Tauopathy in the $APP_{swe}/PSI_{A\varepsilon9}$ mouse model of familial Alzheimer’s disease

Athanasios Metaxas$^{1*}$, Camilla Thygesen$^{1,2†}$, Stefan J. Kempf$^{2}$, Marco Anzalone$^{1}$, Ramanan Vaitheeswaran$^{1}$, Sussanne Petersen$^{1}$, Anne M. Landau$^{3,4}$, Hélène Audrain$^{3}$, Jessica L. Teeling$^{5}$, Sultan Darvesh$^{6,7}$, David J. Brooks$^{3,8}$, Martin R. Larsen$^{2}$, Bente Finsen$^{1}$

Affiliations:

$^1$Institute of Molecular Medicine, University of Southern Denmark, Odense C, Denmark.

$^2$Department of Biochemistry and Molecular Biology, University of Southern Denmark, Odense M, Denmark.

$^3$Department of Nuclear Medicine and PET Centre, Aarhus University and Hospital, Denmark.

$^4$Translational Neuropsychiatry Unit, Aarhus University and Hospital, Denmark.

$^5$Biological Sciences, University of Southampton, United Kingdom.

$^6$Department of Medical Neuroscience, Dalhousie University, Halifax, NS, Canada.

$^7$Department of Medicine (Neurology and Geriatric Medicine), Dalhousie University, Halifax, NS, Canada.

$^8$Division of Neuroscience, Department of Medicine, Newcastle University, United Kingdom.

†Shared first authorship

*To whom correspondence should be addressed:
ametaxas@health.sdu.dk; a.metaxas@hotmail.com

One Sentence Summary: Neurofibrillary tangles in amyloidosis mice
Abstract

Despite compelling evidence that the accumulation of amyloid-beta (Aβ) promotes cortical MAPT (tau) aggregation in familial and idiopathic Alzheimer’s disease (AD), murine models of cerebral amyloidosis are not considered to develop tau-associated pathology. The absence of neurofibrillary lesions in amyloidosis mice remains a challenge for the amyloidocentric paradigm of AD pathogenesis. It has resulted in the generation of transgenic mice harboring mutations in their tau gene, which may be inappropriate for studying a disease with no known TAU mutations, such as AD. Here, we have used APPswe/PS1ΔE9 mice to show that tau pathology can develop spontaneously in murine models of familial AD. Tauopathy was abundant around Aβ deposits, with Gallyas- and thioflavin-S-positive perinuclear inclusions accumulating in the APPswe/PS1ΔE9 cortex by 18 months of age. Age-dependent increases in Gallyas signal correlated positively with binding levels of the paired helical filament (PHF) ligand [18F]Flortaucipir, in all brain areas examined. Sarkosyl-insoluble PHFs were visualized by electron microscopy. Tandem mass tag proteomics identified sequences of hyperphosphorylated tau in transgenic mice, along with signs of RNA missplicing, ribosomal dysregulation and disturbed energy metabolism. Human frontal gyrus tissue was used to validate these findings, revealing primarily quantitative differences between the tauopathy observed in AD patient vs. transgenic mouse tissue. Levels of tau mRNA were not different between APPswe/PS1ΔE9 and littermate control animals. As physiological levels of endogenous, ‘wild-type’ tau aggregate secondarily to Aβ in transgenic mice, this study demonstrates that amyloidosis is both necessary and sufficient to drive tauopathy in experimental models of familial AD.
Introduction

Genetically-inherited and sporadic forms of Alzheimer’s disease (AD) are characterized by a common set of hallmark brain lesions, which include the accumulation of amyloid-β (Aβ) peptides into plaques, neuroinflammation, aggregation of hyperphosphorylated MAPT (tau) into neurofibrillary tangles (NFTs), and neurodegeneration. Transgenic mouse models that reproduce aspects of the aforementioned lesions have been generated based on mutations in the amyloid precursor protein (APP) and presenilin 1 (PSEN1) and 2 (PSEN2) genes, which are known to cause familial AD (1). Despite playing important roles in evaluating APP processing, Aβ toxicity, and amyloid-targeting therapeutic strategies, transgenic mice are not being regarded as models that can replicate the full spectrum of AD histopathology (2). In particular, while the overexpression of mutant APP and APP/PSEN1 has been shown to yield amyloidosis (3), neuroinflammation (4) and neurodegeneration (5) in mice, it is generally not considered to promote the conversion of endogenous tau into neurofibrillary structures (6).

To address the in vivo role of tau hyperphosphorylation and NFT formation in AD pathogenesis, human MAPT (TAU) has been introduced into the mouse genome, either mutated or non-mutated, on a Tau-knockout background (7, 8). TAU overexpressing mice demonstrate progressive neurofibrillary pathology, albeit in the marked absence of cerebral amyloidosis, which is required for a neuropathological diagnosis of AD. Moreover, mutations in TAU have been linked to non-AD tauopathies, most commonly frontotemporal lobar degeneration [FTLD; (9)], a condition with neuropathological hallmarks distinct from AD. Thus, murine models of amyloidosis and combined amyloidosis-tauopathy models have been widely criticized for their translational relevance to the human condition. It has been argued that virtually all existing
murine models would be considered as ‘not’ AD (10) according to the ABC scoring system of neuropathology (11). The inability of amyloidosis mice to develop neurofibrillary lesions is thought to contribute to the poor translation of preclinical research into clinical benefits (12), and has raised concern about the amyloidocentric model of AD pathogenesis (13).

Two principal explanations have been put forward for the lack of tau-associated pathology in amyloidosis mice (14). First, adult mice express fewer isoforms of the tau protein than humans (three vs. six), which might render them less liable to the post-translational modifications (PTMs) that are associated with the accumulation of tau into NFTs, such as phosphorylation (15). However, murine tau has been shown to readily fibrillize in vitro upon treatment with polyanionic factors, including RNA (16), and there is ample evidence of tau hyperphosphorylation in the transgenic mouse brain [(17), Table S1], indicating that no differences exist in the propensity of murine and human tau for aggregation and PTMs. A second reason that is often cited for the absence of tauopathy in amyloidosis models is that the murine lifespan may be too short for the complete sequence of neurofibrillary pathology to unfold in transgenic mice. Although age scaling studies suggest otherwise (18), the aging factor has been neglected in the design of preclinical studies.

Transgenic Fischer rats (TgF344-AD), expressing human APP harboring the Swedish double mutations (KM670/671NL) and PSEN1 lacking exon 9 (APP<sub>swe</sub>/PS1<sub>ΔE9</sub>), both under control of the mouse prion protein promoter, develop progressive neurofibrillary pathology (19). In this study, transgenic APP<sub>swe</sub>/PS1<sub>ΔE9</sub> mice that were constructed in an identical manner as TgF344-AD rats were used to demonstrate neurofibrillary pathology in aging amyloidosis mice.
Results

Neurofibrillary pathology in aging APPswe/PS1ΔE9 mice

Fresh-frozen brain sections from 3-, 6-, 12-, 18- and 24-month-old APPswe/PS1ΔE9 transgenic (TG) mice and their wild-type (WT) counterparts were processed for the detection of neurofibrillary alterations with the Gallyas silver stain (n=6/group). Thioflavin-S and DAPI (4’,6-diamidino-2-phenylindole) were used to detect perinuclear β-pleated structures. Co-staining for amyloid and Gallyas was used to probe the relationship between amyloidosis and tau-associated pathology in aging TG animals. Fresh-frozen sections of the middle frontal gyrus from a patient with definite AD were processed in parallel with sections from APPswe/PS1ΔE9 mice, to compare Gallyas-positive structures in mouse vs. human tissue.

Aβ deposition was the predominant lesion in the 6-month-old APPswe/PS1ΔE9 brain (Fig. 1A&B), with age-dependent increases in argyrophilic density observed exclusively in TG mice (Fig. 1C-F). Only mild and diffuse silver staining was observed in the neocortex of 6-month-old animals (Fig. 1G). Densely-labeled, round structures, surrounded by a halo of argyrophilic staining, constituted the majority of Gallyas-positive signal in the neuropil of the neocortex and hippocampus at 12-24 months of age (Fig. 1H&I). In addition, diffuse and compact argyrophilic staining was observed surrounding red-stained nuclei in the neocortex of 18- and 24-month-old APPswe/PS1ΔE9 mice (Fig. 1J&K). The perinuclear structures were positive for thioflavin-S (Fig. 1L-N), which colocalized with nuclear DAPI (Fig. 1O) and was further detected in cell-sized structures lacking a stainable nucleus (Fig. 1P). There were no apparent differences in morphology between the argyrophilic structures in brain tissue from 24-month-old TG mice (Fig 1Q-U) and AD-confirmed patient material (Fig. 1V-Z), although neuropil threads were detected
exclusively in AD tissue (Fig. 1Q-Z). Coronal brain sections of 20-month-old Tg2576 mice, harboring the Swedish double mutations, were used to examine 6E10- and Gallyas-positive pathology in a second mouse model of amyloidosis (Fig. 1AA-AD). Amorphous argyrophilic signal (AC) and perinuclear lesions (AD) were also present in the Tg2576 mouse brain, albeit at lower levels compared to 18-month-old $\textit{APP}_{\text{swe}}/\textit{PSI}_{\Delta E9}$ mice.

The fraction of brain tissue occupied by Gallyas-positive staining in aging $\textit{APP}_{\text{swe}}/\textit{PSI}_{\Delta E9}$ mice is shown in Fig. S1A. Conformationally-altered tau was detected with the MC-1 monoclonal antibody (Fig. S1B). Vascular and meningeal lesions were present in 18- and 24-month-old animals (Fig. S1C).
Fig. 1. Neurofibrillary alterations in amyloidosis mice. (A&B) Sagittal brain sections of 6-month-old $APP_{swe}/PSI_{AE9}$ mice, processed for 6E10 immunohistochemistry (A) and the Gallyas silver stain (B). Silver-labeled sections were counterstained with nuclear fast red. β-amyloidosis dominates over argyrophilic pathology in 6-month-old $APP_{swe}/PSI_{AE9}$ mice. (C-F) Progressive increase in Gallyas-positive signal in 12- (C), 18- (D), and 24-month-old transgenic mice (E). Wild-type animals showed no silver deposition up to 24 months of age (F). (G-P) All photomicrographs are from the neocortex of $APP_{swe}/PSI_{AE9}$ mice. Argyrophilic signal was scarce in 6-month-old TG animals (G). Gallyas-positive structures in 18- (H) and 24-month-old animals (I), likely of neuritic nature. Gallyas silver (J & K) and thioflavin-S stainings (L-P), showing perinuclear and intranuclear signal in 18- and 24-month-old transgenic mice. The insert in J shows compact Gallyas staining in the absence of nuclear fast red. Note potential fragmented nuclei in (M) and (N), intranuclear signal in (O), and absence of DAPI signal in (P). (Q-Z) Gallyas/6E10 doubly-labeled sections from a 24-month-old transgenic mouse (Q-U) and an AD patient (V-Z),
showing dense-core plaques (Q & V), teardrop-shaped structures (R & W, arrows), tuft-shaped filaments (S & X, arrows), and globose structures in close proximity (T & Y) and over 200 µm afar from Aβ deposits (U & Z). (AA-AD) 6E10/Gallyas- (AA) and Gallyas-labeled (AB-AD) sections of 20-month-old Tg2576 mice. Scale bar is 2 mm for A&B, 1 mm for C-F, 10 µm for G-I, 5 µm for J-K, L-P, 10 µm for Q & V, 20 µm for R-U & W-Z, 200 µm for AA&AB, 20 µm for AC, and 5 µm for AD.

[^F]Flortaucipir autoradiography

The paired helical filament (PHF) ligand [[^F]Flortaucipir ([[^F]AV-1451, [[^F]T807] was used to quantify tau pathology in aging APP_{swe}/PSI_{ΔE9} TG mice by autoradiography (Table 1). Increased binding was observed in the neocortex, hippocampus, amygdala and the cerebellum of 12-month-old APP_{swe}/PSI_{ΔE9} mice, compared to age-matched WT, 3- and 6-month-old TG animals (P<0.001 for all regions; Bonferroni post-hoc tests). [[^F]Flortaucipir binding was further elevated in the visual (P<0.001), somatosensory (P<0.001), motor cortex (P<0.001), and the amygdala (P<0.05) of 18- vs. 12-month-old APP_{swe}/PSI_{ΔE9} TG mice. Increased binding over age-matched WT mice was first observed in the thalamus of TG animals at 18 months of age (P<0.001). In 24-month-old APP_{swe}/PSI_{ΔE9} mice, [[^F]Flortaucipir signal had increased in all brain regions examined compared to age-matched controls. Three-way ANOVA confirmed genotype- [F(1,476)=2603.1, P<0.001], age- [F(4,476)=457.3, P<0.001] and brain region-specific increases in the binding levels of [[^F]Flortaucipir [F(9,476)=42.9, P<0.001], as well as significant age x genotype x region interaction effects [F(36,476)=5.5, P<0.001].

Within each brain area analyzed, there was a positive correlation between the age-dependent increase in the binding levels of [[^F]Flortaucipir and the progressive increases in the density of Gallyas-positive lesions (Pearson r for all brain regions: 0.92, P<0.001; Fig. S2).
Table 1. Autoradiography of [18F]Flortaucipir binding sites in aging APP<sup>swe</sup>/PS1<sup>ΔE9</sup> mice. Fresh-frozen brain sections from APP<sup>swe</sup>/PS1<sup>ΔE9</sup> and age-matched wild-type (WT) animals were incubated with 38.4±9.6 MBq [18F]Flortaucipir for a period of 60 min (specific activity: 145±68 GBq/µmol). Autoradiography data are presented as the mean specific binding of [18F]Flortaucipir (kBq/mL) ± standard error of the mean in brain regions of 5-6 animals/group. By 24 months of age, [18F]Flortaucipir binding in APP<sup>swe</sup>/PS1<sup>ΔE9</sup> mice had increased across all brain areas examined vs. age-matched WT animals. The age-dependent increase in [18F]Flortaucipir binding levels was positively correlated with the progressive increase in Gallyas-positive argyrophilic signal, in all TG brain areas examined.

**P<0.01, ***P<0.001 vs. age-matched littermate control mice, Bonferroni post-hoc tests. Symbols of significant differences between groups of 24 & 18 vs. 3-, 6- and 12-month-old-mice were omitted from the table for clarity of presentation.

| Brain region | 3 months | 6 months | 12 months | 18 months | 24 months | Correlation with Gallyas-positive fraction (Pearson r (Significance)) |
|--------------|----------|----------|-----------|-----------|-----------|---------------------------------------------------------------|
|              | WT APP/PS1 | WT APP/PS1 | WT APP/PS1 | WT APP/PS1 | WT APP/PS1 |                                                          |
| Frontal      | 2.2 ± 0.7 3.6 ± 1.3 | 2.3 ± 0.9 10.0 ± 1.6 | 4.0 ± 1.0 46.7 ± 2.7*** | 4.7 ± 1.1 53.2 ± 3.0 | 4.2 ± 1.0 55.2 ± 5.7 | 0.74 (P<0.001) |
| Motor        | 2.5 ± 0.5 2.8 ± 0.8 | 2.5 ± 0.7 7.3 ± 1.3 | 3.2 ± 0.7 31.0 ± 1.3*** | 3.2 ± 0.8 45.1 ± 2.0 | 4.3 ± 1.1 55.7 ± 2.9 | 0.90 (P<0.001) |
| Somatosensory| 5.2 ± 1.3 5.0 ± 2.0 | 4.0 ± 0.9 11.6 ± 1.9 | 6.7 ± 4.5 34.9 ± 2.6*** | 6.5 ± 1.8 50.3 ± 1.5 | 5.8 ± 1.6 57.8 ± 2.7 | 0.93 (P<0.001) |
| Visual       | 6.8 ± 2.4 4.7 ± 1.4 | 2.4 ± 1.1 11.8 ± 2.5 | 8.2 ± 1.8 35.5 ± 3.2*** | 6.3 ± 1.9 52.9 ± 2.8 | 5.0 ± 1.3 56.4 ± 2.9 | 0.92 (P<0.001) |
| Entorhinal   | 3.2 ± 1.0 2.9 ± 1.0 | 3.3 ± 0.8 8.8 ± 1.1 | 6.7 ± 1.5 29.8 ± 1.9*** | 4.1 ± 2.6 40.6 ± 3.8 | 6.3 ± 1.7 42.8 ± 4.0 | 0.84 (P<0.001) |
| Subcortical  |          |          |           |           |           |                                                          |
| Hippocampus  | 3.1 ± 1.3 2.8 ± 0.8 | 3.0 ± 0.7 7.5 ± 1.3 | 4.3 ± 1.3 31.3 ± 2.4*** | 4.3 ± 1.2 40.9 ± 2.5 | 5.6 ± 1.5 49.1 ± 3.1 | 0.86 (P<0.001) |
| Striatum     | 2.6 ± 1.4 3.1 ± 1.0 | 3.1 ± 0.7 4.8 ± 0.9 | 4.4 ± 1.1 10.9 ± 2.4 | 5.1 ± 1.5 17.2 ± 1.2 | 5.4 ± 1.5 19.7 ± 2.8** | 0.64 (P<0.001) |
| Amygdala     | 1.8 ± 1.5 2.9 ± 0.9 | 3.1 ± 0.7 7.4 ± 1.0 | 4.2 ± 1.1 27.8 ± 2.9*** | 5.2 ± 1.5 40.0 ± 2.5 | 5.2 ± 1.1 47.7 ± 4.8 | 0.79 (P<0.001) |
| Thalamus     | 2.6 ± 0.6 2.2 ± 0.6 | 3.3 ± 1.0 3.5 ± 0.5 | 3.6 ± 0.9 11.2 ± 3.2 | 3.9 ± 1.3 17.5 ± 2.0*** | 4.1 ± 1.0 27.2 ± 4.5 | 0.87 (P<0.001) |
| Cerebellum   | 4.2 ± 0.8 3.1 ± 1.1 | 4.1 ± 1.2 10.3 ± 1.1 | 3.3 ± 1.0 23.0 ± 3.1*** | 4.5 ± 1.5 31.2 ± 3.6 | 5.8 ± 1.6 32.4 ± 3.7 | 0.83 (P<0.001) |
| Mean binding levels (all brain regions) | 3.4 ± 1.1 3.3 ± 1.1 | 3.1 ± 0.9 8.3 ± 1.3 | 4.9 ± 1.5 28.2 ± 2.6 | 4.8 ± 1.5 38.9 ± 2.5 | 5.2 ± 1.3 44.4 ± 3.7 | 0.92 (P<0.001) |
Representative autoradiograms of $[^{18}F]$Flortaucipir binding sites are shown in Fig. 2. Binding was decreased in the presence of 50 µM unlabeled flortaucipir but was not reversed by 1 µM of the amyloid-preferring Pittsburgh compound B (PIB).

**Fig. 2.** Representative autoradiograms of $[^{18}F]$Flortaucipir binding sites. (A) Sagittal brain sections of aging transgenic (top panel) and wild-type mice (WT, lower panel), taken at the level of the entorhinal cortex [lateral 2.88±0.12 mm of the Paxinos and Franklin mouse atlas (74)]. Images were analyzed on a black & white display mode, and presented as a pseudocolor interpretation of black & white pixel intensity, calibrated in kBq/mL of $[^{18}F]$Flortaucipir solution. Age-dependent increases in binding levels were observed exclusively in $APP_{swe}/PS1\Delta E9$ mice. (B) $[^{18}F]$Flortaucipir binding in sections from the middle frontal gyrus of AD-confirmed patients, 18-month-old $APP_{swe}/PS1\Delta E9$ mice and 20-month-old Tg2576 animals, showing the magnitude of tau pathology in patient vs. transgenic mouse tissue. Non-specific binding (NSB) was assessed in the presence of 50 µM ‘cold’ flortaucipir. (C) Binding was not blocked by co-incubating sections with $[^{18}F]$Flortaucipir and 1 µM of the amyloid-targeting agent Pittsburgh Compound B (PIB).
**Mapt expression**

Relative expression of total *Mapt* mRNA was determined by RT-qPCR (Fig. 3). There were no age \([F(4,50)=0.29, \ P>0.05]\), genotype \([F(1,50)=0.93, \ P>0.05]\), or age x genotype interaction effects on the expression levels of *Mapt* \([F(4,50)=1.21, \ P>0.05]\).

![Graph showing expression levels of Mapt mRNA](image)

**Fig. 3. Regulation of Mapt mRNA in aging mice.** Levels of endogenous murine tau mRNA were not altered by age or genotype. PCR products of x4 diluted tau cDNA were determined after 24 cycles. A single peak was obtained by melt-curve analysis, and no signal was detected in the genomic DNA and buffer controls. The efficiency of amplification was 99.2±0.2% for *Hprt1* and 100.3±2.1% for *Mapt*.

**Isolation and Transmission Electron Microscopy (TEM) of sarkosyl-insoluble tau**

The general methods of Sahara et al. (20) and Greenberg and Davies (21) were evaluated for the extraction of PHFs from the 24-month-old *APP_{swd/PS1ΔE9} TG* brain (Fig. S3). Although longer filaments were isolated by the procedure of Sahara et al., the Greenberg and Davies method was chosen for the isolation of sarkosyl-insoluble tau from 3- and 24-month-old mice, based on immunoblotting experiments, solubility considerations, and to allow for comparisons with literature data (22). Soluble and insoluble tau levels were measured in mouse brain homogenates.
by using the mouse Total Tau Meso Scale kit (Meso Scale Diagnostics LLC). TEM was used to visualize filaments in the sarkosyl-insoluble extracts from the TG mouse and AD patient brains by negative staining.

Tau protein levels increased with age in the pellet obtained by centrifuging WT and APP<sub>swe</sub>/PSI<sub>ΔE9</sub> homogenates at 27,000 x g [Fig. 4A; age effect: F<sub>(1,18)=50.0, P<0.001</sub>; genotype effect: F<sub>(1,18)=2.4, P>0.05</sub>]. Levels of tau in the supernatant fraction were not different between 3- and 24-month old, WT and APP<sub>swe</sub>/PSI<sub>ΔE9</sub> TG animals [age: F<sub>(1,16)=0.6, P>0.05</sub>; genotype: F<sub>(1,16)=0.0, P>0.05</sub>]. Treatment of the supernatant with 1% sarkosyl for 2 h at 37°C increased the concentration of tau in the detergent-soluble fraction by >3-fold. Sarkosyl-soluble tau levels were lower in the 24- vs. 3-month-old mouse brain [F<sub>(1,16)=12.5, P<0.01</sub>], irrespective of genotype [F<sub>(1,16)=0.5, P>0.05</sub>]. Sarkosyl-insoluble tau was not detected in 3-month-old animals, and its levels were not different between 24-month-old APP<sub>swe</sub>/PSI<sub>ΔE9</sub> and WT mice [t<sub>(8)=0.7, P>0.05</sub>; independent two-tailed Student’s t-test].

Fig. 4B shows negatively-stained filaments in the sarkosyl-insoluble extract from the 24-month-old APP<sub>swe</sub>/PSI<sub>ΔE9</sub> mouse and AD patient brain. Fibrils of mean length 104.9±8.3 nm and width 10.1±0.5 nm were isolated from TG mice. Wider fibrils (~20 nm), with or without a pronounced twist, were readily detected (a & e). Longer filaments (271.7±11.3 nm), with axial periodicities of 78.7±9.8 nm, constituted ~8% and ~34% of the fibril population analyzed in the APP<sub>swe</sub>/PSI<sub>ΔE9</sub> and AD brains, respectively (b & f). Clusters of long filaments, which were denser in AD patient material, were present in the insoluble preparation from APP<sub>swe</sub>/PSI<sub>ΔE9</sub> mice (b & f, inserts). Thin, bent fibrils (c & g) and rod-shaped particles (d & h) were observed in
both 24-month-old APP<sub>swe</sub>/PS1<sub>ΔE9</sub> and AD brains. There were no between-species differences in the dimensions of the isolated filaments [short filaments, length: t(82)=0.1, P>0.05, width: t(82)=1.2, P>0.05; long filaments, length: t(16)=0.3, P>0.05, width: t(16)=0.8, P>0.05; independent two-tailed t-tests].

**Fig. 4. Isolation and electron microscopy of sarkosyl-insoluble tau.** (A) Levels of soluble and insoluble tau were determined with the mouse Total Tau Meso Scale kit. Tau levels increased with age in the pellet obtained by centrifuging brain homogenates at 27,000 x g. The resulting supernatant was treated with 1% sarkosyl and centrifuged at 200,000 x g. The solubility of tau in sarkosyl was decreased with age, irrespective of genotype. (B) Overview of negatively-stained filament types in the sarkosyl-insoluble fraction from 24-month-old APP<sub>swe</sub>/PS1<sub>ΔE9</sub> and AD brain tissue. Fibrils of ~20 nm in width, appearing as straight filaments (a) or as two intertwined fibrils (e), each with a diameter of ~10 nm. PHFs with axial periodicities of ~80 nm (b & f; arrows) were present in APP<sub>swe</sub>/PS1<sub>ΔE9</sub> mice, and more frequently observed in AD patient material. The inserts show ‘stacked’ PHFs, which
were denser in the AD preparation. Structures commonly identified in the detergent-insoluble fractions of the mouse and human brain included bent fibrils of ~7 nm in width (c & g), and rod-shaped particles (d & h; arrows). Scale bars: 200 nm (a, b, e, f), 100 nm (c, d, g, h).

**Proteomics of sarkosyl-insoluble tau**

The sarkosyl-insoluble fractions extracted from 3- and 24-month-old mouse brain, AD and non-AD individuals, were pooled and digested with trypsin & Lys-C. The peptides were labeled with Tandem Mass Tags (TMT), fractionated, and analyzed by nanoLiquid Chromatography-Electrospray Ionization Mass Spectrometry (LC-ESI MS/MS).

A list of tau-associated proteins quantified in the sarkosyl-insoluble proteome is shown in Table 2. Lists of between-group abundance ratios for all regulated proteins are shown in Data File S1. There were 583 proteins identified in the sarkosyl-insoluble mouse proteome, of which 456 were also present in the human samples. Isoforms of tau with three (3R) and four (4R) microtubule-binding repeats were extracted from both human and the murine brain. In mice, all isoforms collapsed under the term microtubule associated protein (MAP; UniProt accession number: B1AQW2). Mouse MAP was regulated by age, rather than genotype. The protein was enriched 2.1-fold in 24- vs. 3-month-old TG mice, and 1.8-fold in 24- vs. 3-month-old WT mice. Genotype-specific enrichment was observed for mouse tau isoform-B (UniProt accession number: P10637-3), a 3R isoform of tau with an extended C-terminal domain, which was identified by the sequence \(^{205}\text{KVQIVYKPVDSLKV}^{218}\). Tau isoform-B increased 3.2-fold in 24-month-old TG vs. WT mice, and 4.5-fold in 24- vs. 3-month-old TG animals. Human MAP (UniProt accession number: A0A0G2JMX7), containing tau isoforms P10637-2, -4, -6 & -8, was 37-fold enriched in the sarkosyl-insoluble fraction of AD compared to non-AD brain.
Table 2. Proteomics of sarkosyl-insoluble tau. Tau-associated proteins quantified in the detergent-insoluble fractions of the mouse and human brain. The presented proteins have been selected for their documented roles in the regulation and binding of tau.

| UniProt Accession Number | Protein(s) | Involvement | TG vs. WT 3 months | TG vs. WT 24 months | TG 24 vs. 3 months | WT 24 vs. 3 months | AD vs. non-AD |
|--------------------------|------------|-------------|--------------------|---------------------|-------------------|-------------------|--------------|
| B1AQW2                   | Microtubule-associated protein | Tau       | 0.86               | 1.00                | 2.06              | 1.77              | 37.15        |
| P10637-3                 | Microtubule-associated protein tau | Tau Isoform-B | 0.61               | 3.21                | 4.52              | 0.86              | Fetal form present |
| Multiple                 | Small nuclear ribonucleoproteins (snRPN) | Core spliceosomal components | Age- and genotype-specific regulation (Data File S1) |
| Multiple                 | Heterogeneous nuclear ribonucleoproteins | Exon 10 splicing regulation | Multiple proteins regulated (Data File S1) |
| Q8BL97                   | Serine/arginine-rich splicing factor 7 | Exon 10 exclusion | 0.82               | 1.05                | 1.11              | 0.87              | 0.69        |
| Q9Z0H4                   | CUGBP Elav-like family member 2 | Exon 10 exclusion | 0.40               | 1.85                | 1.94              | 0.42              | 1.49        |
| P62996                   | Transformer-2 protein homolog beta | Exon 10 inclusion | 0.85               | 1.13                | 0.74              | 0.56              | Not identified |
| Multiple                 | Tubulin | Tau binding partner | Alpha & beta chains regulated (Data File S1) |
| P60710                   | Actin, cytoplasmic 1 | Tau binding partner | 0.80               | 0.53                | 1.43              | 2.16              | 0.71        |
| P08551, P08553, P19246   | Neurofilament | Tau binding partner | Light, medium & heavy polypeptides regulated (Data File S1) |
| Multiple                 | Ribosomal proteins 60S, 40S | Tau binding partner | Age- and genotype-specific changes, particularly in the acidic proteins of the 60S subunit (Data File S1) |
| O08788                   | Dynactin | Tau binding partner | 1.01               | 1.34                | 0.79              | 0.59              | Not identified |
| P28738                   | Kinesin | Tau binding partner | 0.92               | 0.75                | 1.03              | 1.28              | 0.90        |
| P11499, Q80Y52, Q3UAD6   | Heat shock protein 90 | Tau binding partner | Isoforms alpha & beta identified (Data File S1) |
| P48722, P17156, Q3U2G2, Q8K0U4 | Heat shock protein 70 | Tau binding partner | Members 2 & 4 common in mice & humans (Data File S1) |
| P0DP26                   | Calmodulin-1 | Tau binding partner | 1.68               | 0.31                | 0.68              | 3.63              | 0.93        |
| Q3UY00                   | S100β | Tau binding partner | 0.99               | 0.52                | 1.27              | 2.44              | 0.34        |
| O55042                   | α-Synuclein | Tau binding partner | 0.81               | 0.70                | 1.29              | 1.49              | 0.79        |
| A8IP69, P68510, F6VW30, Q9CQV8, P63101 | 14-3-3 proteins | Tau binding partner | Isoform-specific changes (Data File S1) |
| Q3TXU4                   | Apolipoprotein E | Tau binding partner/AD risk factor | 0.65               | 3.58                | 7.51              | 1.37              | Not identified |
| Q3T259                   | Bin1 | Tau binding partner/AD risk factor | 2.11               | 0.44                | 0.71              | 3.41              | 1.44        |
| Q549A5                   | Clusterin | Tau interacting partner/AD risk factor | 1.17               | 1.82                | 1.87              | 1.20              | Not identified |
| P11798, Q923T9, A0A0G2JGS4 | Cu2+/calmodulin-dependent protein kinase II | Tau kinase | Multiple subunits identified (Data File S1) |
| P63318                   | Protein kinase C, gamma type | Tau kinase | 0.71               | 1.48                | 1.30              | 0.62              | 1.05        |
| P31324                   | cyclic AMP-dependent protein kinase II | Tau kinase | 0.57               | 0.91                | 1.61              | 1.01              | 0.84        |
| Q63810                   | Calcineurin subunit B type I | Tau phosphatase | 1.36               | 0.34                | 0.96              | 3.84              | Not identified |
| Q76MZ3                   | Serine/threonine-protein phosphatase 2A | Tau phosphatase | 1.25               | 0.58                | 0.87              | 1.88              | 0.73        |
The mouse MAP sequence $^{174}\text{KVAVVRTPPKSPSSAKS}^{190}$, phosphorylated at Threonine (T) 180 and Serine (S) 188, was more than 20-fold enriched in 24-month-old TG, compared to age-matched WT and 3-month-old $APP_{swe}/PSI_{\Delta E9}$ mice. The peptide sequence was not regulated in aging WT animals. An orthologous sequence of the human MAP was phosphorylated at Threonine (T) 566 and Serine (S) 573 ($^{560}\text{KVAVVRTPPKSPSSAKS}^{576}$). The reported phosphorylation sites correspond to amino acids (aa) T231 and S238 of the human tau isoform with 441 aa. Indications of additional phosphorylation sites were obtained by searching modified peptides against tau isoform- and species-specific databases. Phosphorylated S396, S400 and S404 on the conserved sequence $^{396}\text{SPVSVGDTSPR}^{406}$ of the human 441 aa isoform were identified in the sarkosyl-insoluble mouse proteome. Phosphorylation at S404 in 24-month-old TG mice was confirmed by immunoblotting (Fig. S4). In addition to phosphorylation, murine MAP was deamidated at Asparagine (N) 44, a site on the N-terminal domain of tau that is not conserved in humans ($^{34}\text{AEEAGIGDTPNQEDQAAGHVTQAR}^{57}$). Human MAP was deamidated at position N484, corresponding to N167 of the 441 aa tau isoform ($^{473}\text{GAAPPGQKGQANATRIPAK}^{491}$).

The database for annotation, visualization and integrated discovery (DAVID, v6.8) was used for gene ontology (GO) enrichment analysis of the sarkosyl-insoluble proteome (23, 24). RNA splicing, mRNA processing and translation were among the 10 most enriched biological processes associated with protein upregulation in 24-month-old $APP_{swe}/PSI_{\Delta E9}$ vs. WT mice and AD vs. non-AD subjects. Ribonucleoprotein complexes, ribosomes, and exosomes were among the 10 most enriched cellular components in the insoluble extracts from the mouse and human brain (Fig. 5A). The top 10 molecular functions of the enriched proteins were associated with
poly(A) RNA binding, as well as binding of molecules contributing to the structural integrity of ribosomes and the cytoskeleton (Fig. 5B). Pathway-based enrichment analysis of upregulated proteins in 24-month-old \( APP_{swd}/PS1_{\Delta E9} \) vs. WT mice involved GO terms such as Alzheimer’s and Huntington’s disease, long-term depression, cholinergic, serotonergic and glutamatergic synapse (Fig. 5C). Glycolysis/gluconeogenesis and the Krebs cycle were among the top 10 pathways for downregulated proteins (Fig. 5D).

Fig. 5. Gene Ontology (GO) enrichment analysis of the sarkosyl-insoluble proteome. (A) Enriched cellular components; (B) Enriched molecular functions; (C) Top 10 enriched pathways based on protein upregulation in 24-month-old TG vs. WT mice, according to the Kyoto Encyclopedia of Genes and Genomes (KEGG); (D) Top 10 enriched KEGG pathways based on protein downregulation in 24-month-old TG vs. WT mice. Functional annotation clustering was generated by using DAVID software. Maximum enrichment probability (\( P \) value) was based on an EASE score threshold value of 0.05.
Discussion

The present study describes tauopathy in murine models of familial AD. Neurofibrillary alterations in \( APP_{swe}/PSI_{AE9} \) and Tg2576 mice were demonstrated by a set of tools that are currently used for the evaluation of pathological tau clinically, such as the Gallyas silver stain and \([^{18}F]Flortaucipir\). The presence of PHF tau was confirmed by TEM of sarkosyl-insoluble preparations from the \( APP_{swe}/PSI_{AE9} \) mouse brain. As murine tau possesses a remarkably high number of 76 potential serine/threonine and 4 tyrosine phosphorylation sites, an antibody-free proteomics approach was used for the detection of tauopathy-related epitopes. Of the five hyperphosphorylated sites identified, S404 has been associated with the intraneuronal and extracellular deposition of NFTs in AD (25). The pathology observed in the present study occurred at physiological levels of endogenous tau, as there was no difference in total tau mRNA and protein between \( APP_{swe}/PSI_{AE9} \) and WT mice. Hence, in addition to progressive amyloidosis (3), neuroinflammation (4) and neurodegeneration (5), \( APP_{swe}/PSI_{AE9} \) mice develop progressive neurofibrillary pathology of the AD type, mimicking a range of AD pathologies, in a translationally-relevant manner. The observation that endogenous tau accumulates secondarily to \( A\beta \) in models of cerebral amyloidosis is entirely consistent with post-mortem (26) and in vivo imaging data (27), showing that the development of cortical tau pathology in AD patients is associated with, and may depend on, pre-existing amyloid pathology.

Current approaches to induce tauopathy in mice have been criticized for generating models that poorly recapitulate the situation in the AD brain, as \( TAU \) in AD is neither overexpressed, nor mutated (28). FLTD-linked mutations, in particular, induce tauopathy that is not only morphologically different than that of AD (e.g. Pick bodies), but further characterized by distinct
neurodegenerative processes. For example, cholinergic neurons are extensively lost in AD, but not in FTLD (29). Acetylcholinesterase inhibitors, which are prescribed for the symptomatic relief of cognitive impairment in AD, are largely ineffective in FTLD and may even worsen its symptoms (30). Thus, the pathophysiology that differentiates AD from primary tauopathies is unlikely to be modeled in mutant TAU models. Moreover, neurofibrillary alterations in TAU overexpressing mice occur in the absence of Aβ deposition, which is a defining feature of AD histopathology. The present results indicate that amyloidosis models may overcome these limitations, by reproducing both the neurofibrillary pathology of familial AD and the molecular heterogeneity that is associated with it. In addition to the spontaneous aggregation of tau in APPswel/PS1ΔE9 and Tg2576 mice, analysis of the sarkosyl-insoluble APPswel/PS1ΔE9 proteome identified proteins that have been strongly linked to AD pathogenesis, in general, and tau pathology in particular. Among them, APOE and BIN1 are encoded by genes whose variants are known to increase the risk of late-onset AD, through pathways involving interactions with both APP (31, 32) and tau (33-35). Core components of the spliceosome, on the other hand, particularly Sm-D1 and Sm-D2, are closely related to the deposition of NFTs, but not plaques in familial AD (36). This literature implicates multiple mechanisms in AD tauopathy, which occur downstream of Aβ processing in cases of autosomal dominant AD (ADAD) and, as shown here, APPswel/PS1ΔE9 mice.

Although the sporadic and familial forms of AD share common clinical and histopathological features, it is becoming increasingly recognized that they are not precisely equivalent (37). Positron emission tomography (PET) with [11C]PIB demonstrates accumulation of Aβ in the cerebellum of familial AD cases, which is not typical of sporadic AD (38). Cerebellar deposition
of hyperphosphorylated tau has been observed in ADAD cases harboring the \textit{PSEN1} E280A mutation, but not in sporadic AD (39). Thus, the pronounced cerebellar involvement in \textit{APP_{swe}/PSI_{AE9}} mice, which are known to accumulate \(\text{A}\beta\) in this region (40), suggests that the model mimics familial, rather than the sporadic forms of AD. Reports of cerebellar pathology in ADAD cases and \textit{APP_{swe}/PSI_{AE9}} mice warrant caution in using the cerebellum as a reference region for the quantification of \(^{11}\text{C}\)PIB and \(^{18}\text{F}\)Flortaucipir PET (41, 42), as this is likely to underestimate cortical \(\text{A}\beta\) and tau pathology, respectively.

Unlike the imbalance in \(\text{A}\beta\) homeostasis, which is thought to be central in the pathogenesis of AD, gross changes in tau production and clearance were not observed in this study. On the one hand, Gallyas-, \(^{18}\text{F}\)Flortaucipir- and thioflavin-S-positive signal was observed in the vasculature of 18-24-month-old \textit{APP_{swe}/PSI_{AE9}} mice. Moreover, there were age- and genotype-specific changes in multiple components of the phagosome and proteasome in TG vs. WT animals (Data File S1). On the other hand, total tau mRNA and protein levels were not different between 24-month-old WT and TG mice, as evidenced by tau mesoscale, proteomics and PCR. Moreover, age-dependent decreases in the solubility of tau were equally observed in \textit{APP_{swe}/PSI_{AE9}} and control animals. Notwithstanding that the contribution of individual pathways to tau degradation was not assessed in this study, these findings suggest that the neurofibrillary alterations observed in \textit{APP_{swe}/PSI_{AE9}} mice are not mediated by an imbalance between the production and clearance of tau. It is important to note that, unlike in TG mice, sarkosyl-insoluble tau was increased in AD vs. non-AD tissue, a finding that is consistent with literature data on the regulation of human tau in AD (43). It might be that the increased concentration of brain tau in late-stage AD is associated with heavily impaired clearance pathways or pronounced neuronal damage, processes
that may not be modeled in 24-month-old \( \text{APP}_{\text{swd}}/\text{PS1}_{\Delta E9} \) mice. Alternatively, the present data may highlight the involvement of transcriptional and translational mechanisms, rather than production and clearance pathways, in the assembly of PHF tau.

A prevalence of 3R isoforms in the composition of NFTs has been observed in the AD hippocampus by immunohistochemical and biochemical methods (44). Moreover, a shift from 4R to 3R isoforms has been associated with the morphological evolution of tau-positive neurons from a pre-tangle to the NFT state (45). Although the literature on the regulation of tau isoforms in AD remains scarce, the present results support the notion that an imbalance in tau isoform ratio is involved in the neurofibrillary alterations of AD, with 3R isoforms being preferentially sequestered into the insoluble tau fraction. The identification of tau isoform-B, a 3R isoform that is predominantly expressed in the fetal mouse brain, supports the suggestion that immature tau isoforms participate in AD tauopathy (46), and implicates aberrant transcription and translation mechanisms in the disease process. A re-induction of fetal tau may be attributed to the deregulation of core splicing machinery, which was marked in this study and considered to occur early and selectively in AD (47). Moreover, as the selection of splice sites is determined by canonical sequences encoded into the genome, the re-expression of fetal isoforms might be a consequence of aberrant DNA replication during cell cycle re-entry (48). Cell cycle proteins that were deregulated in an age- and genotype-specific manner in this study include Sub1, cdc42, CEND1, Histone H3 and nucleolin (Data File S1). Clearly, the exact mechanisms underlying tauopathy in AD cannot be resolved by the present set of experiments. The data demonstrate, however, that the formation of PHF tau is associated with loss of regulatory control over \( \tau \) splicing \textit{in vivo}, which may have important implications for the origins and management of
tauopathy in AD. It is tempting to speculate that tau hyperphosphorylation may partly be due to
the re-emergence of fetal isoforms, which are known to be over-phosphorylated compared to
adult tau (49). Moreover, it is plausible that an imbalance in tau isoform ratio mediates protein
misllocalization from the axonal to the somatodendritic compartment, as distinct tau isoforms are
differentially sorted across the cell (50). Of note, cofilin-dependent, ‘classical’ pathways of tau
missorting (51) may also be involved in the pathology observed in this study, as cofilin was
reduced in the sarkosyl-insoluble proteome of 24-month-old APP<sub>swe</sub>/PS1<sub>ΔE9</sub> mice. Collectively,
these data highlight the relevance of amyloidosis models for studying the diverse macroscopic
and molecular aspects of AD tauopathy.

The limitations associated with models overexpressing APP and PSEN mutations have been
discussed previously (2). To exclude the possibility that tauopathy is an artefact of APP or PSEN
overexpression, it would be important to determine whether it develops in second-generation
amyloidosis models, carrying AD-related mutations in endogenous genes. Moreover, as there is
evidence of [18F]Flortaucipir binding to monoamine oxidases (MAO; 52), signal quantification in
the presence of MAO inhibitors is warranted to determine the extent of off-target binding, if any
(53). Practical considerations in using amyloidosis mice to study tauopathy include long waiting
times for the accumulation of endogenous murine tau, mouse-on-mouse antibody issues, and the
low abundance of pathology as compared to human AD. While ~30% of all Nissl-positive cells
in the prefrontal cortex of Braak stage V-VI brains may contain NFTs (54), Gallyas-positive
signal in this study occupied ~1% of the frontal cortex of 24-month-old APP<sub>swe</sub>/PS1<sub>ΔE9</sub> mice, neuritic structures included. Nevertheless, cognitive impairment in AD is known to correlate
with the spread of tau pathology, and the number of brain areas containing at least one NFT has
been shown to be the best explanatory variable of intellectual status in AD (55). In this context, it is worth evaluating whether measurements of tauopathy in aging $APP_{swe}/PSI_{A49}$ mice correlate with the progressive cognitive impairment that these animals exhibit in the Barnes maze assay (56).

**Materials and Methods**

*Study design*

Mice were grouped according to age and genotype. Sample numbers were based on preliminary studies, showing absence of Gallyas and $[^{18}\text{F}]$Flortaucipir signal in 18-month-old WT vs. TG animals. (Immuno)histochemistry, autoradiography, the isolation of sarkosyl-insoluble tau, and electron microscopy studies were repeated at least three independent times. Tau Meso Scale was performed two independent times. Remaining samples were pooled and subjected to proteomics. To avoid cross-contamination during the isolation of sarkosyl-insoluble tau, glassware was washed in ultrapure de-ionized H$_2$O (dH$_2$O, Ultra Clear™, Siemens), followed by rinses in formic acid (FA, 98-100%; Merck Millipore), dH$_2$O, ethanol (99%; VWR International) and dH$_2$O. No samples were excluded from data analysis, which was performed in an unblinded manner. To compare tau pathology in transgenic mouse vs. human brain, tissue from the middle frontal gyrus of an AD-confirmed patient [BB08-002, Female, 80 years old, *post-mortem* interval (PMI): 9 h] and a non-AD subject (BB16-023, Female, 83 years old, PMI unknown) were processed along with the murine samples for the Gallyas silver stain, autoradiography, electron microscopy and proteomics experiments. The AD and non-AD samples were chosen for their abundance and complete lack of tau pathology respectively, as assessed by Gallyas silver
staining and [$^{18}$F]Flortaucipir autoradiography. To avoid confounding effects of anesthesia on tau phosphorylation, mice were euthanized by cervical dislocation.

**Ethical statement**

Mouse tissue: All procedures complied with Danish law (Dyreværnsloven-Protection of Animals Act, nr 344/2005) and European Union directive 2010/63/EU, regulating animal research. Ethical permission was granted by the Animal Ethics Inspectorate of Denmark (nr 2011/561-1950).

Human tissue: Fresh-frozen samples from the middle frontal gyrus were obtained from the Maritime Brain Tissue Bank, Department of Medical Neuroscience, Faculty of Medicine, Dalhousie University, Sir Charles Tupper Building, 5850 College Street, Halifax Nova Scotia B3H 4R2. Ethical approval was obtained from the Nova Scotia Health Authority Research Board in Halifax, Canada, and the Danish Biomedical Research Ethical Committee of the region of Southern Denmark (Project ID: S-20070047). Informed, written consent forms were obtained for all subjects.

**Animals and tissue sectioning**

$\text{APP}_\text{swe}/\text{PSI}_{\Delta E9}$ mice (57), originally purchased from the Jackson Laboratories (MMRRC Stock No: 34832-JAX), were bred and maintained on a C57BL/6J background. The animals were group-housed (4-8/cage) in a temperature (21±1°C) and humidity controlled environment (45-65%), under a 12:12 h light:dark cycle (lights on: 7 am). Food and water were available *ad libitum*. Female $\text{APP}_\text{swe}/\text{PSI}_{\Delta E9}$ mice were used at 3, 6, 12, and 18 months of age. Sex- and age-matched WT littermates were used as control. Both male and female mice were used in the 24-
month-old groups (n=6/genotype & age-group, total animal number: 60). The animals were euthanized by cervical dislocation, and brains immediately removed and bisected along the midline. Right hemispheres were frozen in isopentane on dry-ice (-30°C). The olfactory bulb, striatum, cortex, hippocampus, diencephalon, brainstem and cerebellum from the left hemisphere were dissected on a petri dish on ice, collected in Eppendorf® tubes, and frozen on dry-ice. The tissue was stored at -80°C until use.

Sectioning was carried out at -17°C using a Leica CM3050S cryostat (Leica Biosystems GmbH). Series of 20 µm-thick sagittal sections were collected at 300 µm intervals. The sections were mounted onto ice-cold Superfrost™ Plus slides (Thermo Fisher Scientific), dried at 4°C in a box containing silica gel for at least 2 h, and stored at -80°C for future experiments. Every 13th and 14th section was collected in Eppendorf® tubes for RNA extraction with Trizol™.

Fresh-frozen coronal brain sections of male and female, 20-month-old Tg2576 and WT mice were provided by the Centre for Biological Sciences, University of Southampton, U.K.

*(Immuno)histochemistry, autoradiography and proteomics*

The Gallyas silver stain was performed according to Kuninaka et al. (58), thioflavin-S according to Sun et al. (59), [18F]Flortaucipir autoradiography according to Marquié et al. (60), proteomics according to Kempf et al. (61). Protocol details are provided in Supplementary Materials and Methods.
Statistical analysis

Parametric testing was employed following inspection of the data for normality with the Kolmogorov-Smirnov test in Prism (v6.01; GraphPad Software). Data sets were analyzed by Statistica™ v10 (TIBCO Software Inc., USA). The effects of age, genotype and brain region on the binding levels of [18F]Flortaucipir were analyzed by three-way ANOVA. Gallyas-positive area fraction and tau gene/protein levels were analyzed by two-way ANOVA for the independent factors age and brain region or genotype, respectively. Where ANOVA yielded significant effects, Bonferroni post-hoc comparisons were used to detect between-group regional and age-dependent differences. Levels of sarkosyl-insoluble tau between 24-month-old TG and WT mice, and PHF dimensions extracted from TG vs. AD brain were compared by two-tailed independent Student’s t-tests. Significance was set at $\alpha=0.05$. A 1.3-fold change cut-off value for all TMT ratios was used to rank proteins as up- or down-regulated in the proteomics study (62).

Supplementary Materials

Materials and Methods.

Fig. S1. Quantification of Gallyas-positive lesions, photomicrographs of MC-1 immunoreactivity and vascular pathology in $APP_{swe}/PSI_{\Delta E9}$ mice.

Fig. S2. Correlation between Gallyas-positive area fraction and [18F]Flortaucipir binding levels.

Fig. S3. Evaluation of methods for extracting sarkosyl-insoluble tau.

Fig. S4. pS404 immunoblot.

Table S1. Evidence of tau hyperphosphorylation in $APP_{swe}/PSI_{\Delta E9}$ mice.

Data file S1. Regulated proteins in the sarkosyl-insoluble fraction.
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Author contributions: AM designed the project and wrote the manuscript, performed (immuno)histochemistry, autoradiography, tau isolation studies, and assisted with TEM. CT and SJK performed proteomics and immunoblotting. MA and RV performed tissue sectioning, (immuno)histochemistry, autoradiography and tau filament analysis. SP performed PCR and tau Meso Scale. AML organized and performed autoradiography. HA synthesized $[^{18}\text{F}]$Flortaucipir. JLT performed (immuno)histochemistry and provided Tg2576 tissue, SD provided human tissues and critically reviewed the manuscript. DJB, MRL and BF supervised the project and contributed to its design. All authors assisted with data interpretation, participated in drafting the manuscript and approved its final version.

Competing interests: None related to the design and completion of this study.

Data and materials availability: The proteomics data have been deposited to the ProteomeXchange Consortium (63) via the PRIDE partner repository with the dataset identifier.
PXD009306 [username: reviewer39090@ebi.ac.uk; password: HdJxxVxU (64)]. The MC-1 antibody, and material for the synthesis of $[^{18}F]$Flortaucipir were obtained through an MTA.
Supplementary Materials:

Materials and Methods

Gallyas silver staining

The Kuninaka et al. simplification of the modified Gallyas method was used to examine neurofibrillary pathology (58, 65). Fresh-frozen sections were directly immersed in 4% neutral buffered formalin (NBF) at 4°C for 24 h. The sections were thoroughly washed in ultrapure deionized H2O (dH2O; Ultra Clear™, Siemens), dried at room temperature (RT) for 10 min and defatted for 1 h in a solution of chloroform/99% ethanol (1:1) in the dark. Following hydration through a series of graded ethanols into dH2O (2 x 1 min: 99%, 96%, 70%), slides were immersed into an aqueous solution of 0.25% potassium permanganate (20 min), washed in dH2O (1 min), and incubated in 1% oxalic acid (2 min). After washing in dH2O (2 x 5 min), sections were transferred into the alkaline silver iodide solution (1 min), washed with 0.5% acetic acid (2 x 5 min), and developed in a water bath at 15°C, until the appearance of a brownish shade (12-14 min). The developed sections were washed in 0.5% acetic acid (3 min), toned with 0.1% gold chloride (10 min), fixed with 1% sodium thiosulfate (5 min), and counterstained with 0.1% nuclear fast red (3 min). Ethanol and chloroform were from VWR International. The remaining chemicals were from Sigma-Aldrich Co.

Aβ immunohistochemistry on silver-stained sections

The biotinylated 6E10 antibody (SIG-39340, Nordic BioSite) was used to investigate the association between neurofibrillary pathology and Aβ load in APP<sub>swe/PS1<sub>ΔE9</sub></sub> mice. Clone 6E10 is raised against amino acids 1-16 of human Aβ, recognizing multiple amyloid peptides and precursor forms (manufacturer information). Silver-stained sections were immersed in 70%
formic acid for 30 min, rinsed for 10 min in 50 mM Tris-buffered saline (TBS, pH 7.4), and further washed/permeabilised in TBS containing 1% Triton X-100 (3 x 15 min). Sections were subsequently blocked for 30 min in TBS, containing 10% fetal bovine serum (FBS). Incubation with the 6E10 anti-β-amyloid antibody was carried out overnight at 4°C, in TBS containing 10% FBS (1:500 dilution of stock). Adjacent, negative control sections were incubated with biotin-labeled mouse IgG1 (MG115, Thermo Fisher Scientific), diluted to the same protein concentration as the primary antibody. Following incubation with 6E10, the sections were adjusted to RT for 30 min and washed in TBS+1% Triton X-100 (3 x 15 min). Endogenous peroxidase activity was quenched for 20 min in a solution of TBS/methanol/H₂O₂ (8:1:1). After washing in TBS+1% Triton X-100 (3 x 15 min), sections were incubated for 3 h with HRP-streptavidin in TBS/10% FBS (1:200; GE Healthcare Life Sciences). After a final wash in TBS (3 x 10 min), peroxidase activity was visualised with 0.05% 3,3′diaminobenzidine (DAB) in TBS buffer, containing 0.01% H₂O₂ (Sigma Aldrich Co.).

**MC-1 immunohistochemistry**

Fresh-frozen sections were directly immersed in 4% NBF at 4°C for 24 h. The sections were thoroughly washed in dH₂O, dried at RT for 10 min, and defatted for 1 h in a solution of chloroform/99% ethanol (1:1) in the dark. Following hydration through a series of graded ethanols into dH₂O (2 x 1 min: 99%, 96%, 70%), endogenous peroxidase activity was quenched for 30 min with 1.5% H₂O₂ in TBS. The sections were washed and blocked for 1 h at RT using 10% FBS in 0.05% Triton X-100 (TBS-Tx; blocking buffer). The mouse anti-human MC-1 antibody, a generous gift from Dr. Peter Davies, was diluted in blocking buffer (1:10 dilution of stock). Negative control sections were incubated in blocking buffer with mouse IgG1 (1:100;
MG100, Thermo Fisher Scientific). Following overnight incubation at 4°C, the sections were washed in TBS-Tx (4 x 5 min) and incubated at RT for 3 h with biotin-labeled goat anti-mouse IgG1 (abcam, ab97238), diluted 1:300 in TBS-Tx, containing 50% Superblock (Thermo Fisher Scientific; #37580). After washing in TBS-Tx (4 x 5 min), sections were incubated for 1 h with HRP-streptavidin, diluted 1:200 in TBS-Tx containing 50% Superblock. The sections were washed in TBS (4 x 5 min) and developed with 50 mg DAB and 0.01% H₂O₂, in TBS containing 10 mM imidazole and 0.5% nickel ammonium hexahydrate (pH 7.4).

For all light microscopy studies, the developed sections were thoroughly washed in dH₂O, dehydrated in graded alcohols, cleared in xylene, and cover-slipped with PERTEX® (Histolab Products AB).

**Thioflavin-S staining**

Thioflavin-S staining was performed according to Sun et al. (59). Fresh-frozen sections were directly immersed in 4% NBF at 4°C for 24 h. The sections were thoroughly washed in ultrapure dH₂O, dried at RT for 10 min, and defatted for 1 h in a solution of chloroform/99% ethanol (1:1) in the dark. Following hydration through a series of graded ethanols into dH₂O (2 x 1 min: 99%, 96%, 70%), slides were immersed into an aqueous solution of 0.25% potassium permanganate (5 min), washed in dH₂O (1 min), and incubated in 1% oxalic acid (2 min). After washing in dH₂O (2 x 2.5 min), the sections were incubated with freshly-prepared 0.25% NaBH₄ (2 x 5 min), washed in dH₂O (5 x 2 min), and transferred into a 0.1% thioflavin-S solution (8 min; dark incubation). The sections were differentiated in 80% ethanol (2 x 10 s), washed in dH₂O (3 x 5 dips), and incubated for 30 min at 4°C in the dark with high-concentration phosphate buffer, to
prevent photobleaching (411 mM NaCl, 8.1 mM KCl, 30 mM Na₂HPO₄; 5.2 mM KH₂PO₄). Following a dip in dH₂O, the sections were counterstained with DAPI (30 µM) for 10 min and mounted with Aquatex® mounting medium (Sigma Aldrich Co.).

Immuno(histochemistry) images were acquired with an Olympus DP71 digital camera, mounted on an Olympus BX51 microscope equipped for Epi-Fluorescence illumination, or an Olympus DP80 Dual Monochrome CCD camera, mounted on a motorized BX63 Olympus microscope.

[^18F]Flortaucipir autoradiography
Autoradiography experiments were conducted at the Department of Nuclear Medicine and PET-centre, Aarhus University, Denmark.[^18F]Flortaucipir was synthesised in Aarhus using previously detailed methods (66).

[^18F]Flortaucipir autoradiography was performed as described previously (60), with minor modifications. Sections were thawed to RT for 20 min and fixed/permeabilised in 100% methanol for 20 min. The sections were incubated for a period of 60 min in a 160 mL bath of 10 mM phosphate buffered saline (PBS, pH 7.4), containing 38.4±9.6 MBq[^18F]Flortaucipir (specific activity: 145±68 GBq/µmol). A series of adjacent brain sections was incubated with identical amounts of radioligand in the presence of 50 µM ‘cold’ flortaucipir, to assess non-specific binding (NSB). Following incubation, sections were serially washed in PBS (1 min), 70% ethanol in PBS (2 x 1min), 30% ethanol in PBS (1 min) and PBS (1 min). After rapid drying under a stream of cold air, the sections were placed in light-tight cassettes and exposed against FUJI multi-sensitive phosphor screens for 30 min (BAS-IP SR2025, GE Healthcare Life
Sciences). To allow quantification, standards of known radioactive concentration were prepared by serial dilution of the \[^{18}F\]Flortaucipir incubation solution, and exposed along with the sections. Images were developed in a BAS-5000 phosphor-imager at 25 µm resolution.

For image analysis, the intensity values produced by the \(^{18}\)F standards were entered with their corresponding radioactivity values (kBq/mL) into a calibration table, and the relationship between radioactivity and intensity determined by using ImageJ software (v. 1.51c; National Institutes of Health, USA). Adjustments were undertaken to allow for the radioactive decay of \[^{18}F\]Flortaucipir. Values of specific binding were derived after subtraction of NSB from total binding images.

Isolation of sarkosyl-insoluble Tau

The general procedure by Greenberg and Davies (21) was used to isolate PHFs. Left brain hemispheres from two mice per group were pooled and weighed (467.1±3.1 mg). The tissue was thoroughly homogenised with a motor driven Potter-Elvehjem tissue grinder (WHEATON), in a 5-fold excess (v/w) of 10 mM Tris-HCl buffer (pH 7.4), containing 800 mM NaCl, 1 mM EGTA, 10% sucrose, protease inhibitors (cOmplete\textsuperscript{TM} Protease Inhibitor; Roche Diagnostics) and phosphatase inhibitors (PhosSTOP\textsuperscript{TM}; Roche Diagnostics; H buffer). The homogenate was centrifuged at 4°C for 20 min in a refrigerated ultracentrifuge (27,000 x g; Sorvall RC M150 GX). The supernatant was decanted and kept on ice, the pellet (P1) suspended in 5 vol of H-buffer and re-centrifuged at 27,000 x g for 20 min (4°C). The combined supernatants (S1) were brought to 1% sarkosyl in H buffer and incubated for 2 h at 37°C in a C24 incubator shaker (100 rpm; New Brunswick Scientific). Following centrifugation at 200,000 x g for 40 min (4°C), the
sarkosyl-soluble fraction was decanted and kept on ice, and the sarkosyl-insoluble pellet suspended in H buffer, containing 1% CHAPS hydrate (Sigma Aldrich Co.). After filtering through acetate cellulose filters (0.45 µm; VWR International), the filtrates were centrifuged at 200,000 g for 70 min, and the final pellet suspended in 250 µL dH₂O. Aliquots of 150 µL from the P1, S1, sarkosyl soluble and insoluble fractions were kept for determining Tau protein levels. Samples were stored at -80°C until further processed.

**Tau Meso Scale**

Tau protein concentration in soluble and insoluble fractions was measured with the mouse Total Tau kit (K151DSD-1; Mesoscale Diagnostics LLC). The anti-mouse monoclonal antibody used for detection binds between amino acids 150-200 of Tau, but the clone number and exact epitope recognition site(s) are proprietary. Plates were processed in a SECTOR® Imager 6000 plate reader (Meso Scale Diagnostics LLC), and data acquired with Discovery Workbench software (v.4.0; Meso Scale Diagnostics LLC). Results are presented as pg of Tau/mg of total protein, the latter measured at A562 nm with a Pierce™ BCA protein kit and bovine serum albumin as standard (Thermo Fisher Scientific).

**Transmission electron microscopy (TEM)**

Electron microscopy was performed in the Core Facility for Integrated Microscopy, Faculty of Health and Medical Sciences, University of Copenhagen, Denmark. Carbon-coated copper grids (200 mesh; Ted Pella Inc.) were glow-discharged with a Leica EM ACE 200 (Leica Biosystems Nussloch GmbH), and loaded with 6 µL of sarkosyl-insoluble sample. The sample was adsorbed for 1 min, blotted and stained with 2% phosphotungstic acid in dH₂O for 2 min. After blotting
and a quick wash with d\(\text{H}_2\text{O}\), the samples were examined with a Philips CM 100 TEM (Koninklijke Philips N.V.), operated at an accelerating voltage of 80 kV. Digital images were acquired at a nominal magnification of x180,000, by using an OSIS Veleta digital slow scan 2k x 2k CCD camera and the iTEM software package (Olympus Corporation). Filaments shorter and longer than 200 µm were analyzed in at least two fields of view with ImageJ software. Reported values are mean ± SEM of 70 and 32 PHFs for \(\text{APP}_\text{swe}/\text{PSI}_{\Delta \text{E}9}\) and AD tissue, respectively.

**Mass spectrometry-based proteomics**

**Reduction, alkylation and enzymatic digestion**

Sarkosyl-insoluble samples were dried down and denatured at RT with 6 M Urea, 2 M Thiourea and 10 mM dithiothreithol (DTT; Sigma-Aldrich Co.) in d\(\text{H}_2\text{O}\) (pH 7.5), supplemented with cOmplete™ protease inhibitors and PhosSTOP™ phosphatase inhibitors (Roche Diagnostics). After vortexing and sonication, 100 µg total protein/condition was alkylated in 20 mM iodoacetamide (IAA) for 20 min in the dark. A total of 2 µL of endoproteinase Lys-C was added to the protein sample (6 µg/µL; Wako Chemicals GmbH), and the solution incubated for 2 h at RT. The sample was then diluted 10 times with 20 mM TEAB, pH 7.5, and digested with trypsin overnight (1:50 w/w trypsin:protein). The enzymatic digestion was stopped with 5% formic acid (FA) and the peptide sample cleared by centrifugation (14,000 x g, 15 min). Protein and peptide quantification was performed by Qubit™ fluorometric quantitation (Invitrogen™).

**Tandem Mass Tag (TMT) labeling**

A total of 100 µg tryptic peptides were dried and desalted with R2/R3 columns, before TMT-10plex labeling (AB Sciex Pte. Ltd.). The desalting procedure is detailed below. Labeling was
performed according to manufacturer instructions: TMT-126 for WT-3 months(1), TMT-127N WT-3 months(2), TMT-127C Tg-3 months(1), TMT-128N Tg-3 months(2), TMT-128C for WT-24 months(1), TMT-129N for WT-24 months(2), TMT-129C for Tg-24 months(1), 130N for Tg-24 months(2), TMT-130C for human non-AD and TMT-131 for human AD. The labeled peptides from all groups were mixed 1:1, dried down and stored for further enrichment and analysis. Human AD and non-AD samples were included for validation, as well as for taking advantage of the stacking effect of the TMT10-plex, in order to increase identification rates.

**Enrichment of phosphopeptides and formerly sialylated N-linked glycopeptides (deglycosylated)**

Multi- and mono-phosphorylated peptides, as well as sialylated N-linked glycopeptides, were separated from unmodified peptides by using a TiO2 workflow (67). Modified peptides bind to TiO2 beads because the phospho and sialic groups are acidic and retained on the column, whereas unmodified peptides flow-through. The eluted modified peptides were deglycosylated to remove N-linked glycans (68). Hydrophilic interaction chromatography (HILIC) was used for sample fractionation prior to nano liquid chromatography-tandem mass spectrometry [LC-MS/MS; (67)].

Briefly, the combined labelled peptides (~1000 µg) were dissolved in TiO2 loading buffer [80% acetonitrile (ACN), 5% trifluoroacetic acid (TFA), 1 M glycolic acid] and incubated for 30 min at RT with 6 mg of TiO2 beads (5020 Titansphere™ TiO2, 5 µm; gift from GL Sciences). The beads were sequentially washed with TiO2 loading buffer, 80% ACN/1% TFA and 10% ACN/0.1% TFA. Modified peptides were eluted with 1.5% ammonium hydroxide solution, pH 11.3, and dried-down in a vacuum centrifuge. The unbound TiO2 fraction and the combined
washing fractions contain unmodified peptides. The dried modified peptides were deglycosylated at 37°C overnight in 20 mM TEAB buffer, pH 8.0, containing N-glycosidase F (P0705L, New England Biolabs Inc.) and Sialidase A™ (GK80046, ProZyme). Unmodified and modified peptides were dried and desalted on micro-columns before capillary HILIC fractionation.

Sample desalting with R2/R3 micro-column

Samples were desalted by using home-made P200 tip-based columns, packed with equal ratios of reversed-phase resin material Poros R2 (Oligo R2 Reversed Phase Resin 1-1112-46, Thermo Fisher Scientific) and Poros R3 (OligoR3 Reversed Phase Resin 1-1339-03, Thermo Fisher Scientific). The end of the tip was blocked with C8 material (Model 2314, 3m Empore™ C8). The column was prepared by short centrifugation (1000 x g) of the R3 reversed-phase resin (100% ACN), equilibrated with 0.1% TFA, and centrifuged again. The acidified samples were loaded onto the columns and washed three times with 0.1% TFA. Peptides were eluted with 50% ACN, 0.1% TFA and dried by vacuum centrifugation.

HILIC fractionation

The fractions containing unmodified peptides were fractionated prior to nanoLC-MS/MS analysis using HILIC, as described previously (69, 70). Peptides were dissolved in 90% ACN, 0.1% TFA (solvent B), and loaded onto a 450 μm OD x 320 μm ID x 17 cm micro-capillary column packed with TSK Amide-80 (3 μm; Tosoh Bioscience LLC). The peptides were separated on a 1200 Series HPLC (Agilent Technologies) over 30 min, by using a gradient from 100–60% solvent B (A = 0.1% TFA), at a flow-rate of 6 μL/min. Fractions were collected every
1 min based on the UV chromatogram. Subsequently, the peptide fractions were dried by vacuum centrifugation.

**Reversed-phase nanoLC-ESI-MS/MS**

The peptides were resuspended in 0.1% FA, and automatically injected on a ReproSil-Pur C18 AQ, in-house packed-trap column (Dr. Maisch GmbH; 2 cm x 100 µm inner diameter; 5 µm). The peptides were separated by reversed phase chromatography at 250 nL/min on an analytical ReproSil-Pur C18 AQ column (Dr. Maisch GmbH), packed in-house (17 cm x 75 µm; 3 µm), which was operated on an EASY-nanoLC system (Thermo Fisher Scientific). Mobile phase was 95% ACN/ 0.1% FA (B) and water/0.1% FA (A). The gradient was from 1% to 30% B over 80 min for mono-phosphorylated, deglycosylated and unmodified peptides, and 1% to 30% solvent B over 110 min for multi-phosphorylated peptides, followed by 30 - 50% B over 10 min, 50 - 100% B over 5 min, and 8 min at 100% B. The nano-LC was connected online to a Q Exactive HF Hybrid Quadrupole-Orbitrap mass spectrometer (Thermo Fisher Scientific), operating in positive ion mode and using data-dependent acquisition. The eluent was directed toward the ion transfer tube of the Orbitrap instrument by dynamic electrospray ionization. The Orbitrap acquired the full MS scan with an automatic gain control target value of 3x10^6 ions and a maximum fill time of 100 ms. Each MS scan was acquired in the Orbitrap at high-resolution [120,000 full-width half maximum (FWHM)] at m/z 200 with a mass range of 400-1400 Da. The 12 most abundant peptide ions were selected from the MS for higher energy collision-induced dissociation fragmentation (collision energy: 34 V) if they were at least doubly-charged. Fragmentation was performed at high resolution (60,000 FWHM) for a target of 1x10^5.
maximum injection time of 60 ms using an isolation window of 1.2 m/z and a dynamic exclusion of 20 s.

**Data search & analysis**

Raw data were searched against the *mus musculus* or *homo sapiens* reference databases from swissprot and uniprot via Mascot (v2.3.02, Matrix Science) and Sequest HT search engines, respectively, using Proteome Discoverer (v2.1, Thermo Fisher Scientific). A precursor mass tolerance of 20 ppm and a product ion mass tolerance of 0.05 Da was applied, allowing two missed cleavages for trypsin. Fixed modifications included carboxamidomethylation of Cys/Arg and TMT-10plex labeling for Lys and N-termini. Variable modifications contained phosphorylation on Ser/Thr/Tyr, acetylation on the N-termini, oxidation of Met and deamidation of Asn. The TMT datasets were quantified using the centroid peak intensity with the ‘reporter ions quantifier’ node. To ensure high-confident identification, the Mascot percolator algorithm (q value filter set to 0.01), Mascot and Sequest HT peptide rank 1, a cut-off Mascot score value of ≥18, and a Sequest HT∆Cn of 0.1 were used. Only high confident peptides were used for further analysis. The peptides were filtered against a Decoy database resulting into a false discovery rate (FDR) of <0.01. Two murine biological replicates per group without missing values were considered for the analysis, and normalization was performed on the protein median. Based on the mean technical variation from repetitive measurements of murine brain samples (61, 62), the threshold for determining regulated proteins was set to 1.3-fold, i.e. proteins with TMT ratios >1.30 were considered upregulated and <0.77 downregulated. Tau isoform-specific searches were performed by creating a Uniprot database of isoform sequences for mouse Tau (Uniprot ID: P10637-1, -2, -3, -4, -5, -6) and human Tau (Uniprot ID: P10636-1, -2, -3, -4, -5, -6, -7, -8, -9),
as performed by Morris et al. (71). Moderate confidence peptides (FDR<0.05) were included in the isoform-specific search.

RT-qPCR

For reverse transcription, quantitative polymerase chain reaction (RT-qPCR), Trizol™-isolated RNA (2 μg) from brain sections of WT and TG mice was reverse-transcribed to cDNA, by using the Applied Biosystems™ high-capacity cDNA transcription kit (Thermo Fisher Scientific). Samples were analyzed in triplicate on a StepOnePlus™ Real-Time PCR system (Applied Biosystems™, Thermo Fisher Scientific). Each 20 μL sample contained nuclease-free H₂O (Thermo Fisher Scientific), 1x Maxima SYBR® green/probe master mix (Thermo Fisher Scientific), 500 nM forward and reverse primers (TAG Copenhagen A/S), 4x diluted cDNA for Mapt and 10x diluted cDNA for hypoxanthine phosphoribosyltransferase (Hprt1), which was used as a reference gene. Hprt1 sequences (72) and mouse-specific Mapt primers spanning exon 10 have been described previously (73). Conventional PCR cycling conditions were used [95°C (10 min), followed by 40 cycles of 95°C (15s)/60°C (1 min)], followed by a melt curve. After normalization to Hprt1, data were expressed as fold change from the mean value of the 3-month-old WT samples. Nuclease-free H₂O and genomic DNA were used as controls.

Immunoblotting of sarkosyl-insoluble Tau

Ten μg of lysed, denatured protein were separated on 4-12% Bolt Bis-Tris gradient gels (NW04125Box, Novex®), and transferred to polyvinylidene fluoride (PVDF) membranes using the Trans-Blot SD Semi-Dry Transfer Cell system (Bio-Rad Laboratories Inc.). Protein content on the PVDF membranes was visualized with PonceauS. Following washing (10 min) and blocking for 1 h in Roti®-Block (Carl Roth GmbH), the membranes were incubated overnight at
4°C in blocking solution, containing rabbit anti-tau (1:1000; A0024, Dako Agilent) or rabbit anti-phopshoSer404 primary antibodies (1:200; OAAF07796, Aviva Systems Biology). The blots were washed in TBS+1% Triton X-100 (3 x 15 min; TBS-Tx) and incubated for 2 h with horseradish peroxidase-conjugated secondary antibody (anti-rabbit IgG, HRP-linked antibody, #7074; Cell Signaling Technology®). After a final wash in TBS-Tx (3 x 15 min), the blots were developed with enhanced chemiluminescent substrate (ECL), according to manufacturer instructions (Luminata™ Forte Western HRP Substrate, WBLUF0100, Merck Millipore).
Fig. S1. (A) Quantification of Gallyas-positive signal in aging *APP<sup>swe</sup>/PS<sub>IΔE9</sub> mice. Regions of interest were manually drawn by reference to the mouse brain atlas of Paxinos and Franklin (74). Gallyas-positive particles were measured with the particle analysis plugin in ImageJ, after thresholding ROIs on a black and white image display mode, by using default software settings. Data are presented as the mean area fraction occupied by Gallyas-positive particles ± standard error of the mean (SEM), in brain regions of 5-6 animals/group. Asterisks denote the age when
Gallyas signal was first increased compared to 3-month old \textit{APP}_{swe}/\textit{PSI}_{\Delta E9} mice (**\(P<0.01\), ***\(P<0.001\), Bonferroni post-hoc tests). Increased silver deposition across all brain areas analyzed was detected in 12- vs. 3- and 6-month-old \textit{APP}_{swe}/\textit{PSI}_{\Delta E9} mice (\(P<0.001\)), with additional accumulation occurring in 18- vs. 12- (\(P<0.001\)), and 24- vs. 18-month-old TG animals (\(P<0.05\), Bonferroni post hoc tests). Two-way ANOVA confirmed significant main effects of age [\(F(4,245)=169.9, P<0.001\)] and brain region [\(F(9,245)=11.4, P<0.001\)], as well as significant age x region interaction effects on the fraction of brain tissue bearing Gallyas-positive signal [\(F(36,245)=3.2, P<0.001\)]. (B) MC-1 immunoreactivity in the neocortex of 24-month-old TG and WT mice. Indications of conformationally modified tau were obtained by using the conformation-dependent MC-1 antibody. In mice, part of the MC-1 signal may be derived from non-specific binding to mouse immunoglobulin 1 (IgG1). Scale bar: 20 µm. (C) Vascular and meningeal lesions in 18-month-old \textit{APP}_{swe}/\textit{PSI}_{\Delta E9} mice. Gallyas/6E10- (a) and thioflavin-S-positive vascular pathology (b). The arrows in (c) & (d) respectively point to thioflavin-S and Gallyas signal in the meninges of the cerebellum. Scale bars: 10 µm (a & b), 200 µm (c & d).
Fig. S2. Correlation between Gallyas-positive area fraction and \(^{18}\text{F}\)Flortaucipir binding levels. Signals from the Gallyas silver stain and \(^{18}\text{F}\)Flortaucipir autoradiography monitor the propagation of identical pathology, most likely tau-associated lesions. Each dot represents values from a single TG animal.
Fig. S3. Evaluation of methods for extracting sarkosyl-insoluble tau. TEM and immunoblotting of sarkosyl-insoluble tau, extracted according to (A) Sahara et al. (20) and (B) Greenberg and Davies (21). A triplet of immunoreactive bands in the 55-70 kDa range was detected by both methods, by using a rabbit antibody directed to the C-terminal domain of unmodified tau (aa 243-441; A0024, Dako Agilent). (C) Bands in A & B were spliced from gel in C, showing total tau immunoreactivity in the following groups: (1) TG 24 months, (6) WT 24 months (Greenberg and Davies method). (2) WT 24 months, (3) Human AD, (4) TG 18 months, (5) TG 24 months (Sahara et al. method).
**Fig. S4.** pS404 immunoblot. The accumulation of sarkosyl-insoluble tau hyperphosphorylated at pS404 in 24-month-old transgenic (TG) mice was confirmed with a rabbit anti-phosphoSer404 antibody (1:200; OAAF07796, Aviva Systems Biology).
| Background strain | Age (Months) | Gender | Method of Euthanasia | Method of Tau Evaluation | Antibody/Epitope | Brain Region | Reference |
|-------------------|-------------|--------|----------------------|--------------------------|-----------------|-------------|-----------|
| B6.C3             | 12          | Female | Anesthesia           | IHC                      | pS262           | NCx         | (75)      |
| B6.C3             | ~9          | Male   | Not reported         | IF & WB                  | pS396           | NCx & Hip   | (76)      |
| B6.C3             | ~7.5        | Male & Female | Anesthesia | IF                      | AT8 (pS202/pT205) | NCx & Hip   | (77)      |
| B6.C3             | 6 to >24    | Male   | Anesthesia           | IHC                      | PHF1, CP13, pT231, p262, pS396, pS422 | Entire Brain | (78)      |
| B6.C3             | 8           | Not reported | Anesthesia | IHC                      | AT8 (pS202/pT205) | NCx & Hip   | (79)      |
| B6.C3             | 11 & 18     | Male   | Not reported         | WB & Gallyas             | AT8 (pS202/pT205) | Entire Brain | (80)      |
| B6.C3             | 11          | Male   | Not reported         | IHC                      | AB1518 (not reported) | Hip        | (81)      |
| B6.C3             | 6 to >24    | Male   | Anesthesia           | IHC                      | PHF1 (pS396/pS404) | NCx & Hip   | (82)      |
| B6.C3             | ~7.5        | Male   | Anesthesia           | IF & IHC                 | AT8 (pS202/pT205) | NCx & Hip   | (83)      |
| B6.C3             | ~7          | Male   | Anesthesia           | WB                       | pS199, pS202, pS235, pS396, pS404 | FrCx & Hip | (84)      |
| C57BL/6           | 6           | Female | Cervical dislocation | WB & IHC                | pT205, pS396, pS404 | Hip        | (85)      |
| C57BL/6J          | 22          | Female | Anesthesia           | WB & IHC                | pS199, pS396    | NCx & Entire Brain | (86) |
| C57BL/6J          | 7           | Male   | Not reported         | IF                       | pS199           | NCx & Hip   | (87)      |
| C57BL/6J          | 3-12        | Not reported | Not reported | WB                      | PHF1 (pS396/pS404) | FrCx        | (88)      |
| C57BL/6J          | 12          | Male   | Cervical dislocation | Proteomics & Gallyas | N/A            | NCx & Hip, Olf. Bulb, Brainstem | (61) |
| C57BL/6           | ~9          | Female | Anesthesia           | WB                       | pS235, pT205    | Entire Brain | (89)      |
| C57BL/6J          | ~7.5        | Male   | Not reported         | WB                       | pS262           | NCx & Hip   | (90)      |
| C57BL/6           | 7           | Male   | Decapitation         | WB                       | PHF1 (pS396/pS404) | Hip        | (91)      |
| C57BL/6           | ~12         | Female | Anesthesia           | WB                       | pS235, pT205    | NCx & Hip   | (92)      |
| C57BL/6           | 3 & 6       | Male   | Not reported         | WB                       | pS199, pT205, pS396, pS404 | Hip        | (93)      |
| C57BL/6J          | ~7.5        | Male   | Not reported         | IF                       | pT181           | NCx & Hip   | (94)      |
| C57BL/6J          | 6 & 9       | Male   | Anesthesia           | IF                       | pS199, pS202, pS262, pT181 | NCx        | (95)      |
| C57BL/6           | 6-7         | Not reported | Anesthesia | IHC                      | AT8 (pS202/pT205) | Amygdala    | (96)      |
| C57BL/6J          | 12          | Not reported | Anesthesia | IHC/IF                   | AT8 (pS202/pT205) | PHF1 (pS396/pS404) | N/C        | (5)       |
| Not reported      | ~12         | Male   | Anesthesia           | WB                       | pS235, pT205    | Entire Brain | (97)      |
| Not reported      | 3-12        | Not reported | Anesthesia | WB                       | pS199, pT205, pS396, pS404 | Entire Brain | (98)      |
| Not reported      | 6           | Not reported | Anesthesia | WB                       | AT8 (pS202/pT205) | NCx        | (99)      |
| Not reported      | 7           | Not reported | Anesthesia | WB                       | pS396           | Brain hemisphere | (100) |
| Not reported      | ~7          | Not reported | Anesthesia | WB                       | AT8 (pS202/pT205) | NCx        | (101)     |
| Not reported      | >18         | Not reported | Anesthesia | IHC                      | pS199, pT231    | Cerebellum   | (102)     |
| Not reported      | ~2-3        | Male   | Anesthesia           | WB                       | PHF1 (pS396/pS404) | NCx & Hip   | (103)     |
| Not reported      | 2           | Male   | Anesthesia           | WB                       | AT8 (pS202/pT205) | PHF1 (pS396/pS404) | Subventricular zone, NCx & Hip | (104) |

**Table S1.** Evidence of tau hyperphosphorylation in APP<sub>swe</sub>/PSI<sub>ΔE9</sub> mice. Abbreviations: IHC: Immunohistochemistry; WB: Western Blot; IF: Immunofluorescence; NCx: Neocortex; Fr Cx: Frontal Cortex; Hip: Hippocampus.
| Accession | Description                                                                 | Abundance Ratio: (TG3) / (WT3) |
|-----------|------------------------------------------------------------------------------|--------------------------------|
| Q3YV117   | ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1                       | 5,526                          |
| Q3TTY5    | Keratin, type II cytoskeletal 2 epidermal OS=Mus musculus GN=Krt2 PE=1 SV=1  | 2,979                          |
| Q8BL66    | Early endosome antigen 1 OS=Mus musculus GN=Seal1 PE=1 SV=2                 | 2,834                          |
| B1AQ77    | Keratin 15, isoform CRA_a OS=Mus musculus GN=Krt15 PE=1 SV=1                | 2,777                          |
| Q3P0P4    | Keratin 5 OS=Mus musculus GN=Krt5 PE=2 SV=2                                 | 2,716                          |
| Q4VW25    | Acyl-CoA-binding protein OS=Mus musculus GN=Dbi PE=1 SV=1                   | 2,416                          |
| Q61782    | Type I epidermal keratin mRNA, 3'end (Fragment) OS=Mus musculus PE=2 SV=1    | 2,363                          |
| Q91VB8    | Alpha globin 1 OS=Mus musculus GN=haemoglobin alpha PE=1 SV=1               | 2,309                          |
| Q3UBP6    | Putative uncharacterized protein OS=Mus musculus GN=Actb PE=2 SV=1          | 2,147                          |
| D3YXH0    | Immunoglobulin superfamily member 5 OS=Mus musculus GN=Igsf5 PE=4 SV=1       | 2,139                          |
| Q08539    | Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1   | 2,109                          |
| Q3UV17    | Keratin, type II cytoskeletal 2 oral OS=Mus musculus GN=Krt76 PE=2 SV=1     | 2,096                          |
| P63005    | Platelet-activating factor acetylhydrolase IB subunit alpha OS=Mus musculus GN=Palh1b1 PE=1 SV=2 | 2,078                          |
| Q548F2    | Guanine deaminase OS=Mus musculus GN=Gda PE=2 SV=1                          | 1,997                          |
| Q6E902    | MCG10343, isoform CRA_b OS=Mus musculus GN=Slc25a3 PE=1 SV=1                | 1,993                          |
| Q9DCW4    | Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfb PE=1 SV=3 | 1,984                          |
| Q14929    | Histone cluster 1, H1d OS=Mus musculus GN=Hist1h1d PE=2 SV=1                | 1,883                          |
| Q62W42    | Thymosin, beta 4, X chromosome OS=Mus musculus GN=Tmsb4x PE=2 SV=1           | 1,832                          |
| B1AWD9    | Clathrin light chain A OS=Mus musculus GN=Clta PE=1 SV=1                    | 1,816                          |
| Q08331    | Calretinin OS=Mus musculus GN=Calb2 PE=1 SV=3                               | 1,814                          |
| P14115    | 60S ribosomal protein L27a OS=Mus musculus GN=Rpl27a PE=2 SV=5              | 1,809                          |
| P84086    | Complexin-2 OS=Mus musculus GN=Cplx2 PE=1 SV=1                              | 1,806                          |
| P02802    | Metallothionein-1 OS=Mus musculus GN=Mt1 PE=1 SV=1                          | 1,796                          |
| Q9043     | Myosin light chain 6B OS=Mus musculus GN=Mylb PE=2 SV=1                     | 1,771                          |
| P47962    | 60S ribosomal protein L5 OS=Mus musculus GN=Rpl5 PE=1 SV=3                  | 1,757                          |
| A8DUK4    | Beta-globin OS=Mus musculus GN=Hbbt1 PE=1 SV=1                              | 1,749                          |
| P99024    | Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1                     | 1,713                          |
| Q546G4    | Albumin 1 OS=Mus musculus GN=Alb PE=2 SV=1                                  | 1,688                          |
| P30065    | Thymosin beta-4 OS=Mus musculus GN=Tmsb4a PE=1 SV=1                         | 1,682                          |
| P62717    | 60S ribosomal protein L18a OS=Mus musculus GN=Rpl18a PE=1 SV=1              | 1,688                          |
| P62204    | Calmodulin OS=Mus musculus GN=Calm1 PE=1 SV=2                               | 1,677                          |
| P19157    | Glutathione S-transferase P 1 OS=Mus musculus GN=Gstp1 PE=1 SV=2            | 1,651                          |
| Q90P9     | Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Mus musculus GN=Uch1 PE=1 SV=1 | 1,647                          |
| Q8VD05    | Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4                                  | 1,624                          |
| Q0EQUS5-2 | Isoform 2 of Protein SET OS=Mus musculus GN=Set                             | 1,604                          |
| P17742    | Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2      | 1,595                          |
| Q810U4    | Neuronal cell adhesion molecule OS=Mus musculus GN=Nrcam PE=1 SV=2           | 1,586                          |
| Q6FX2     | Keratin, type I cytoskeletal 42 OS=Mus musculus GN=Krt42 PE=1 SV=1           | 1,586                          |
| P14869    | 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3          | 1,576                          |
| Q9WV69    | Dematin OS=Mus musculus GN=Dmnt PE=1 SV=1                                   | 1,561                          |
| Accession | Protein Name | Organism | Gene Name | Protein Feature | Entry Count |
|-----------|--------------|----------|-----------|----------------|-------------|
| Q5BLK1    | 40S ribosomal protein S6 | Mus musculus | Rps6 | PE=1 SV=1 | 3072 |
| 17751     | Triosephosphate isomerase | Mus musculus | Tpi1 | PE=1 SV=4 | 1556 |
| P99027    | 60S acidic ribosomal protein P2 | Mus musculus | Rplp2 | PE=1 SV=3 | 1519 |
| P55091    | Protein IMPACT | Mus musculus | Impact | PE=1 SV=2 | 1514 |
| P98086    | Complement C1q subcomponent subunit A | Mus musculus | C1qa | PE=1 SV=2 | 1493 |
| E9Q557    | Desmoplakin | Mus musculus | Dsp | PE=1 SV=1 | 1474 |
| P98086    | Complement C1q subcomponent subunit B | Mus musculus | C1qb | PE=2 SV=1 | 1429 |
| Q2RCZ8    | Secerin-1 | Mus musculus | Scrn1 | PE=1 SV=1 | 1415 |
| Q9D8J1    | Phosphoglycerate mutase 1 | Mus musculus |Pgaml | PE=1 SV=3 | 1411 |
| P68510    | 14-3-3 protein eta | Mus musculus | Ywhah | PE=1 SV=2 | 1394 |
| Q8K183    | Pyridoxal kinase | Mus musculus | Pdxk | PE=1 SV=1 | 1391 |
| Q3UR55    | ATPase, Na+/K+ transporting, beta 2 polypeptide | Mus musculus | Atp1b2 | PE=2 SV=1 | 1366 |
| Q63810    | Calcinurin subunit B type 1 | Mus musculus | Ppp3r1 | PE=1 SV=3 | 1355 |
| Q55866    | Splicing factor 3B subunit 1 | Mus musculus | Sf3b1 | PE=1 SV=2 | 1353 |
| P01352    | cAMP-dependent protein kinase catalytic subunit alpha | Mus musculus | Prkaca | PE=1 SV=3 | 1349 |
| Q8K2O8    | Cytochrome b-c1 complex subunit 6, mitochondrial | Mus musculus | Uqcrh | PE=1 SV=2 | 1367 |
| Q3U857    | Myosin-10 | Mus musculus | Myh10 | PE=1 SV=1 | 132 |
| Q79863    | 60S ribosomal protein L13 | Mus musculus | Rpl13 | PE=1 SV=3 | 1319 |
| Q80YN3    | Breast carcinoma-amplified sequence 1 homolog | Mus musculus | Bcas1 | PE=1 SV=3 | 1312 |
| Q5X7F6    | Ribosomal protein O | Mus musculus | Rpl10a | PE=1 SV=1 | 1302 |
| Q90X10    | Tenascin | Mus musculus | Tnc | PE=1 SV=1 | 775 |
| Q99K10    | Aconitate hydratase, mitochondrial | Mus musculus | Aco2 | PE=1 SV=1 | 773 |
| Q52K1C    | Eukaryotic translation initiation factor 4A2 | Mus musculus | Elf4a2 | PE=2 SV=1 | 772 |
| Q919V5    | Brain acid soluble protein 1 | Mus musculus | Basp1 | PE=1 SV=3 | 771 |
| Q548L4    | Glutamate decarboxylase X | Mus musculus | Gad2 | PE=2 SV=1 | 771 |
| A0A075B5P2 | Protein Igk (Fragment) | Mus musculus | Igk | PE=1 SV=1 | 779 |
| Q80Y1X    | Tenascin-O | Mus musculus | Tnc | PE=1 SV=1 | 769 |
| V9G7X6    | Unconventional myosin-VI | Mus musculus | Myo6 | PE=1 SV=1 | 768 |
| P63163    | Small nuclear ribonucleoprotein-associated protein N | Mus musculus | Snrnp | PE=2 SV=1 | 766 |
| S4R1P5    | Dystonin | Mus musculus | Dst | PE=1 SV=1 | 765 |
| P670766   | Cell division control protein 42 homolog | Mus musculus | Cdc42 | PE=1 SV=2 | 765 |
| Q9C213    | Cytochrome b-c1 complex subunit 1 | Mus musculus | Uqcrbc1 | PE=1 SV=2 | 764 |
| P61264    | Syntaxin-1B | Mus musculus | Stxb1 | PE=1 SV=1 | 764 |
| P40336    | Vacuolar protein sorting-associated protein 26A | Mus musculus | Vps26a | PE=1 SV=1 | 763 |
| B2RTL5    | Aldehyde dehydrogenase family 1, subfamily A7 | Mus musculus | Aldh1a7 | PE=2 SV=1 | 76 |
| E9Q455    | Tropomyosin alpha-1 chain | Mus musculus | Tpm1 | PE=1 SV=1 | 759 |
| Q92ZT6    | Keratin, type II cuticular Hb5 | Mus musculus | Krt85 | PE=2 SV=2 | 758 |
| Accession Number | Description                                                                 | E-Value | Score |
|------------------|------------------------------------------------------------------------------|---------|-------|
| Q9CZU6           | Citrate synthase, mitochondrial OS=Mus musculus GN=Cs PE=1 SV=1              | 0,757   |       |
| P62858           | 40S ribosomal protein S28 OS=Mus musculus GN=Rps28 PE=1 SV=1                 | 0,757   |       |
| P26883           | Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Mus musculus GN=Fkbp1a PE=1 SV=2 | 0,755   |       |
| P53395           | Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Mus musculus GN=Dbt PE=1 SV=2 | 0,755   |       |
| Q61838           | Alpha-2-macroglobulin OS=Mus musculus GN=A2m PE=1 SV=3                      | 0,754   |       |
| Q3TL9P           | RAS-related C3 botulinum substrate 1, isoform CRA_a OS=Mus musculus GN=Rac1 PE=1 SV=1 | 0,753   |       |
| Q9HU4            | Cytoplasmic dyn1 1 heavy chain 1 OS=Mus musculus GN=Dynclh1 PE=1 SV=2        | 0,753   |       |
| S4R349           | Ankyrin-2 OS=Mus musculus GN=Ank2 PE=1 SV=1                                 | 0,753   |       |
| Q9EF6            | Dihydropyrimidinase-related protein 5 OS=Mus musculus GN=Dpy5s1 PE=1 SV=1   | 0,746   |       |
| F6TY7            | Myelin basic protein (Fragment) OS=Mus musculus GN=Mbpe PE=1 SV=1            | 0,745   |       |
| QWUM4            | Coronin-1C OS=Mus musculus GN=Coro1c PE=1 SV=2                              | 0,744   |       |
| Q9WUB3           | Glycogen phosphorylase, muscle form OS=Mus musculus GN=Pygm PE=1 SV=3        | 0,744   |       |
| Q8CE0            | Sodium/potassium-transporting ATPase subunit alpha OS=Mus musculus GN=Atpa1a3 PE=1 SV=1 | 0,74   |       |
| P17427           | AP-2 complex subunit alpha-2 OS=Mus musculus GN=Ap2a2 PE=1 SV=2             | 0,739   |       |
| Q8C94            | Glycogen phosphorylase, brain form OS=Mus musculus GN=Pgpb PE=1 SV=3         | 0,737   |       |
| Q3U2G2           | Heat shock 70 kDa protein 4 OS=Mus musculus GN=Hspa4 PE=1 SV=1               | 0,736   |       |
| P3S4G8           | Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1 | 0,735   |       |
| Q9JLM8           | Serine/threonine-protein kinase DCLK1 OS=Mus musculus GN=Dclk1 PE=1 SV=1     | 0,731   |       |
| Q5XR6            | Clathrin heavy chain OS=Mus musculus GN=Cltc PE=1 SV=1                      | 0,73    |       |
| Q5S22            | Endonuclease domain-containing 1 protein OS=Mus musculus GN=Endod1 PE=1 SV=2 | 0,729   |       |
| Q9JK6            | Cell cycle exit and neuronal differentiation protein 1 OS=Mus musculus GN=Cend1 PE=1 SV=1 | 0,725   |       |
| B2RTM0           | Histone H4 OS=Mus musculus GN=Hist2h4 PE=2 SV=1                             | 0,725   |       |
| P63276           | 40S ribosomal protein S17 OS=Mus musculus GN=Rps17 PE=1 SV=2                 | 0,724   |       |
| Q62621           | Sprectin beta chain, non-erythrocytic 1 OS=Mus musculus GN=Sptb3 PE=1 SV=2   | 0,724   |       |
| A2AUKS           | Band 4.1-like protein 1 OS=Mus musculus GN=Epb41I1 PE=1 SV=1                | 0,722   |       |
| Q8BV14           | Dihydropyrimidinase reductase OS=Mus musculus GN=Qdpr PE=1 SV=2              | 0,72    |       |
| P47857           | ATP-dependent 6-phosphofructokinase, muscle type OS=Mus musculus GN=Pfkme PE=1 SV=3 | 0,72    |       |
| P60202           | Myelin proteolipid protein OS=Mus musculus GN=Plp1 PE=1 SV=2                 | 0,719   |       |
| E9Q7Q3           | Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=1                  | 0,718   |       |
| Q5SYD0           | Unconventional myosin-7d OS=Mus musculus GN=Myo1d PE=1 SV=1                  | 0,718   |       |
| Q9QLW7           | Keratin, type I cytoskeletal 17 OS=Mus musculus GN=Krt17 PE=1 SV=3           | 0,71    |       |
| P84078           | ADP-ribosylation factor 1 OS=Mus musculus GN=Art1 PE=1 SV=2                  | 0,71    |       |
| P43274           | Histone H1.4 OS=Mus musculus GN=Hist1h1e PE=1 SV=2                           | 0,71    |       |
| Q9WW92           | Band 4.1-like protein 3 OS=Mus musculus GN=Ep41I13 PE=1 SV=1                 | 0,709   |       |
| G5E924           | Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Mus musculus GN=Hnrnpl PE=1 SV=1 | 0,708   |       |
| P63318           | Protein kinase C gamma type OS=Mus musculus GN=Prkcg PE=1 SV=1               | 0,707   |       |
| Q9CZY3           | Ubiquitin-conjugating enzyme E2 variant 1 OS=Mus musculus GN=Ube2v1 PE=1 SV=1 | 0,707   |       |
| P48771           | Cytochrome c oxidase subunit 7A2, mitochondrial OS=Mus musculus GN=Cox7a2 PE=1 SV=2 | 0,706   |       |
| Q3T10S           | Chaperonin containingTcp1, subunit 6a (Zeta) OS=Mus musculus GN=Cct6a PE=2 SV=1 | 0,706   |       |
| B2RXK2           | Serine/threonine-protein phosphatase OS=Mus musculus GN=Ppp3ca PE=2 SV=1      | 0,704   |       |
| Q9DOM3           | Cytochrome c1, heme protein, mitochondrial OS=Mus musculus GN=Cyc1 PE=1 SV=1  | 0,701   |       |
| P56399           | Ubiquitin carboxyl-terminal hydrolase 5 OS=Mus musculus GN=Usp5 PE=1 SV=1     | 0,701   |       |
| Q543Y7           | Putative uncharacterized protein OS=Mus musculus GN=Pacs1 PE=2 SV=1          | 0,7     |       |
| Q9DCD0           | 6-phosphogluconate dehydrogenase, decarboxylating OS=Mus musculus GN=Pgd PE=1 SV=3 | 0,693   |       |
| Accession | Protein Name                                      | Gene Name   | Organism          | PE | SV |
|-----------|--------------------------------------------------|-------------|-------------------|----|----|
| A0A0MQA5  | Tubulin alpha chain (Fragment)                   | Tuba4a      | Mus musculus      | 1  | 1  |
| P46097    | Synaptotagmin-2                                  | Syt2        | Mus musculus      | 1  | 1  |
| P39053    | Dynamin-1                                        | Dnm1        | Mus musculus      | 1  | 2  |
| Q21G4     | V-type proton ATPase subunit a isoform 1         | Ap6v0a1     | Mus musculus      | 1  | 3  |
| Q2CX86    | Heterogeneous nuclear ribonucleoprotein A0        | Hnrnpa0     | Mus musculus      | 1  | 1  |
| P26645    | Myristoylated alanine-rich C-kinase substrate     | Marcks      | Mus musculus      | 1  | 1  |
| Q7Z28J    | MGC22989, isoform CRA_b                          | Rab11b      | Mus musculus      | 1  | 2  |
| Q4R001    | Microtubule-associated protein RP/EB family member| Mapre2      | Mus musculus      | 1  | 1  |
| P11798    | Calcium/calmodulin-dependent protein kinase type II| Camk2a     | Mus musculus      | 1  | 1  |
| Q33UV7    | Putative uncharacterized protein                  | Mlf2        | Mus musculus      | 1  | 2  |
| E9Q401    | Ryanodine receptor 2                              | Ryr2        | Mus musculus      | 1  | 1  |
| Q9D051    | Pyruvate dehydrogenase E1 component subunit beta | Pdhb        | Mus musculus      | 1  | 1  |
| Q2UMU9    | Hepatoma-derived growth factor-related protein    | Ral7        | Mus musculus      | 1  | 2  |
| Q92Z19    | Succinate-CoA ligase [ADP-forming] subunit beta   | Scl2a       | Mus musculus      | 1  | 2  |
| P14148    | 60S ribosomal protein L7                         | Rpl7        | Mus musculus      | 1  | 2  |
| P62317    | Small nuclear ribonucleoprotein Sm D2             | Snpd2       | Mus musculus      | 3  | 1  |
| Q92Z26    | Tetraspanin-2                                    | Tspan2      | Mus musculus      | 1  | 1  |
| Q19001    | Keratin, type I cytoskeletal 19                   | Krt19       | Mus musculus      | 1  | 1  |
| Q27318    | Band 4.1-like protein 2                           | Ebp4112     | Mus musculus      | 1  | 2  |
| Q923T9    | Calcium/calmodulin-dependent protein kinase type II| Camk2g     | Mus musculus      | 1  | 1  |
| A0A0G2JFT8| Protein RUFY3                                    | Rufy3       | Mus musculus      | 1  | 1  |
| Q3UHL1    | CaM kinase-like vesicle-associated protein       | Camk4v      | Mus musculus      | 1  | 2  |
| P62305    | Small nuclear ribonucleoprotein E                | Snrpe       | Mus musculus      | 1  | 1  |
| Q5DQ3     | Capping protein (Actin filament) muscle Z-line, alpha 2, isoform CRA_c | Capza2 | Mus musculus | 2 | 1 |
| Q7TSI2    | Microtubule-associated protein 6                   | Map6        | Mus musculus      | 1  | 2  |
| Q92B13    | 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1 | Plcb1 | Mus musculus | 1 | 2 |
| Q3UYK6    | Amino acid transporter                            | Sc1a2       | Mus musculus      | 2  | 1  |
| B2RXY7    | Carbonyl reductase 1                              | Cbr1        | Mus musculus      | 2  | 1  |
| P52480-2  | Isoform M1 of Pyruvate kinase PKM                 | Pkm         | Mus musculus      | 1  | 1  |
| Q3TXU4    | Apolipoprotein E, isoform CRA_h                   | Apoe        | Mus musculus      | 2  | 1  |
| P62715    | Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform | Ppp2cb | Mus musculus | 1 | 1 |
| P80313    | T-complex protein 1 subunit eta                   | Cct7        | Mus musculus      | 1  | 1  |
| P61255    | 60S ribosomal protein L26                         | Rpl26       | Mus musculus      | 1  | 1  |
| Q4FX4     | Csrp1 protein OS=Mus musculus                    | Csrp1       | Mus musculus      | 1  | 1  |
| Q8VEK3    | Heterogeneous nuclear ribonucleoprotein U         | Hnrnpu      | Mus musculus      | 1  | 1  |
| Q3UAD6    | Heat shock protein 90kDa beta (Grp94)             | Hsp90b1     | Mus musculus      | 1  | 2  |
| Q90UM9    | Proteasome subunit alpha-6 OS=Mus musculus       | Poma6       | Mus musculus      | 1  | 1  |
| P47757    | F-actin-capping protein subunit beta OS=Mus musculus | Capzb | Mus musculus | 1 | 2 |
| Q9R1P1    | Proteasome subunit beta-3 OS=Mus musculus        | Psmb3       | Mus musculus      | 1  | 1  |
| P12382    | ATP-dependent 6-phosphofructokinase, liver type OS=Mus musculus | Pfk1 | Mus musculus | 1 | 1 |
| Q88MS1    | Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus | Hadha | Mus musculus | 1 | 1 |
| E9PYH0    | Versican core protein OS=Mus musculus            | Vcan        | Mus musculus      | 1  | 1  |
| P27773    | Protein disulfide-isomerase A3 OS=Mus musculus    | Pdla3       | Mus musculus      | 1  | 1  |
| Q8BG05    | Heterogeneous nuclear ribonucleoprotein A3        | Hnrnpa3     | Mus musculus      | 1  | 1  |
| Accession  | Name and Description                                                                 | Score |
|------------|--------------------------------------------------------------------------------------|-------|
| P00920     | Carbonic anhydrase 2 OS=Mus musculus GN=Ca2 PE=1 SV=4                                | 0.626 |
| E9QA2X     | Unconventional myosin-XVIIIA OS=Mus musculus GN=Myo18a PE=1 SV=1                     | 0.625 |
| P19246     | Neurofilament heavy polypeptide OS=Mus musculus GN=Nefh PE=1 SV=3                    | 0.623 |
| P17426     | AP-2 complex subunit alpha-1 OS=Mus musculus GN=Ap2a1 PE=1 SV=1                      | 0.623 |
| Q68FL4     | Putative adenosylhomocysteinase 3 OS=Mus musculus GN=Ahcy2 PE=1 SV=1                 | 0.619 |
| Q2PFD7     | PH and SEC7 domain-containing protein 3 OS=Mus musculus GN=Psd3 PE=1 SV=2             | 0.615 |
| Q3UYY1     | Myelin-oligodendrocyte glycoprotein OS=Mus musculus GN=Mog PE=1 SV=1                 | 0.614 |
| P10637-3   | Isomorph Tau-B of Microtubule-associated protein tau OS=Mus musculus GN=Mapt         | 0.611 |
| Q88F92     | Elin-2 OS=Mus musculus GN=Elin2 PE=1 SV=1                                             | 0.610 |
| E9PVP0     | PCTP-like protein OS=Mus musculus GN=Stard10 PE=1 SV=1                                | 0.609 |
| Q8R0Y6     | Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh111 PE=1 SV=1 | 0.608 |
| Q62182     | Aggreca core protein OS=Mus musculus GN=Acan PE=1 SV=2                                 | 0.607 |
| O09061     | Proteasome subunit beta type-1 OS=Mus musculus GN=Psmb1 PE=1 SV=1                    | 0.599 |
| Q542X7     | Chaperonin subunit 2 (Beta), isoform CRA_b OS=Mus musculus GN=Cct2 PE=2 SV=1           | 0.597 |
| O55143     | Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus GN=Atpa2a PE=2 SV=2 | 0.591 |
| Q5FW9      | Adaptor protein complex CP2, mu1 OS=Mus musculus GN=Ap2m1 PE=2 SV=2                   | 0.587 |
| Q7M6W1     | Reticulin OS=Mus musculus GN=Rtn1 PE=1 SV=1                                           | 0.587 |
| P50066     | Neurocan core protein OS=Mus musculus GN=Ncan PE=2 SV=1                                | 0.584 |
| Q8BY9Y     | Tenasin-C OS=Mus musculus GN=Tnr PE=1 SV=2                                            | 0.584 |
| Q9JL3      | Methylglutacol-CoA hydtratase, mitochondrial OS=Mus musculus GN=Auh PE=1 SV=1           | 0.58  |
| P62307     | Small nuclear ribonucleoprotein F OS=Mus musculus GN=Snrfp PE=1 SV=1                  | 0.58  |
| Q544E3     | Phosphatidylinositol-4-phosphate 5-kinase, type II, alpha OS=Mus musculus GN=Pipk2a PE=2 SV=1 | 0.579 |
| P48036     | Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1                                        | 0.573 |
| P31324     | cAMP-dependent protein kinase type II-beta regulatory subunit OS=Mus musculus GN=Prkra2b PE=1 SV=3 | 0.572 |
| Q99M71     | Mammalian epipodemin-related protein 1 OS=Mus musculus GN=Epdr1 PE=2 SV=1             | 0.571 |
| P70202     | Latexin OS=Mus musculus GN=Lx1 PE=1 SV=2                                              | 0.57  |
| P12023     | Amyloid beta A4 protein OS=Mus musculus GN=App PE=1 SV=3                                | 0.57  |
| Q9QUP5     | Hyaluronan and proteoglycan link protein 1 OS=Mus musculus GN=Hapln1 PE=1 SV=1         | 0.568 |
| Q04690     | Neurofibromin OS=Mus musculus GN=NT1 PE=1 SV=1                                        | 0.566 |
| Q9CU62     | Structural maintenance of chromosomes protein 1A OS=Mus musculus GN=Smc1a PE=1 SV=4    | 0.566 |
| Q9QYC0     | Alpha-actinin OS=Mus musculus GN=Adc1 PE=1 SV=2                                        | 0.564 |
| Q9ES5M     | Hyaluronan and proteoglycan link protein 2 OS=Mus musculus GN=Hapln2 PE=1 SV=1         | 0.563 |
| Q5BLK0     | MCG18564, isoform CRA_a OS=Mus musculus GN=Rpl12 PE=2 SV=1                            | 0.56  |
| P31550     | Sodium- and chloride-dependent GABA transporter 3 OS=Mus musculus GN=Scl6a11 PE=1 SV=2 | 0.56  |
| Q9R19P     | Proteasome subunit alpha type-4 OS=Mus musculus GN=Psma4 PE=1 SV=1                    | 0.56  |
| Q9QX51     | Plectin OS=Mus musculus GN=Plec PE=1 SV=3                                             | 0.559 |
| Q92331     | Keratin, type II cytoskeletal 6B OS=Mus musculus GN=Krt6b PE=1 SV=3                    | 0.558 |
| P09528     | Ferritin heavy chain OS=Mus musculus GN=Fth1 PE=1 SV=2                                 | 0.558 |
| P11881     | Inositol 1,4,5-trisphosphate receptor type 1 OS=Mus musculus GN=Itrp1 PE=1 SV=2        | 0.557 |
| F8WB81     | Calcium-transporting ATPase OS=Mus musculus GN=Atp2b2 PE=1 SV=1                       | 0.556 |
| P97300     | Neuroplastin OS=Mus musculus GN=Nptn PE=1 SV=3                                        | 0.555 |
| Q5SS83     | Flotillin 2, isoform CRA_b OS=Mus musculus GN=Flot2 PE=1 SV=1                          | 0.555 |
| Q912X7     | Prolow-density lipoprotein receptor-related protein 1 OS=Mus musculus GN=Lrp1 PE=1 SV=1 | 0.554 |
| Q3TQ70     | Beta1 subunit of GTP-binding protein OS=Mus musculus GN=Gnb1 PE=2 SV=1                | 0.549 |
| Gene ID   | Description                                                                 | Species       | Gene ID   | Description                                                                 | Species       |
|-----------|-----------------------------------------------------------------------------|---------------|-----------|-----------------------------------------------------------------------------|---------------|
| Q60692    | Proteasome subunit beta type-6 OS=Mus musculus GN=Psmb6 PE=1 SV=3            |               | A6H611    | Mitochondrial intermediate peptidase OS=Mus musculus GN=Mipep PE=1 SV=1     |               |
| Q9CX54    | Centromere protein V OS=Mus musculus GN=Centp PE=1 SV=2                     |               | Q922U0    | Proteasome subunit alpha type-7 OS=Mus musculus GN=Psma7 PE=1 SV=1          |               |
| Q8C605    | ATP-dependent 6-phosphofructokinase OS=Mus musculus GN=Pfkp PE=1 SV=1       |               | P48722    | Heat shock 70 kDa protein 4L OS=Mus musculus GN=Hspa4l PE=1 SV=2             |               |
| P63011    | Ras-related protein Rab-3A OS=Mus musculus GN=Rab3a PE=1 SV=1               |               | A0A0G2JG54| Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Mus musculus GN=Camk2d PE=4 SV=1 |               |
| P17156    | Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV=2      |               | P99026    | Proteasome subunit beta type-4 OS=Mus musculus GN=Psmb4 PE=1 SV=1            |               |
| Q9R1P4    | Proteasome subunit alpha type-1 OS=Mus musculus GN=Poma1 PE=1 SV=1          |               | P01592    | Immunoglobulin J chain OS=Mus musculus GN=Igj PE=2 SV=4                    |               |
| P35235    | Tyrosine-protein phosphatase non-receptor type 11 OS=Mus musculus GN=Ptpn11 PE=1 SV=2 |               | Q99PUS    | Long-chain-fatty-acid-CoA ligase ACSBG1 OS=Mus musculus GN=Acsbg1 PE=1 SV=1 |               |
| P60879    | Synaptosomal-associated protein 25 OS=Mus musculus GN=Snap25 PE=1 SV=1       |               | P80TL4    | PHD finger protein 24 OS=Mus musculus GN=Phf24 PE=1 SV=2                   |               |
| Q545X8    | 40S ribosomal protein S4 OS=Mus musculus GN=Rps4x PE=2 SV=1                 |               | Q9QYX7    | Protein piccolo OS=Mus musculus GN=Pclo PE=1 SV=4                          |               |
| D0VYV6    | Erythrocyte protein band 4.1-like 3 isoform B OS=Mus musculus GN=Epb4.13 PE=2 SV=1 |               | Q88VE3    | V-type proton ATPase subunit H OS=Mus musculus GN=Atp6v1h PE=1 SV=1         |               |
| Q08917    | Flotillin-1 OS=Mus musculus GN=Flot1 PE=1 SV=1                              |               | Q9WT4     | Insulin-receptor-related protein OS=Mus musculus GN=Insr PE=2 SV=2          |               |
| P21460    | Cystatin-C OS=Mus musculus GN=Cst3 PE=1 SV=2                                |               | P62814    | V-type proton ATPase subunit B, brain isoform OS=Mus musculus GN=Atp6v1b2 PE=1 SV=1 |               |
| A0A076FRG6| KCC2a variant 1 OS=Mus musculus GN=Slc12a5 PE=2 SV=1                       |               | O55234    | Proteasome subunit beta type-5 OS=Mus musculus GN=Psmb5 PE=1 SV=3           |               |
| P49722    | Proteasome subunit alpha type-2 OS=Mus musculus GN=Psma2 PE=1 SV=3          |               | Q0D2G2    | Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Mus musculus GN=Dist PE=1 SV=1 |               |
| Q9CPX4    | Ferritin OS=Mus musculus GN=Fht1 PE=1 SV=1                                 |               | Q9BGT8    | Phytanoyl-CoA hydroxylase-interacting protein-like OS=Mus musculus GN=Phyhipl PE=2 SV=1 |               |
| Q8BF4     | Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Mus musculus GN=Slc9a3r1 PE=1 SV=3 |               | Q0VF55    | Calcium-transporting ATPase OS=Mus musculus GN=Atp2b3 PE=1 SV=1             |               |
| P63085    | Mitogen-activated protein kinase 1 OS=Mus musculus GN=Mapk1 PE=1 SV=3       |               | Q2UGC8    | Propionyl-Coenzyme A carboxylase, alpha polypeptide, isoform CRA_b OS=Mus musculus GN=Pcca PE=2 SV=1 |               |
| Q22U1     | Proteasome subunit alpha type-5 OS=Mus musculus GN=Psma5 PE=1 SV=1          |               | P62827    | GTP-binding nuclear protein Ran OS=Mus musculus GN=Ran PE=1 SV=3             |               |
| Q0RSS5    | Synaptic vesicle glycoprotein 2A OS=Mus musculus GN=Svga2a PE=1 SV=1        |               | Q9R1P3    | Proteasome subunit beta type-2 OS=Mus musculus GN=Psmb2 PE=1 SV=1            |               |
| Q9QOZ8    | Core histone macro-H2A.1 OS=Mus musculus GN=H2afy PE=1 SV=3                 |               | Q9V1E0    | Long-chain fatty acid transport protein 4 OS=Mus musculus GN=Cla27a4 PE=1 SV=1 |               |
| O35955    | Proteasome subunit beta type-10 OS=Mus musculus GN=Psmb10 PE=1 SV=1         |               | O35962    | Barrier-to-autointegration factor OS=Mus musculus GN=Banf1 PE=1 SV=1         |               |
| A2AWN8    | YTH domain family 1, isoform CRA_a OS=Mus musculus GN=Ythdf1 PE=1 SV=1     |               | P70195    | Proteasome subunit beta type-7 OS=Mus musculus GN=Psmb7 PE=1 SV=1            |               |
| Accession | Description                                                                 | Organism   | Gene Name | Peptide | Score |
|-----------|------------------------------------------------------------------------------|------------|-----------|---------|-------|
| P14106    | Complement C1q subcomponent subunit B                                     | Mus musculus | C1qb      | PE=1    | 0.441 |
| Q8BKZ9    | Pyruvate dehydrogenase protein X component, mitochondrial                    | Mus musculus | Pdhx      | PE=1    | 0.438 |
| Q91ZU6    | Dystonin                                                                     | Mus musculus | Dst       | PE=1    | 0.438 |
| Q8R016    | Bleomycin hydrolase                                                         | Mus musculus | Blmh      | PE=1    | 0.438 |
| Q3U7E0    | Putative uncharacterized protein                                            | Mus musculus | Atp6v1g1  | PE=2    | 0.436 |
| A2CEK3    | Phosphoglucomutase-2                                                        | Mus musculus | Pgm2      | PE=1    | 0.431 |
| B9EIC7    | MCG3853                                                                     | Mus musculus | Pdhx      | PE=2    | 0.421 |
| L9PUA3    | IQ motif and SEC7 domain-containing protein                                 | Mus musculus | Iqsec1    | PE=1    | 0.407 |
| Q88MF4    | Dihydropolylysine-residue acetyltransferase component of pyruvate dehydrogenase complex | Mus musculus | Dlat     | PE=1    | 0.407 |
| P42669    | Transcriptional activator protein Pur-alpha                                 | Mus musculus | Pura      | PE=1    | 0.398 |
| Q9ZO4H    | CUGBP Elav-like family member 2                                            | Mus musculus | Celh2     | PE=1    | 0.395 |
| Q58EV4    | Proteasome subunit alpha type                                               | Mus musculus | Psma3     | PE=2    | 0.393 |
| Q920E0    | Neurochondrin                                                              | Mus musculus | Ncdn      | PE=1    | 0.39  |
| Q58EA6    | MCG10725, isoform CRA_a                                                    | Mus musculus | Rps25     | PE=2    | 0.366 |
| P11983    | T-complex protein 1 subunit alpha                                           | Mus musculus | Tcp1      | PE=1    | 0.365 |
| Q9JM93    | ADP-ribosylation factor-like protein 6-interacting protein 4                | Mus musculus | Arl6ip4   | PE=1    | 0.34  |
| Q5SQX6    | Cytoplasmic FMR1-interacting protein 2                                      | Mus musculus | Cyfip2    | PE=1    | 0.327 |
| F6VYP7    | Protein Gm10260                                                             | Mus musculus | Gm10260   | PE=3    | 0.286 |
| F6VPT0    | Protein Ccdc163 (Fragment)                                                  | Mus musculus | Ccdc163   | PE=4    | 0.284 |
| Q02105    | Complement C1q subcomponent subunit C                                       | Mus musculus | C1qc      | PE=2    | 0.274 |
| Q99MN9    | Propionyl-CoA carboxylase beta chain, mitochondrial                         | Mus musculus | Pccb      | PE=1    | 0.229 |
| Q3V0Q1    | Dynein heavy chain 12, axonemal                                             | Mus musculus | Dnah12    | PE=1    | 0.227 |
| Q3TVK3    | Aspartyl aminopeptidase                                                      | Mus musculus | Dnpep     | PE=1    | 0.224 |
| Q9D8B3    | Charged multivesicular body protein 4b                                      | Mus musculus | Chmp4b    | PE=1    | 0.201 |
| Q8R184    | Eukaryotic translation initiation factor 3 subunit C                        | Mus musculus | Eif3c     | PE=1    | 0.189 |
## DATA FILE S1
### REGULATED PROTEINS 24 MONTHS: TG vs. WT

| Accession   | Description                                                                 | Description | Abundance Ratio: (TG24) / (WT24) |
|-------------|-----------------------------------------------------------------------------|-------------|----------------------------------|
| P12023      | Amyloid beta A4 protein OS=Mus musculus GN=App PE=1 SV=3                   |             | 14,021                           |
| Q35Y5       | Keratin 16 OS=Mus musculus GN=Krt16 PE=2 SV=1                              |             | 8,4                              |
| Q9Z31       | Keratin, type II cytoskeletal 6B OS=Mus musculus GN=Krt6b PE=1 SV=3        |             | 5,956                            |
| Q6IFX2      | Keratin, type I cytoskeletal 42 OS=Mus musculus GN=Krt42 PE=1 SV=1         |             | 5,635                            |
| Q9IM93      | ADP-ribosylation factor-like protein 6-interacting protein 4 OS=Mus musculus GN=Arl6ip4 PE=1 SV=1 |             | 5,486                            |
| Q61782      | Type I epidermal keratin mRNA, 3’end (Fragment) OS=Mus musculus PE=2 SV=1 |             | 4,628                            |
| Q9QW17      | Keratin, type I cytoskeletal 17 OS=Mus musculus GN=Krt17 PE=1 SV=3         |             | 4,351                            |
| Q99MN9      | Propionyl-CoA carboxylase beta chain, mitochondrial OS=Mus musculus GN=Pccb PE=1 SV=2 |             | 3,96                             |
| Q9CZY3      | Ubiquitin-conjugating enzyme E2 variant 1 OS=Mus musculus GN=Ube2v1 PE=1 SV=1 |             | 3,89                             |
| Q9WTL4      | Insulin receptor-related protein OS=Mus musculus GN=Insr PE=1 SV=2         |             | 3,852                            |
| P62715      | Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Mus musculus GN=Ppp2cb PE=1 SV=1 |             | 3,674                            |
| Q61781      | Keratin, type I cytoskeletal 14 OS=Mus musculus GN=Krt14 PE=1 SV=2         |             | 3,606                            |
| P19001      | Keratin, type I cytoskeletal 19 OS=Mus musculus GN=Krt19 PE=1 SV=1         |             | 3,598                            |
| Q3TXU4      | Apolipoprotein E, isoform CRA_h OS=Mus musculus GN=Apoe PE=2 SV=1          |             | 3,577                            |
| P43276      | Histone H1.5 OS=Mus musculus GN=Hist1h1b PE=1 SV=2                        |             | 3,402                            |
| P10637-3    | Isoform Tau-B of Microtubule-associated protein tau OS=Mus musculus GN=Mapt |             | 3,212                            |
| P14685      | 26S proteasome non-ATPase regulatory subunit 3 OS=Mus musculus GN=Psmd3 PE=1 SV=3 |             | 3,164                            |
| Q9D0M3      | Cytochrome c1, heme protein, mitochondrial OS=Mus musculus GN=Cyc1 PE=1 SV=1 |             | 2,935                            |
| Q80Y1       | Tenascin OS=Mus musculus GN=Tnc PE=1 SV=1                                 |             | 2,749                            |
| Q9JLM8      | Serine/threonine-protein kinase DCLK1 OS=Mus musculus GN=Dclk1 PE=1 SV=1   |             | 2,726                            |
| AOA140T8K6  | 60S ribosomal protein L36 OS=Mus musculus GN=Rpl36-ps3 PE=3 SV=1           |             | 2,694                            |
| P12787      | Cytochrome c oxidase subunit 5A, mitochondrial OS=Mus musculus GN=Cox5a PE=1 SV=2 |             | 2,555                            |
| Q3V0Q1      | Dynein heavy chain 12, axonemal OS=Mus musculus GN=Dnah12 PE=1 SV=2        |             | 2,526                            |
| Q91VE0      | Long-chain fatty acid transport protein 4 OS=Mus musculus GN=Slc27a4 PE=1 SV=1 |             | 2,47                             |
| Q6S4G0      | Guanylate kinase OS=Mus musculus GN=Guk1 PE=1 SV=1                        |             | 2,384                            |
| Q8R366      | Immunoglobulin superfamily member 8 OS=Mus musculus GN=Igsf8 PE=1 SV=2    |             | 2,374                            |
| E9Q5S7      | Desmoplakin OS=Mus musculus GN=Dsp PE=1 SV=1                              |             | 2,319                            |
| Q9D0823     | 60S ribosomal protein L37 OS=Mus musculus GN=Rpl37 PE=3 SV=3              |             | 2,302                            |
| P62855      | 40S ribosomal protein S26 OS=Mus musculus GN=Rps26 PE=1 SV=3              |             | 2,296                            |
| Q3P204      | Keratin 5 OS=Mus musculus GN=Krt5 PE=2 SV=2                               |             | 2,268                            |
| Q8R1B4      | Eukaryotic translation initiation factor 3 subunit C OS=Mus musculus GN=If3c PE=1 SV=1 |             | 2,204                            |
| Q8C1Y8      | Vacuolar fusion protein CCZ1 homolog OS=Mus musculus GN=Ccz1 PE=1 SV=1    |             | 2,201                            |
| V9G6X76     | Unconventional myosin-VI OS=Mus musculus GN=Myo6 PE=1 SV=1                |             | 2,143                            |
| Q9CXS4      | Centromere protein V OS=Mus musculus GN=Cenpv PE=1 SV=2                   |             | 2,142                            |
| Q9QX51      | Plectin OS=Mus musculus GN=Plec PE=1 SV=3                                 |             | 2,138                            |
| P62717      | 60S ribosomal protein L18a OS=Mus musculus GN=Rpl18a PE=1 SV=1            |             | 2,133                            |
| P62307      | Small nuclear ribonucleoprotein F OS=Mus musculus GN=Snrpf PE=1 SV=1      |             | 2,066                            |
| Q9CYR0      | Single-stranded DNA-binding protein, mitochondrial OS=Mus musculus GN=Ssbp1 PE=1 SV=1 |             | 2,033                            |
| Accession | Description                                                                 | Organism  | Gene Name | Protein Entry | Similarity Score |
|-----------|-----------------------------------------------------------------------------|-----------|-----------|----------------|------------------|
| Q8C522    | Endonuclease domain-containing 1 protein OS=Mus musculus GN=Endod1 PE=1 SV=2 | Mus musculus | Endod1    | 2,031          |                  |
| P97499    | Telomerase protein component 1 OS=Mus musculus GN=Tep1 PE=1 SV=1             | Mus musculus | Tep1      | 2,01           |                  |
| Q9R062    | Glycogenin-1 OS=Mus musculus GN=Gyg1 PE=1 SV=3                               | Mus musculus | Gyg1      | 1,985          |                  |
| Q9QW6     | SRC kinase signaling inhibitor 1 OS=Mus musculus GN=Srcin1 PE=1 SV=2         | Mus musculus | Srcin1    | 1,98           |                  |
| P63163    | Small nuclear ribonucleoprotein-associated protein OS=Mus musculus GN=Snrp PE=2 | Mus musculus | Snrp      | 1,948          |                  |
| P17427    | AP-2 complex subunit alpha-2 OS=Mus musculus GN=Ap2a2 PE=1 SV=2             | Mus musculus | Ap2a2     | 1,948          |                  |
| Q5BKL0    | MCG1B564, isoform CRA-a OS=Mus musculus GN=Rpl12 PE=2 SV=1                   | Mus musculus | Rpl12     | 1,948          |                  |
| J3QMG3    | Voltage-dependent anion-selective channel protein OS=Mus musculus GN=Vdac3 PE=1 | Mus musculus | Vdac3   | 1,911          |                  |
| Q9DCW4    | Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfb PE=1 SV=3 | Mus musculus | Etfb      | 1,906          |                  |
| Q5BEW0    | 60S ribosomal protein L18 OS=Mus musculus GN=Rpl18 PE=2 SV=2                 | Mus musculus | Rpl18     | 1,886          |                  |
| Q8BFM4    | Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Mus musculus GN=DiOS=Mus musculus GN=Di | Mus musculus | Di | 1,856          |                  |
| Q9Z0H4    | CUGBP Elav-like family member 2 OS=Mus musculus GN=Cell2 PE=1 SV=1           | Mus musculus | Cell2    | 1,845          |                  |
| P46660    | Alpha-internexin OS=Mus musculus GN=Ina PE=1 SV=3                           | Mus musculus | Ina     | 1,828          |                  |
| P08752    | Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Mus musculus GN=Gna2 PE=1 SV=5 | Mus musculus | Gna2 | 1,823          |                  |
| Q549A5    | Clusterin OS=Mus musculus GN=Cli PE=2 SV=1                                  | Mus musculus | Clu     | 1,822          |                  |
| Q8BTI8    | Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3 | Mus musculus | Srrm2 | 1,819          |                  |
| Q3TI05    | Chaperonin containing Tcp1, subunit 6a (Zeta) OS=Mus musculus GN=Cct6a PE=2 SV=1 | Mus musculus | Cct6a | 1,814          |                  |
| OS5091    | Protein IMPACT OS=Mus musculus GN=Impact PE=1 SV=2                         | Mus musculus | Impact | 1,778          |                  |
| F6TBY7    | Myelin basic protein (Fragment) OS=Mus musculus GN=Mbp PE=1 SV=1            | Mus musculus | Mbp     | 1,776          |                  |
| Q04690    | Neurofilament OS=Mus musculus GN=Nf1 PE=1 SV=1                              | Mus musculus | Nf1     | 1,722          |                  |
| P03995    | Gial fibrillary acidic protein OS=Mus musculus GN=Gfap PE=1 SV=4             | Mus musculus | Gfap    | 1,694          |                  |
| E9Q401    | Ryanodine receptor 2 OS=Mus musculus GN=Ryr2 PE=1 SV=1                      | Mus musculus | Ryr2    | 1,689          |                  |
| Q5BLL9    | 60S ribosomal protein L27 OS=Mus musculus GN=Rpl27 PE=1 SV=1                | Mus musculus | Rpl27   | 1,688          |                  |
| A2CEK3    | Phosphoglucomutase-2 OS=Mus musculus GN=Pgm2 PE=1 SV=1                      | Mus musculus | Pgm2   | 1,675          |                  |
| P61514    | 60S ribosomal protein L37a OS=Mus musculus GN=Rpl37a PE=3 SV=2             | Mus musculus | Rpl37a | 1,667          |                  |
| Q5OSA8    | MCG17585 OS=Mus musculus GN=Rpl39 PE=2 SV=1                                | Mus musculus | Rpl39   | 1,64           |                  |
| P11983    | T-complex protein 1 subunit alpha OS=Mus musculus GN=Tcp1 PE=1 SV=3         | Mus musculus | Tcp1   | 1,637          |                  |
| Q9DO5M5   | Dynein light chain 2, cytoplasmic OS=Mus musculus GN=Dynl2 PE=1 SV=1        | Mus musculus | Dynl2 | 1,626          |                  |
| Q5MR98    | MCG13936 OS=Mus musculus GN=Rpl28 PE=2 SV=1                                | Mus musculus | Rpl28 | 1,621          |                  |
| P31938    | Dual specificity mitogen-activated protein kinase 1 OS=Mus musculus GN=Map2k1 PE=1 SV=2 | Mus musculus | Map2k1 | 1,596          |                  |
| Q8BG78    | Phytanoyl-CoA hydroxylase-interacting protein-like OS=Mus musculus GN=Phyhipl PE=2 SV=1 | Mus musculus | Phyhipl | 1,584          |                  |
| E9PYK3    | Poly [ADP-ribose] polymerase OS=Mus musculus GN=Parp4 PE=1 SV=1             | Mus musculus | Parp4  | 1,583          |                  |
| Q4VAG4    | MCG12304 OS=Mus musculus GN=Rpl22 PE=2 SV=1                                 | Mus musculus | Rpl22 | 1,575          |                  |
| Q8BL66    | Early endosome antigen 1 OS=Mus musculus GN=Eea1 PE=1 SV=2                  | Mus musculus | Eea1   | 1,564          |                  |
| P11881    | Inositol 1,4,5-trisphosphate receptor type 1 OS=Mus musculus GN=Itpr1 PE=1 SV=2 | Mus musculus | Itpr1 | 1,562          |                  |
| P12382    | ATP-dependent 6-phosphofructokinase, liver type OS=Mus musculus GN=Pfk1 PE=1 SV=4 | Mus musculus | Pfk1 | 1,544          |                  |
| P62320    | Small nuclear ribonucleoprotein 5m D3 OS=Mus musculus GN=Snrpd3 PE=1 SV=1   | Mus musculus | Snrpd3 | 1,523          |                  |
| A0A0A0MHAQ5 | Tubulin alpha chain (Fragment) OS=Mus musculus GN=Tub4a4a PE=1 SV=1      | Mus musculus | Tub4a4a | 1,516          |                  |
| Q2PFD7    | PH and SEC7 domain-containing protein 3 OS=Mus musculus GN=Ps3 PE=1 SV=2    | Mus musculus | Ps3    | 1,487          |                  |
| Q9JHU4    | Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dynch1 PE=1 SV=2      | Mus musculus | Dynch1 | 1,48           |                  |
| P63318    | Protein kinase C gamma type OS=Mus musculus GN=Prkgc PE=1 SV=1              | Mus musculus | Prkgc | 1,476          |                  |
| P14106    | Complement C1q subcomponent subunit B OS=Mus musculus GN=C1qb PE=1 SV=2     | Mus musculus | C1qb  | 1,473          |                  |
| Accession | Description                                      | Organism   | Gene Name | Protein ID  | Evidence Level | Start Position | End Position |
|-----------|--------------------------------------------------|------------|-----------|-------------|----------------|----------------|--------------|
| P01592    | Immunoglobulin J chain                           | Mus musculus | Igj       | PE=2        | SV=4           | 1,472          |             |
| Q8VD05    | Myosin-9                                          | Mus musculus | Myh9      | PE=1        | SV=4           | 1,471          |             |
| Q3TG70    | Beta1 subunit of GTP-binding protein              | Mus musculus | Gnb1      | PE=2        | SV=1           | 1,468          |             |
| P62918    | 60S ribosomal protein L8                          | Mus musculus | Rpl8      | PE=1        | SV=2           | 1,461          |             |
| P66048    | 60S ribosomal protein L10-like                    | Mus musculus | Rpl10i    | PE=2        | SV=1           | 1,461          |             |
| Q8BM51    | Trifunctional enzyme subunit alpha, mitochondrial| Mus musculus | Hadha     | PE=1        | SV=1           | 1,458          |             |
| P14148    | 60S ribosomal protein L7                          | Mus musculus | Rpl7      | PE=1        | SV=2           | 1,449          |             |
| Q9CSR7    | 60S ribosomal protein L14                          | Mus musculus | Rpl14     | PE=1        | SV=3           | 1,443          |             |
| Q9EQK5    | Major vault protein                               | Mus musculus | Mvpp      | PE=1        | SV=4           | 1,426          |             |
| A0A097PUG4| Anti-lox-1 15C4 light chain                       | Mus musculus | P2777    | PE=2        | SV=1           | 1,416          |             |
| Q9WU34    | MAGUK p55 subfamily member 2                       | Mus musculus | Mpp2      | PE=1        | SV=1           | 1,391          |             |
| P27659    | 60S ribosomal protein L3                          | Mus musculus | Rpl3      | PE=1        | SV=3           | 1,384          |             |
| Q8HS58    | TIP41-like protein                                | Mus musculus | Tipr1     | PE=1        | SV=1           | 1,384          |             |
| P62267    | 40S ribosomal protein S23                         | Mus musculus | Rps23     | PE=1        | SV=3           | 1,379          |             |
| Q9CQV8    | 14-3-3 protein beta alpha                         | Mus musculus | Ywhab     | PE=1        | SV=3           | 1,378          |             |
| Q99104    | Unconventional myosin-Va                          | Mus musculus | Myo5a     | PE=1        | SV=2           | 1,378          |             |
| Q4FJX4    | Crsp1 protein                                     | Mus musculus | Crsp1     | PE=2        | SV=1           | 1,375          |             |
| Q9WU83    | Glycogen phosphorylase, muscle form               | Mus musculus | Pygm      | PE=1        | SV=3           | 1,374          |             |
| Q3JUV7    | Putative uncharacterized protein                   | Mus musculus | Mlf2      | PE=2        | SV=1           | 1,373          |             |
| P20152    | Vimentin                                          | Mus musculus | Vim       | PE=1        | SV=3           | 1,368          |             |
| P62880    | Guanine nucleotide-binding protein (G)/G(S)/G(T) subunit beta-2 | Mus musculus | Gnb2     | PE=1        | SV=3           | 1,368          |             |
| Q3U7E0    | Putative uncharacterized protein                   | Mus musculus | Atp6v1g1  | PE=2        | SV=1           | 1,364          |             |
| P49722    | Proteasome subunit alpha type-2                   | Mus musculus | Psma2     | PE=1        | SV=3           | 1,356          |             |
| P19096    | Fatty acid synthase                               | Mus musculus | Fasn      | PE=1        | SV=2           | 1,355          |             |
| Q9DAK9    | 14 kDa phosphohistidine phosphate                 | Mus musculus | Phept1    | PE=1        | SV=1           | 1,355          |             |
| P62827    | GTP-binding nuclear protein Ran                   | Mus musculus | Ran       | PE=1        | SV=3           | 1,343          |             |
| O08778    | Dynactin subunit 1                                | Mus musculus | Dctn1     | PE=1        | SV=3           | 1,341          |             |
| P29341    | Polyadenylate-binding protein 1                    | Mus musculus | Pabpc1    | PE=1        | SV=2           | 1,341          |             |
| P56480    | ATP synthase subunit beta, mitochondrial          | Mus musculus | Atp5b     | PE=1        | SV=2           | 1,335          |             |
| Q3UJS9    | Myosin-10                                         | Mus musculus | Myh10     | PE=1        | SV=1           | 1,334          |             |
| Q497E9    | 40S ribosomal protein S8                          | Mus musculus | Rps8      | PE=2        | SV=1           | 1,325          |             |
| P62305    | Small nuclear ribonucleoprotein E                 | Mus musculus | Snrpe     | PE=1        | SV=1           | 1,322          |             |
| Q61838    | Alpha-2-macroglobulin                             | Mus musculus | A2m       | PE=1        | SV=3           | 1,321          |             |
| Q5SQX6    | Cytoplasmic FMR1-interacting protein 2            | Mus musculus | Cyfip2    | PE=1        | SV=2           | 1,319          |             |
| P68040    | Receptor of activated protein C kinase 1          | Mus musculus | Rack1     | PE=1        | SV=3           | 1,313          |             |
| O70318    | Band 4.1-like protein 2                            | Mus musculus | Epb41l2   | PE=1        | SV=2           | 1,311          |             |
| Gene ID | Description                                                                 | Species          | Gene Symbol | Protein Accession | Protein Description | Description | Score |
|---------|------------------------------------------------------------------------------|------------------|-------------|-------------------|--------------------|-------------|-------|
| Q9OZQ8  | Core histone macro-H2A.1                                                     | Mus musculus     | H2afy       | Q8VEK3            | Heterogeneous nuclear ribonucleoprotein U | OS=Mus musculus | 1,308 |
| Q9JIS5  | Synaptic vesicle glycoprotein 2A                                              | Mus musculus     | Sv2a        |                   |                    | OS=Mus musculus | 1,302 |
| Q548L4  | Glutamate decarboxylase                                                      | Mus musculus     | Gad2        | P19253            | 60S ribosomal protein L13a | OS=Mus musculus | 0,774 |
| Q91V12-2| Isoform A of Cytosolic acyl coenzyme A thioster hydrolase OS=Mus musculus   | GN=Acot7         |             |                   |                    | 0,772 |
| A0A075B6A0 | Ig mu chain C region (Fragment) OS=Mus musculus GN=Ighm PE=1 SV=2          | Mus musculus     |             |                   |                    | 0,77 |
| P60202  | Myelin proteolipid protein OS=Mus musculus GN=Plp1 PE=1 SV=2                | Mus musculus     |             |                   |                    | 0,77 |
| P47963  | 60S ribosomal protein L13 OS=Mus musculus GN=Rpl13 PE=1 SV=3                | Mus musculus     |             |                   |                    | 0,763 |
| P06745  | Glucose-6-phosphate isomerase OS=Mus musculus GN=Gpi PE=1 SV=4              | Mus musculus     |             |                   |                    | 0,762 |
| Q5YLW3  | Ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=2 SV=1                      | Mus musculus     |             |                   |                    | 0,762 |
| P47962  | 60S ribosomal protein L5 OS=Mus musculus GN=Rpl5 PE=1 SV=3                  | Mus musculus     |             |                   |                    | 0,762 |
| B2RTM0  | Histone H4 OS=Mus musculus GN=H2ht4 PE=2 SV=1                               | Mus musculus     |             |                   |                    | 0,753 |
| Q9D051  | Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Mus musculus GN=Fdhb PE=1 SV=1 | 0,753 |
| P17710  | Hexokinase-1 OS=Mus musculus GN=Hk1 PE=1 SV=3                               | Mus musculus     |             |                   |                    | 0,749 |
| P28738  | Kinesin heavy chain isoform 5C OS=Mus musculus GN=Kif5c PE=1 SV=3           | Mus musculus     |             |                   |                    | 0,746 |
| P62281  | 405 ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=1 SV=2                | Mus musculus     |             |                   |                    | 0,743 |
| P21460  | Cystatin-C OS=Mus musculus GN=Cst3 PE=1 SV=2                                | Mus musculus     |             |                   |                    | 0,742 |
| O08553  | Dihydropyrimidinase-related protein 2 OS=Mus musculus GN=Dyps12 PE=1 SV=2   | Mus musculus     |             |                   |                    | 0,735 |
| P97351  | 405 ribosomal protein S3a OS=Mus musculus GN=Rps3a PE=1 SV=3                | Mus musculus     |             |                   |                    | 0,735 |
| P35486  | Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1 | 0,734 |
| Q9CPU0  | Lactoylglutathione lyase OS=Mus musculus GN=Glo1 PE=1 SV=3                  | Mus musculus     |             |                   |                    | 0,732 |
| Q7TJS2  | Microtubule-associated protein 6 OS=Mus musculus GN=Map6 PE=1 SV=2          | Mus musculus     |             |                   |                    | 0,732 |
| Q8OYN3  | Breast carcinoma-amplified sequence 1 homolog OS=Mus musculus GN=Bcat1 PE=1 SV=3 | 0,731 |
| P62137  | Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Mus musculus GN=Ppp1ca PE=1 SV=1 | 0,731 |
| Q8K183  | Pyridoxal kinase OS=Mus musculus GN=Pdk1 PE=1 SV=1                           | Mus musculus     |             |                   |                    | 0,729 |
| Q02105  | Complement C1q subcomponent subunit C OS=Mus musculus GN=C1qc PE=2 SV=2     | Mus musculus     |             |                   |                    | 0,728 |
| Q90883  | Charged multisvesicular body protein 4B OS=Mus musculus GN=Chmp4b PE=1 SV=2 | Mus musculus     |             |                   |                    | 0,728 |
| Q3TVK3  | Aspartyl aminopeptidase OS=Mus musculus GN=Dnpep PE=1 SV=1                  | Mus musculus     |             |                   |                    | 0,727 |
| Q7TMM9  | Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1                   | Mus musculus     |             |                   |                    | 0,724 |
| B9EHNO  | Ubiquitin-activating enzyme E1, Chr X OS=Mus musculus GN=Uba1 PE=2 SV=1     | Mus musculus     |             |                   |                    | 0,721 |
| P70349  | Histidine triad nucleotide-binding protein 1 OS=Mus musculus GN=Hnt1 PE=1 SV=3 | 0,716 |
| Q8OYS2  | Heat shock protein 90, alpha (Cytosolic), class A member 1 OS=Mus musculus GN=Hsp90a1a PE=2 SV=2 | 0,716 |
| G5E902  | MCG10343, isoform CRA_b OS=Mus musculus GN=Slc25a3 PE=1 SV=1                | Mus musculus     |             |                   |                    | 0,71 |
| H38KH6  | S-formylglutathione hydrolase OS=Mus musculus GN=Esrd PE=1 SV=1              | Mus musculus     |             |                   |                    | 0,709 |
| P63017  | Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1         | Mus musculus     |             |                   |                    | 0,708 |
| F6RSK3  | Protein Gm17430 OS=Mus musculus GN=Gm17430 PE=4 SV=1                         | Mus musculus     |             |                   |                    | 0,705 |
| Q7M6W1  | Reticulin OS=Mus musculus GN=Rtn1 PE=1 SV=1                                 | Mus musculus     |             |                   |                    | 0,705 |
| O5S042  | Alpha-synuclein OS=Mus musculus GN=Snca PE=1 SV=2                            | Mus musculus     |             |                   |                    | 0,704 |
| F6YVP7  | Protein Gm10260 OS=Mus musculus GN=Gm10260 PE=3 SV=2                         | Mus musculus     |             |                   |                    | 0,704 |
| Q546G4  | Albumin 1 OS=Mus musculus GN=Alb PE=2 SV=1                                 | Mus musculus     |             |                   |                    | 0,703 |
| P70202  | Lactein OS=Mus musculus GN=Lxm PE=1 SV=2                                   | Mus musculus     |             |                   |                    | 0,703 |
P50396 Rab GDP dissociation inhibitor alpha OS=Mus musculus GN=Gdi1 PE=1 SV=3 0,701
Q810U4 Neuronal cell adhesion molecule OS=Mus musculus GN=Cam1 OS=1 SV=2 0,699
P11499 Heat shock protein 90-beta OS=Mus musculus GN=Hspa1a PE=1 SV=3 0,699
Q542X7 Chaperonin subunit 2 (Beta), isoform CRA_a OS=Mus musculus GN=Cc2 PE=2 SV=1 0,699
Q642L7 MCI1 OS=Mus musculus GN=Rps27a PE=2 SV=1 0,692
A2ARP8 Microtubule-associated protein 1A OS=Mus musculus GN=Map1a PE=1 SV=1 0,692
P99028 Cytochrome b-c1 complex subunit 6, mitochondrial OS=Mus musculus GN=Uqcrf1 PE=1 SV=2 0,691
Q3UMU9 Hepatoma-derived growth factor-related 0 OS=Mus musculus GN=Hdgfrp2 PE=1 SV=1 0,69
D0VYV6 Erythrocyte protein band 4.1-like 3 OS=Mus musculus GN=Epb4.13 PE=2 SV=1 0,689
P77780 Alpha-actinin-4 OS=Mus musculus GN=Actn4 PE=1 SV=1 0,686
A2ALV3 Endophilin-A1 OS=Mus musculus GN=Sh3gl2 PE=1 SV=1 0,68
Q92204 Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Mus musculus GN=Hnrnc PE=1 SV=1 0,679
Q91V88 Alpha globin 1 OS=Mus musculus GN=Haemoglobin alpha 2 PE=1 SV=1 0,67
P17742 Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=1 0,669
Q92ZG4 V-type proton ATPase 116 kDa subunit a OS=Mus musculus GN=Atp6v0a1 PE=1 SV=3 0,669
Q01853 Transitional endoplasmic reticulum ATPase OS=Mus musculus GN=Vcpe PE=1 SV=4 0,668
Q3V117 ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1 0,665
Q9ERD7 Tubulin beta-3 chain OS=Mus musculus GN=Tubb3 PE=1 SV=1 0,665
P28651 Carbonic anhydrase-related protein OS=Mus musculus GN=Ga3 PE=1 SV=5 0,664
Q92ZT6 Keratin, type II cuticular OS=Mus musculus GN=Krt8 Pe=1 SV=2 0,66
P52480 Pyruvate kinase PMI OS=Mus musculus GN=Pkm PE=1 SV=4 0,659
Q58864 Elongation factor 1-alpha OS=Mus musculus GN=Eef1a1 PE=2 SV=1 0,658
Q906R2 Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Mus musculus GN=Idh3a PE=1 SV=1 0,657
Q60829 Protein phosphatase 1 regulatory subunit 1B OS=Mus musculus GN=Ppp1r1b PE=2 SV=2 0,656
Q77Q02 Tubulin polymerization-promoting protein OS=Mus musculus GN=Tppp PE=1 SV=1 0,656
A0A087WQN2 Prothymosin alpha (Fragment) OS=Mus musculus GN=Ptma PE=1 SV=1 0,654
P62082 40S ribosomal protein S7 OS=Mus musculus GN=Rps7 PE=2 SV=1 0,654
B0QZ5N Vesicle-associated membrane protein 2 OS=Mus musculus GN=Vamp2 PE=1 SV=1 0,648
P68369 Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1 0,648
Q8331 Calretinin OS=Mus musculus GN=Cale2 PE=1 SV=3 0,647
P26443 Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus GN=Giud1 PE=1 SV=1 0,646
P01787 Ig heavy chain V regions TEP1 OS=S/M107/HPCM1/HPCM2/HPCM3 OS=Mus musculus PE=1 SV=1 0,644
P61255 60S ribosomal protein L26 OS=Mus musculus GN=Rpl26 PE=1 SV=1 0,644
D32722 40S ribosomal protein S19 OS=Mus musculus GN=Rps19 PE=1 SV=1 0,637
B9EK81 Receptor-type tyrosine-protein phosphatase zeta OS=Mus musculus GN=Ptprz1 PE=1 SV=1 0,635
P63005 Platelet-activating factor acetylhydrolase IB subunit alpha OS=Mus musculus GN=Pafah1b1 PE=1 SV=2 0,629
Q55XR6 Clathrin heavy chain OS=Mus musculus GN=Clcte PE=1 SV=1 0,621
P18872 Guanine nucleotide-binding protein G(o) subunit alpha OS=Mus musculus GN=Gnao1 PE=1 SV=1 0,619
Q60864 Stress-induced phosphoprotein 1 OS=Mus musculus GN=Stip1 PE=1 SV=1 0,612
P62889 60S ribosomal protein L30 OS=Mus musculus GN=Rpl30 PE=1 SV=2 0,611
F6RT34 Myelin basic protein (Fragment) OS=Mus musculus GN=Mbp PE=1 SV=1 0,61
O54962 Barrier-to-autoinhibition factor OS=Mus musculus GN=Banf1 PE=1 SV=1 0,608
| UniProt ID | Description                                                                 |物种   | GN          | PE | SV | Score |
|-----------|------------------------------------------------------------------------------|--------|-------------|----|----|-------|
| A8DUK4    | Beta-globin OS=Mus musculus GN=Hbbt1 PE=1 SV=1                              |0,603  |
| P62259    | 14-3-3 protein epsilon OS=Mus musculus GN=Ywhea PE=1 SV=1                  |0,603  |
| Q9D6F9    | Tubulin beta-4A chain OS=Mus musculus GN=Tubb4a PE=1 SV=3                  |0,6   |
| Q99PT1    | Rho GDP-dissociation inhibitor 1 OS=Mus musculus GN=Arhgdia PE=1 SV=3      |0,596  |
| Q91L23    | Methylglutaconyl-CoA hydratase, mitochondrial OS=Mus musculus GN=Auh PE=1 SV=1|0,596  |
| Q9QXY7    | Protein piccolo OS=Mus musculus GN=Pclo PE=1 SV=4                          |0,596  |
| Q04447    | Creatine kinase B-type OS=Mus musculus GN=Ckb PE=1 SV=1                    |0,595  |
| Q8K0U4    | Heat shock 70 kDa protein 12A OS=Mus musculus GN=Hspa12a PE=1 SV=1         |0,595  |
| F6VW30    | 14-3-3 protein theta (Fragment) OS=Mus musculus GN=Ywhaq PE=1 SV=1         |0,594  |
| P14873    | Microtubule-associated protein 18 OS=Mus musculus GN=Map1b PE=1 SV=2      |0,591  |
| Q548F2    | Guanine deaminase OS=Mus musculus GN=Gda PE=2 SV=1                         |0,59   |
| A0A075B5P2| Protein Igk (Fragment) OS=Mus musculus GN=Igk PE=1 SV=1                   |0,59   |
| A0A0AYWX6 | Protein Igfa (Fragment) OS=Mus musculus GN=Igfa PE=1 SV=1                 |0,589  |
| F8WGL3    | Cofilin-1 OS=Mus musculus GN=Cfl1 PE=1 SV=1                                |0,584  |
| Q76MZ3    | Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Mus musculus GN=Ppp2r1a PE=1 SV=3 |0,584  |
| P09411    | Phosphoglycerate kinase 1 OS=Mus musculus GN=Pgk1 PE=1 SV=4               |0,584  |
| P05063    | Fructose-bisphosphate aldolase C OS=Mus musculus GN=Aldoc PE=1 SV=4        |0,583  |
| PS8252    | Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2                      |0,583  |
| Q6WQ83    | Purkinje cell protein 4-like protein 1 OS=Mus musculus GN=Pcp4l1 PE=1 SV=1|0,582  |
| Q9DBJ1    | Phosphoglycerate mutase 1 OS=Mus musculus GN=Pgam1 PE=1 SV=3               |0,579  |
| Q99K10    | Aconitase hydratase, mitochondrial OS=Mus musculus GN=Aco2 PE=1 SV=1       |0,579  |
| P27661    | Histone H2AX OS=Mus musculus GN=H2afx PE=1 SV=2                           |0,577  |
| P60766    | Cell division control protein 42 homolog OS=Mus musculus GN=Cdc42 PE=1 SV=2|0,577  |
| P52760    | Ribonuclease UK114 OS=Mus musculus GN=Hrsp12 PE=1 SV=3                    |0,576  |
| Q5EBQ2    | MCG7941, isoform CRA_f OS=Mus musculus GN=Pebp1 PE=2 SV=1                 |0,576  |
| Q545B6    | Stathmin OS=Mus musculus GN=Stmn1 PE=2 SV=1                               |0,574  |
| P20357    | Microtubule-associated protein 2 OS=Mus musculus GN=Map2 PE=2 SV=2        |0,574  |
| P62858    | 40S ribosomal protein S28 OS=Mus musculus GN=Rps28 PE=1 SV=1               |0,574  |
| Q545P0    | ATPase, Na+/K+ transporting, beta 1 polypeptide OS=Mus musculus GN=Atplb1 PE=2 SV=1 |0,565  |
| A0A087WP80 | Limbic system-associated membrane protein OS=Mus musculus GN=Lsamp PE=1 SV=1 |0,559  |
| Q9R0V5    | Adenylate kinase isozyme 1 OS=Mus musculus GN=Ak1 PE=1 SV=1               |0,559  |
| Q3UL22    | Chaperonin subunit 8 (Theta), isoform CRA_a OS=Mus musculus GN=Cct8 PE=2 SV=1|0,557  |
| P35700    | Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1                        |0,556  |
| P16125    | L-lactate dehydrogenase B chain OS=Mus musculus GN=Ldhb PE=1 SV=2         |0,552  |
| P16049    | Glutathione S-transferase Mu 1 OS=Mus musculus GN=Gstm1 PE=1 SV=2         |0,55   |
| D3Z4B2    | Gamma-soluble NSF attachment protein (Fragment) OS=Mus musculus GN=Nagp PE=1 SV=1 |0,545  |
| P98086    | Complement C1q subcomponent subunit A OS=Mus musculus GN=C1qa PE=1 SV=2   |0,542  |
| P08249    | Malate dehydrogenase, mitochondrial OS=Mus musculus GN=Mdh2 PE=1 SV=3     |0,542  |
| Q61361    | Brevican core protein OS=Mus musculus GN=Bcan PE=1 SV=2                   |0,54   |
| P63101    | 14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhae PE=1 SV=1              |0,537  |
| E9PV0     | PCTP-like protein OS=Mus musculus GN=Stard10 PE=1 SV=1                    |0,537  |
| Q91Z3     | Beta-synuclein OS=Mus musculus GN=Sncb PE=1 SV=1                          |0,535  |
| Accession  | Description                                                                 | Species       | Gene Name                  | Protein Entrez | Spectrum Entrez |
|------------|------------------------------------------------------------------------------|---------------|---------------------------|----------------|-----------------|
| P62631     | Elongation factor 1-alpha 2                                                  | Mus musculus  | Eef1a2                    | 1              | 1               |
| Q90DB63    | AP-2 complex subunit beta                                                    | Mus musculus  | Ap2b1                     | 1              | 1               |
| P51863     | V-type proton ATPase subunit d                                               | Mus musculus  | Atp6v0d1                  | 2              | 1               |
| P60710     | Actin, cytoplasmic 1                                                         | Mus musculus  | Actb                       | 1              | 1               |
| P68433     | Histone H3.1                                                                | Mus musculus  | Hist1h3a                   | 2              | 1               |
| Q3U1Y0     | Protein S100 OS=Mus musculus 1                                               | Mus musculus  | S100b                     | 2              | 1               |
| Q3U1N0     | Coronin                                                                      | Mus musculus  | Coro1a                     | 2              | 1               |
| Q5FW97     | Enolase 1 alpha non-neuron                                                    | Mus musculus  | EG433182                   | 2              | 1               |
| E9P2F0     | Nucleoside diphosphate kinase                                                | Mus musculus  | Gm20390                    | 3              | 1               |
| A6ZI44     | Fructose-bisphosphate aldolase                                               | Mus musculus  | Aldoa                      | 1              | 1               |
| Q3U2G2     | Heat shock 70 kDa protein 4                                                  |Mus musculus  | Hspa4                      | 1              | 1               |
| P90405     | Nucleolin                                                                   | Mus musculus  | Ncl                        | 2              | 1               |
| P61922     | 4-aminobutyrate aminotransferase, mitochondrial                             | Mus musculus  | Abat                       | 1              | 1               |
| Q2Z2D6-2   | Isoform B of Methyl-CpG-binding protein 2                                    | Mus musculus  | Mecp2                      |                |                 |
| P80313     | T-complex protein 1 subunit eta                                              | Mus musculus  | Cct7                       | 1              | 1               |
| Q14929     | Histone cluster 1, H1d                                                       | Mus musculus  | Hist1h1d                   | 2              | 1               |
| P17755     | Triosephosphate isomerase                                                    | Mus musculus  | Tpi1                       | 4              | 1               |
| Q9R0P9     | Ubiquitin carboxyl-terminal hydrolase isoyzme                               | Mus musculus  | Uchli                      | 1              | 1               |
| Q8EQU-2    | Isoform 2 of Protein SET                                                     | Mus musculus  | Set                        |                |                 |
| Q8C2Q7     | Heterogeneous nuclear ribonucleoprotein H                                   | Mus musculus  | Hrnnp1                     | 1              | 1               |
| Q8JVU-2    | Profilin-2 OS=Mus musculus                                                   | Mus musculus  | Phn2                       | 3              |                 |
| P68372     | Tubulin beta-4B chain                                                        | Mus musculus  | Tubb4b                     | 1              | 1               |
| Q60668     | Heterogeneous nuclear ribonucleoprotein D10                                 | Mus musculus  | Hnrnpd                     | 2              |                 |
| Q8BV4     | Dihydropteridine reductase                                                   | Mus musculus  | Qdpr                       | 2              |                 |
| Q543Y7     | Putative uncharacterized protein                                             | Mus musculus  | Pascin1                    | 2              |                 |
| P28474     | Alcohol dehydrogenase class-3                                               | Mus musculus  | Adh5                       | 3              |                 |
| P14869     | 60S acidic ribosomal protein P0                                               | Mus musculus  | Riplp0                      | 3              |                 |
| P61979     | Heterogeneous nuclear ribonucleoprotein K                                   | Mus musculus  | Hnrnpk                     | 1              |                 |
| Q6GT24     | Peroxiredoxin 6 OS=Mus musculus                                              | Mus musculus  | Prdx6                      | 1              |                 |
| P26883     | Peptidyl-prolyl cis-trans isomerase FKB1A                                    | Mus musculus  | Fkbp1a                     | 2              |                 |
| P84086     | Complexin-2 OS=Mus musculus                                                  | Mus musculus  | Cplx2                      | 1              |                 |
| O8B569     | Heterogeneous nuclear ribonucleoprotein A2/B1                                | Mus musculus  | Hnrnpa2b1                  | 2              |                 |
| Q9J1M7     | Protein FAM49B OS=Mus musculus                                               | Mus musculus  | Fam49b                     | 2              |                 |
| P20029     | 78 kDa glucose-regulated protein                                             | Mus musculus  | Hspa5                      | 2              |                 |
| Q9CZC8     | Secerin-1 OS=Mus musculus                                                    | Mus musculus  | Scrn1                      | 1              |                 |
| P99024     | Tubulin beta-5 chain                                                         | Mus musculus  | Tubb5                      | 1              |                 |
| P42669     | Transcriptional activator protein Pur-alpha                                   | Mus musculus  | Pura                       | 1              |                 |
| P68510     | 14-3-3 protein eta                                                          | Mus musculus  | Ywhae                      | 2              |                 |
| B2RTK3     | Histone H2B OS=Mus musculus                                                  | Mus musculus  | Hist1h2bm                  | 2              |                 |
| A0A0A0M0QF6| Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus                     | Mus musculus  | Gapdh                      | 1              |                 |
| Q99PU5     | Long-chain-fatty-acid-CoA ligase ANS1OS=Mus musculus                          | Mus musculus  | Acslb1                     | 1              |                 |
| O0B539     | Myc box-dependent-interacting protein 1 OS=Mus musculus                      | Mus musculus  | Bin1                       | 1              |                 |
| Accession | Description                                                                 | Organism          | Gene Name | Protein Name | Score |
|-----------|------------------------------------------------------------------------------|-------------------|-----------|--------------|-------|
| P19157    | Glutathione S-transferase P 1                                                | Mus musculus      | Gstp1     | Gstp1        | 0.438 |
| Q9CZ13    | Cytochrome b-c1 complex subunit 1, mitochondrial                            | Mus musculus      | Uqcrcl    | Uqcrcl1      | 0.438 |
| Q9QYCO    | Alpha-2uCinin OS=Mus musculus GN=Add1 P1 SV=2                               |                   |           |              | 0.437 |
| A2AWN8    | YTH domain family 1, isoform CRA_a                                         | Mus musculus      | Ythd1    | Ythd1        | 0.434 |
| Q9WTT4    | V-type proton ATPase subunit G 2                                             | Mus musculus      | Atp6v1g2  | Atp6v1g2     | 0.432 |
| Q61598    | Rab GDP dissociation inhibitor beta OS=Mus musculus GN=Gdi2 PE=1 SV=1        |                   |           |              | 0.432 |
| P50518    | V-type proton ATPase subunit E 1                                             | Mus musculus      | Atp6v1e1  | Atp6v1e1     | 0.428 |
| P12658    | Calbindin OS=Mus musculus GN=Calb1 PE=1 SV=2                                |                   |           |              | 0.427 |
| P14152    | Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Mdh1 PE=1 SV=3         |                   |           |              | 0.419 |
| B2RSH2    | Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Mus musculus GN=Gna1 PE=1 SV=1 | | | 0.419 |
| Q92216    | Tetraspanin-2 OS=Mus musculus GN=Tspan2 PE=1 SV=1                          |                   |           |              | 0.417 |
| P48722    | Heat shock 70 kDa protein 4L OS=Mus musculus GN=Hspa4l PE=1 SV=2            |                   |           |              | 0.417 |
| Q60631    | Growth factor receptor-bound protein 2 OS=Mus musculus GN=Grb2 PE=1 SV=1    |                   |           |              | 0.409 |
| A0A076FRG6| KCC2a variant 1 OS=Mus musculus GN=Slc12a5 PE=2 SV=1                       |                   |           |              | 0.407 |
| Q80TL4    | PHD finger protein 24 OS=Mus musculus GN=Phf24 PE=1 SV=2                   |                   |           |              | 0.403 |
| Q7TQ3     | Ubiquitin thioesterase OTUB1 OS=Mus musculus GN=Otub1 PE=1 SV=2             |                   |           |              | 0.394 |
| P63038    | 60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspa1d1 PE=1 SV=1 | | | 0.393 |
| P06837    | Neumodulin OS=Mus musculus GN=Gap43 PE=1 SV=2                              |                   |           |              | 0.381 |
| P62774    | Myotrophin OS=Mus musculus GN=Mtnp PE=1 SV=2                               |                   |           |              | 0.379 |
| A0A0G2JFTB| Protein RUFY3 OS=Mus musculus GN=Rufy3 PE=1 SV=1                           |                   |           |              | 0.372 |
| Q9CPW4    | Actin-related protein 2/3 complex subunit 5 OS=Mus musculus GN=Arpc5 PE=2 SV=3 | | | 0.371 |
| Q68FL4    | Putative adenosylhomocysteinase 3 OS=Mus musculus GN=Ahcy12 PE=1 SV=1      |                   |           |              | 0.368 |
| Q61R5U5   | Clathrin light chain B OS=Mus musculus GN=Cltb PE=1 SV=1                   |                   |           |              | 0.366 |
| P31650    | Sodium- and chloride-dependent GABA transporter 3 OS=Mus musculus GN=Slc6a11 PE=1 SV=2 | | | 0.366 |
| P60761    | Neurogranin OS=Mus musculus GN=Nrgn PE=1 SV=1                              |                   |           |              | 0.364 |
| O08749    | Dihydrolipoil dehydrogenase, mitochondrial OS=Mus musculus GN=Old PE=1 SV=2 | | | 0.362 |
| P99027    | 60s acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3          |                   |           |              | 0.355 |
| P08228    | Superoxide dismutase [Cu-Zn] OS=Mus musculus GN=Sod1 PE=1 SV=2             |                   |           |              | 0.346 |
| Q9JKD3    | Secretory carrier-associated membrane protein 5 OS=Mus musculus GN=Tscamp5 PE=1 SV=1 | | | 0.34 |
| P48036    | Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1                              |                   |           |              | 0.339 |
| Q9CX86    | Heterogeneous nuclear ribonucleoprotein A0 OS=Mus musculus GN=Hnrnpo0 PE=1 SV=1 | | | 0.338 |
| Q63810    | Calcineurin subunit B type 1 OS=Mus musculus GN=Ppp3r1 PE=1 SV=3            |                   |           |              | 0.337 |
| P63040    | Complexin-1 OS=Mus musculus GN=Cpx1 PE=1 SV=1                              |                   |           |              | 0.335 |
| P32848    | Parvalbumin alpha OS=Mus musculus GN=Pvalb PE=1 SV=3                       |                   |           |              | 0.327 |
| Q4VWZ5    | Acyl-CoA-binding protein OS=Mus musculus GN=Dbi PE=1 SV=1                   |                   |           |              | 0.324 |
| F6VPT0    | Protein Ccdc163 (Fragment) OS=Mus musculus GN=Cdc163 PE=4 SV=1             |                   |           |              | 0.323 |
| P02802    | Metallothionein-1 OS=Mus musculus GN=Mt1 PE=1 SV=1                         |                   |           |              | 0.322 |
| P62204    | Calmodulin OS=Mus musculus GN=Calm1 PE=1 SV=2                              |                   |           |              | 0.313 |
| D3YXH0    | Immunoglobulin superfamily member 5 OS=Mus musculus GN=Igsf5 PE=4 SV=1     |                   |           |              | 0.311 |
| Q90D309   | ATP synthase subunit delta, mitochondrial OS=Mus musculus GN=Atpsd PE=1 SV=1 | | | 0.297 |
| Q91XV3    | Brain acid soluble protein 1 OS=Mus musculus GN=Basp1 PE=1 SV=3             |                   |           |              | 0.284 |
| Q9CRB6    | Tubulin polymerization-promoting protein family member 3 OS=Mus musculus GN=Tppp3 PE=1 SV=1 | | | 0.274 |
| Accession  | Gene Name                        | Organism   | Gene Symbol | Protein Expression | Score |
|------------|---------------------------------|------------|-------------|--------------------|-------|
| P26645     | Myristoylated alanine-rich C-kinase substrate | Mus musculus | Marcks      | PE=1 SV=2          | 0.273 |
| Q9WV69     | Dematin                          | Mus musculus | Dmtn        | PE=1               | 0.269 |
| Q9JKC6     | Cell cycle exit and neuronal differentiation protein 1 | Mus musculus | Cend1       | PE=1 SV=1          | 0.269 |
| P43274     | Histone H1.4                     | Mus musculus | Hist1h1e    | PE=1 SV=2          | 0.256 |
| B1AWD9     | Clathrin light chain A            | Mus musculus | Clta        | PE=1 SV=1          | 0.255 |
| Q8CI43     | Myosin light chain 6B             | Mus musculus | Myl6b       | PE=2 SV=1          | 0.252 |
| P61089     | Ubiquitin-conjugating enzyme E2 N | Mus musculus | Ube2n       | PE=1 SV=1          | 0.249 |
| G5E8N5     | L-lactate dehydrogenase           | Mus musculus | Ldha        | PE=1 SV=1          | 0.248 |
| Q6ZWX2     | Thymosin, beta 4, X chromosome    | Mus musculus | Tmsb4x      | PE=2 SV=1          | 0.239 |
| P13595     | Neural cell adhesion molecule 1   | Mus musculus | Ncam1       | PE=1 SV=3          | 0.224 |
| E9PYN1     | Cell adhesion molecule 1          | Mus musculus | Cadm1       | PE=1 SV=1          | 0.212 |
| P28663     | Beta-soluble NSF attachment protein | Mus musculus | Napb        | PE=1 SV=2          | 0.21  |
| P20065     | Thymosin beta-4                  | Mus musculus | Tmsb4x      | PE=1 SV=1          | 0.207 |
| P60904     | DnaJ homolog subfamily C member 5 | Mus musculus | Dnajc5      | PE=1 SV=1          | 0.204 |
| Accession | Description |
|-----------|-------------|
| P43276    | Histone H1.5 OS=Mus musculus GN=H1h1b PE=1 SV=2 |
| Q02331    | Keratin, type II cytoskeletal 68 OS=Mus musculus GN=Krt6b PE=1 SV=3 |
| Q552A3    | Histone cluster 1, H1c OS=Mus musculus GN=H1h1c PE=2 SV=1 |
| P12023    | Amyloid beta A4 protein OS=Mus musculus GN=Abp PE=1 SV=3 |
| Q35YP5    | Keratin 16 OS=Mus musculus GN=Krt16 PE=2 SV=1 |
| Q8R1B4    | Eukaryotic translation initiation factor 3 subunit C OS=Mus musculus GN=Eif3c PE=1 SV=1 |
| Q2105     | Complement C1q subcomponent subunit C OS=Mus musculus GN=C1qc PE=2 SV=2 |
| Q04690    | Neurofibromin OS=Mus musculus GN=Nf1 PE=1 SV=1 |
| Q37TX4    | Apolipoprotein E, isoform CRA_h OS=Mus musculus GN=ApoE PE=2 SV=1 |
| P14106    | Complement C1q subcomponent subunit B OS=Mus musculus GN=C1qb PE=1 SV=2 |
| P01592    | Immunoglobulin J chain OS=Mus musculus GN=Igj PE=2 SV=4 |
| J3QM63    | Voltage-dependent anion-selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=1 SV=1 |
| Q9WTL4    | Insulin receptor-related protein OS=Mus musculus GN=Insr PE=1 SV=2 |
| P28651    | Carbonic anhydrase-related protein OS=Mus musculus GN=Ca8 PE=1 SV=5 |
| Q3U7E0    | Putative uncharacterized protein OS=Mus musculus GN=Atp6v1g1 PE=2 SV=1 |
| Q617B2    | Type I epidermal keratin mRNA, 3'end (Fragment) OS=Mus musculus PE=2 SV=1 |
| Q9ESM3    | Hyaluronan and proteoglycan link protein 2 OS=Mus musculus GN=Hapl2 PE=1 SV=1 |
| Q9WUL7    | Keratin, type I cytoskeletal 17 OS=Mus musculus GN=Krt17 PE=1 SV=3 |
| Q88GT8    | Phytanoyl-CoA hydroxylase-interacting protein-like OS=Mus musculus GN=Phyhipl PE=2 SV=1 |
| P10637-3  | Isoform Tau-B of Microtubule-associated protein tau OS=Mus musculus GN=Mapt |
| E9Q7G3    | Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=1 |
| A6H611    | Mitochondrial intermediate peptidase OS=Mus musculus GN=Mipep PE=1 SV=1 |
| P21460    | Cystatin-C OS=Mus musculus GN=Cst3 PE=1 SV=2 |
| Q61282    | Aggrecan core protein OS=Mus musculus GN=Acan PE=1 SV=2 |
| Q99MN9    | ADP-ribosylation factor-like protein 6-interacting protein 4 OS=Mus musculus GN=Ar6ip4 PE=1 SV=1 |
| Q9QUP5    | Hyaluronan and proteoglycan link protein 1 OS=Mus musculus GN=Hapl1 PE=1 SV=1 |
| E9P9Y0    | Versican core protein OS=Mus musculus GN=Vcan PE=1 SV=1 |
| F6YVP7    | Protein Gm10260 OS=Mus musculus GN=Gm10260 PE=3 SV=2 |
| Q903D9    | ATP synthase subunit delta, mitochondrial OS=Mus musculus GN=Atpd5 PE=1 SV=1 |
| P11983    | T-complex protein 1 subunit alpha OS=Mus musculus GN=Tcpl1 PE=1 SV=3 |
| P10922    | Histone H1.0 OS=Mus musculus GN=H1f0 PE=2 SV=4 |
| P28663    | Beta-soluble NSF attachment protein OS=Mus musculus GN=Napb PE=1 SV=2 |
| P28184    | Metallothionein-3 OS=Mus musculus GN=Mt3 PE=1 SV=1 |
| Q99MN9    | Propionyl-CoA carboxylase beta chain, mitochondrial OS=Mus musculus GN=Pccb PE=1 SV=2 |
| E9Q905    | Protein Gm20425 OS=Mus musculus GN=Gm20425 PE=4 SV=1 |
| Q88MS1    | Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1 |
| P17156    | Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV=2 |
| Q564G0    | Guanylate kinase OS=Mus musculus GN=Guk1 PE=1 SV=1 |
| P55066    | Neurocan core protein OS=Mus musculus GN=Ncan PE=2 SV=1 |
| P19001    | Keratin, type I cytoskeletal 19 OS=Mus musculus GN=Krt19 PE=1 SV=1 |
| Accession | Description                                                                 | Species          | Gene Name | Peptide | Spectrum Value |
|-----------|------------------------------------------------------------------------------|------------------|-----------|----------|----------------|
| P09920    | Carbonic anhydrase 2                                                         | Mus musculus     | Ca2       | PE=1     | SV=4           |
| Q9QYC0    | Alpha-adducin                                                                | Mus musculus     | Add1      | PE=1     | SV=2           |
| Q9QCD0    | 6-phosphogluconate dehydrogenase, decarboxylating                           | Mus musculus     | Pgd       | PE=1     | SV=3           |
| Q58EA6    | MCG10725, isoform CRA_a                                                     | Mus musculus     | Rps25     | PE=2     | SV=1           |
| P26883    | Peptidyl-prolyl cis-trans isomerase FKBPIA                                  | Mus musculus     | Fkbpi1a   | PE=1     | SV=2           |
| P63040    | Complexin-1                                                                  | Mus musculus     | Cplx1     | PE=1     | SV=1           |
| Q9CK54    | Centromere protein V                                                         | Mus musculus     | Cenpv     | PE=1     | SV=2           |
| Q2UJV7    | Putative uncharacterized protein OS=Mus musculus GN=MIF2 PE=2 SV=1           | Mus musculus     | MIF2      | PE=2     | SV=1           |
| P70441    | Na(+)/H(+) exchange regulatory cofactor NHE-RF1                              | Mus musculus     | Slc9a3r1  | PE=2     | SV=1           |
| Q06781    | Keratin, type I cytoskeletal 14                                              | Mus musculus     | Krt14     | PE=1     | SV=2           |
| B9EJC7    | MCG3853                                                                      | Mus musculus     | Phyp     | PE=2     | SV=1           |
| Q4FJK9    | Superoxide dismutase                                                         | Mus musculus     | Sod2      | PE=2     | SV=1           |
| P26645    | Myristoylated alanine-rich C-kinase substrate                                | Mus musculus     | Marcks    | PE=1     | SV=2           |
| Q60829    | Protein phosphatase 1 regulatory subunit 18                                  | Mus musculus     | Ppp1r1b   | PE=2     | SV=2           |
| A0A075B6A0| Ig mu chain C region (Fragment)                                             | Mus musculus     | Igmm1     | PE=1     | SV=2           |
| Q0AA0G2FE8| Amphilophysin                                                                | Mus musculus     | Amphil    | PE=1     | SV=1           |
| Q8BVI4    | Dihydropteridine reductase                                                   | Mus musculus     | Qdpr      | PE=1     | SV=2           |
| A2CEK3    | Phosphoglucomutase-2                                                         | Mus musculus     | Pgm2      | PE=1     | SV=1           |
| A0A075B5P2| Protein IgkC (Fragment)                                                      | Mus musculus     | IgkC      | PE=1     | SV=1           |
| B2RXY7    | Carbonyl reductase 1                                                         | Mus musculus     | Cbr1      | PE=2     | SV=1           |
| P61089    | Ubiquitin-conjugating enzyme E2 N OS=Mus musculus GNA=Ube2n PE=1 SV=1        | Mus musculus     | Ube2n     | PE=1     | SV=1           |
| Q5347Y    | Putative uncharacterized protein OS=Mus musculus GN=Pacsin1 PE=2 SV=1        | Mus musculus     | Pacsin1   | PE=2     | SV=1           |
| Q9CZU6    | Citrate synthase, mitochondrial                                              | Mus musculus     | Cs        | PE=1     | SV=1           |
| P62827    | GTP-binding nuclear protein Ran OS=Mus musculus GN=Ran PE=1 SV=3             | Mus musculus     | Ran       | PE=1     | SV=3           |
| Q6FX2     | Keratin, type I cytoskeletal 42                                              | Mus musculus     | Krt42     | PE=1     | SV=1           |
| Q92ZT6    | Keratin, type II cuticular Hb5                                               | Mus musculus     | KrtB5     | PE=2     | SV=2           |
| Q60692    | Proteasome subunit beta type-6                                              | Mus musculus     | Psmb6     | PE=1     | SV=3           |
| Q9CPW4    | Actin-related protein 2/3 complex subunit 5                                 | Mus musculus     | Arpc5     | PE=2     | SV=3           |
| Q9CZY3    | Ubiquitin-conjugating enzyme E2 variant 1                                   | Mus musculus     | Ube2v1    | PE=1     | SV=1           |
| P12382    | ATP-dependent 6-phosphofructokinase, liver type OS=Mus musculus GN=PfkA    | Mus musculus     | PfkA      | PE=1     | SV=4           |
| Q9R062    | Glycogenin-1 OS=Mus musculus GN=Gygl PE=1 SV=3                              | Mus musculus     | Gygl      | PE=1     | SV=3           |
| E9PYN1    | Cell adhesion molecule 1 OS=Mus musculus GN=Cadm1                            | Mus musculus     | Cadm1     | PE=1     | SV=1           |
| Q9KD3     | Secretory carrier-associated membrane protein 5 OS=Mus musculus GN=Scamp5   | Mus musculus     | Scamp5    | PE=1     | SV=1           |
| Q74MV1    | Reticulon OS=Mus musculus GN=Rtn1                                            | Mus musculus     | Rtn1      | PE=1     | SV=1           |
| P43274    | Histone H1.4 OS=Mus musculus GN=Hist1h1e                                    | Mus musculus     | Hist1h1e  | PE=1     | SV=2           |
| Q92Z04    | Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Mus musculus GN=Hnmpc    | Mus musculus     | Hnmpc     | PE=1     | SV=1           |
| P12787    | Cytochrome c oxidase subunit 5, mitochondrial                               | Mus musculus     | Cox5a     | PE=1     | SV=2           |
| P62774    | Myotrophin OS=Mus musculus GN=Mtrpn                                            | Mus musculus     | Mtrpn     | PE=1     | SV=2           |
| Q05201    | Aspartate aminotransferase, cytoplasmic OS=Mus musculus GN=Got1               | Mus musculus     | Got1      | PE=1     | SV=3           |
| Q5155     | Schematic vesicle glycoprotein 2A OS=Mus musculus GN=Vva2                   | Mus musculus     | Vva2      | PE=1     | SV=1           |
| Q9R0Y6    | Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh11l1| Mus musculus     | Aldh11l1  | PE=1     | SV=1           |
| P13707    | Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS=Mus musculus GN=Gpd1| Mus musculus     | Gpd1      | PE=1     | SV=3           |
| A0A087WQCN2| Prothymosin alpha (Fragment) OS=Mus musculus GN=Ptmalpha                    | Mus musculus     | Ptmalpha  | PE=1     | SV=1           |
| Q8BVE3    | V-type proton ATPase subunit H OS=Mus musculus GN=Atp6v1h                     | Mus musculus     | Atp6v1h   | PE=1     | SV=1           |
| Accession | Description                                                                 | Species      | Entrez ID | SV | PE |
|-----------|------------------------------------------------------------------------------|--------------|-----------|----|----|
| Q91VE0    | Long-chain fatty acid transport protein 4                                    | Mus musculus | 2,134     | 1  | 1  |
| Q53955    | Proteasome subunit beta type-10                                               | Mus musculus | 2,112     | 1  | 1  |
| AA0A97PU8G4 | Anti-lox-1 15C4 light chain                                                  | Mus musculus | 2,103     | 2  | 1  |
| P19783    | Cytochrome c oxidase subunit 4 isofrom 1, mitochondrial                      | Mus musculus | 2,101     | 2  | 1  |
| Q9QZQ0    | Core histone macro-H2A.1                                                     | Mus musculus | 2,087     | 3  | 1  |
| AA0A75BSP3 | Protein lghg2b (Fragment)                                                    | Mus musculus | 2,086     | 1  | 1  |
| Q7S8J8    | MCGG29889, isofrom CRA b                                                    | Mus musculus | 2,07      | 2  | 1  |
| Q920E0    | Neurochordin OS                                                               | Mus musculus | 2,07      | 1  | 1  |
| B1AQW2    | Microtubule-associated protein OS                                             | Mus musculus | 2,064     | 1  | 1  |
| OS0901    | Protein IMPACT OS                                                            | Mus musculus | 2,043     | 2  | 1  |
| P08228    | Superoxide dismutase [Cu-Zn] OS                                              | Mus musculus | 2,017     | 1  | 1  |
| P62305    | Small nuclear ribonucleoprotein E                                            | Mus musculus | 2,004     | 1  | 1  |
| P61979    | Heterogeneous nuclear ribonucleoprotein K OS                                 | Mus musculus | 2,001     | 1  | 1  |
| Q8WF0     | Succinate-semialdehyde dehydrogenase, mitochondrial OS                       | Mus musculus | 1,992     | 1  | 1  |
| Q9OXS1    | Plectin OS                                                                   | Mus musculus | 1,992     | 3  | 1  |
| Q3T7Q0    | Beta1 subunit of GTP-binding protein OS                                       | Mus musculus | 1,987     | 2  | 1  |
| Q8BT18    | Serine/arginine repetitive matrix protein 2 OS                               | Mus musculus | 1,98      | 3  | 1  |
| P56399    | Ubiquitin carboxyl-terminal hydrolase 5 OS                                   | Mus musculus | 1,973     | 1  | 1  |
| E9Q557    | Desmoplakin OS                                                               | Mus musculus | 1,968     | 1  | 1  |
| P68040    | Receptor of activated protein C kinase 1 OS                                  | Mus musculus | 1,968     | 1  | 1  |
| Q9WUB8    | Glycogen phosphorylase, muscle form OS                                       | Mus musculus | 1,957     | 3  | 1  |
| Q9QY7X    | Protein piccolo OS                                                           | Mus musculus | 1,957     | 4  | 1  |
| D3L722    | 40S ribosomal protein S19                                                    | Mus musculus | 1,947     | 1  | 1  |
| Q2Z6G4    | V-type proton ATPase 116 kDa subunit a isofrom 1 OS                          | Mus musculus | 1,947     | 1  | 1  |
| Q2Z0H4    | CUGBP Elav-like family member 2 OS                                            | Mus musculus | 1,944     | 1  | 1  |
| P62715    | Serine/threonine-protein phosphatase 2A catalytic subunit beta isofrom OS   | Mus musculus | 1,938     | 1  | 1  |
| Q3ULD5    | Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS                  | Mus musculus | 1,928     | 1  | 1  |
| P46460    | Vesicle-fusing ATPase OS                                                     | Mus musculus | 1,902     | 2  | 1  |
| Q9OXXV0   | ProSAAS OS                                                                  | Mus musculus | 1,901     | 2  | 1  |
| G61838    | Alpha-2-macroglobulin OS                                                     | Mus musculus | 1,893     | 3  | 1  |
| E9PFAA3   | IQ motif and SEC7 domain-containing protein 1 OS                             | Mus musculus | 1,891     | 1  | 1  |
| Q3UYK6    | Amino acid transporter OS                                                    | Mus musculus | 1,882     | 1  | 1  |
| Q97300    | Neuroplastin OS                                                              | Mus musculus | 1,877     | 1  | 1  |
| Q6GT24    | Peroxiredoxin 6 OS                                                           | Mus musculus | 1,869     | 2  | 1  |
| Q9D7M5    | Dynein light chain 2, cytoplasmic OS                                         | Mus musculus | 1,852     | 1  | 1  |
| Q564G5    | Clusterin OS                                                                 | Mus musculus | 1,851     | 2  | 1  |
| P62814    | V-type proton ATPase subunit B, brain isofrom OS                             | Mus musculus | 1,851     | 2  | 1  |
| Q4FJX4    | Crsp1 protein OS                                                             | Mus musculus | 1,846     | 1  | 1  |
| Q8RRO1    | Microtubule-associated protein RP/EB family member 2 OS                     | Mus musculus | 1,821     | 1  | 1  |
| Q3UY2J    | Myelin-oligodendrocyte glycoprotein OS                                       | Mus musculus | 1,821     | 1  | 1  |
| P63726    | 40S ribosomal protein S17 OS                                                  | Mus musculus | 1,818     | 1  | 1  |
| Q9D2G2    | Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate | Mus musculus | 1,81     | 1  | 1  |
| Q2Z1G3    | V-type proton ATPase subunit C 1 OS                                           | Mus musculus | 1,805     | 4  | 1  |
| Q3TVK3    | Aspartyl aminopeptidase OS                                                   | Mus musculus | 1,8      | 1  | 1  |
| P48036 | Annexin A5 | OS=Mus musculus | GN=Anxa5 | PE=1 | SV=1 | 1,795 |
| P62858 | 40S ribosomal protein S28 | OS=Mus musculus | GN=Rps28 | PE=1 | SV=1 | 1,794 |
| Q92ZD6-2 | Isoform B of Methyl-CpG-binding protein 2 | OS=Mus musculus | GN=Mecp2 | PE=1 | SV=1 | 1,784 |
| F6VP70 | Protein Ccdc163 [Fragment] | OS=Mus musculus | GN=Ccdc163 | PE=4 | SV=1 | 1,783 |
| E9P2F0 | Nucleoside diphosphate kinase | OS=Mus musculus | GN=Gn20390 | PE=3 | SV=1 | 1,782 |
| E9Q4J5 | Tropomyosin alpha-1 chain | OS=Mus musculus | GN=Tpm1 | PE=1 | SV=1 | 1,78 |
| Q8BG05 | Heterogeneous nuclear ribonucleoprotein A3 | OS=Mus musculus | GN=Hnmpa3 | PE=1 | SV=1 | 1,778 |
| Q7TSJ2 | Microtubule-associated protein 6 | OS=Mus musculus | GN=Map6 | PE=1 | SV=2 | 1,777 |
| P11881 | Inositol 1,4,5-trisphosphate receptor type 1 | OS=Mus musculus | GN=Itr1 | PE=1 | SV=2 | 1,774 |
| P05202 | Aspartate aminotransferase, mitochondrial | OS=Mus musculus | GN=Got2 | PE=1 | SV=1 | 1,772 |
| Q9D0M3 | Cytochrome c, heme protein, mitochondrial | OS=Mus musculus | GN=Cyc1 | PE=1 | SV=1 | 1,764 |
| Q9C6E0 | ATP-dependent 6-phosphofructokinase | OS=Mus musculus | GN=Pkf | PE=1 | SV=1 | 1,751 |
| Q9PT1 | Rh GDP-dissociation inhibitor 1 | OS=Mus musculus | GN=Arhgdia | PE=1 | SV=3 | 1,738 |
| P47857 | ATP-dependent 6-phosphofructokinase, muscle type | OS=Mus musculus | GN=Pkm | PE=1 | SV=3 | 1,736 |
| Q91L23 | Methylglutaconyl-CoA hydratase, mitochondrial | OS=Mus musculus | GN=Auh | PE=1 | SV=1 | 1,714 |
| Q8BY1 | Tenasin-R | OS=Mus musculus | GN=Tnr | PE=1 | SV=2 | 1,703 |
| Q2Z2I9 | Succinate-CoA ligase [ADP-forming] subunit beta, mitochondrial | OS=Mus musculus | GN=Sucld2 | PE=1 | SV=2 | 1,691 |
| Q6ZWX2 | Thymosin, beta 4, X chromosome | OS=Mus musculus | GN=Tmsb4x | PE=2 | SV=1 | 1,688 |
| O5S143 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 | OS=Mus musculus | GN=Atp2a2 | PE=1 | SV=2 | 1,68 |
| P57780 | Alpha-actinin-4 | OS=Mus musculus | GN=Actn4 | PE=1 | SV=1 | 1,674 |
| Q0VF55 | Calcium-transporting ATPase | OS=Mus musculus | GN=Atp2b3 | PE=1 | SV=1 | 1,674 |
| Q9C0PU | Lactoylglutathione lyase | OS=Mus musculus | GN=Glo1 | PE=1 | SV=3 | 1,664 |
| B2RTE | Aldehyde dehydrogenase family 1, subfamily A7 | OS=Mus musculus | GN=Aldh1a7 | PE=2 | SV=1 | 1,663 |
| Q3UM9 | Hepatoma-derived growth factor-related protein 2 | OS=Mus musculus | GN=Hdgfrp2 | PE=1 | SV=1 | 1,66 |
| Q3VQ0 | Dynein heavy chain 12, axonemal | OS=Mus musculus | GN=Dnah12 | PE=1 | SV=2 | 1,655 |
| Q9DBG3 | AP-2 complex subunit beta OS | Mus musculus | GN=Ap2b1 | PE=1 | SV=1 | 1,651 |
| P47757 | F-actin-capping protein subunit beta | OS=Mus musculus | GN=Capzb | PE=1 | SV=3 | 1,641 |
| Q9R01 | Bleomycin hydrolase | OS=Mus musculus | GN=Blmh | PE=1 | SV=1 | 1,639 |
| G5E924 | Heterogeneous nuclear ribonucleoprotein L (Fragment) | OS=Mus musculus | GN=Hnmp1 | PE=1 | SV=1 | 1,636 |
| P1422 | Calreticulin OS | Mus musculus | GN=Calr | PE=1 | SV=1 | 1,616 |
| P80316 | T-complex protein 1 subunit epsilon | OS=Mus musculus | GN=Cct5 | PE=1 | SV=1 | 1,613 |
| P31324 | cAMP-dependent protein kinase type II-beta regulatory subunit OS | Mus musculus | GN=Prkar2b | PE=1 | SV=3 | 1,608 |
| H38KH6 | S-formylglutathione hydrolase OS | Mus musculus | GN=Esd | PE=1 | SV=1 | 1,605 |
| P61922 | 4-aminobutyrate aminotransferase, mitochondrial | OS=Mus musculus | GN=Abat | PE=1 | SV=1 | 1,589 |
| Q99KIO | Acotinate hydratase, mitochondrial | OS=Mus musculus | GN=Aco2 | PE=1 | SV=1 | 1,588 |
| Q99M71 | Mammalian ependymin-related protein 1 | OS=Mus musculus | GN=Eprd1 | PE=2 | SV=1 | 1,587 |
| O61598 | Rab GDP dissociation inhibitor beta OS | Mus musculus | GN=Gdi2 | PE=1 | SV=1 | 1,586 |
| Q542X7 | Chaperonin subunit 2 (Beta), isoform CRA_a OS | Mus musculus | GN=Cct2 | PE=2 | SV=1 | 1,584 |
| P70 | Importin subunit beta-1 OS | Mus musculus | GN=Kpnb1 | PE=1 | SV=2 | 1,574 |
| Q8K2C9 | Very-long-chain (3R)-3-hydroxyacyl-Coa dehydratase | OS=Mus musculus | GN=Hcad3 | PE=1 | SV=2 | 1,574 |
| Q88MF4 | Dihydrolipoamide-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial | OS=Mus musculus | GN=Diat | PE=1 | SV=2 | 1,574 |
| P48771 | Cytochrome c oxidase subunit 7A2, mitochondrial | OS=Mus musculus | GN=Cox7a2 | PE=2 | SV=1 | 1,573 |
| E0CYV0 | Protein-L-isoaspartate O-methyltransferase | OS=Mus musculus | GN=Pcm1 | PE=1 | SV=1 | 1,568 |
| P08249 | Malate dehydrogenase, mitochondrial | OS=Mus musculus | GN=Mdh2 | PE=1 | SV=3 | 1,566 |
Q3TGU7  Proliferation-associated 2G4 OS=Mus musculus GN=Pa2g4 PE=2 SV=1  1,565
P63011  Ras-related protein Rab-3A OS=Mus musculus GN=Rab3a PE=1 SV=1  1,565
P40336  Vacuolar protein sorting-associated protein 26A OS=Mus musculus GN=Vps26a PE=1 SV=1  1,562
Q99P5U  Long-chain-fatty-acid--CoA ligase ACSBG1 OS=Mus musculus GN=Acsbg1 PE=1 SV=1  1,561
Q9D8B3  Charged multivesicular body protein 4b OS=Mus musculus GN=Chmp4b PE=1 SV=2  1,557
A2AWN8  YTH domain family 1, isoform CRA_a OS=Mus musculus GN=Ythdf1 PE=1 SV=1  1,554
Q5A4E3  Phosphatidylinositol-4-phosphate 5-kinase, type II, alpha OS=Mus musculus GN=Pip4k2a PE=2 SV=1  1,552
Q61361  Breccin core protein OS=Mus musculus GN=Bcan PE=1 SV=2  1,544
P60335  Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1  1,542
E9Q8N8  Anion exchange protein OS=Mus musculus GN=Sclc4a4 PE=1 SV=1  1,539
Q3U1N0  Coronin OS=Mus musculus GN=Coro1a PE=2 SV=1  1,538
Q5B8X0  MCG18564, isoform CRA_a OS=Mus musculus GN=Rpl12 PE=2 SV=1  1,528
Q61900  Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 PE=1 SV=1  1,52
P20357  Microtubule-associated protein 12 OS=Mus musculus GN=Ct12 PE=2 SV=1  1,508
P50396  Rab GDP dissociation inhibitor alpha OS=Mus musculus GN=Rdi1 PE=1 SV=3  1,501
P14148  60S ribosomal protein L7 OS=Mus musculus GN=Rpl7 PE=1 SV=2  1,5
Q01853  Transitional endoplasmic reticulum ATPase OS=Mus musculus GN=Cp PE=1 SV=4  1,493
Q9IZU6  Dystonin OS=Mus musculus GN=Dst PE=1 SV=2  1,493
P05063  Fructose-bisphosphatase aldolase C OS=Mus musculus GN=Aldc PE=1 SV=4  1,492
Q68FL4  Putative adenosylhomocysteinase 3 OS=Mus musculus GN=Ahcy3 PE=1 SV=1  1,485
P35235  Tyrosine-protein phosphatase non-receptor type 11 OS=Mus musculus GN=Ptpn11 PE=1 SV=2  1,484
Q61711  Peroxiredoxin-2 OS=Mus musculus GN=Prdx2 PE=1 SV=3  1,483
P51190  Ras-related protein Rab-7a OS=Mus musculus GN=Rab7a PE=1 SV=2  1,473
Q80YX1  Tenascin OS=Mus musculus GN=Tnc PE=1 SV=1  1,473
Q2PF07  PH and SEC7 domain-containing protein 3 OS=Mus musculus GN=Psdc3 PE=1 SV=2  1,473
Q91ZZ3  Beta-synuclein OS=Mus musculus GN=Sncb PE=1 SV=1  1,469
Q7TQD2  Tubulin polymerization-promoting protein OS=Mus musculus GN=Tpp1 PE=1 SV=1  1,468
Q9IK65  Cell cycle exit and neuronal differentiation protein 1 OS=Mus musculus GN=Cend1 PE=1 SV=1  1,468
B2RRX2  Serine/threonine-protein phosphatase OS=Mus musculus GN=Ppp2ca PE=2 SV=1  1,464
Q3UAD6  Heat shock protein 90kDa beta (Grp94), member 1 OS=Mus musculus GN=Hsp90b1 PE=1 SV=2  1,462
Q5M9B8  MCG13936 OS=Mus musculus GN=Rpl28 PE=2 SV=1  1,458
Q52C1C  Eukaryotic translation initiation factor 4A2 OS=Mus musculus GN=Elf4a2 PE=2 SV=1  1,458
P60761  Neurilin OS=Mus musculus GN=Nrgn PE=1 SV=1  1,457
P01552  Vimentin OS=Mus musculus GN=Vim PE=1 SV=3  1,454
Q5DOQ5  Capping protein (Actin filament) muscle Z-line, alpha 2, isoform CRA_a OS=Mus musculus GN=Capza2 PE=2 SV=1  1,45
P52760  Ribonuclease U114 OS=Mus musculus GN=Hrps12 PE=1 SV=3  1,449
P63085  Mitogen-activated protein kinase 1 OS=Mus musculus GN=Mapk1 PE=1 SV=3  1,448
F8WHB1  Calcium-transporting ATPase OS=Mus musculus GN=Atp2b2 PE=1 SV=1  1,441
P27661  Histone H2AX OS=Mus musculus GN=H2afx PE=1 SV=2  1,438
Q9D0A9  14 kDa phosphohistidine phosphatase OS=Mus musculus GN=Phpt1 PE=1 SV=1  1,437
P60710  Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1  1,43
P70349  Histidine triad nucleotide-binding protein 1 OS=Mus musculus GN=Hnt1 PE=1 SV=3  1,429
Q9CPX4  Ferritin OS=Mus musculus GN=Fth1 PE=1 SV=1  1,423
P31650  Sodium- and chloride-dependent GABA transporter 3 OS=Mus musculus GN=Slc6a11 PE=1 SV=2 1,42
O08749  Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus musculus GN=Dld PE=1 SV=2 1,419
Q80TL4  PHD finger protein 24 OS=Mus musculus GN=Phf24 PE=1 SV=2 1,417
P61264  Syntaxin-1B OS=Mus musculus GN=Stx1b PE=1 SV=1 1,414
B9HN0  Ubiquitin-activating enzyme E1, Chr X OS=Mus musculus GN=Uba1 PE=2 SV=1 1,398
P15105  Glutamine synthetase OS=Mus musculus GN=Glul PE=1 SV=6 1,392
Q9R1P0  Proteasome subunit alpha type-4 OS=Mus musculus GN=Psmα4 PE=1 SV=1 1,392
QV0CE0  Sodium/potassium-transporting ATPase subunit alpha OS=Mus musculus GN=Atpα1a1 PE=1 SV=1 1,39
Q8CBQ4  Glycogen phosphorylase, brain form OS=Mus musculus GN=Pygb PE=1 SV=3 1,385
O83842  WD repeat-containing protein 1 OS=Mus musculus GN=Wdr1 PE=1 SV=3 1,383
P68369  Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1 1,378
Q8VDN2  Sodium/potassium-transporting ATPase subunit alpha-1 OS=Mus musculus GN=Atpα1a1 PE=1 SV=1 1,377
A2ARP8  Microtubule-associated protein 1A OS=Mus musculus GN=Mapα1a PE=1 SV=1 1,372
Q8VEK3  Heterogeneous nuclear ribonucleoprotein U OS=Mus musculus GN=Hnrnpu PE=1 SV=1 1,37
Q912X7  Proline-density lipoprotein receptor-related protein 1 OS=Mus musculus GN=Lrp1 PE=1 SV=1 1,368
P58252  Elongation factor 2 OS=Mus musculus GN=Efε2 PE=1 SV=2 1,364
Q9C213  Cytochrome b-c1 complex subunit 1, mitochondrial OS=Mus musculus GN=Uqrc1 PE=1 SV=2 1,363
A0A0AMQA5  Tubulin alpha chain (Fragment) OS=Mus musculus GN=Tuba4a PE=1 SV=1 1,353
P84078  ADP-ribosylation factor 1 OS=Mus musculus GN=Arfα1 PE=1 SV=2 1,352
P08752  Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Mus musculus GN=Gna12 PE=1 SV=5 1,35
Q90051  Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Mus musculus GN=Pdhβ PE=1 SV=1 1,345
Q9WTT4  V-type proton ATPase subunit G OS=Mus musculus GN=Atpβ1g2 PE=3 SV=1 1,344
G5E902  MCG10343, isoform CRA_b OS=Mus musculus GN=Slc25a3 PE=1 SV=1 1,338
P62317  Small nuclear ribonucleoprotein Sm D2 OS=Mus musculus GN=Snrdp2 PE=3 SV=1 1,331
A0A0G2JFT8  Protein RUFY3 OS=Mus musculus GN=Rufy3 PE=1 SV=1 1,328
F6R5K3  Protein Gm17430 OS=Mus musculus GN=Gm17430 PE=4 SV=1 1,325
P55088  Aquaporin-4 OS=Mus musculus GN=Aqp4 PE=1 SV=2 1,323
P11031  Activated RNA polymerase II transcriptional coactivator p15 OS=Mus musculus GN=Gsub1 PE=1 SV=3 1,321
Q8C522  Endonuclease domain-containing 1 protein OS=Mus musculus GN=Endод1 PE=1 SV=2 1,321
Q8X0T0  Reticulin-1 OS=Mus musculus GN=Rtn1 PE=1 SV=1 1,321
A8I6P9  14-3-3 protein gamma subtype OS=Mus musculus GN=Ywhag PE=2 SV=1 1,308
P63318  Protein kinase C gamma type OS=Mus musculus GN=PrkγC PE=1 SV=1 1,304
Q60668  Heterogeneous nuclear ribonucleoprotein D0 OS=Mus musculus GN=Hnrnpd PE=1 SV=2 1,303
Q0R1F4  Proteasome subunit alpha type-1 OS=Mus musculus GN=Psmα1 PE=1 SV=1 1,301
Q546D4  Albumin 1 OS=Mus musculus GN=Ab PE=2 SV=1 0,775
P47915  60S ribosomal protein L29 OS=Mus musculus GN=Rpl29 PE=2 SV=2 0,76
Q9C6U2  Structural maintenance of chromosomes protein 1A OS=Mus musculus GN=Smcα1a PE=1 SV=4 0,757
P62855  40S ribosomal protein S26 OS=Mus musculus GN=Rps26 PE=1 SV=3 0,752
Q3TT94  Serine/threonine-protein phosphatase 2A OS=Mus musculus GN=Pp2ra2 PE=2 SV=1 0,751
P01831  Thy-1 membrane glycoprotein OS=Mus musculus GN=Thy1 PE=1 SV=1 0,75
P83882  60S ribosomal protein L36a OS=Mus musculus GN=Rpl36a PE=1 SV=2 0,744
P62996  Transformer-2 protein homolog beta OS=Mus musculus GN=Tra2b PE=1 SV=1 0,744
Q91VB8  Alpha globin 1 OS=Mus musculus GN=Haemoglobin alpha 2 PE=1 SV=1 0,733
D32AB2  Gamma-soluble NSF attachment protein (Fragment) OS=Mus musculus GN=Napg PE=1 SV=1 0,726
| Gene ID       | Description                                                                 | Organism              | Protein ID | Expression |
|--------------|------------------------------------------------------------------------------|-----------------------|------------|------------|
| O08539       | Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1    | 0,711                 | P18872     | 0,709      |
| Q99P00       | Pre-mRNA-processing-splicing factor B OS=Mus musculus GN=Prp8 PE=1 SV=2     |                       |            |            |
| P18872       | Guanine nucleotide-binding protein G1 alpha OS=Mus musculus GN=Gnao1 PE=1 SV=3|                       |            |            |
| D0V066       | Erythocyte protein band 4.1-like isoform B OS=Mus musculus GN=Epba13 PE=2 SV=1|                       |            | 0,708      |
| Q9WUM5       | Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Mus musculus GN=Succlg1 PE=1 SV=4|                      |            | 0,705      |
| Q31LP8       | RAS-related C3 botulinum substrate 1, isoform CRA_a OS=Mus musculus GN=Rac1 PE=1 SV=1|                      |            | 0,693      |
| P02802       | Metallothionein-1 OS=Mus musculus GN=Mt1 PE=1 SV=1                         | 0,689                 | P36308     |            |
| P17742       | Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Pinpe PE=2 SV=2    | 0,681                 |            |            |
| P12970       | 60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=1 SV=2               | 0,68                   |            |            |
| P62204       | Calmodulin OS=Mus musculus GN=Calm1 PE=1 SV=2                              | 0,679                 |            |            |
| B1AQ20       | Septin-8 OS=Mus musculus GN=Sept8 PE=1 SV=1                               | 0,678                 |            |            |
| P68510       | 14-3-3 protein eta OS=Mus musculus GN=Ywhah PE=1 SV=2                     | 0,677                 |            |            |
| Q9CVB6       | Actin-related protein 2/3 complex subunit 2 OS=Mus musculus GN=Arpc2 PE=1 SV=3| 0,665                 |            |            |
| P08551       | Neurofilament light polypeptide OS=Mus musculus GN=Neft PE=1 SV=5          | 0,66                   |            |            |
| P99024       | Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1                   | 0,659                 |            |            |
| O09167       | 60S ribosomal protein L21 OS=Mus musculus GN=Rpl21 PE=1 SV=3               | 0,659                 |            |            |
| Q6IR05       | Clathrin light chain B OS=Mus musculus GN=Cltb PE=1 SV=1                   | 0,657                 |            |            |
| E9Q05Q       | Kinesin-like protein KIF21A OS=Mus musculus GN=Kif21a PE=1 SV=2            | 0,657                 |            |            |
| P20065       | Thymosin beta-4 OS=Mus musculus GN=Tmsb4x PE=1 SV=1                        | 0,656                 |            |            |
| Q54GL4       | Glutamate decarboxylase OS=Mus musculus GN=Gad2 PE=2 SV=1                  | 0,655                 |            |            |
| F8WGL3       | Cofilin-1 OS=Mus musculus GN=Cfl1 PE=1 SV=1                               | 0,651                 |            |            |
| Q8BK29       | Pyruvate dehydrogenase protein X component, mitochondrial OS=Mus musculus GN=Pdhx PE=1 SV=1 | 0,643                 |            |            |
| Q8CQ27       | Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnmp1 PE=1 SV=1 | 0,627                 |            |            |
| Q5SM9M5      | MCIG10806 OS=Mus musculus GN=Rpl23a PE=2 SV=1                             | 0,624                 |            |            |
| P99028       | Cytochrome b-c1 complex subunit 6, mitochondrial OS=Mus musculus GN=Uqcrh PE=1 SV=2 | 0,622                 |            |            |
| P99027       | 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3         | 0,62                   |            |            |
| P63163       | Small nuclear ribonucleoprotein-associated protein N OS=Mus musculus GN=Snrnp PE=2 SV=1 | 0,612                 |            |            |
| Q9CQZ8       | Secerin-1 OS=Mus musculus GN=Srn1 PE=1 SV=1                               | 0,61                   |            |            |
| P63017       | Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1       | 0,61                   |            |            |
| Q921M7       | Protein FAM49B OS=Mus musculus GN=Fam49b PE=2 SV=1                        | 0,61                   |            |            |
| P27659       | 60S ribosomal protein L3 OS=Mus musculus GN=Rpl3 PE=1 SV=3                 | 0,606                 |            |            |
| O08599       | Syntaxin-binding protein 1 OS=Mus musculus GN=Stxbp1 PE=1 SV=2             | 0,606                 |            |            |
| P08553       | Neurofilament medium polypeptide OS=Mus musculus GN=Nefm PE=1 SV=4         | 0,604                 |            |            |
| Q8R366       | Immunoglobulin superfamily member 8 OS=Mus musculus GN=Igfbf PE=1 SV=2    | 0,592                 |            |            |
| Q80YN3       | Breast carcinoma-amplified sequence 1 homolog OS=Mus musculus GN=Bcas1 PE=1 SV=3 | 0,59                  |            |            |
| F6RT34       | Myelin basic protein (Fragment) OS=Mus musculus GN=Mbp PE=1 SV=1           | 0,58                   |            |            |
| P06837       | Neuronomulbin OS=Mus musculus GN=Gap43 PE=1 SV=1                           | 0,58                   |            |            |
| Q99104       | Unconventional myosin-Va OS=Mus musculus GN=Myos1a PE=1 SV=2               | 0,58                   |            |            |
| Q3UR55       | ATPase, Na+/K+ transporting, beta 2 polypeptide, isoform CRA_b OS=Mus musculus GN=Atp1b2 PE=2 SV=1 | 0,573                 |            |            |
| Q54BF2       | Guanine deaminase OS=Mus musculus GN=Gda PE=2 SV=1                         | 0,567                 |            |            |
| Q6ZWV7       | 60S ribosomal protein L35 OS=Mus musculus GN=Rpl35 PE=1 SV=1               | 0,561                 |            |            |
| Q923T9       | Calcium/calmodulin-dependent protein kinase type II subunit gamma OS=Mus musculus GN=Camk2g PE=1 SV=1 | 0,556                 |            |            |
| Q60631       | Growth factor receptor-bound protein 2 OS=Mus musculus GN=Ghrb2 PE=1 SV=1  | 0,553                 |            |            |
| GeneID  | Protein Name                        | OS          | GN      | PE  | SV  | Score |
|--------|-------------------------------------|-------------|---------|-----|-----|-------|
| Q08331 | Calretinin                          | Mus musculus| Calb2   | 1   | 3   | 0.551 |
| P62267 | 40S ribosomal protein S23           | Mus musculus| Rps23   | 1   | 3   | 0.549 |
| P68433 | Histone H3.1                        | Mus musculus| Hist1h3a| 1   | 2   | 0.544 |
| G5E866 | Splicing factor 3B subunit 1       | Mus musculus| Sf3b1   | 1   | 1   | 0.533 |
| P12658 | Calbindin                           | Mus musculus| Calb1   | 1   | 2   | 0.525 |
| Q6CQK5 | Major vault protein                 | Mus musculus| Mvp     | 1   | 4   | 0.525 |
| Q9WV69 | Dematin                             | Mus musculus| Dmnt    | 1   | 1   | 0.524 |
| P29341 | Polyadenylate-binding protein 1     | Mus musculus| Pabp1   | 1   | 2   | 0.522 |
| Q9CR57 | Myosin-10                           | Mus musculus| Myh10   | 1   | 1   | 0.520 |
| Q3UH59 | Small nuclear ribonucleoprotein F   | Mus musculus| Snrpf   | 1   | 1   | 0.519 |
| P62307 | Flotillin 2, isoform CRA_a          | Mus musculus| Flot2   | 1   | 1   | 0.519 |
| P62911 | 60S ribosomal protein L32           | Mus musculus| Rpl32   | 1   | 2   | 0.506 |
| Q51078 | Ribosomal protein L19               | Mus musculus| Rpl19   | 2   | 1   | 0.506 |
| Q9CRB6 | Tubulin polymerization-promoting protein family member 3 | Mus musculus| Tppp3  | 1   | 1   | 0.5   |
| P97499 | Telomerase protein component 1     | Mus musculus| Tep1    | 1   | 1   | 0.499 |
| Q9R1T4 | Septin-6                            | Mus musculus| Sept6   | 1   | 4   | 0.493 |
| Q8BL66 | Early endosome antigen 1           | Mus musculus| Eea1    | 1   | 2   | 0.487 |
| Q3TYV5 | Cyclic nucleotide phosphodiesterase 1, isoform CRA_b | Mus musculus| Cnp    | 2   | 1   | 0.487 |
| Q9CYR0 | Single-stranded DNA-binding protein, mitochondrial OSMus musculus | Mus musculus| Ssbp1  | 1   | 1   | 0.487 |
| P20029 | 78 kDa glucose-regulated protein OSMus musculus | Hspa5   | 1   | 3   | 0.48  |
| Q4VWZ5 | Acyl-CoA-binding protein OSMus musculus | Dbi    | 1   | 1   | 0.461 |
| Q497E9 | 40S ribosomal protein S8 OSMus musculus | Rps8    | 2   | 1   | 0.457 |
| P63101 | 14-3-3 protein zeta/delta OSMus musculus | Ywhaz   | 1   | 1   | 0.456 |
| Q50SA8 | MCG17585 OSMus musculus | Rpl39   | 2   | 1   | 0.456 |
| Q7TQ13 | Ubiquitin thioesterase OTUB1 OSMus musculus | Otub1  | 1   | 2   | 0.456 |
| P47911 | 60S ribosomal protein L6 OSMus musculus | Rpl6    | 1   | 3   | 0.452 |
| Q8VDD5 | Myosin-9                             | Mus musculus| Myh9    | 1   | 4   | 0.451 |
| Q60864 | Stress-induced-phosphoprotein 1 OSMus musculus | Stip1   | 1   | 1   | 0.448 |
| E9QA2  | Ribosomal protein L15 OSMus musculus | Gm10020  | 3   | 1   | 0.447 |
| P14869 | 60S acidic ribosomal protein P0 OSMus musculus | Rplp0   | 1   | 3   | 0.438 |
| Q5S64E | Ribosomal protein L4 OSMus musculus | Rpl4    | 2   | 1   | 0.437 |
| P32067 | Lupus La protein homolog OSMus musculus | Srb    | 1   | 1   | 0.425 |
| P47963 | 60S ribosomal protein L13 OSMus musculus | Rpl13   | 1   | 3   | 0.414 |
| Q2UBP6 | Putative uncharacterized protein OSMus musculus | Actb   | 2   | 1   | 0.407 |
| P62264 | 40S ribosomal protein S14 OSMus musculus | Rps14   | 1   | 3   | 0.399 |
| P63005 | Platelet-activating factor acetylhydrolase IB subunit alpha OSMus musculus | Pafah1b1 | 1   | 2   | 0.396 |
| Q8CI43 | Myosin light chain 6B OSMus musculus | Myl6b    | 2   | 1   | 0.388 |
| B2RSH2 | Guanine nucleotide-binding protein G1 subunit alpha-1 OSMus musculus | Gna1    | 1   | 1   | 0.382 |
| Q5SV10 | Calcium/calmodulin-dependent protein kinase I, beta, isoform CRA_b OSMus musculus | Camk2b  | 1   | 1   | 0.37  |
| B1AQ77 | Keratin 15, isoform CRA_a OSMus musculus | Krt15   | 1   | 1   | 0.367 |
| Q5XJF6 | Ribosomal protein OSMus musculus | Rpl10a   | 1   | 1   | 0.367 |
| P62320 | Small nuclear ribonucleoprotein Sm D3 OSMus musculus | Snrpd3  | 1   | 1   | 0.36  |
| Q9D1R9 | 60S ribosomal protein L34 OSMus musculus | Rpl34   | 1   | 2   | 0.347 |
| Accession | Description | Organism      | Gene Symbol | Protein Description | E-value |
|-----------|-------------|---------------|-------------|---------------------|---------|
| P14115    | 60S ribosomal protein L27a | Mus musculus | Rpl27a      | 60S ribosomal protein L27a | 0.344   |
| Z4Y123    | Fer-1-like protein 4 | Mus musculus | Fer1l4      | Fer-1-like protein 4 | 0.336   |
| P62889    | 60S ribosomal protein L30 | Mus musculus | Rpl30       | 60S ribosomal protein L30 | 0.319   |
| P62918    | 60S ribosomal protein L8  | Mus musculus | Rpl8        | 60S ribosomal protein L8  | 0.311   |
| Q5BLK1    | 40S ribosomal protein S6  | Mus musculus | Rps6        | 40S ribosomal protein S6  | 0.298   |
| Q8CAK3    | UPF0515 protein C19orf66 homolog | Mus musculus | Snrpd1  | UPF0515 protein C19orf66 homolog | 0.292   |
| P62315    | Small nuclear ribonucleoprotein Sm D1 | Mus musculus | Snrpd1  | Small nuclear ribonucleoprotein Sm D1 | 0.275   |
| P62717    | 60S ribosomal protein L18a | Mus musculus | Rpl18a | 60S ribosomal protein L18a | 0.245   |
| P60904    | DnaJ homolog subfamily C member 5 | Mus musculus | Dnajc5 | DnaJ homolog subfamily C member 5 | 0.231   |
| Q8C1Y8    | Vacuolar fusion protein CCZ1 homolog | Mus musculus | Ccz1 | Vacuolar fusion protein CCZ1 homolog | 0.217   |
| P47962    | 60S ribosomal protein L5 | Mus musculus | Rpl5 | 60S ribosomal protein L5 | 0.203   |
| Q3V117    | ATP-citrate synthase | Mus musculus | Acly | ATP-citrate synthase | 0.173   |
# DATA FILE S1

## REGULATED PROTEINS WT: 24 vs. 3 months

| Accession | Description | Abundance Ratio: (WT24) / (WT3) |
|-----------|-------------|---------------------------------|
| P28663    | Beta-soluble NSF attachment protein OS=Mus musculus GN=Napb PE=1 SV=2 | 17,199 |
| Q6ZWX2    | Thymosin, beta 4, X chromosome OS=Mus musculus GN=Tmsb4x PE=2 SV=1 | 12,952 |
| E9PYN1    | Cell adhesion molecule 1 OS=Mus musculus GN=Cadm1 PE=1 SV=1 | 11,645 |
| Q9D309    | ATP synthase subunit delta, mitochondrial OS=Mus musculus GN=Atpsd PE=1 SV=1 | 10,358 |
| P28651    | Carbonic anhydrase-related protein OS=Mus musculus GN=Ca8 PE=1 SV=5 | 9,736 |
| P61089    | Ubiquitin-conjugating enzyme E2 N OS=Mus musculus GN=Ube2n PE=1 SV=1 | 9,43 |
| Q55ZA3    | Histone cluster 1, H1c OS=Mus musculus GN=Hist1h1c PE=2 SV=1 | 8,966 |
| Q9JKD3    | Secretory carrier-associated membrane protein 5 OS=Mus musculus GN=Scamp5 PE=1 SV=1 | 7,509 |
| P63040    | Complexin-1 OS=Mus musculus GN=Cplx1 PE=1 SV=1 | 6,894 |
| Q9CPW4    | Actin-related protein 2/3 complex subunit 5 OS=Mus musculus GN=Arpc5 PE=2 SV=3 | 6,543 |
| P26645    | Myristoylated alanine-rich C-kinase substrate OS=Mus musculus GN=Marcks PE=1 SV=2 | 6,515 |
| B1AWD9    | Clathrin light chain A OS=Mus musculus GN=CltA PE=1 SV=1 | 6,296 |
| D3YXH0    | Immunoglobulin superfamily member 5 OS=Mus musculus GN=Igsf5 PE=4 SV=1 | 6,247 |
| P43274    | Histone H1.4 OS=Mus musculus GN=Hist1h1e PE=1 SV=2 | 6,212 |
| P20065    | Thymosin beta-4 OS=Mus musculus GN=Tmsb4x PE=1 SV=1 | 5,338 |
| P08228    | Superoxide dismutase [Cu-Zn] OS=Mus musculus GN=Sod1 PE=1 SV=2 | 5,303 |
| P43276    | Histone H1.5 OS=Mus musculus GN=Hist1h1b PE=1 SV=2 | 5,115 |
| P62774    | Myotrophin OS=Mus musculus GN=Mtpn PE=1 SV=2 | 5,082 |
| P60761    | Neurogranin OS=Mus musculus GN=Nrgn PE=1 SV=1 | 4,966 |
| P26883    | Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Mus musculus GN=Fkbp1a PE=1 SV=2 | 4,695 |
| Q14927    | Histone cluster 1, H1d OS=Mus musculus GN=Hist1h1d PE=2 SV=1 | 4,689 |
| P84086    | Complexin-2 OS=Mus musculus GN=Cplx2 PE=1 SV=1 | 4,52 |
| Q60829    | Protein phosphatase 1 regulatory subunit 1B OS=Mus musculus GN=Ppp1r1b PE=2 SV=2 | 4,487 |
| Q6GT24    | Peroxiredoxin 6 OS=Mus musculus GN=Prdx6 PE=1 SV=1 | 4,479 |
| P13595    | Neural cell adhesion molecule 1 OS=Mus musculus GN=Ncam1 PE=1 SV=3 | 4,18 |
| Q08749    | Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus musculus GN=Dld PE=1 SV=2 | 4,18 |
| P61979    | Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrnpk PE=1 SV=1 | 4,093 |
| Q9JK6C    | Cell cycle exit and neuronal differentiation protein 1 OS=Mus musculus GN=Cend1 PE=1 SV=1 | 3,964 |
| P02802    | Metallothionein-1 OS=Mus musculus GN=Mt1 PE=1 SV=1 | 3,841 |
| accession  | description                                                                 | organism       | protein | gene | symbol | version | length |
|------------|------------------------------------------------------------------------------|----------------|---------|------|--------|---------|--------|
| Q63810     | Calcineurin subunit B type 1                                                 | Mus musculus   | Ppp3r1  | GN   | Ppp3r1 | 3        | 3,837  |
| Q8BVI4     | Dihydropteridine reductase                                                   | Mus musculus   | Qdpr    | GN   | Qdpr   | 2        | 3,815  |
| Q9QYC0     | Alpha-adducin                                                                | Mus musculus   | Add1    | GN   | Add1   | 1        | 3,773  |
| G5E902     | MCG10343, isoform CRA_b                                                      | Mus musculus   | Slc25a3 | GN   | Slc25a3| 1        | 3,754  |
| P32848     | Parvalbumin alpha                                                           | Mus musculus   | Pvvalb  | GN   | Pvvalb | 3        | 3,748  |
| P28184     | Metallothionein-3                                                           | Mus musculus   | Mt3     | GN   | Mt3    | 1        | 3,637  |
| P62204     | Calmodulin                                                                  | Mus musculus   | Calm1   | GN   | Calm1  | 1        | 3,634  |
| Q543Y7     | Putative uncharacterized protein                                            | Mus musculus   | Pacsin1 | GN   | Pacsin1| 2        | 3,629  |
| Q92ZD6-2   | Isoform B of Methyl-CpG-binding protein                                      | Mus musculus   | MeCP2   | GN   | MeCP2  | 2        | 3,602  |
| G5E8N5     | L-lactate dehydrogenase                                                       | Mus musculus   | Ldha    | GN   | Ldha   | 1        | 3,561  |
| Q9WWT4     | V-type proton ATPase subunit G                                               | Mus musculus   | Atp6v1g2| GN   | Atp6v1g2| 3        | 3,54   |
| A0A087WQN2 | Prothymosin alpha (Fragment)                                                | Mus musculus   | Ptm1    | GN   | Ptm1   | 1        | 3,536  |
| Q61361     | Brevican core protein                                                        | Mus musculus   | Bcan    | GN   | Bcan   | 1        | 3,507  |
| P19157     | Glutathione S-transferase P                                                 | Mus musculus   | Gstp1   | GN   | Gstp1  | 1        | 3,447  |
| Q4VWZ5     | Acyl-CoA-binding protein                                                     | Mus musculus   | Dbi     | GN   | Dbi    | 1        | 3,436  |
| Q3TTY5     | Keratin, type II cytoskeletal 2 epidermal                                   | Mus musculus   | Krt2    | GN   | Krt2   | 1        | 3,424  |
| O08539     | Myc box-dependent-interacting protein                                        | Mus musculus   | BIn1    | GN   | BIn1   | 1        | 3,412  |
| P10922     | Histone H1.0                                                                 | Mus musculus   | H1f0    | GN   | H1f0   | 2        | 3,345  |
| P08249     | Malate dehydrogenase, mitochondrial                                         | Mus musculus   | Mdha    | GN   | Mdha   | 2        | 3,329  |
| Q91XV3     | Brain acid soluble protein                                                   | Mus musculus   | Basp1   | GN   | Basp1  | 1        | 3,237  |
| A0A075B5P2 | Protein Igkc (Fragment)                                                      | Mus musculus   | Igkc    | GN   | Igkc   | 1        | 3,216  |
| E9Q035     | Protein Gm20425                                                              | Mus musculus   | Gm20425 | GN   | Gm20425| 4        | 3,149  |
| Q99PT1     | Rho GDP-dissociation inhibitor                                               | Mus musculus   | Arhgdia | GN   | Arhgdia| 1        | 3,105  |
| E9PZF0     | Nucleoside diphosphate kinase                                                | Mus musculus   | Gm20390 | GN   | Gm20390| 3        | 3,097  |
| P52760     | Ribonuclease UK114                                                           | Mus musculus   | Hrsp12  | GN   | Hrsp12 | 1        | 3,075  |
| Q9WV69     | Dematin                                                                      | Mus musculus   | Dmtn    | GN   | Dmtn   | 1        | 3,036  |
| P48036     | Annexin A5                                                                  | Mus musculus   | Anxa5   | GN   | Anxa5  | 1        | 3,036  |
| Q02105     | Complement C1q subcomponent subunit C                                       | Mus musculus   | C1qc    | GN   | C1qc   | 2        | 3,033  |
| O88569     | Heterogeneous nuclear ribonucleoproteins A2/B1                               | Mus musculus   | Hnrrnpa2b1| GN   | Hnrrnpa2b1| 2        | 2,987  |
| P27661     | Histone H2AX                                                                 | Mus musculus   | H2afx   | GN   | H2afx  | 1        | 2,98   |
| Q9DBJ1     | Phosphoglycerate mutase 1                                                    | Mus musculus   | Pgam1   | GN   | Pgam1  | 1        | 2,963  |
| Q9ESM3     | Hyaluronan and proteoglycan link protein                                     | Mus musculus   | Hapln2  | GN   | Hapln2 | 1        | 2,956  |
| Q9Z204     | Heterogeneous nuclear ribonucleoproteins C1/C2                              | Mus musculus   | Hnrrnpc | GN   | Hnrrnpc| 1        | 2,944  |
| Accession | Protein Name | Organism     | Gene Name | Protein Expression | Sequence Variation |
|-----------|--------------|--------------|-----------|--------------------|--------------------|
| P61922    | 4-aminobutyrate aminotransferase, mitochondrial | Mus musculus | Abat      | PE=1               | SV=1               |
| P17751    | Triosephosphate isomerase | Mus musculus | Tpi1      | PE=1               | SV=4               |
| Q9DBG3    | AP-2 complex subunit beta | Mus musculus | Ap2b1     | PE=1               | SV=1               |
| Q61598    | Rab GDP dissociation inhibitor beta | Mus musculus | Gdi2      | PE=1               | SV=1               |
| A0A075B6A0 | Ig mu chain C region (Fragment) | Mus musculus | Ighm      | PE=1               | SV=2               |
| P05063    | Fructose-bisphosphate aldolase C | Mus musculus | Aldoc     | PE=1               | SV=4               |
| P21460    | Cystatin-C | Mus musculus | Cst3      | PE=1               | SV=2               |
| P50518    | V-type proton ATPase subunit E | Mus musculus | Atp6v1e1  | PE=1               | SV=2               |
| E9Q7Q3    | Tropomyosin alpha-3 chain | Mus musculus | Tpm3      | PE=1               | SV=1               |
| Q61782    | Type I epidermal keratin mRNA, 3'end (Fragment) | Mus musculus | Alp35     | PE=2               | SV=1               |
| Q8CI43    | Myosin light chain 6B | Mus musculus | Myl6b     | PE=2               | SV=1               |
| Q9Z2T6    | Keratin, type II cuticular Hb5 | Mus musculus | Krt85     | PE=2               | SV=2               |
| A0A0G2JEG8 | Amphiphysin | Mus musculus | Amph      | PE=1               | SV=1               |
| Q9R0P9    | Ubiquitin carboxyl-terminal hydrolase isozyme | Mus musculus | Uchl1     | PE=1               | SV=1               |
| P98086    | Complement C1q subcomponent subunit A | Mus musculus | C1qa      | PE=1               | SV=2               |
| Q8BWFF0   | Succinate-semialdehyde dehydrogenase, mitochondrial | Mus musculus | Aldh5a1   | PE=1               | SV=1               |
| P99027    | 60S acidic ribosomal protein P2 | Mus musculus | Rplp2     | PE=1               | SV=3               |
| Q60668    | Heterogeneous nuclear ribonucleoprotein D0 | Mus musculus | Hnmpd     | PE=1               | SV=2               |
| Q9EQUS-2  | Isoform 2 of Protein SET | Mus musculus | Set       |                   |                    |
| Q91VB8    | Alpha globin 1 | Mus musculus | Hbalpha   | PE=1               | SV=1               |
| P14152    | Malate dehydrogenase, cytoplasmic | Mus musculus | Mdh1      | PE=1               | SV=3               |
| P99024    | Tubulin beta-5 chain | Mus musculus | Tubb5     | PE=1               | SV=1               |
| Q6BFL4    | Putative adenosylhomocysteinase 3 | Mus musculus | Ahcy1     | PE=1               | SV=1               |
| Q04690    | Neurofibromin | Mus musculus | Nf1       | PE=1               | SV=1               |
| D3Z722    | 40S ribosomal protein S19 | Mus musculus | Rps19     | PE=1               | SV=1               |
| Q9DCD0    | 6-phosphogluconate dehydrogenase, decarboxylating | Mus musculus | Pgd       | PE=1               | SV=3               |
| P28474    | Alcohol dehydrogenase class-3 | Mus musculus | Adh5      | PE=1               | SV=3               |
| B2RTK3    | Histone H2B | Mus musculus | Hist1h2bm | PE=2               | SV=1               |
| Q3UY00    | Protein S100 | Mus musculus | S100b     | PE=2               | SV=1               |
| Q6W8Q3    | Purkinje cell protein 4-like | Mus musculus | Pcp4l1    | PE=1               | SV=1               |
| P62259    | 14-3-3 protein epsilon | Mus musculus | Ywthae    | PE=1               | SV=1               |
| A8DUK4    | Beta-globin | Mus musculus | Hbhb1     | PE=1               | SV=1               |
| H3BKH6    | S-formylglutathione hydrolase | Mus musculus | Esd       | PE=1               | SV=1               |
| Accession  | Description                                                                                                                                                                                                 | Mus musculus | Gene Name | Protein Number | SV  |
|------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------|-----------|----------------|-----|
| J3QMG3     | Voltage-dependent anion-selective channel protein 3                                                                                                                                                    | 2,378        | Vdac3     | 1              | 1   |
| Q9CZ13     | Cytochrome b-c1 complex subunit 1, mitochondrial                                                                                                                                                    | 2,378        | Uqcr1     | 1              | 2   |
| A0A0G2JFT8 | Protein RUFY3                                                                                                                                                                                            | 2,374        | Rufy3     | 1              | 1   |
| Q4FI9X     | Superoxide dismutase                                                                                                                                  | 2,373        | Sod2      | 2              | 1   |
| P62858     | 40S ribosomal protein S28                                                                                                                                  | 2,364        | Rps28     | 1              | 1   |
| P09405     | Nucleolin                                                                                                                                                                                                 | 2,353        | Ncl       | 1              | 2   |
| Q91ZZ3     | Beta-synuclein                                                                                                                                             | 2,347        | Sncl      | 1              | 1   |
| Q3ULD5     | Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial                                                                                                           | 2,338        | Mccc2     | 1              | 1   |
| Q3U1N0     | Coronin                                                                                                                                                    | 2,33         | Coro1a    | 1              | 2   |
| Q54B6      | Stathmin                                                                                                                                                                                                  | 2,29         | Stmn1     | 1              | 1   |
| Q5EBQ2     | MCG7941, isoform CRA_f                                                                                                                                                                                   | 2,28         | Pebp1     | 2              | 1   |
| E9PYH0     | Versican core protein                                                                                                                                                                                        | 2,276        | Vcan      | 1              | 1   |
| Q6IRU5     | Clathrin light chain B                                                                                                                                                                                      | 2,269        | Cltb      | 1              | 1   |
| Q61282     | Aggrecan core protein                                                                                                                                                                                       | 2,244        | Acan      | 1              | 2   |
| P05201     | Aspartate aminotransferase, cytoplasmic                                                                                                                                                                   | 2,22         | Got1      | 1              | 3   |
| P20357     | Microtubule-associated protein 2                                                                                                                     | 2,209        | Map2      | 1              | 1   |
| A0A0A0MQF6 | Glyceraldehyde-3-phosphate dehydrogenase                                                                                                              | 2,205        | Gapdh     | 1              | 1   |
| P10649     | Glutathione S-transferase Mu 1                                                                                                                       | 2,176        | Gstm1     | 1              | 1   |
| P31650     | Sodium- and chloride-dependent GABA transporter 3                                                                                                                                                           | 2,176        | Slc6a11   | 1              | 1   |
| P60710     | Actin, cytoplasmic 1                                                                                                                                       | 2,161        | Actb      | 1              | 1   |
| Q99K0      | Aconitase hydratase, mitochondrial                                                                                                                        | 2,121        | Aco2      | 1              | 1   |
| P14873     | Microtubule-associated protein 1B                                                                                                                      | 2,117        | Map1b     | 1              | 1   |
| P68510     | 14-3-3 protein eta                                                                                                                                             | 2,114        | Ywha      | 1              | 2   |
| P01592     | Immunoglobulin J chain                                                                                                                                       | 2,078        | Igj       | 2              | 1   |
| Q9CX86     | Heterogeneous nuclear ribonucleoprotein A0                                                                                                                | 2,055        | Hnnapa0   | 1              | 1   |
| P60335     | Poly(rC)-binding protein 1                                                                                                                                    | 2,049        | Pcbp1     | 1              | 1   |
| P51863     | V-type proton ATPase subunit d 1                                                                                                                                | 2,047        | Atp6v0d1  | 1              | 1   |
| Q92Z1G3    | V-type proton ATPase subunit C 1                                                                                                                                | 2,041        | Atp6v1c1  | 1              | 1   |
| Q9CRB6     | Tubulin polymerization-promoting protein family member 3                                                                                                   | 2,031        | Tppp3     | 1              | 1   |
| P50396     | Rab GDP dissociation inhibitor alpha                                                                                                                          | 2,031        | Gdi1      | 1              | 3   |
| Q77Q2D2    | Tubulin polymerization-promoting protein                                                                                                                     | 2,02         | Tppp      | 1              | 1   |
| Q9CPU0     | Lactoylglutathione lyase                                                                                                                                         | 2,019        | Glo1      | 1              | 3   |
| Q810U4     | Neuronal cell adhesion molecule                                                                                                                                   | 2,014        | Nrcam     | 1              | 1   |
| Accession | Description                                                                 | Species          | Gene Name | Protein Name                  | Score |
|-----------|------------------------------------------------------------------------------|------------------|-----------|-------------------------------|-------|
| Q9Z1G4    | V-type proton ATPase 116 kDa subunit a isoform 1                            | Mus musculus     | Atp6v0a1  |                               | 2,005 |
| Q9JJV2    | Profilin-2                                                                   | Mus musculus     | Pfn2      |                               | 1,989 |
| P17156    | Heat shock-related 70 kDa protein 2                                          | Mus musculus     | Hspa2     |                               | 1,973 |
| P06745    | Glucose-6-phosphate isomerase                                                | Mus musculus     | Gpi       |                               | 1,963 |
| Q01853    | Transitional endoplasmic reticulum ATPase                                   | Mus musculus     | Vcp       |                               | 1,962 |
| P68372    | Tubulin beta-4B chain                                                        | Mus musculus     | Tubb4b    |                               | 1,96  |
| Q3UL22    | Chaperonin subunit 8 (Theta), isoform CRA_a                                 | Mus musculus     | Cct8      |                               | 1,946 |
| A6ZI44    | Fructose-bisphosphate aldolase                                               | Mus musculus     | Aldoa     |                               | 1,942 |
| P57780    | Alpha-actinin-4                                                              | Mus musculus     | Actn4     |                               | 1,93  |
| Q9R0V5    | Adenylate kinase isoenzyme 1                                                | Mus musculus     | Ak1       |                               | 1,925 |
| P13707    | Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic                     | Mus musculus     | Gpd1      |                               | 1,92  |
| Q546F2    | Guanine deaminase                                                            | Mus musculus     | Gda       |                               | 1,919 |
| Q9CZC8    | Secernin-1                                                                   | Mus musculus     | Scrn1     |                               | 1,909 |
| P35700    | Peroxiredoxin-1                                                             | Mus musculus     | Prdx1     |                               | 1,904 |
| P05202    | Aspartate aminotransferase, mitochondrial                                   | Mus musculus     | Got2      |                               | 1,903 |
| P16125    | L-lactate dehydrogenase B chain                                              | Mus musculus     | Ldhb      |                               | 1,882 |
| P14106    | Complement C1q subcomponent subunit B                                       | Mus musculus     | C1qb      |                               | 1,876 |
| Q76M23    | Serine/threonine-protein phosphatase A 65 kDa regulatory subunit A alpha isoform | Mus musculus     |                       |                               | 1,875 |
| Q7M6W1    | Reticulin                                                                    | Mus musculus     | Rtn1      |                               | 1,87  |
| Q546G4    | Albumin 1                                                                    | Mus musculus     | Alb       |                               | 1,863 |
| F6VW30    | 14-3-3 protein theta (Fragment)                                              | Mus musculus     | Ywhaq     |                               | 1,861 |
| Q9QUP5    | Hyaluronan and proteoglycan link protein 1                                   | Mus musculus     | Hapl1     |                               | 1,85  |
| Q99P05    | Long-chain-fatty-acid--CoA ligase ACSBG1                                     | Mus musculus     | Acsg1     |                               | 1,847 |
| P00920    | Carbonic anhydrase 2                                                         | Mus musculus     | Ca2       |                               | 1,834 |
| P58252    | Elongation factor 2                                                          | Mus musculus     | Eef2      |                               | 1,833 |
| Q80TL4    | PHD finger protein 24                                                         | Mus musculus     | Phf24     |                               | 1,832 |
| P46460    | Vesicle-fusing ATPase                                                        | Mus musculus     | Nsf       |                               | 1,825 |
| D3Z4B2    | Gamma-soluble NSF attachment protein (Fragment)                              | Mus musculus     | Napp      |                               | 1,823 |
| Q8C2Q7    | Heterogeneous nuclear ribonucleoprotein H                                    | Mus musculus     | Hnrnph1   |                               | 1,819 |
| Q64L7     | MCG13441                                                                     | Mus musculus     | Rps27a    |                               | 1,815 |
| Q5FW97    | Enolase 1, alpha non-neuron                                                   | Mus musculus     | EG433182  |                               | 1,814 |
| P63038    | 60 kDa heat shock protein, mitochondrial                                     | Mus musculus     | Hspa4     |                               | 1,812 |
| Q3U2G2    | Heat shock 70 kDa protein 4                                                  | Mus musculus     | Hspa4     |                               | 1,806 |
| Accession | Name                                                                 | Species         | Gene Symbol | Peptide | Spectrum Count |
|-----------|----------------------------------------------------------------------|-----------------|-------------|----------|----------------|
| A6H611    | Mitochondrial intermediate peptidase                                  | Mus musculus    | Mipep       | PE=1     | 1,805          |
| B2RXY7    | Carbonyl reductase 1                                                 | Mus musculus    | Cbr1        | PE=2     | 1,802          |
| A2ALV3    | Endophilin-A1                                                        | Mus musculus    | Sh3gl2      | PE=1     | 1,796          |
| P11031    | Activated RNA polymerase II transcriptional coactivator p15          | Mus musculus    | Sub1        | PE=1     | 1,789          |
| B1AQW2    | Microtubule-associated protein                                       | Mus musculus    | Mapt        | PE=1     | 1,773          |
| Q8K183    | Pyridoxal kinase                                                     | Mus musculus    | Pdxk        | PE=1     | 1,772          |
| B0QZN5    | Vesicle-associated membrane protein 2                                | Mus musculus    | Vamp2       | PE=1     | 1,764          |
| P26443    | Glutamate dehydrogenase 1, mitochondrial                            | Mus musculus    | Glud1       | PE=1     | 1,759          |
| Q9CZU6    | Citrate synthase, mitochondrial                                      | Mus musculus    | Cs           | PE=1     | 1,753          |
| Q78J18    | MCG22989, isoform CRA_b                                             | Mus musculus    | Rab11b      | PE=2     | 1,747          |
| O55091    | Protein IMPACT                                                      | Mus musculus    | Impact      | PE=1     | 1,743          |
| A0A097PUG4| Anti-15C4 light chain OS=Mus musculus                                 | Mus musculus    | Polc        | PE=1     | 1,734          |
| Q3U7E0    | Putative uncharacterized protein                                     | Mus musculus    | Atp6v1g1    | PE=2     | 1,72           |
| Q3UV17    | Keratin, type II cytoskeletal 2 oral                                  | Mus musculus    | Krt76       | PE=2     | 1,71           |
| Q9QYX7    | Protein piccolo                                                      | Mus musculus    | Pcoo        | PE=1     | 1,702          |
| B9EKK1    | Receptor-type tyrosine-protein phosphatase zeta                      | Mus musculus    | Ptprz1      | PE=1     | 1,687          |
| P70349    | Histidine triad nucleotide-binding protein 1                         | Mus musculus    | Hint1       | PE=1     | 1,683          |
| A2ARP8    | Microtubule-associated protein 1A                                     | Mus musculus    | Map1a       | PE=1     | 1,663          |
| Q9JLZ3    | Methylglutaconyl-CoA hydratase, mitochondrial                        | Mus musculus    | Auh         | PE=1     | 1,669          |
| P68369    | Tubulin alpha-1A chain OS=Mus musculus                               | Mus musculus    | Tuba1a      | PE=1     | 1,656          |
| A0A087WP80| Limbic system-associated membrane protein OS=Mus musculus            | Mus musculus    | Lsamp       | PE=1     | 1,649          |
| Q9Z2J6    | Tetraspanin-2                                                         | Mus musculus    | Tspan2      | PE=1     | 1,635          |
| Q9D6F9    | Tubulin beta-4A chain OS=Mus musculus                                | Mus musculus    | Tubb4a      | PE=1     | 1,627          |
| P17742    | Peptidyl-prolyl cis-trans isomerase A                                 | Mus musculus    | Ppia        | PE=1     | 1,624          |
| Q3UMU9    | Hepatoma-derived growth factor-related protein 2                     | Mus musculus    | Hdgfrp2     | PE=1     | 1,622          |
| A2AWN8    | YTH domain family 1, isoform CRA_a                                   | Mus musculus    | Ythdf1      | PE=1     | 1,601          |
| Q9QXV0    | ProSAAS OS=Mus musculus                                               | Mus musculus    | Pcsk1n      | PE=1     | 1,6       |
| Q7TSJ2    | Microtubule-associated protein 6                                      | Mus musculus    | Map6        | PE=1     | 1,596          |
| F8WGL3    | Cofilin-1 OS=Mus musculus                                             | Mus musculus    | Cfl1        | PE=1     | 1,593          |
| F6RSK3    | Protein Gm17430                                                       | Mus musculus    | Gm17430     | PE=4     | 1,587          |
| P56399    | Ubiquitin carboxyl-terminal hydrolase 5                              | Mus musculus    | Usp5        | PE=1     | 1,586          |
| P55066    | Neurocan core protein OS=Mus musculus                                | Mus musculus    | Ncan        | PE=2     | 1,586          |
| A0A075B5P3| Protein lghg2b (Fragment) OS=Mus musculus                            | Mus musculus    | Lghg2b      | PE=1     | 1,586          |
| Accession | Description                                                                 | Species   | Description | Peptide | Spectrum Count |
|-----------|------------------------------------------------------------------------------|-----------|-------------|----------|----------------|
| P14211    | Calreticulin OS=Mus musculus GN=Calr PE=1 SV=1                               | 1,577     |             |          |                |
| Q04447    | Creatine kinase B-type OS=Mus musculus GN=Ckb PE=1 SV=1                     | 1,576     |             |          |                |
| F6VPT0    | Protein Ccdc163 (Fragment) OS=Mus musculus GN=Ccdc163 PE=4 SV=1             | 1,571     |             |          |                |
| Q61171    | Peroxiredoxin-2 OS=Mus musculus GN=Prdx2 PE=1 SV=3                         | 1,57      |             |          |                |
| P05132    | cAMP-dependent protein kinase catalytic subunit alpha OS=Mus musculus GN=Prkaca PE=1 SV=3 | 1,568    |             |          |                |
| P62137    | Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Mus musculus GN=Ppp1ca PE= | 1,565    |             |          |                |
| P12658    | Calbindin OS=Mus musculus GN=Calb1 PE=1 SV=2                                | 1,561     |             |          |                |
| B9EHN0    | Ubiquitin-activating enzyme E1, Chr X OS=Mus musculus GN=Uba1 PE=2 SV=1     | 1,554     |             |          |                |
| Q08331    | Calretinin OS=Mus musculus GN=Calb2 PE=1 SV=3                               | 1,545     |             |          |                |
| A8IP69    | 14-3-3 protein gamma subtype OS=Mus musculus GN=Ywhag PE=2 SV=1             | 1,537     |             |          |                |
| P80316    | T-complex protein 1 subunit epsilon OS=Mus musculus GN=Cct5 PE=1 SV=1       | 1,536     |             |          |                |
| F6YVP7    | Protein Gm10260 OS=Mus musculus GN=Gm10260 PE=3 SV=2                        | 1,53      |             |          |                |
| P63276    | 40S ribosomal protein S17 OS=Mus musculus GN=Rps17 PE=1 SV=2                | 1,523     |             |          |                |
| P09411    | Phosphoglycerate kinase 1 OS=Mus musculus GN=Pgk1 PE=1 SV=4                 | 1,521     |             |          |                |
| Q3U4U6    | T-complex protein 1 subunit gamma OS=Mus musculus GN=Cct3 PE=2 SV=1         | 1,52      |             |          |                |
| P47857    | ATP-dependent 6-phosphofructokinase, muscle type OS=Mus musculus GN=Pfkem PE=1 SV=3 | 1,517    |             |          |                |
| Q55X6     | Clathrin heavy chain OS=Mus musculus GN=Cltc PE=1 SV=1                      | 1,512     |             |          |                |
| E0CYV0    | Protein-L-isooaspartate O-methyltransferase OS=Mus musculus GN=PCmt1 PE=1 SV=1 | 1,491    |             |          |                |
| P14869    | 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3          | 1,486     |             |          |                |
| O55042    | Alpha-synuclein OS=Mus musculus GN=Snca PE=1 SV=2                          | 1,486     |             |          |                |
| P01787    | Ig heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3 OS=Mus musculus PE=1 SV=1 | 1,482    |             |          |                |
| Q8BG78    | Phytanoyl-CoA hydroxylase-interacting protein-like OS=Mus musculus GN=Phyhipl PE=2 SV=1 | 1,481    |             |          |                |
| P40142    | Transketolase OS=Mus musculus GN=Tkt PE=1 SV=1                             | 1,476     |             |          |                |
| Q3U5Y6    | Amino acid transporter OS=Mus musculus GN=Slci2a2 PE=2 SV=1                 | 1,465     |             |          |                |
| Q8C187    | Septin-11 OS=Mus musculus GN=Sept11 PE=1 SV=4                              | 1,454     |             |          |                |
| P19783    | Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Mus musculus GN=Cox4i1 PE=1 SV=2 | 1,454    |             |          |                |
| A0A0A6YXW6 | Protein Igha (Fragment) OS=Mus musculus GN=Igha PE=1 SV=1                  | 1,442     |             |          |                |
| O88342    | WD repeat-containing protein 1 OS=Mus musculus GN=Wdr1 PE=1 SV=3            | 1,437     |             |          |                |
| Q3V117    | ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1                      | 1,434     |             |          |                |
| Q92219    | Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Mus musculus GN=Sucl2 PE=1 | 1,429    |             |          |                |
| P52480    | Pyruvate kinase PKM OS=Mus musculus GN=Pkm PE=1 SV=4                        | 1,422     |             |          |                |
| Q921M7    | Protein FAM49B OS=Mus musculus GN=Fam49b PE=2 SV=1                         | 1,415     |             |          |                |
| Q8BMS1    | Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1 | 1,406    |             |          |                |
| Accession   | Description                                                                 | Organism       | Gene Name | Protein Name          | Accession | Description                                                                 | Organism       | Gene Name | Protein Name       | Accession | Description                                                                 | Organism       | Gene Name | Protein Name       | Accession | Description                                                                 | Organism       | Gene Name | Protein Name       | Accession | Description                                                                 | Organism       | Gene Name | Protein Name       | Accession | Description                                                                 | Organism       | Gene Name | Protein Name       | Accession | Description                                                                 | Organism       | Gene Name | Protein Name       | Accession |
|------------|------------------------------------------------------------------------------|----------------|-----------|------------------------|-----------|------------------------------------------------------------------------------|----------------|-----------|----------------------|-----------|------------------------------------------------------------------------------|----------------|-----------|----------------------|-----------|------------------------------------------------------------------------------|----------------|-----------|----------------------|-----------|------------------------------------------------------------------------------|----------------|-----------|----------------------|-----------|------------------------------------------------------------------------------|----------------|-----------|----------------------|-----------|------------------------------------------------------------------------------|----------------|-----------|----------------------|-----------|------------------------------------------------------------------------------|----------------|-----------|----------------------|-----------|------------------------------------------------------------------------------|----------------|-----------|----------------------|-----------|------------------------------------------------------------------------------|----------------|-----------|----------------------|-----------|------------------------------------------------------------------------------|----------------|-----------|----------------------|-----------|------------------------------------------------------------------------------|----------------|-----------|----------------------|-----------|------------------------------------------------------------------------------|----------------|-----------|----------------------|-----------|
| Q8K0T0     | Reticulon-1 OS=Mus musculus GN=Rtn1 PE=1 SV=1                               | 1,403          | P70168    | Importin subunit beta-1 OS=Mus musculus GN=Kpnb1 PE=1 SV=2        | 1,402     | P545V3  Enolase 2, gamma neuronal, isoform CRA_a OS=Mus musculus GN=Eno2 PE=2 SV=1 | 1,399          | Q62631    | Elongation factor 1-alpha 2 OS=Mus musculus GN=Eef1a2 PE=1 SV=1              | 1,398          | Q56A15 Cytochrome c OS=Mus musculus GN=Cytc PE=2 SV=1                        | 1,378          | P17710    | Hexokinase-1 OS=Mus musculus GN=Hk1 PE=1 SV=3                               | 1,369          | Q3TXU4  Apolipoprotein E, isoform CRA_h OS=Mus musculus GN=Apoe PE=2 SV=1   | 1,369          | Q3UNV7  Putative uncharacterized protein OS=Mus musculus GN=Mif2 PE=2 SV=1   | 1,367          | Q9ERD7  Tubulin beta-3 chain OS=Mus musculus GN=Tubb3 PE=1 SV=1              | 1,361          | Q9D6R2  Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Mus musculus GN=Idh3a PE=1 | 1,355          | Q542X7  Chaperonin subunit 2 (Beta), isoform CRA_a OS=Mus musculus GN=Cct2 PE=2 SV=1 | 1,355          | P40336  Vacular protein sorting-associated protein 26A OS=Mus musculus GN=Vps26a PE=1 | 1,348          | Q586E4  Elongation factor 1-alpha OS=Mus musculus GN=Eef1a1 PE=2 SV=1            | 1,342          | P48722  Heat shock 70 kDa protein 4L OS=Mus musculus GN=Hspa4l PE=1 SV=2      | 1,338          | O08553  Dihydropyrimidinase-related protein 2 OS=Mus musculus GN=Dpsy1 PE=1 SV=2 | 1,333          | A0A076FRG6  KCC2a variant 1 OS=Mus musculus GN=S12a5 PE=2 SV=1               | 1,332          | Q5YLW3  Ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=2 SV=1              | 1,322          | Q3UY21  Myelin-oligodendrocyte glycoprotein OS=Mus musculus GN=Mog PE=1 SV=1 | 1,309          | P97300  Neuroplastin OS=Mus musculus GN=Nptn PE=1 SV=3                           | 1,309          | P63005  Platelet-activating factor acetylhydrolase IB subunit alpha OS=Mus musculus GN=Pafah1b1 PE=1 | 1,308          | P63101  14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1            | 1,308          | Q9DCW4  Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfa PE=1 SV=3 | 1,303          | Q61990  Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 PE=1 SV=1               | 1,303          | P06837  Neurmodulin OS=Mus musculus GN=Gap43 PE=1 SV=1                         | 1,302          | P60766  Cell division control protein 42 homolog OS=Mus musculus GN=Cdc42 PE=1 SV=2 | 1,3  | P62880  Guanine nucleotide-binding protein G(i)/G(S)/G(T) subunit beta-2 OS=Mus musculus GN=Gnb2 PE=1 S                      | 0,749          | P46097  Synaptotagmin-2 OS=Mus musculus GN=Syt2 PE=1 SV=1                    | 0,746          | P97427  Dihydropyrimidinase-related protein 1 OS=Mus musculus GN=Crmp1 PE=1 SV=1 | 0,743          | Q3TQ70  Beta1 subunit of GTP-binding protein OS=Mus musculus GN=Gnb1 PE=2 SV=1 | 0,743          | A2AQR0  Glycerol-3-phosphate dehydrogenase OS=Mus musculus GN=Gpd2 PE=1 SV=1     | 0,738          | D32656  Synaptotanin-1 OS=Mus musculus GN=Syn1 PE=1 SV=1                     | 0,733          | Q9C8V6  Actin-related protein 2/3 complex subunit 2 OS=Mus musculus GN=Arpc2 PE=1 SV=3 | 0,732          | Q9WTL4  Insulin receptor-related protein OS=Mus musculus GN=Insrr PE=1 SV=2       | 0,731          |
| Accession | Description                                                                 | Organism     | Gene Symbol | Peptide Count |
|-----------|------------------------------------------------------------------------------|--------------|-------------|---------------|
| Q9QZQ8    | Core histone macro-H2A.1                                                     | Mus musculus | H2afy       | 3             |
| P52480-2  | Isoform M1 of Pyruvate kinase PKM                                           | Mus musculus | Pkm         | 1             |
| P47963    | 60S ribosomal protein L13                                                    | Mus musculus | Rpl13       | 3             |
| O54962    | Barrier-to-autointegration factor                                             | Mus musculus | Banf1       | 1             |
| Q912U6    | Dystonin                                                                     | Mus musculus | Dst         | 2             |
| Q99M71    | Mammalian ependymin-related protein 1                                        | Mus musculus | Epdr1       | 2             |
| Q9CX54    | Centromere protein V                                                          | Mus musculus | Cenpv       | 2             |
| P12787    | Cytochrome c oxidase subunit 5A, mitochondrial                               | Mus musculus | Cox5a       | 2             |
| P08752    | Guanine nucleotide-binding protein G(i) subunit alpha-2                      | Mus musculus | Gna1i       | 5             |
| P35235    | Tyrosine-protein phosphatase non-receptor type 11                            | Mus musculus | Ptpn11      | 2             |
| Q8R1B4    | Eukaryotic translation initiation factor 3 subunit C                          | Mus musculus | Eif3c       | 1             |
| Q9EQF6    | Dihydropyrimidinase-related protein 5                                         | Mus musculus | Dpysl5      | 1             |
| Q9WV34    | MAGUK p55 subfamily member 2                                                 | Mus musculus | Mpp2        | 1             |
| P14148    | 60S ribosomal protein L7                                                      | Mus musculus | Rpl7        | 2             |
| P19096    | Fatty acid synthase                                                           | Mus musculus | Fasn        | 1             |
| Q9R1P1    | Proteasome subunit beta type-3                                               | Mus musculus | Psmb3       | 1             |
| E9PUA3    | IQ motif and SEC7 domain-containing protein 1                                 | Mus musculus | Iqsec1      | 1             |
| Q8BFZ9    | Erlin-2                                                                      | Mus musculus | Erlin2      | 1             |
| Q8VEK3    | Heterogeneous nuclear ribonucleoprotein U                                    | Mus musculus | Hnrnpu      | 1             |
| Q62WNS    | 40S ribosomal protein S9                                                      | Mus musculus | Rps9        | 3             |
| Q6IFX2    | Keratin, type I cytoskeletal 42                                              | Mus musculus | Krt42       | 1             |
| Q9WUM5    | Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial           | Mus musculus | Suclg1      | 1             |
| Q9R1P4    | Proteasome subunit alpha type-1                                              | Mus musculus | Psma1       | 1             |
| S4R249    | Ankyrin-2                                                                    | Mus musculus | Ank2        | 1             |
| E9OAX2    | Unconventional myosin-XVIIIa subunit alpha                                    | Mus musculus | Myo18a      | 1             |
| Q9Z1B3    | 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1             | Mus musculus | Plcb1       | 1             |
| Q548L4    | Glutamate decarboxylase                                                       | Mus musculus | Gad2        | 2             |
| P47915    | 60S ribosomal protein L29                                                     | Mus musculus | Rpl29       | 2             |
| A2CEK3    | Phosphoglucomutase-2                                                          | Mus musculus | Pgm2        | 1             |
| A0A0G2JGS4| Calcium/calmodulin-dependent protein kinase type II subunit delta             | Mus musculus | Camk2d      | 1             |
| P14115    | 60S ribosomal protein L27a                                                   | Mus musculus | Rpl27a      | 2             |
| G5E866    | Splicing factor 3B subunit 1                                                 | Mus musculus | Sf3b1       | 1             |
| O09061    | Proteasome subunit beta type-1                                               | Mus musculus | Psmb1       | 1             |
| Accession | Description                                                                 | Species   | Gene   | Peptide | Score |
|----------|------------------------------------------------------------------------------|-----------|--------|---------|-------|
| Q3TVK3   | Aspartyl aminopeptidase OS=Mus musculus GN=Dnpep PE=1 SV=1                   |           |        |         | 0.555 |
| Q3TLP8   | RAS-related C3 botulinum substrate 1, isoform CRA_a OS=Mus musculus GN=Rac1 PE=1 SV=1 |           |        |         | 0.552 |
| D0VYV6   | Erythrocyte protein band 4.1-like 3 isoform B OS=Mus musculus GN=Epb4.1l3 PE=2 SV=1 |           |        |         | 0.532 |
| Q545X8   | 40S ribosomal protein S4 OS=Mus musculus GN=Rps4x PE=2 SV=1                  |           |        |         | 0.527 |
| Q9R1T4   | Septin-6 OS=Mus musculus GN=Sept6 PE=1 SV=4                                |           |        |         | 0.526 |
| P60879   | Synaptosomal-associated protein 25 OS=Mus musculus GN=Snap25 PE=1 SV=1      |           |        |         | 0.525 |
| Q9QWI6   | SRC kinase signaling inhibitor 1 OS=Mus musculus GN=Srclin1 PE=1 SV=2       |           |        |         | 0.522 |
| P62264   | 40S ribosomal protein S14 OS=Mus musculus GN=Rps14 PE=1 SV=3                |           |        |         | 0.521 |
| Q9QXS1   | Plectin OS=Mus musculus GN=Plec PE=1 SV=3                                  |           |        |         | 0.521 |
| P47911   | 60S ribosomal protein L6 OS=Mus musculus GN=Rpl6 PE=1 SV=3                  |           |        |         | 0.52  |
| P63085   | Mitogen-activated protein kinase 1 OS=Mus musculus GN=Mapk1 PE=1 SV=3       |           |        |         | 0.516 |
| Q3UH59   | Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=1                               |           |        |         | 0.514 |
| Q9QUM9   | Proteasome subunit alpha type-6 OS=Mus musculus GN=Psma6 PE=1 SV=1          |           |        |         | 0.514 |
| Q08599   | Syntaxin-binding protein 1 OS=Mus musculus GN=Stxbp1 PE=1 SV=2             |           |        |         | 0.513 |
| Q92U1    | Proteasome subunit alpha type-5 OS=Mus musculus GN=Psma5 PE=1 SV=1          |           |        |         | 0.507 |
| P19246   | Neurofilament heavy polypeptide OS=Mus musculus GN=Nefh PE=1 SV=3           |           |        |         | 0.505 |
| O09167   | 60S ribosomal protein L21 OS=Mus musculus GN=Rpl21 PE=1 SV=3                |           |        |         | 0.504 |
| Q8VDD5   | Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4                                 |           |        |         | 0.498 |
| E9QAZ2   | Ribosomal protein L15 OS=Mus musculus GN=Gm10020 PE=3 SV=1                  |           |        |         | 0.497 |
| Q3TI05   | Chaperonin containing Tcp1, subunit 6a (Zeta) OS=Mus musculus GN=Cct6a PE=2 SV=1 |           |        |         | 0.491 |
| A0A140T8K6| 60S ribosomal protein L36 OS=Mus musculus GN=Rpl36-ps3 PE=3 SV=1           |           |        |         | 0.49  |
| P90026   | Proteasome subunit beta type-4 OS=Mus musculus GN=Psmb4 PE=1 SV=1           |           |        |         | 0.49  |
| P27659   | 60S ribosomal protein L3 OS=Mus musculus GN=Rpl3 PE=1 SV=3                  |           |        |         | 0.485 |
| P31938   | Dual specificity mitogen-activated protein kinase kinase 1 OS=Mus musculus GN=Map2k1 PE=1 SV=2 |           |        |         | 0.484 |
| P53395   | Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mi |           |        |         | 0.477 |
| Q9JHU4   | Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dync1h1 PE=1 SV=2     |           |        |         | 0.475 |
| Q8C522   | Endonuclease domain-containing 1 protein OS=Mus musculus GN=Endod1 PE=1 SV=2 |           |        |         | 0.474 |
| O70318   | Band 4.1-like protein 2 OS=Mus musculus GN=Epb41l2 PE=1 SV=2                |           |        |         | 0.474 |
| P47962   | 60S ribosomal protein L5 OS=Mus musculus GN=Rpl5 PE=1 SV=3                  |           |        |         | 0.471 |
| E9Q401   | Ryanodine receptor 2 OS=Mus musculus GN=Ryr2 PE=1 SV=1                     |           |        |         | 0.466 |
| Q50T8    | Ribosomal protein L19 OS=Mus musculus GN=Rpl19 PE=2 SV=1                   |           |        |         | 0.447 |
| Q9Z2U0   | Proteasome subunit alpha type-7 OS=Mus musculus GN=Psma7 PE=1 SV=1          |           |        |         | 0.441 |
| Q5BLK0   | MCG18564, isoform CRA_a OS=Mus musculus GN=Rpl12 PE=2 SV=1                 |           |        |         | 0.44  |
| Accession | Description | Organism | Gene Name | Protein Name | Peptide | Spectrum | Score |
|-----------|-------------|----------|-----------|--------------|---------|---------|-------|
| P62911    | 60S ribosomal protein L32 | Mus musculus | Rpl32 | 0.439 |
| E9PYK3    | Poly [ADP-ribose] polymerase | Mus musculus | Parp4 | 0.439 |
| Q4VAG4    | MCG12304 | Mus musculus | Rpl22 | 0.439 |
| P12023    | Amyloid beta A4 protein | Mus musculus | App | 0.432 |
| Q9D8B3    | Charged multivesicular body protein 4b | Mus musculus | Chmp4b | 0.431 |
| P49722    | Proteasome subunit alpha type-2 | Mus musculus | Psma2 | 0.425 |
| Q9CZY3    | Ubiquitin-conjugating enzyme E2 variant 1 | Mus musculus | Ube2v1 | 0.423 |
| Q9D0M3    | Cytochrome c1, heme protein, mitochondrial | Mus musculus | Cyc1 | 0.421 |
| Q9R1P3    | Proteasome subunit beta type-2 | Mus musculus | Psmb2 | 0.419 |
| Q58EW0    | 60S ribosomal protein L18 | Mus musculus | Rpl18 | 0.416 |
| Q9Z0H4    | CUGBP Elav-like family member 2 | Mus musculus | Celf2 | 0.416 |
| Q5BLJ9    | 60S ribosomal protein L27 | Mus musculus | Rpl27 | 0.414 |
| Q497E9    | 40S ribosomal protein S8 | Mus musculus | Rps8 | 0.412 |
| Q80YX1    | Tenascin | Mus musculus | Tnc | 0.412 |
| Q5BLK1    | 40S ribosomal protein S6 | Mus musculus | Rps6 | 0.411 |
| Z4YL23    | Fer-1-like protein 4 | Mus musculus | Fer1l4 | 0.399 |
| Q923T9    | Calcium/calmodulin-dependent protein kinase II subunit gamma | Mus musculus | Camk2g | 0.399 |
| O08917    | Flotillin-1 | Mus musculus | Flot1 | 0.399 |
| Q91VE0    | Long-chain fatty acid transport protein 4 | Mus musculus | Slc27a4 | 0.392 |
| Q50SA8    | MCG17585 | Mus musculus | Rpl39 | 0.389 |
| P46660    | Alpha-internexin | Mus musculus | Ina | 0.389 |
| Q5SVJ0    | Calcium/calmodulin-dependent protein kinase II, beta, isoform CRA_b | Mus musculus | Camk2b | 0.386 |
| P62267    | 40S ribosomal protein S23 | Mus musculus | Rps23 | 0.383 |
| P29341    | Polyadenylate-binding protein 1 | Mus musculus | Pabpc1 | 0.38 |
| P08553    | Neurofilament medium polypeptide | Mus musculus | Nefm | 0.377 |
| Q9CU62    | Structural maintenance of chromosomes protein 1A | Mus musculus | Smc1a | 0.376 |
| O55234    | Proteasome subunit beta type-5 | Mus musculus | Psmb5 | 0.376 |
| P17427    | AP-2 complex subunit alpha-2 | Mus musculus | Ap2a2 | 0.371 |
| Q9D1R9    | 60S ribosomal protein L34 | Mus musculus | Rpl34 | 0.37 |
| P09528    | Ferritin heavy chain | Mus musculus | Fth1 | 0.369 |
| Q564E8    | Ribosomal protein L4 | Mus musculus | Rpl4 | 0.367 |
| P14685    | 26S proteasome non-ATPase regulatory subunit 3 | Mus musculus | Psmd3 | 0.367 |
| Q8BKZ9    | Pyruvate dehydrogenase protein X component, mitochondrial | Mus musculus | Pdhx | 0.362 |
| Accession | Description                                                                 | Organism       | Gene Name | Protein Description                                                                 | Score |
|-----------|------------------------------------------------------------------------------|----------------|-----------|-------------------------------------------------------------------------------------|-------|
| P32067    | Lupus La protein homolog OS=Mus musculus GN=Ssb PE=1 SV=1                   |                |           |                                                                                    | 0.358 |
| Q58E4     | Proteasome subunit alpha type OS=Mus musculus GN=Psma3 PE=2 SV=1             |                |           |                                                                                    | 0.353 |
| Q8BFM4    | Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial |                |           |                                                                                    | 0.345 |
| P62715    | Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Mus musculus GN=Ppp2c |                |           |                                                                                    | 0.344 |
| Q99104    | Unconventional myosin-Va OS=Mus musculus GN=Myo5a PE=1 SV=2                  |                |           |                                                                                    | 0.337 |
| F6TB7     | Myelin basic protein (Fragment) OS=Mus musculus GN=Mbp PE=1 SV=1             |                |           |                                                                                    | 0.334 |
| Q9JLM8    | Serine/threonine-protein kinase DCLK1 OS=Mus musculus GN=Dclk1 PE=1 SV=1     |                |           |                                                                                    | 0.321 |
| P62855    | 40S ribosomal protein S26 OS=Mus musculus GN=Rps26 PE=1 SV=3                 |                |           |                                                                                    | 0.316 |
| Q9CR57    | 60S ribosomal protein L14 OS=Mus musculus GN=Rpl14 PE=1 SV=3                 |                |           |                                                                                    | 0.313 |
| P70195    | Proteasome subunit beta type-7 OS=Mus musculus GN=Psmb7 PE=1 SV=1            |                |           |                                                                                    | 0.31  |
| Q9D823    | 60S ribosomal protein L37 OS=Mus musculus GN=Rpl37 PE=3 SV=3                 |                |           |                                                                                    | 0.305 |
| Q9EQ5     | Major vault protein OS=Mus musculus GN=Mvp PE=1 SV=4                         |                |           |                                                                                    | 0.292 |
| Q5SXS6    | Cytoplasmic FMR1-interacting protein 2 OS=Mus musculus GN=Cyfip2 PE=1 SV=2  |                |           |                                                                                    | 0.291 |
| V9GX76    | Unconventional myosin-VI OS=Mus musculus GN=Myo6 PE=1 SV=1                   |                |           |                                                                                    | 0.285 |
| P97499    | Telomerase protein component 1 OS=Mus musculus GN=Tep1 PE=1 SV=1             |                |           |                                                                                    | 0.273 |
| Q9JNM3    | ADP-ribosylation factor-like protein 6-interacting protein 4 OS=Mus musculus GN=Arl6ip4 PE=1 SV=1 |                |           |                                                                                    | 0.251 |
| Q5SS83    | Flotillin 2, isoform CRA_a OS=Mus musculus GN=Flot2 PE=1 SV=1                |                |           |                                                                                    | 0.25  |
| P62918    | 60S ribosomal protein L8 OS=Mus musculus GN=Rpl8 PE=1 SV=2                   |                |           |                                                                                    | 0.244 |
| P63163    | Small nuclear ribonucleoprotein-associated protein N OS=Mus musculus GN=Snrpn PE=2 SV=1 |                |           |                                                                                    | 0.241 |
| Q8R366    | Immunoglobulin superfamily member 8 OS=Mus musculus GN=Igsf8 PE=1 SV=2       |                |           |                                                                                    | 0.234 |
| Q8AC8K3   | UPF0515 protein C19orf66 homolog OS=Mus musculus PE=2 SV=1                   |                |           |                                                                                    | 0.229 |
| Q9CYR0    | Single-stranded DNA-binding protein, mitochondrial OS=Mus musculus GN=Ssbp1 PE=1 SV=1 |                |           |                                                                                    | 0.205 |
| P62320    | Small nuclear ribonucleoprotein Sm D3 OS=Mus musculus GN=Snrd3 PE=1 SV=1     |                |           |                                                                                    | 0.204 |
| P62315    | Small nuclear ribonucleoprotein Sm D1 OS=Mus musculus GN=Snrd1 PE=1 SV=1     |                |           |                                                                                    | 0.203 |
| P62717    | 60S ribosomal protein L18a OS=Mus musculus GN=Rpl18a PE=1 SV=1              |                |           |                                                                                    | 0.193 |
| Q99MN9    | Propionyl-CoA carboxylase beta chain, mitochondrial OS=Mus musculus GN=Pccb PE=1 SV=2 |                |           |                                                                                    | 0.187 |
| Q3V0Q    | Dynein heavy chain 12, axonemal OS=Mus musculus GN=Dnah12 PE=1 SV=2           |                |           |                                                                                    | 0.149 |
| P62307    | Small nuclear ribonucleoprotein F OS=Mus musculus GN=Snrfp PE=1 SV=1         |                |           |                                                                                    | 0.146 |
| Q8C1Y8    | Vacuolar fusion protein CCZ1 homolog OS=Mus musculus GN=Ccz1 PE=1 SV=1       |                |           |                                                                                    | 0.126 |
| Accession | Description                                                                                                                                                                                                 | Abundance Ratio: (AD) / (non-AD) |
|-----------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------|
| P10636-6  | Isoform of P10636, Isoform Tau-D of Microtubule-associated protein tau OS=Homo sapiens GN=MAPT                                                                                                              | 60,425                           |
| P10636-4  | Isoform of P10636, Isoform Tau-B of Microtubule-associated protein tau OS=Homo sapiens GN=MAPT                                                                                                              | 43,146                           |
| A0A0G2JMX7| Microtubule-associated protein OS=Homo sapiens GN=MAPT PE=1 SV=1                                                                                                                                          | 37,151                           |
| P62979    | Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2                                                                                                                                   | 8,079                            |
| Q13867    | Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1                                                                                                                                                      | 7,447                            |
| Q727K6    | Centromere protein V OS=Homo sapiens GN=CENPV PE=1 SV=1                                                                                                                                                   | 5,332                            |
| P63244    | Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3                                                                                                                                  | 4,905                            |
| P08670    | Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4                                                                                                                                                                  | 4,749                            |
| Q99747    | Gamma-soluble NSF attachment protein OS=Homo sapiens GN=NAPG PE=1 SV=1                                                                                                                                     | 4,461                            |
| A0A087WV75| Isoform of P13591, Neural cell adhesion molecule 1 OS=Homo sapiens GN=NCAM1 PE=1 SV=1                                                                                                                     | 4,26                             |
| P11182    | Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4                                                                 | 3,851                            |
| B726Z4    | Isoform of P60660, Myosin light polypeptide 6 OS=Homo sapiens GN=MV6 PE=1 SV=1                                                                                                                              | 3,766                            |
| Q9UBB6    | Neurochondrin OS=Homo sapiens GN=NCDN PE=1 SV=1                                                                                                                                                            | 3,646                            |
| A0A087X165| Isoform of Q9C0H9, SRC kinase-signaling inhibitor 1 OS=Homo sapiens GN=SRCIN1 PE=1 SV=1                                                                                                                     | 3,564                            |
| P05067    | Amyloid beta A4 protein OS=Homo sapiens GN=APP PE=1 SV=3                                                                                                                                                  | 2,998                            |
| P61927    | 60S ribosomal protein L37 OS=Homo sapiens GN=RPL37 PE=1 SV=2                                                                                                                                                | 2,831                            |
| Q01813    | ATP-dependent 6-phosphofructokinase, platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2                                                                                                                     | 2,762                            |
| Q13509    | Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2                                                                                                                                                | 2,732                            |
| P11021    | 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSP55 PE=1 SV=2                                                                                                                                      | 2,656                            |
| P0DME0    | Protein SETSIP OS=Homo sapiens GN=SETPSIP PE=1 SV=1                                                                                                                                                         | 2,477                            |
| G8JLB6    | Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNP1 PE=1 SV=1                                                                                                                               | 2,471                            |
| P02144    | Myoglobin OS=Homo sapiens GN=MB PE=1 SV=2                                                                                                                                                                  | 2,414                            |
| P30044    | Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4                                                                                                                                         | 2,327                            |
| P52306    | Rap1 GTPase-GDP dissociation stimulator 1 OS=Homo sapiens GN=RAP1GDS1 PE=1 SV=3                                                                                                                           | 2,291                            |
| P19338    | Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3                                                                                                                                                                 | 1,952                            |
| P62888    | 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2                                                                                                                                                | 1,935                            |
| P0C055    | Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2                                                                                                                                                           | 1,784                            |
| Q00839    | Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNP1 PE=1 SV=6                                                                                                                            | 1,71                             |
| Q9UQ80    | Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3                                                                                                                                  | 1,702                            |
| P50990  | T-complex protein 1 subunit theta  OS=Homo sapiens GN=CCT8 PE=1 SV=4 | 1,702 |
| P61513  | 60S ribosomal protein L37a OS=Homo sapiens GN=RPL37A PE=1 SV=2 | 1,693 |
| P62266  | 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 | 1,689 |
| P02792  | Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 | 1,674 |
| Q13243  | Serine/arginine-rich splicing factor 5 OS=Homo sapiens GN=SRSF5 PE=1 SV=1 | 1,643 |
| Q07954  | Proline-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2 | 1,633 |
| P07737  | Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2 | 1,567 |
| P62318  | Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=1 SV=1 | 1,522 |
| P15531  | Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 | 1,504 |
| Q9NQ66  | 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1 OS=Homo sapiens GN=PLCB1 PE=1 | 1,499 |
| P39019  | 40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2 | 1,495 |
| P04899  | Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3 | 1,493 |
| A0A0J9YXJ0 | Isoform of O95319, CUGBP Elav-like family member 2 OS=Homo sapiens GN=CELF2 PE=1 SV=1 | 1,488 |
| H0YKD8  | Isoform of P46779, 60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=1 | 1,469 |
| P06454  | Prothymosin alpha OS=Homo sapiens GN=PTMA PE=1 SV=2 | 1,456 |
| P31146  | Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4 | 1,451 |
| O00499  | Myc box-dependent-interacting protein 1 OS=Homo sapiens GN=BIN1 PE=1 SV=1 | 1,439 |
| A0A075B767 | Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=LOC105371242 PE=3 SV=1 | 1,439 |
| P21291  | Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRIP1 PE=1 SV=3 | 1,437 |
| Q01484  | Ankyrin-2 OS=Homo sapiens GN=ANK2 PE=1 SV=4 | 1,429 |
| O60636  | Tetraspanin-2 OS=Homo sapiens GN=TSPAN2 PE=1 SV=2 | 1,427 |
| P78386  | Keratin, type II cuticular Hb5 OS=Homo sapiens GN=KRT85 PE=1 SV=1 | 1,404 |
| P14678  | Small nuclear ribonucleoprotein-associated proteins B and B’ OS=Homo sapiens GN=SNRPB PE=1 SV=2 | 1,403 |
| P39023  | 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2 | 1,389 |
| U3KQK0  | Isoform of Q99877, Histone H2B OS=Homo sapiens GN=HIST1H2BN PE=1 SV=1 | 1,376 |
| P18621-3 | Isoform of P18621, Isoform 3 of 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 | 1,375 |
| Q9UQ35  | Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2 | 1,366 |
| Q9ULV4  | Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 | 1,36 |
| Q92599  | Septin-8 OS=Homo sapiens GN=SEPT8 PE=1 SV=4 | 1,359 |
| P53396  | ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 | 1,344 |
| P61254  | 60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1 | 1,343 |
| P51991  | Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2 | 1,332 |
| P35080  | Profilin-2 OS=Homo sapiens GN=PFN2 PE=1 SV=3 | 0,774 |
| P55072 | Transitional endoplasmic reticulum ATPase | OS=Homo sapiens | GN=VCP | PE=1 | SV=4 | 0.771 |
|--------|-----------------------------------------|-----------------|--------|------|------|------|
| P62195 | 26S protease regulatory subunit 8 | OS=Homo sapiens | GN=PSMC5 | PE=1 | SV=1 | 0.767 |
| P48426 | Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha | OS=Homo sapiens | GN=PIP4K2A | PE=1 | SV=2 | 0.755 |
| P12277 | Creatine kinase B-type | OS=Homo sapiens | GN=CKB | PE=1 | SV=1 | 0.751 |
| P14625 | Endoplasmin | OS=Homo sapiens | GN=HSP90B1 | PE=1 | SV=1 | 0.748 |
| A0A01RRH7 | Histone H2A | OS=Homo sapiens | PE=3 | SV=1 | 0.746 |
| Q86Y23 | Hornerin | OS=Homo sapiens | GN=HRNR | PE=1 | SV=2 | 0.746 |
| P16615 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 | OS=Homo sapiens | GN=ATP2A2 | PE=1 | SV=1 | 0.738 |
| A0A087WUS0 | 40S ribosomal protein S24 | OS=Homo sapiens | GN=RPS24 | PE=1 | SV=1 | 0.734 |
| P53597 | Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial | OS=Homo sapiens | GN=SUCLG1 | PE=1 | SV=1 | 0.733 |
| P00558 | Phosphoglycerate kinase 1 | OS=Homo sapiens | GN=PGK1 | PE=1 | SV=3 | 0.733 |
| P35219 | Carbonic anhydrase-related protein | OS=Homo sapiens | GN=CA8 | PE=1 | SV=3 | 0.731 |
| P63151 | Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform | OS=Homo sapiens | PE=1 | SV=2 | 0.729 |
| Q08554 | Desmocollin-1 | OS=Homo sapiens | GN=DSC1 | PE=1 | SV=2 | 0.725 |
| P17600 | Synapsin-1 | OS=Homo sapiens | GN=SYN1 | PE=1 | SV=3 | 0.719 |
| Q15366 | Poly(rC)-binding protein 2 | OS=Homo sapiens | GN=PCBP2 | PE=1 | SV=1 | 0.719 |
| P08621 | U1 small nuclear ribonucleoprotein 70 kDa | OS=Homo sapiens | GN=SNRNP70 | PE=1 | SV=2 | 0.716 |
| P23528 | Cofilin-1 | OS=Homo sapiens | GN=CFL1 | PE=1 | SV=3 | 0.714 |
| P60709 | Actin, cytoplasmic 1 | OS=Homo sapiens | GN=ACTB | PE=1 | SV=1 | 0.709 |
| P13797 | Plastin-3 | OS=Homo sapiens | GN=PLS3 | PE=1 | SV=4 | 0.707 |
| P62937 | Peptidyl-prolyl cis-trans isomerase A | OS=Homo sapiens | GN=PPIA | PE=1 | SV=2 | 0.707 |
| P61764 | Syntaxin-binding protein 1 | OS=Homo sapiens | GN=STXB1 | PE=1 | SV=1 | 0.703 |
| Q16143 | Beta-synuclein | OS=Homo sapiens | GN=SNCB | PE=1 | SV=1 | 0.701 |
| Q8TAC9 | Secretory carrier-associated membrane protein 5 | OS=Homo sapiens | GN=SCAMP5 | PE=1 | SV=1 | 0.698 |
| Q5JXB2 | Putative ubiquitin-conjugating enzyme E2 N-like | OS=Homo sapiens | GN=UBE2NL | PE=1 | SV=1 | 0.692 |
| P40925 | Malate dehydrogenase, cytoplasmic | OS=Homo sapiens | GN=MDH1 | PE=1 | SV=4 | 0.692 |
| P20336 | Ras-related protein Rab-3A | OS=Homo sapiens | GN=RAB3A | PE=1 | SV=1 | 0.691 |
| P40227 | T-complex protein 1 subunit zeta | OS=Homo sapiens | GN=CCT6A | PE=1 | SV=3 | 0.691 |
| Q16629 | Serine/arginine-rich splicing factor 7 | OS=Homo sapiens | GN=SRSF7 | PE=1 | SV=1 | 0.687 |
| P11766 | Alcohol dehydrogenase class-3 | OS=Homo sapiens | GN=ADH5 | PE=1 | SV=4 | 0.683 |
| P05771 | Protein kinase C beta type | OS=Homo sapiens | GN=PRKCB | PE=1 | SV=4 | 0.68 |
| P07900 | Heat shock protein HSP 90-alpha | OS=Homo sapiens | GN=HSP90AA1 | PE=1 | SV=5 | 0.679 |
| Q9Y2J2 | Band 4.1-like protein 3 | OS=Homo sapiens | GN=EPB41L3 | PE=1 | SV=2 | 0.678 |
| Accession | Description                                                                 | Organism            | Gene Name | Protein Name | Score |
|-----------|------------------------------------------------------------------------------|---------------------|-----------|--------------|-------|
| Q04837    | Single-stranded DNA-binding protein, mitochondrial                         | Homo sapiens       | SSBP1     | SSBP1        | 0.674 |
| P06576    | ATP synthase subunit beta, mitochondrial                                     | Homo sapiens       | ATP5B     | ATP synthase subunit beta | 0.674 |
| Q8NCB2    | CaM kinase-like vesicle-associated protein                                   | Homo sapiens       | CAMKV     | CAMKV        | 0.672 |
| Q02413    | Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2                             | Homo sapiens       | DSG1      | Desmoglein-1 | 0.671 |
| Q14982    | Opioid-binding protein/cell adhesion molecule                               | Homo sapiens       | OPCML     | OPCML        | 0.671 |
| P21579    | Synaptotagmin-1 OS=Homo sapiens GN=SYT1 PE=1 SV=1                          | Homo sapiens       | SYT1      | Synaptotagmin-1 | 0.669 |
| P19367    | Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3                              | Homo sapiens       | HK1       | Hexokinase-1     | 0.667 |
| P10412    | Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2                         | Homo sapiens       | HIST1H1E  | Histone H1.4   | 0.666 |
| P02768    | Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2                            | Homo sapiens       | ALB       | Serum albumin  | 0.665 |
| P18669    | Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2               | Homo sapiens       | PGAM1     | Phosphoglycerate mutase-1 | 0.663 |
| Q05639    | Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1            | Homo sapiens       | EEF1A2    | Elongation factor-1-alpha-2 | 0.662 |
| Q7Z456    | Kinesin-like protein KIF21A OS=Homo sapiens GN=KIF21A PE=1 SV=2            | Homo sapiens       | KIF21A    | Kinesin-like protein KIF21A | 0.662 |
| P18124    | 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1                 | Homo sapiens       | RPL7      | 60S ribosomal protein L7 | 0.661 |
| P61981    | 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2                   | Homo sapiens       | YWHAG     | 14-3-3 protein gamma | 0.655 |
| Q92598    | Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1              | Homo sapiens       | HSPH1     | Heat shock protein 105 kDa | 0.655 |
| Q9UJ21    | Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1 | Homo sapiens       | STOML2    | Stomatin-like protein 2 | 0.654 |
| A0A1B0GTW6| Isoform of Q9H4G0, Band 4.1-like protein 1 (Fragment) OS=Homo sapiens GN=EPB41L1 PE=1 SV=1 | Homo sapiens       | EPB41L1   | Isoform of Q9H4G0, Band 4.1-like protein 1 | 0.65 |
| P17858    | ATP-dependent 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 | Homo sapiens       | PFKL      | ATP-dependent 6-phosphofructokinase, liver type | 0.65 |
| P49720    | Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2          | Homo sapiens       | PSMB3     | Proteasome subunit beta type-3 | 0.648 |
| P46777    | 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3                 | Homo sapiens       | RPL5      | 60S ribosomal protein L5 | 0.641 |
| Q14141    | Septin-6 OS=Homo sapiens GN=SEPT6 PE=1 SV=4                               | Homo sapiens       | SEPT6     | Septin-6 | 0.639 |
| O15075    | Serine/threonine-protein kinase DCLK1 OS=Homo sapiens GN=DCLK1 PE=1 SV=2  | Homo sapiens       | DCLK1     | Serine/threonine-protein kinase DCLK1 | 0.631 |
| E7EQ64    | Isoform of P07477, Trypsin-1 OS=Homo sapiens GN=PRSS1 PE=1 SV=1            | Homo sapiens       | PRSS1     | Isoform of P07477, Trypsin-1 | 0.63 |
| Q9Y277    | Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 | Homo sapiens       | VDAC3     | Voltage-dependent anion-selective channel protein 3 | 0.628 |
| H3BR70    | Isoform of P14618, Pyruvate kinase OS=Homo sapiens GN=PKM PE=1 SV=1        | Homo sapiens       | PKM       | Isoform of P14618, Pyruvate kinase | 0.627 |
| P35908    | Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2| Homo sapiens       | KRT2      | Keratin, type II cytoskeletal 2 epidermal | 0.625 |
| Q15773    | Myeloid leukemia factor 2 OS=Homo sapiens GN=MLF2 PE=1 SV=1                | Homo sapiens       | MLF2      | Myeloid leukemia factor 2 | 0.623 |
| A0A0B4J2C3| Translational-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1   | Homo sapiens       | TPT1      | Translational-controlled tumor protein | 0.622 |
| Q6ZN40    | Tropomyosin 1 (Alpha), isoform CRA_f OS=Homo sapiens GN=TPM1 PE=1 SV=1    | Homo sapiens       | TPM1      | Tropomyosin 1 (Alpha), isoform CRA_f | 0.621 |
| Q6PUV4    | Complexin-2 OS=Homo sapiens GN=CPLX2 PE=2 SV=2                            | Homo sapiens       | CPLX2     | Complexin-2 | 0.621 |
| P60201    | Myelin proteolipid protein OS=Homo sapiens GN=PLP1 PE=1 SV=2               | Homo sapiens       | PLP1      | Myelin proteolipid protein | 0.614 |
| Q15365    | Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2              | Homo sapiens       | PCBP1     | Poly(rC)-binding protein 1 | 0.612 |
| P28070    | Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4          | Homo sapiens       | PSMB4     | Proteasome subunit beta type-4 | 0.61 |
| Accession | Description | OS | GN | PE | SV |
|-----------|-------------|----|----|----|----|
| A0A024RA52 | Proteasome subunit alpha type | Homo sapiens | PSMA2 | 1 | 1 |
| P13929 | Beta-enolase | Homo sapiens | ENO3 | 1 | 5 |
| O14818 | Proteasome subunit alpha type-7 | Homo sapiens | PSMA7 | 1 | 1 |
| P62316 | Small nuclear ribonucleoprotein Sm D2 | Homo sapiens | SNRPD2 | 1 | 1 |
| P07195 | L-lactate dehydrogenase B chain | Homo sapiens | LDHB | 1 | 2 |
| Q14683 | Structural maintenance of chromosomes protein 1A | Homo sapiens | SMC1A | 1 | 2 |
| P13647 | Keratin, type II cytoskeletal | Homo sapiens | KRT5 | 1 | 3 |
| P28066 | Proteasome subunit alpha type-5 | Homo sapiens | PSMA5 | 1 | 3 |
| P09471 | Guanine nucleotide-binding protein G(o) subunit alpha | Homo sapiens | GNAO1 | 1 | 4 |
| P58546 | Myotrophin | Homo sapiens | MTPN | 1 | 1 |
| Q92752 | Tenascin-R | Homo sapiens | TNR | 1 | 3 |
| P13645 | Keratin, type I cytoskeletal 10 | Homo sapiens | KRT10 | 1 | 6 |
| P20930 | Filaggrin | Homo sapiens | FLG | 1 | 3 |
| Q9BP6U6 | Dihydropyrimidinase-related protein 5 | Homo sapiens | DPYSL5 | 1 | 1 |
| P62750 | 60S ribosomal protein L23a | Homo sapiens | RPL23A | 1 | 1 |
| P51149 | Ras-related protein Rab-7a | Homo sapiens | RAB7A | 1 | 1 |
| Q9Y639 | Neuroplastin | Homo sapiens | NPTN | 1 | 2 |
| P02538 | Keratin, type II cytoskeletal 6A | Homo sapiens | KRT6A | 1 | 3 |
| O00330 | Pyruvate dehydrogenase protein X component, mitochondrial | Homo sapiens | PDHX | 1 | 1 |
| P50395 | Rab GDP dissociation inhibitor beta | Homo sapiens | GDI2 | 1 | 2 |
| P07910 | Heterogeneous nuclear ribonucleoproteins C1/C2 | Homo sapiens | HNRNPC | 1 | 4 |
| P21796 | Voltage-dependent anion-selective channel protein 1 | Homo sapiens | VDAC1 | 1 | 2 |
| E7EMK3 | Isoform of Q14254, Flotillin-2 | Homo sapiens | FLOT2 | 1 | 1 |
| P25705 | ATP synthase subunit alpha, mitochondrial | Homo sapiens | ATP5A1 | 1 | 1 |
| F5GYJ8 | Isoform of Q96FW1, Ubiquitin thioesterase OTUB1 | Homo sapiens | OTUB1 | 1 | 1 |
| P07437 | Tubulin beta chain | Homo sapiens | TUBB | 1 | 2 |
| P05388 | 60S acidic ribosomal protein P0 | Homo sapiens | RPLP0 | 1 | 1 |
| P22676 | Calretinin | Homo sapiens | CALB2 | 1 | 2 |
| P07305 | Histone H1.0 | Homo sapiens | H1F0 | 1 | 3 |
| O76013 | Keratin, type I cuticular Ha6 | Homo sapiens | KRT36 | 1 | 2 |
| O75390 | Citrate synthase, mitochondrial | Homo sapiens | CS | 1 | 2 |
| Q9Y2T3 | Guanine deaminase | Homo sapiens | GDA | 1 | 1 |
| P04350 | Tubulin beta-4A chain | Homo sapiens | TUBB4A | 1 | 2 |
| Accession | Description                                                                 | GO ID | Score |
|-----------|------------------------------------------------------------------------------|-------|-------|
| P30153    | Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform |       | 0.561 |
| Q7L0J3    | Synaptic vesicle glycoprotein 2A OS=Homo sapiens GN=SV2A PE=1 SV=1            |       | 0.559 |
| F8WF69    | Isoform of P09496, Clathrin light chain A OS=Homo sapiens GN=CLTA PE=1 SV=1  |       | 0.559 |
| H7BY58    | Isoform of P22061, Protein-L-isopropyl side-chain O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=4 |       | 0.559 |
| Q04695    | Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2            |       | 0.555 |
| P06702    | Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1                          |       | 0.554 |
| P05387    | 60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1            |       | 0.552 |
| P28072    | Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4            |       | 0.55  |
| A0A1C7CYX9| Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1   |       | 0.548 |
| P31946    | 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3                 |       | 0.545 |
| P46459    | Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3                      |       | 0.544 |
| Q9UPV7    | PHD finger protein 24 OS=Homo sapiens GN=PHF24 PE=1 SV=2                     |       | 0.539 |
| A0A0B4J231| Isoform of B9A064, Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=1 SV=1 |       | 0.531 |
| P46821    | Microtubule-associated protein 1B OS=Homo sapiens GN=MAP1B PE=1 SV=2         |       | 0.529 |
| E7EPK1    | Isoform of Q16181, Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2               |       | 0.525 |
| P09936    | Ubiquitin carboxyl-terminal hydrolase isoform L1 OS=Homo sapiens GN=UCHL1 PE=1 SV=2 |       | 0.525 |
| P61266    | Syntaxin-1B OS=Homo sapiens GN=STX1B PE=1 SV=1                               |       | 0.52  |
| P62701    | 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2       |       | 0.52  |
| P21281    | V-type proton ATPase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3 |       | 0.514 |
| P17987    | T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1          |       | 0.512 |
| P08779    | Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4           |       | 0.51  |
| Q14194    | Dihydropyrimidinase-related protein 1 OS=Homo sapiens GN=CRMP1 PE=1 SV=1    |       | 0.509 |
| Q12860    | Contactin-1 OS=Homo sapiens GN=CNTN1 PE=1 SV=1                               |       | 0.503 |
| P40926    | Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3        |       | 0.502 |
| Q9NZT1    | Calmodulin-like protein 5 OS=Homo sapiens GN=CALML5 PE=1 SV=2                |       | 0.501 |
| P23396    | 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2                   |       | 0.501 |
| P02533    | Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4           |       | 0.493 |
| Q9BY11    | Protein kinase C and casein kinase substrate in neurons protein 1 OS=Homo sapiens GN=PACSIN1 PE=1 SV=1 |       | 0.489 |
| P11142    | Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1         |       | 0.487 |
| Q16720    | Plasma membrane calcium-transporting ATPase 3 OS=Homo sapiens GN=ATP2B3 PE=1 SV=3 |       | 0.483 |
| P04264    | Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6             |       | 0.481 |
| P31944    | Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2                               |       | 0.48  |
| P81605    | Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2                                  |       | 0.479 |
| Accession | Description                                                                 | Organism       | Gene Name | Protein Name | Ensembl Transcript ID | Score |
|-----------|-----------------------------------------------------------------------------|----------------|-----------|--------------|-----------------------|-------|
| P04075    | Fructose-bisphosphate aldolase A                                             | Homo sapiens   | ALDOA     | Fructose-bisphosphate aldolase A | 0.478    |
| P63104    | 14-3-3 protein zeta/delta                                                  | Homo sapiens   | YWHAZ     | 14-3-3 protein zeta/delta      | 0.474    |
| P04259    | Keratin, type II cytoskeletal 6B                                           | Homo sapiens   | KRT6B     | Keratin, type II cytoskeletal 6B | 0.473    |
| A0A0A0MT26| Isoform of P13637, Sodium/potassium-transporting ATPase subunit alpha-3   | Homo sapiens   | AT        | Sodium/potassium-transporting ATPase subunit alpha-3 | 0.472    |
| P30101    | Protein disulfide-isomerase A                                              | Homo sapiens   | PDIA3     | Protein disulfide-isomerase A  | 0.472    |
| P32119    | Peroxiredoxin-2 OS                                                        | Homo sapiens   | PRDX2     | Peroxiredoxin-2 OS            | 0.467    |
| P14136    | Glial fibrillary acidic protein OS                                         | Homo sapiens   | GFAP      | Glial fibrillary acidic protein OS | 0.466    |
| P13646    | Keratin, type I cytoskeletal 13                                              | Homo sapiens   | KRT13     | Keratin, type I cytoskeletal 13 | 0.461    |
| P69905    | Hemoglobin subunit alpha OS                                                | Homo sapiens   | HBA1      | Hemoglobin subunit alpha OS    | 0.46     |
| P68366    | Tubulin alpha-4A chain OS                                                  | Homo sapiens   | TUBA4A    | Tubulin alpha-4A chain OS      | 0.457    |
| P27797    | Calreticulin OS                                                            | Homo sapiens   | CALR      | Calreticulin OS                | 0.454    |
| P35527    | Keratin, type I cytoskeletal 9                                              | Homo sapiens   | KRT9      | Keratin, type I cytoskeletal 9  | 0.452    |
| D6RER5    | Isoform of Q9NVA2, Septin-11 OS                                            | Homo sapiens   | SEPT11    | Isoform of Q9NVA2, Septin-11 OS | 0.452    |
| P27348    | 14-3-3 protein theta OS                                                     | Homo sapiens   | YWHAQ     | 14-3-3 protein theta OS         | 0.451    |
| Q04917    | 14-3-3 protein eta OS                                                      | Homo sapiens   | YWHAH     | 14-3-3 protein eta OS           | 0.45     |
| Q14103    | Heterogeneous nuclear ribonucleoprotein D0 OS                              | Homo sapiens   | HNRNPD    | Heterogeneous nuclear ribonucleoprotein D0 OS | 0.443    |
| P20618    | Proteasome subunit beta type-1 OS                                          | Homo sapiens   | PSMB1     | Proteasome subunit beta type-1 OS | 0.441    |
| P34932    | Heat shock 70 kDa protein 4 OS                                              | Homo sapiens   | HSPA4     | Heat shock 70 kDa protein 4 OS   | 0.434    |
| V9G217    | Isoform of Q9NY65, Tubulin alpha-8 chain (Fragment) OS                     | Homo sapiens   | TUBA8     | Isoform of Q9NY65, Tubulin alpha-8 chain (Fragment) OS | 0.431    |
| P43004    | Excitatory amino acid transporter 2 OS                                     | Homo sapiens   | SLC1A2    | Excitatory amino acid transporter 2 OS | 0.429    |
| P61978    | Heterogeneous nuclear ribonucleoprotein K OS                              | Homo sapiens   | HNRNPK    | Heterogeneous nuclear ribonucleoprotein K OS | 0.425    |
| P47914    | 60S ribosomal protein L29 OS                                                | Homo sapiens   | RPL29     | 60S ribosomal protein L29 OS    | 0.424    |
| G3V5Z7    | Isoform of P60900, Proteasome subunit alpha type OS                        | Homo sapiens   | PSMA6     | Isoform of P60900, Proteasome subunit alpha type OS | 0.422    |
| Q99436    | Proteasome subunit beta type-7 OS                                          | Homo sapiens   | PSMB7     | Proteasome subunit beta type-7 OS | 0.417    |
| Q96IE9    | Microtubule-associated protein 6 OS                                        | Homo sapiens   | MAP6      | Microtubule-associated protein 6 OS | 0.412    |
| Q13825    | Methylglutaconyl-CoA hydratase, mitochondrial OS                           | Homo sapiens   | AUH       | Methylglutaconyl-CoA hydratase, mitochondrial OS | 0.406    |
| P00918    | Carbonic anhydrase 2 OS                                                    | Homo sapiens   | CA2       | Carbonic anhydrase 2 OS         | 0.403    |
| P45880    | Voltage-dependent anion-selective channel protein 2 OS                     | Homo sapiens   | VDAC2     | Voltage-dependent anion-selective channel protein 2 OS | 0.403    |
| P54652    | Heat shock-related 70 kDa protein 2 OS                                     | Homo sapiens   | HSPA2     | Heat shock-related 70 kDa protein 2 OS | 0.403    |
| Q9H3Z4    | DnaJ homolog subfamily C member 5 OS                                       | Homo sapiens   | DNAJC5    | DnaJ homolog subfamily C member 5 OS | 0.399    |
| P61313    | 60S ribosomal protein L15 OS                                               | Homo sapiens   | RPL15     | 60S ribosomal protein L15 OS    | 0.396    |
| Q96F2J    | Dynein light chain 2, cytoplasmic OS                                       | Homo sapiens   | DYNLL2    | Dynein light chain 2, cytoplasmic OS | 0.395    |
| O14594    | Neurocan core protein OS                                                  | Homo sapiens   | NCAN      | Neurocan core protein OS        | 0.38     |
| P55087 | Aquaporin-4 OS=Homo sapiens GN=AQP4 PE=1 SV=2 | 0,379 |
| P68871 | Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 | 0,378 |
| O75822 | Eukaryotic translation initiation factor 3 subunit J OS=Homo sapiens GN=EIF3J PE=1 SV=2 | 0,375 |
| A0A0D9SGF6 | Isoform of Q13813, Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=2 | 0,371 |
| Q96HN2 | Adenosylhomocysteinase 3 OS=Homo sapiens GN=AHCYL2 PE=1 SV=1 | 0,367 |
| P49721 | Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1 | 0,358 |
| P36543 | V-type proton ATPase subunit E 1 OS=Homo sapiens GN=ATP6V1E1 PE=1 SV=1 | 0,358 |
| P46776 | 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 | 0,355 |
| P36871 | Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1 SV=3 | 0,353 |
| A0A087WZQ7 | Isoform of Q9H115, Beta-soluble NSF attachment protein OS=Homo sapiens GN=NAPB PE=1 SV=1 | 0,35 |
| P21283 | V-type proton ATPase subunit C 1 OS=Homo sapiens GN=ATP6V1C1 PE=1 SV=4 | 0,347 |
| P15104 | Glutamine synthetase OS=Homo sapiens GN=GLUL PE=1 SV=1 | 0,345 |
| P04271 | Protein S100-B OS=Homo sapiens GN=S100B PE=1 SV=2 | 0,344 |
| P62942 | Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens GN=FKBP1A PE=1 SV=2 | 0,341 |
| P78371 | T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 | 0,332 |
| A0A087WUZ3 | Spectrin beta chain OS=Homo sapiens GN=SPTBN1 PE=1 SV=1 | 0,326 |
| Q93050 | V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1 PE=1 SV=3 | 0,314 |
| O95670 | V-type proton ATPase subunit G 2 OS=Homo sapiens GN=ATP6V1G2 PE=2 SV=1 | 0,313 |
| P50993 | Sodium/potassium-transporting ATPase subunit alpha-2 OS=Homo sapiens GN=ATP1A2 PE=1 SV=1 | 0,305 |
| F5GYQ1 | Isoform of P61421, V-type proton ATPase subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=1 SV=1 | 0,304 |
| H7BYR8 | Isoform of P02686, Myelin basic protein OS=Homo sapiens GN=MBP PE=1 SV=1 | 0,299 |
| P52209 | 6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3 | 0,286 |
| Q08380 | Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1 | 0,284 |
| P02686 | Myelin basic protein OS=Homo sapiens GN=MBP PE=1 SV=3 | 0,284 |
| P80723 | Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2 | 0,271 |
| P46976 | Glycogenin-1 OS=Homo sapiens GN=GYG1 PE=1 SV=4 | 0,269 |
| Q15907 | Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4 | 0,268 |
| P05026 | Sodium/potassium-transporting ATPase subunit beta-1 OS=Homo sapiens GN=ATP1B1 PE=1 SV=1 | 0,267 |
| P62873 | Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=1 | 0,267 |
| H3BNQ7 | Isoform of P80404, 4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 | 0,266 |
| P09543 | 2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens GN=CNP PE=1 SV=2 | 0,265 |
| P30041 | Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3 | 0,263 |
| E7EX88 | Aggrecan core protein OS=Homo sapiens GN=ACAN PE=1 SV=2 | 0,257 |
| Accession | Description                                                                 | Organism       | Gene       | Protein       | Version | Score  |
|-----------|------------------------------------------------------------------------------|----------------|------------|---------------|---------|--------|
| Q96GW7    | Brevican core protein                                                        | Homo sapiens   | BCAN       | PE=1          | SV=2    | 0.255  |
| Q9Y2A7    | Nck-associated protein 1                                                     | Homo sapiens   | NCKAP1     | PE=1          | SV=1    | 0.213  |
| Q5D862    | Filaggrin-2                                                                 | Homo sapiens   | FLG2       | PE=1          | SV=1    | 0.209  |
| Q9HCC0    | Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial                    | Homo sapiens   | MCCC2      | PE=1          | SV=1    | 0.207  |
| Q92747    | Actin-related protein 2/3 complex subunit 1A                                | Homo sapiens   | ARPC1A     | PE=1          | SV=2    | 0.204  |
| A0A0G2JHM8| Myelin-oligodendrocyte glycoprotein                                         | Homo sapiens   | MOG        | PE=1          | SV=1    | 0.2    |
| Q9GZV7    | Hyaluronan and proteoglycan link protein 2                                  | Homo sapiens   | HAPLN2     | PE=2          | SV=1    | 0.187  |
| Q13404    | Ubiquitin-conjugating enzyme E2 variant                                    | Homo sapiens   | UBE2V1     | PE=1          | SV=2    | 0.178  |
| P10915    | Hyaluronan and proteoglycan link protein 1                                  | Homo sapiens   | HAPLN1     | PE=2          | SV=2    | 0.155  |
| H3BLU2    | Limbic system-associated membrane protein (Fragment)                       | Homo sapiens   | LSAMP      | PE=1          | SV=1    | 0.15   |
| P00441    | Superoxide dismutase [Cu-Zn]                                                | Homo sapiens   | SOD1       | PE=1          | SV=2    | 0.146  |
| P41222    | Prostaglandin-H2 D-isomerase                                                | Homo sapiens   | PTGDS      | PE=1          | SV=1    | 0.141  |
| A0A075B6H6| Isoform of P01834, Ig kappa chain C region (Fragment)                       | Homo sapiens   | IGKC       | PE=1          | SV=1    | 0.125  |
| P40306    | Proteasome subunit beta type-10                                              | Homo sapiens   | PSMB10     | PE=1          | SV=1    | 0.098  |
| P00738    | Haptoglobin                                                                | Homo sapiens   | HP         | PE=1          | SV=1    | 0.079  |
| P13611    | Versican core protein                                                        | Homo sapiens   | VCAN       | PE=1          | SV=3    | 0.075  |
| A0A180GUA9| Isoform of P01871, Ig mu chain C region (Fragment)                          | Homo sapiens   | IGHM       | PE=1          | SV=1    | 0.06   |