow-Wilcoxon test, which gives more weight to early onset deaths [20], suggests a p-value of 0.0462 when comparing survival curves from the inception of the treatment. This implies a potential effect of α-KB on early onset deaths in female mice. Further experiments are required to clarify whether α-KB increases early onset deaths and to assess its impact on maximum lifespan of female mice, particularly given the small sample size and the insignificant *P* value from the Kolmogorov-Smirnov test comparing death distributions between the control and treated groups (P = 0.0707). Metformin, a diabetic drug known to activate AMPK and promote longevity across various species [21-25], has been shown to regulate development and metabolism in a sex-specific manner in rodent pups [26]. While additional studies are needed to confirm its effects on lifespan extension in rodents, one study reported a 5.83% increase in lifespan in male mice when metformin treatment was initiated in midlife at 12 months of age [27, 28]. As for female mice, another study showed that the 14% mean lifespan extension were only observed with early treatment initiation at 3 months old [29]. The longevity effects from metformin

drastically declined if the treatment on female mice started later, with mean lifespan extension of 6% at 9 months and no effects at 15 months [29]. Interestingly, another study even found that supplementation of metformin decreased the median lifespan of aged female mice treated from 20 months old [30]. These findings suggested an age-dependent response of metformin, at least in female mice. Given that both metformin and α-KB activate AMPK, further investigations are needed to explore α-KB's effects on female lifespan with earlier treatment initiation.

The findings from this dissertation hold promise for developing therapeutic strategies using endogenous metabolites to combat aging and age-related diseases. α-KB not only extends the mean lifespan, but also increases the maximum lifespan. In most of our lifespan experiments in *C. elegans*, α-KB did not alter the slope shape of the lifespan curves where death events began to occur. This suggests that all populations, including both originally short- and long-lived ones, responded to α-KB treatment and received longevity benefits to a similar extent. In some lifespan results, α-KB did increase the death rate towards the end of the lifespan curves, suggesting that, in these instances, the lifespan extensions were primarily due to the prevention of early onset deaths. It would be valuable to investigate whether α-KB, in addition to its general longevity effects, can reduce specific causes of early onset death, such as pharyngeal pathogenic infections [31]. Future research directions for this study include exploring the timing of treatment initiation, examining sex-specific responses, evaluating the influence on stress resistance, and investigating potential synergistic effects of drug combinations to further promote longevity.

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