The endosome is a master regulator of plasma membrane collagen fibril assembly

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Keywords: collagen-I, endocytosis, extracellular matrix, fibril, fibrillogenesis, integrin-α11, trafficking, VPS33b,

[abstract] [149 word max]

Collagen fibrils are the principal supporting elements in vertebrate tissues. They account for 25% of total protein mass, exhibit a broad range of size and organisation depending on tissue and stage of development, and can be under circadian clock control. Here we show that the remarkable dynamic pleomorphism of collagen fibrils is underpinned by a mechanism that distinguishes between collagen secretion and initiation of fibril assembly, at the plasma membrane. Collagen fibrillogenesis occurring at the plasma membrane requires vacuolar protein sorting (VPS) 33b (which is under circadian clock control), collagen-binding integrin-α11 subunit, and is reduced when endocytosis is inhibited. Fibroblasts lacking VPS33b secrete soluble collagen without assembling fibrils, whereas constitutive over-expression of VPS33b increases fibril number with loss of fibril rhythmicity. In conclusion, our study has identified the mechanism that switches secretion of collagen (without forming new fibrils) to new collagen fibril assembly, at the plasma membrane.

A primary function of vertebrate cells is to synthesise the matrisome, which is an ensemble of 1000+ genes encoding extracellular matrix (ECM) and ECM-associated proteins [1]. The ECM, which can account for up to 70% of the mass of vertebrates, is essential for metazoan development because it provides attachment sites for cell migration and provides biomechanical support and protection against crushing and tensile forces. However, synthesis of the matrisome is, in itself, insufficient to generate a functional ECM; scaffolding proteins, such as collagens, are assembled into defined numbers of elongated fibrils that are organised into precise three-dimensional architectures [2-4] to give tissues and organs their physical form, polarity, mechanical properties, and adaptability to environmental stimuli. Collagen fibrils are the largest (up to centimetres in length[5]) protein polymers in vertebrates and account for ~25% of total body protein mass [6]. They exhibit a characteristic *D*-periodic axial banding pattern (where *D* = 67 nm) [7], are roughly circular in cross section, range in diameter from ~12 nm to ~500 nm [8], and grow in length from their two pointed tips [9,10]. Studies in tendon and cartilage have shown that collagen fibrils are synthesised during development [4] and persist throughout life without turnover (in humans [11] and mice [12]). Therefore, having the right number, length and organisation of collagen fibrils is critical for normal cell behaviour and tissue health.

Collagen can be purified from tissues and reconstituted in neutral buffers to generate fibrils with the same *D*-periodicity as those that occur *in vivo* [7]. However, the fibrils lack a preferred orientation and the control of fibril number and diameter distribution is lost. Collagen fibril length is difficult to ascertain, either *in vivo* or *in vitro*; therefore, it is unknown if the centimetre lengths that are attained *in vivo* are reproduced *in vitro*. Considering that collagen can self-assemble into fibrils, but that higher-order assemblies are lost *in vitro*, implies that cells exert control over the fibril assembly process to

produce tissue-specific matrices. We hypothesised that the endosomal system, with its complex collection of vesicles trafficking between the Golgi and the plasma membrane, could contribute to such a mechanism.

Support for this hypothesis comes from a previous report that the assembly of collagen fibrils is under the control of the circadian clock [13] and that vacuolar protein sorting (VPS) 33b (a regulator of SNARE-dependent membrane fusion in the endocytic pathway) is circadian clock regulated. VPS33b forms a distinct complex with VIPAS39 (also known as VIPAR) [14], and mutations in the *VPS33B* gene cause arthrogryposis-renal dysfunction-cholestasis (ARC) syndrome [15], with death usually occurring within the first year of birth with renal insufficiency, jaundice, multiple congenital anomalies, predisposition to infection, and failure to thrive [16]. One proposed disease-causing mechanism is abnormal post-Golgi trafficking of lysyl hydroxylase 3 (LH3, PLOD3), which is essential for collagen homeostasis during development [17]. Additional support for tight cellular control of collagen fibril formation comes from electron microscope observations of collagen fibrils at the plasma membrane of embryonic avian and rodent tendon fibroblasts [18,19]. Here, one of the two tips of newly-formed collagen fibrils is enclosed within a plasma membrane invagination termed a fibripositor [20]. The second tip protrudes into the extracellular matrix. One way in which cells could exert control over collagen fibrillogenesis is by separating initiation of fibril formation (nucleation at the plasma membrane) from longitudinal growth. Nucleation at the plasma membrane would give precise control of fibril number whereas propagation (involving either the proximal or distal tip) would contribute to tissue expansion. However, despite ultrastructural observations, direct mechanistic support for these observations was lacking.

Here, we showed that cells lacking VPS33b did not exhibit fibripositors and could not assemble collagen fibrils, which was in contrast to control cells that exhibited fibripositors and assembled fibrils at their plasma membrane. Instead, VPS33B knockout cells secreted soluble collagen and accumulated collagen in intracellular puncta. Using a split-GFP approach, we showed that collagen-I and VPS33b were contained in vesicles below the plasma membrane. We showed using biotin-surface labelling that col5a1 (a critical chain of collagen-V) and integrin-α11 subunit (a collagen-binding integrin involved in collagen reorganisation [21]) are absent from the surface of VPS33b knockout cells. Together, these results provide insights into the importance of the endosomal system in orchestrating and regulating the assembly of collagen fibrils at the plasma membrane.

Results

Collagen-I is endocytosed and reassembled into fibrils

As a first experiment, we made Cy3 labelled collagen-I (Cy3-colI) using previously described methods [22] and incubated it with freshly isolated tail tendons for 3 days, then imaged the mid-section of the tendon (Figure 1A). Cells in tendon (nuclei marked with Hoechst stain) show a clear uptake of Cy3-colI within the cytoplasm (Figure 1A, yellow box and indicated by yellow arrowheads). Additionally, fibrillar Cy3 fluorescence signals that transverse between cells were also observed (Figure 1A, grey box and indicated by white arrows). Pulse-chase experiments were performed, where Cy3-colI was added to the tendons for 3 days, followed by 5FAM-colI for a further 2 days (Supplementary Figure 1A). The results confirmed that collagen-I can be taken up by cells regardless of the fluorophore used; additionally, there are distinct areas where only Cy3-positivity was observed (Supplementary 1A, yellow box). The persistence of Cy3-colI indicated that not all collagen endocytosed by cells is directed to degradation. 5FAM-positive fibril-like structures were also observed, suggesting that collagen-I taken up by cells is recycled to the matrix (Supplementary 1A, grey box). Next, we added Cy3-colI to

cultured tendon fibroblasts. Immunofluorescence staining indicated co-localisation of endogenous collagen-I with Cy3-labelled collagen-I (Figure 1B). Therefore, endocytosed collagen can be repurposed into fibrils without being targeted for degradation. Taken together, these results demonstrated that exogenous collagen-I can be taken up by cells both *in vitro* and in tendon tissues *ex vivo*.

We considered the possibility that the fluorescent fibril-like structures were the result of Cy3-colI attachment to pre-existing fibres in the extracellular matrix, or to spontaneous cell-free fibrillogenesis. Therefore, we incubated Cy3-colI at concentrations that spanned the 0.4 μg/mL critical concentration for cell-free *in vitro* fibril formation [23], in the presence and absence of cells (Figure 1C). In the absence of cells, Cy3-positive fibrils were observed at 1 μg/mL and 5 μg/mL with no discernible Cy3-positive fibrils at 0.1 μg/mL Cy3-colI (Figure 1C, left panel). However, in the presence of cells, Cy3-positive fibrillar structures were observed at the surfaces of cells at all concentrations of Cy3-colI examined, including 0.1 μg/mL (Figure 1C, right panel and Figure 1D). These results indicated that the cells actively recycled Cy3-colI into fibrils. As a next experiment, we incubated cells with Cy3-colI or Cy5-colI for 1 hr and released the cells from the cell culture plastic. Flow cytometry imaging revealed that tagged collagen-I is endocytosed by the cells into distinct vesicles (Figure 1E). After overnight incubation, flow cytometry analysis revealed ~ 80% of the fibroblasts had taken up Cy3-colI (Figure 1F). Further time course analyses revealed a time-dependent, as well as concentration-dependent, increase of collagen-I uptake (Figure 1G). Similar results were obtained using Cy5-colI, indicating that soluble monomeric collagen-I can be taken up by cells regardless of the fluorophore attached (Supplementary Figure 1B, C).

The endocytic pathway controls collagen-I secretion and fibril assembly

Having shown that cells can take up and recycle collagen-I to extracellular fibrils, we asked if the endocytic process is *required* for collagen deposition or fibril formation. To address this, we first used Dyngo4a (Dyng) to inhibit clathrin-mediated endocytosis. We confirmed that Dyng treatment at 20 μM leads to ~ 60% reduction in Cy3-colI uptake (Figure 2A) and does not affect cell viability even after long periods in culture (Supplementary Figure 2A).

We then investigated the effects of Dyng treatment on the ability of fibroblasts to assemble collagen fibrils. Murine tendon fibroblasts (which are prolific at secreting collagen-I and assembling fibrils) were treated with Dyng for 48 hrs and conditioned media (CM) collected to assess levels of secreted collagen-I. The results showed that the amount of soluble collagen-I secreted was greatly reduced in Dyng-treated cells (Figure 2B). Moreover, this was coupled with a reduction in the number of collagen-I fibres in the cell-derived matrix, as indicated by immunofluorescence (Figure 2C). qPCR analyses revealed that *col1a1* transcripts were significantly reduced in cells treated with Dyng (Figure 2D), suggesting the possible existence of a feedback mechanism between endocytosis and collagen-I secretion. Taken together, these results suggest that inhibiting endocytosis in fibroblasts does not lead to accumulation of soluble collagen-I monomers in the extracellular space. Rather, endocytosis is directly involved in collagen fibrillogenesis, which in turn regulates collagen transcript levels through an unidentified negative feedback loop.

Collagen-I endocytosis is circadian clock regulated

Previously, we have demonstrated that circadian clock-synchronised fibroblasts synthesise collagen fibrils in a circadian clock rhythmic manner [13]; the results here thus far indicate an involvement of endocytosis in collagen fibrillogenesis. Therefore, we tested the hypothesis that collagen-I endocytosis may also be circadian clock regulated. Time-series flow cytometry analyses on fibroblasts

incubated with Cy3-colI revealed that the level of Cy3-colI endocytosed by the cells is rhythmic, with a periodicity of 23.8 hrs as determined by MetaCycle analysis (Figure 2E, left). When corrected to the running average, the rhythmic nature of Cy3-colI uptake is accentuated (Figure 2E, right). We noted that, when compared to the number of fibrils produced over time, the peak time of uptake has an inverse correlation with fibril numbers (Supplementary Figure 2B). This suggested to us that the cells may be endocytosing exogenous collagen and holding it in the endosomal compartment under circadian clock control, then trafficking the collagen to the plasma membrane for fibril formation. A possible function of this delay could be to increase the concentration of collagen-I in readiness for fibril initiation, which is supported by our findings above where fibroblasts can take a starting concentration of Cy3-colI of 0.1 μg/mL (which is lower than the 0.4 μg/mL critical concentration for fibril formation, Figure 1C, D) and concentrate it sufficiently to assemble fibrils.

VPS33b controls collagen fibril homeostasis

VPS33b is situated in the post-Golgi space where it is involved in endosomal trafficking with multiple functions including extracellular vesicle formation [24], modulation of P53 signalling [25], and maintenance of cell polarity [26], dependent on cell type. We previously identified VPS33b to be a circadian-controlled component of the collagen-I secretory pathway in fibroblasts [13]. As a result, we decided to interrogate further its role in endosomal recycling of collagen-I.

We first confirmed our previous finding that CRISPR-knockout of VPS33b (VPSko, as verified by Western blot analysis and qPCR analysis, Supplementary Figure 3A and B) in tendon fibroblasts led to fewer collagen fibrils, as evidenced by both electron microscopy (Figure 3A) and immunofluorescence microscopy (Figure 3B). The impact on matrix deposition was verified by analysis of the decellularized matrices. The results showed that VPSko fibroblasts produced less matrix (by mass) than control cells (Figure 3C, left), which was mirrored by a reduction in hydroxyproline content (Figure 3C, right). This decrease in matrix deposition was not due to changes in cell proliferation (Supplementary Figure 3C).

To further investigate the role of VPS33b in collagen-I homeostasis, we stably overexpressed VPS33b in fibroblasts (VPSoe). Overexpression was confirmed by western blot, qPCR analyses, and flow cytometry of transfected cells (Supplementary Figure 3D, E, F). The mean total matrix and mean total hydroxyproline were higher in VPSoe cultures but not significant (Figure 3D). Immunofluorescence staining of cells after 3 days in culture indicated a greater number of collagen-I fibrils in VPSoe cells (Figure 3E). Vps33b overexpressing cell lines showed equivalent proliferation to controls over the time course of these experiments (Supplementary Figure 3G), suggesting VPSoe enhanced the assembly of collagen fibrils. We then synchronised control and VPSoe fibroblasts and performed time-series immunofluorescence to quantify the number of collagen fibres formed. Similar to our previous finding in primary lung fibroblasts [13], murine tendon fibroblasts exhibited a ~ 24 hrs rhythmic increase and decrease in collagen-I fibre numbers; however, VPSoe cells continuously deposited collagen-I fibres over the 55-hr period (Figure 3F). MetaCycle analyses indicated that the increase and decrease in fibre numbers in control and VPSoe cultures occurred at a periodicity of 22.7 hrs and 28.0 hrs, respectively (Supplementary Figure 3H). This indicates that continuous expression of VPS33b leads to loss of collagen-I fibre circadian homeostasis. Interestingly, when assessing the levels of soluble collagen-I monomers present in the culture medium from control and VPSoe cells, VPSoe cells have lower levels of soluble collagen-I (Figure 3G). In addition, when VPS33b is knocked-down using siRNA, there is an elevation of soluble collagen-I secreted into the CM; siVPS33b on VPSoe cells also increased the levels of collagen-I in CM similar to the level seen in control cells (Supplementary Figure 3I). These findings strongly indicate that VPS33b is not involved in collagen-I secretion per se, but specifically

collagen-I fibre-assembly. The reduction of secreted soluble collagen-I in VPSoe cells suggests that in fibroblasts, VPS33b is directing collagen-I towards fibril assembly.

VPS33b containing vesicles carry collagen-I

To understand the mechanism of VPS33b-directed fibril-assembly, we utilised the split-GFP system [27,28], where the 214-residue N-terminal fragment (GFP1-10) was cloned onto VPS33b, and the 17-residue C-terminal peptide (GFP11) was cloned onto the proα1(I) chain of collagen-I (colI-GFP11, Figure 4A). Using this system, a GFP signal will only be present when VPS33b interacts with collagen-I. We, and others, have previously demonstrated that insertion of tags at the N-terminal of proα2(I) or proα1(I) chain does not interfere with collagen-I folding or secretion [29,30]. To determine which terminus of the VPS33b protein GFP1-10 should be added, we inserted BFP on either the N-terminal (VPSnBFP) and C-terminal (VPScBFP) ends of VPS33b and imaged the cells. In cells with VPSnBFP, the fluorescence signal is diffuse throughout the cell, and in most instances completely excluded from vesicular structures (Supplementary Figure 4A, left). In contrast, VPScBFP-expressing cells have punctate, vesicular-like blue fluorescence signals (Supplementary Figure 4A, right). Further, previous studies investigating VPS33b interactions have also tagged VPS33b at its C-terminal end [14]. Thus, we cloned GFP1-10 into the C-terminus of VPS33b (VPSbarrel). Notably, when VPScBFP was overexpressed in Dendra2-collagen expressing 3T3 cells [31], the number of Dendra2-positive fibrils synthesised by VPScBFP cells significantly increased, again verifying the effects of VPS33b overexpression in fibroblast collagen-I deposition (Supplementary Figure 4B). We noted that the average length of the fibril was not significantly different between control and VPScBFP fibroblasts, suggesting that VPS33b is important in initiating fibrillogenesis and not fibril elongation (Supplementary Figure 4C).

Fibroblasts stably expressing VPSbarrel and ColI-GFP11 were imaged to identify the location of the GFP fluorescence. The results showed puncta throughout the cytoplasm (Figure 4B). Intriguingly, GFP fluorescence was also observed at the cell periphery, sometimes aligned with fibrous elements (Figure 4B, zoom). This distribution was similar to the alignment of collagen fibrils seen in Dendra2-collagen expressing cells (Supplementary figure 4D, yellow arrows), suggesting that VPS33b delivers collagen-I to sites of fibrillogenesis. Immunofluorescence staining of endogenous VIPAS39 (a known VPS33b-interacting partner [14]) also revealed co-localisation of VIPAS39 with collagen-I in vesicular structures (Figure 4C); in particular, in some of the co-localised vesicles, the signal of VIPAS39 is strongest surrounding collagen-I (Figure 4C, zoom), suggesting that VIPAS39 is encasing collagen-I.

We then asked if VPS33b is responsible for the endocytosis of collagen-I. Incubation of cells expressing only the VPSBarrel with culture medium collected from cells expressing only ColI-GFP11 revealed that the GFP signal was detected within cells and mostly in vesicle-like structures. However, no GFP signal was detected along the periphery of the cells, presumably where endocytosis would take place (Figure 4D). In addition, flow cytometry analyses of Cy5-colI endocytosed by control, VPSko, and VPSoe fibroblasts showed that there is no consistent change in uptake by VPSko or VPSoe cells (Figure 4E). This was verified in Cy3-colI uptake analysis of cells over-expressing VPScBFP (Supplementary figure 4E). Taken together, these results suggest that VPS33b is involved in the *delivery* of collagen-I to the extracellular space, and not *endocytosis* per se. VPSko cells replated after Cy3- or Cy5-colI uptake have conspicuously fewer fibrils when compared to control. In contrast, VPSoe cells have shorter and more Cy5-colI fibrils, as well as Cy3-colI fibrils (Figure 4F, Supplementary Figure 4F), highlighting the role of VPS33b in recycling endocytosed collagen-I to fibril assembly sites.

Integrin-α11 mediates VPS33b fibrillogenesis

To help identify other molecules involved in collagen-I fibril formation, we turned to biotin cell surface labelling coupled with mass spectrometry protein identification (LC-MS/MS). Control, VPSko and VPSoe cells were cultured for 3 days prior to biotin-labelling of intact cells in culture, followed by cell lysis, streptavidin-pulldown of biotinylated proteins, and mass spectrometry analysis. We used a "shot-gun" approach to create an overview of protein profiles in control and VPSko and VPSoe cells and visualised the results in a semi-quantitative manner using spectrum counting. In total, 2666 proteins were identified. Comparison between total lysates and biotin-enriched samples demonstrated an enrichment of 742 proteins in the biotin-enriched samples (Supplementary table 1). Gene Ontology (GO) Functional Annotation analysis [32,33] identified the top 25 enriched terms (based on p-values) with the top 5 terms all associated with "extracellular" or "cell surface" (Figure 5A). We took this to indicate that the biotin-labelling procedure had successfully identified proteins at the cell-ECM interface.

We then interrogated the differences between VPSko and control cells. Conspicuously, collagen α1(I) and α1(V) chains were not detected at the surface of VPSko cells (Figure 5B). The absence of α1(V) and α2(V) chains (which constitute type V collagen) from the cell surface supports the long-standing view that collagen-V nucleates collagen-I containing fibrils. Gene ontology pointed to integral components of the plasma membrane, these included multiple integrins. Whilst many integrins were detected in all samples there was an absence of integrin-α1 chain and integrin-α11 chain in VPSko cultures. It is well established that integrins are cell-surface molecules that interact extensively with the ECM [34], with integrin-α11 (partnered with integrin-β1) being a major collagen receptor [35]. Interestingly, whilst the level of integrin-β1 chain detected was also reduced in VPSko cultures, it was not as drastic as the reduction observed for integrin-α11 chain. This is likely due to the promiscuous nature of integrin-β1 subunit, being able to partner with other α subunits for functions other than collagen-I interaction. The absence of integrin-α11 from VPSko cells suggested that VPS33b-mediated collagen fibrillogenesis is mediated through integrin-α11β1.

VPS33b was conspicuous by its absence from control cell samples (Figure 5B and Supplementary Figure 5A). We have previously struggled to detect VPS33b protein using mass spectrometry [13]; therefore, its absence could be due to low abundance. Noteworthy, we detected VPS33b using split-GFP approaches (Figure 4A and B). VPS33b was detected at the cell surface in VPSoe samples (which over-express VPS33b) along with PLOD3 (Supplementary figure 5A), which was previously identified to be delivered by VPS33b [17]. Using a complementary approach, we showed by western blot analysis of total cell lysate that integrin-α11 expression is significantly reduced in VPSko cells and is maintained, and possibly elevated, in VPSoe cells (Figure 5D and Supplementary Figure 5B). This correlation between VPS33b and integrin-α11 expression levels was confirmed at mRNA level (Figure 5E). These findings suggest that the over-abundance of collagen fibrils in VPSoe fibroblasts requires integrin-α11. To confirm this, we performed siRNA against Itga11 on control and VPSoe fibroblasts, and knock-down efficiency was confirmed with qPCR (Supplementary Figure 5C, D). siItga11 in both control and VPSoe cells reduced the level of collagen-I fibrils in culture after 3 days (Figure 5F), confirming that integrin-α11 is required for collagen-I fibrillogenesis, even in the presence of elevated levels of VPS33b. Interestingly, knocking-down integrin-α11 increases exogenous collagen-I uptake as demonstrated by flow cytometry (Supplementary Figure 5E), suggesting that integrin-α11, like VPS33b, is not involved in collagen-I endocytosis; instead, we propose that both VPS33b and integrin-α11 chain are involved in directing collagen-I monomers (endogenous or exogenous) to the formation of collagen-I fibrils.

Discussion

In this study we have identified a molecular mechanism for collagen fibril assembly at the plasma membrane. The major protagonists are collagen-I (the major component of the fibrils), VPS33b (an

endosomal tethering molecule), and integrin-α11 subunit (a collagen-binding transmembrane receptor when partnered with integrin-β1 subunit). VPS33b is under circadian clock regulation and interacts directly with collagen-I in a VIPAS-dependent endosomal compartment (shown schematically in Figure 6). The requirement of VPS33b for fibril assembly explains the previously-observed rhythmicity of collagen fibril formation by fibroblasts, *in vivo* and *in vitro*. A detail of the mechanism is that VPS33b and integrin-α11 subunit are essential for targeting collagen-I to sites of fibril assembly at the plasma membrane but are not needed for collagen uptake.

Whilst collagen fibrils have been located within fibripositors at the plasma membrane by electron microscopy, and cell culture studies have highlighted the importance of extrinsic mechanical forces (e.g. see [36-39]), cell-derived forces [40,41], combined mechanical anchoring and TGFβ1 cell activation [42], and fluid flow [43] in generating an aligned network of collagen fibrils, mechanistic insights into how cells assemble collagen fibrils at the plasma membrane were lacking. Throughout the current study, collagen fibrils and Cy3-colI labelled fibrils were only seen in close proximity to the plasma membrane; fibrils unattached to cells and at distances from cells were not observed. In cells over expressing VPS33b (e.g. see Figure 3E, 4F), in which large numbers of fibrils were generated, all the fibrils were associated with the plasma membrane. Also, in cells in which levels of integrin-α11 subunit had been reduced, the fewer fibrils generated were associated with the plasma membrane (Figure 5F). The results demonstrate that cells exert control over collagen fibril assembly by anchoring one end of the fibril to the plasma membrane, and uses VPS33b to direct collagen-I to fibrogenic sites at the plasma membrane involving integrin-α11 subunit. The critical importance of VPS33b in the fibril assembly process was demonstrated in knockdown and knockout experiments in which its absence led to soluble collagen-I being secreted without new fibril formation.

Previous research on endocytosis of collagen-I in fibroblasts has focussed on degradation or signalling as being the endpoint (e.g., [44-48]). However, our results show that collagen-I endocytosis can also contribute towards fibril formation (Figures 1, 2; Supplementary figure 1). This is highlighted when endocytosis is inhibited and fibroblasts can no longer efficiently assemble collagen-I fibrils (Figure 2C). The decision to flip the endocytosed collagen from degradation to recycling may depend on cell type and on the environment in which the cell finds itself. In complex environments such the site of wound healing, for example, both degradation (of denatured collagen molecules) and recycling (of structurally sound collagen molecules to generate new fibrils) could be beneficial. Nevertheless, we suggest that fibroblasts can either assemble fibrils by a canonical 'inside-out' route using collagen that has been synthesised in the ER and trafficked to the plasma membrane via the Golgi apparatus, or, by an 'outside-in-out' route involving the endocytic pathway.

These results highlight decision-making processes in the endosomal pathway, where endocytosed collagen-I can be switched between degradation to fibril assembly and involves VPS33b and integrin-α11 subunit. We have previously reported that collagen homeostasis is circadian clock controlled. Here, we confirmed that fibroblasts produce collagen-I fibrils in a rhythmic manner *in vitro* (Supplementary Figure 2B, Figure 3F) and went on to show that endocytosis of exogenous collagen-I also fluctuates with time (Figure 2E). Collagen can spontaneously form fibrils in the absence of cells *in vitro*; however, the concentration of collagen must exceed 0.4 μg/mL, which is the critical concentration of fibril formation at 37 °C [23]. Here, we showed that fluorescently-tagged collagen-I can spontaneously assemble into fibril-like structures at concentrations greater than 0.4 μg/mL but the aggregates formed at lower concentrations are short. In contrast, when cells are present, fluorescently-tagged collagen-I assembles into fibrils even at concentrations where spontaneous aggregation does not occur (Figure 1C, D). Further, overlaying the endocytosis profile with fibril numbers profile indicates

a peak of endocytosis prior to a spike in fibril numbers (Supplementary figure 2B); thus, we propose that endocytosis concentrates the collagen-I to facilitate fibrillogenesis.

Our results showed a direct correlation between VPS33b levels and collagen-I fibrils (Figure 3) and that VPS33b delivers collagen-I directly to cell surface fibrillogenic sites (Figure 4). Importantly, secretion of soluble collagen-I and assembly of collagen-I into fibrils are regulated differently; it is possible for cells to secrete soluble collagen without assembling fibrils. Thus, the abundance of collagen-I secretion into the media is not correlated with the level of VPS33b or the number of fibrils. Instead, VPS33b is responsible for directing collagen-I (either endogenous or captured) to fibre assembly sites. The rhythmicity of VPS33b expression in normal fibroblasts determines the rhythmicity of collagen-I fibres, as highlighted by the loss of fibril rhythmicity in VPSoe fibroblast cultures. Conversely, VPSko fibroblasts lack the capacity to recycle labelled collagen-I to assemble fibres, despite still being able to endocytose collagen-I. In turn, VPS33b requires the presence of the collagen-I binding integrin-$\alpha 11\beta 1$ to produce a fibrous collagen-I matrix. Thus, the distinction between secretion of soluble collagen and fibril assembly is important in studies of disease, in which simple measurement of collagen expression or secretion does not equate to fibrogenesis. This distinction between collagen secretion and assembly was also suggested in a recent study on *Pten*-knockout mammary fibroblasts, where SPARC affects collagen fibrillogenesis and not secretion, acting through fibronectin [49]. Of note, whilst SPARC and fibronectin were detected in our previously-reported time-series mass spectrometry analyses (in the SLDOC soluble fraction and high-salt insoluble fractions respectively), they were not circadian clock rhythmic [13].

Finally, whilst previous research has demonstrated that collagen-I can be secreted in a matter of minutes [20], other studies have demonstrated a relatively slow emergence of collagen-I fibres over days [31]. This difference may be due in part to the requirement to concentrate the collagen in the endocytic pathway to a level that supports fibril formation, as discussed above. In addition, nucleation of a fibril is expected to involve collagen-V, a minor fibril-forming collagen that is necessary for the appearance of fibrils containing collagen-I *in vivo* [50]. Another long-standing view is that fibronectin may tether collagen to a fibronectin-binding integrin and thereby function as a proteolytically cleavable anchor (see ref [51] and reviewed by [52]). Whilst this study did not focus on the role of fibronectin, biotin-surface labelling mass spectrometry results indicate that the levels of the major fibronectin-binding integrins (integrin-$\alpha 5\beta 1$ and $\alpha V\beta 3$) were not altered between control, VPSko, and VPSoe fibroblasts (Supplementary table 2), suggesting that the mechanism by which VPS33b modulates collagen fibrillogenesis does not act directly via fibronectin. Interestingly, it was previously demonstrated that in fibronectin knock-out liver cells, exogenous collagen-V could be added to initiate collagen-I fibrillogenesis [53]. Further, whilst collagen $\alpha 1$(V) could only be detected in surface biotin-labelled control and not VPSko or VPSoe cells, collagen $\alpha 2$(V) was only detected in VPSoe cells (Figure 5B). Of note, we have previously shown that collagen $\alpha 2$(V) protein was rhythmic and in phase with collagen $\alpha 1$(I) and collagen $\alpha 2$(I). Whether collagen-V co-traffics with collagen-I in VPS33b vesicles to fibrillogenic sites at the cell periphery, or collagen-V is directed to the nucleation site by another mechanism, is an important question to address in future studies.

Materials and Methods

Cell culture

Unless otherwise stated, all cell culture reagents were obtained from Gibco, and all cells were maintained at 37°C, 5% CO_2 in a humidified incubator. Immortalised mouse tail tendon fibroblasts (iTTF [13]), and NIH3T3 cells with Dendra2-tagged collagen-I expression (Dendra2-3T3 [31]) were cultured

at in DMEM/F12 with sodium bicarbonate and L-glutamine (supplemented with 10% fetal calf serum (FCS), 200 μM L-ascorbate-2-phosphate (Sigma), and 10,000 U/mL penicillin/streptomycin), and DMEM with sodium bicarbonate and L-glutamine (supplemented with 10% new born calf serum, 200 μM L-ascorbate-2-phosphate, and 10,000 U/mL penicillin/streptomycin) media respectively. HEK293T cells were cultured in DMEM with sodium bicarbonate and L-glutamine, supplemented with 10% FCS. Prior to imaging, media was changed to FluoroBrite media with the appropriate supplements.

CRISPR-Cas9-Mediated Knockout

iTTFs were treated with CRISPR-Cas9 to delete *VPS33b* gene as previously described [13]. Gene knockout was confirmed by western blotting and qPCR.

Transfection and stable infection of over-expression vectors in cells

Three different vectors were used to stably over-express VPS33b protein in iTTF and 3T3 cells – untagged VPS33b overexpression (with red fluorescent protein expression as selection), N-terminus BFP-tagged VPS33b overexpression, and C-terminus BFP-tagged VPS33b overexpression. All vectors were cloned onto a pLV vector backbone using Gibson Assembly® (NEB). For split-GFP experiments, vectors expressing GFP11-tagged collagen-I and GFP1-10-tagged VPS33b were ordered from VectorBuilder. Lentiviral particles were generated In HEK293T cells, and cells were infected in the presence of 8 μg/mL polybrene (Millipore). Cells were then sorted using Flow Cytometry to isolate RFP-positive or BFP-positive cells. Alternatively, cells were treated with puromycin (Sigma) or G418 (Sigma) depending on selection marker on the vectors.

Fluorescence labelling of collagen-I

Cy3 or Cy5 NHS-ester dyes (Sigma) were used to fluorescently label rat tail collagen-I (Corning), using a previously described method [22]. Briefly, 3 mg/mL collagen-I gels were made, incubated with 50mM borate buffer (pH 9) for 15 min, followed with incubation with either Cy3-ester or Cy5-ester (Sigma) dissolved in borate buffer in dark overnight at 4°C, gently rocking. Dyes were then aspirated and 50 mM Tris (pH 7.5) were added to quench the dye reaction, and incubated in the dark rocking for 10 min. Gels were washed with PBS (with calcium and magnesium) 6x, incubating for at least 30 min each wash. The gels were then resolubilized using 500 mM acetic acid, and dialyzed in 20 mM acetic acid.

RNA isolation and Quantitative Real-Time PCR

RNA was isolated using TRIzol Reagent (Thermo Fisher Scientific) following manufacturer's protocol, and concentration was measured using a NanoDrop OneC (Thermo Fisher Scientific). Complementary DNA was synthesized from 1 μg RNA using TaqMan™ Reverse Transcription kit (Applied Biosystems) according to manufacturer's instructions.

SensiFAST SYBR kit reagents were used in qPCR reactions. Primer sequences used were as followed:

Col1a1 AGAGCATGACCGATGGAT and AGGCCTCGGTGGACATTA

Itga11 AGATGTCGCAGACTGGCTTT and CCCTAGGTATGCTGCATGGT,

Rplp0 ACTGGTCTAGGACCCGAGAAG and CTCCCACCTTGTCTCCAGTC

Gapdh CAGCCTCGTCCCGTAGACAA and CAATCTCCACTTTGCCACTGC

Vps33b GCATTCACAGACACGGCTAAG and ACACCACCAAGATGAGGCG

Protein extraction and Western blotting

For lysate experiments, proteins were extracted using urea buffer (8M urea, 50mM Tris-HCl pH7.5, supplemented with protease inhibitors and 0.1% β-mercaptoethanol). For conditioned media (CM) media, cells were plated out at 200,000 cells per 6-well plate, and left for 48-72 hrs before 250 μl was

sampled. Samples were mixed with 4xSDS loading buffer with 0.1% β-mercaptoethanol and boiled at 95°C for 5 minutes. The proteins were separated on either NuPAGE Novex 10% polyacrylamide Bis–Tris gels with 1XNuPAGE MOPS SDS buffer or 6% Tris-glycine gels with 1XTris-glycine running buffer (all Thermo Fisher Scientific), and transferred onto polyvinylidene difluoride (PVDF) membranes (GE Healthcare). The membranes were blocked in 5% skimmed milk powder in PBS containing 0.01% Tween 20. Antibodies were diluted in 2.5% skimmed milk powder in PBS containing 0.01% Tween 20. The primary antibodies used were: rabbit polyclonal antibody (pAb) to collagen-I (1:1,000; Gentaur), mouse mAb to vinculin (1:1000; Millipore), rabbit pAb to integrin-α11 (1:1000; from Donald Gulberg) and mouse mAb to VPS33B (1:500; Proteintech). Horseradish-peroxidase-conjugated antibodies and Pierce ECL western blotting substrate (both from Thermo Fisher Scientific) were used and reactivity was detected on GelDoc imager (Biorad). Alternatively, Licor rabbit-anti-mouse 680, mouse-anti-rabbit 800 were used and reactivity detected on an Odyssey Clx imager.

Flow cytometry and imaging

Cy3- or Cy5-tagged collagen was added to cells and incubated at 37°C, 5% CO_2 in a humidified incubator for predetermined lengths of times before washing in PBS, trypsinised, spun down at 2500 rpm for 3 min at 4 °C, and resuspended in PBS on ice. Cells were analysed for Cy3- or Cy5-collagen uptake using LSRFortessa (BD Biosciences). For imaging, cells were prepared as described, and analysed on Amnis® ImageStream®^{X}Mk II (Luminex).

Imaging and immunofluorescence

For fixed immunofluorescence imaging, cells plated on coverslips were fixed with 100% methanol at -20°C and then permeabilized with 0.5% Triton-X in PBS. Primary antibodies used were as follows: rabbit pAb collagen-I (1:400, Gentaur OARA02579), rabbit pAb VIPAS (1:50, Proteintech 20771-1-AP), mouse mAb FN1 (1:400, Sigma F6140 or Abcam ab6328). Secondary antibodies conjugated to Alexa-488, Cy3, and Cy5 were used (ThermoScientific), and nucleus were counterstained with DAPI (Sigma). Coverslips were mounted using Fluoromount G (Southern Biotech). Images were collected using a Leica SP8 inverted confocal microscope (Leica) using an x63/0.50 Plan Fluotar objective. The confocal settings were as follows: pinhole, 1 Airy unit; scan speed, 400 Hz bidirectional; format 1024 x 1024 or 512 x 512. Images were collected using photomultiplier tube detectors with the following detection mirror settings: DAPI, 410-483; Alexa-488, 498-545 nm; Cy3, 565-623 nm; Cy5, 638-750 nm using the 405 nm, 488 nm, 540 nm, 640 nm laser lines. Images were collected in a sequential manner to minimize bleed-through between channels. When acquiring three-dimensional optical stacks, the confocal software was used to determine the optimal number of Z sections.

For fluorescence live-imaging, cells were plated onto Ibidi μ-plates and imaged using Zeiss LSM880 NLO (Zeiss). For split-GFP experiment, cells were seeded for 24h onto Ibidi μ-plates before imaging with an Olympus IXplore SpinSR (Olympus) with 100x oil magnification.

Decellularisation of cells to obtain extracellular matrix

Cells were seeded out at 50,000 in a 6-well plate and cultured for 7 days before decellularization. Extraction buffer (20mM NH_4OH, 0.5% Triton X-100 in PBS) was gently added to cells and incubated for 2 minutes. Lysates were aspirated and the matrix remaining in the dish were washed gently twice with PBS, before being scrapped off into ddH_2O for further processing.

Hydroxyproline Assay

Samples were incubated overnight in 6 M HCl (diluted in ddH_2O (Fluka); approximately 1 mL per 20 mg of sample) in screw-top tubes (StarLab) in a sand-filled heating block at 100 °C covered with aluminium foil. The tubes were then allowed to cool down and centrifuged at 12,000 x*g* for 3 min.

Hydroxyproline standards were prepared (starting at 0.25 mg/mL; diluted in ddH2O) and serially diluted with 6 M HCl. Each sample and standard (50 µL) were transferred into fresh Eppendorf tubes, and 450 µL chloramine T reagent (0.127 g chloramine T in 50% N-propanol diluted with ddH2O; brought up to 10 mL with acetate citrate buffer (120 g sodium acetate trihydrate, 46 g citric acid, 12 mL glacial acetic acid, 34 g sodium hydroxide) adjusted to pH 6.5 and then made to 1 litre with dH_2O; all reagents from Sigma) was added to each tube and incubated at room temperature for 25 min. Ehrlich's reagent (500 µL; 1.5 g 4-dimethylaminobenzaldehyde diluted in 10 mL N-propanol:perchloric acid (2:1)) was added to each reaction tube and incubated at 65 °C for 10 min and then the absorbance at 558 nm was measured for 100 µL of each sample in a 96-well plate format.

Electron Microscopy

Unless otherwise stated, incubation and washes were done at room temperature. Cells were plated on top of ACLAR films and allows to deposit matrix for 7 days. The ACLAR was then fixed in 2% glutaraldehyde/100mM phosphate buffer (pH 7.2) for at least 2 hrs and washed in ddH_2O 3 x 5 min. The samples were then transferred to 2% osmium (v/v)/1.5% potassium ferrocyanide (w/v) in cacodylate buffer (100 mM, pH 7.2) and further fixed for 1 hr, followed by extensive washing in ddH_2O. This was followed by 40 minutes of incubation in 1% tannic acid (w/v) in 100 mM cacodylate buffer, and then extensive washes in ddH_2O. and placed in 2% osmium tetroxide for 40 min. This was followed by extensive washes in ddH_2O. Samples were incubated with 1% uranyl acetate (aqueous) at 4 °C for at least 16 hrs, and then washed again in ddH_2O. Samples were then dehydrated in graded ethanol in the following regime: 30%, 50%, 70%, 90% (all v/v in ddH_2O) for 8 min at each step. Samples were then washed 4 x 8 min each in 100% ethanol, and transferred to pure acetone for 10 min. The samples were the infiltrated in graded series of Agar100Hard in acetone (all v/v) in the following regime: 30% for 1 hr, 50% for 1 hr, 75% for overnight (16 hrs), 100% for 5 hrs. Samples were then transferred to fresh 100% Agar100Hard in labelled moulds and allowed to cure at 60 °C for 72 hrs. Sections (80 nm) were cut and examined using a Tecnai 12 BioTwin electron microscope.

Surface biotinylation-pulldown Mass Spectrometry

Cells were grown in 6 well plates for 72 hrs prior to biotinylation protocol. Briefly, cells around 90% confluence were kept on ice and washed in ice-cold PBS, following with incubation with ice-cold biotinylation reagent (prepared fresh, 200 µg/mL in PBS, pH 7.8) for 30min at 4°C gently shaking. Cells were then washed twice in ice-cold TBS (50 mM Tris, 100 mM NaCl, pH 7.5), and incubated in TBS for 10 min at 4 °C. Cells were then lysed in ice-cold 1% TritonX (in PBS, with protease inhibitors) and lysates cleared by centrifugation at 13,000 x*g* for 10 min at 4 °C. Supernatant was then transferred to a fresh tube and 1/5 of the lysates were kept as a reference sample. Streptavidin-sepharose beads are then aliquoted into each sample and incubated for 30min at 4°C rotating. Beads were then washed 3x in ice cold PBS supplemented with 1% TritonX, followed by one final wash in ice cold PBS and boiled at 95°C for 10min in 2x sample loading buffer, followed by centrifugation at top speed for 5min follow by sample preparation for Mass Spectrometry analysis. The protocol used for sample preparation was as described previously [54]. All MS/MS samples were analyzed using Mascot (Matrix Science, London, UK; version 2.5.1). Mascot was set up to search the SwissProt_2018_01.fasta; Trembl_2018_01 database (selected for Mus musculus, 84416 entries) assuming the digestion enzyme to be non-specific. Mascot was searched with a fragment ion mass tolerance of 0.020 Da and a parent ion tolerance of 10.0 PPM. Carbamidomethyl of cysteine was specified in Mascot as a fixed modification. Oxidation of methionine was specified in Mascot as a variable modification. Scaffold (version Scaffold_4.10.0, Proteome Software Inc., Portland, OR) was used to validate MS/MS based peptide and protein identifications. Peptide identifications were accepted if they could be established at

greater than 50.0% probability by the Peptide Prophet algorithm [55] with Scaffold delta-mass correction. Protein identifications were accepted if they could be established at greater than 95.0% probability and contained at least 2 identified peptides. Protein probabilities were assigned by the Protein Prophet algorithm [56]. Proteins that contained similar peptides and could not be differentiated based on MS/MS analysis alone were grouped to satisfy the principles of parsimony.

Statistics and reproducibility

Data are presented as the mean ± s.e.m. unless otherwise indicated in the figure legends. The sample number (N) indicates the number of independent biological samples in each experiment, and are indicated in the figure legends. Data were analyzed as described in the legends. The data analysis was not blinded, and differences were considered statistically significant at $P<0.05$, using Student's t-test or One-way Anova, unless otherwise stated. Analyses were performed using Graphpad Prism 8 software. Significance levels are: * $P<0.05$; ** $P<0.01$; *** $P<0.005$; ****$P<0.0001$. For periodicity, analysis was performed using the MetaCycle package[57] in the R computing environment [58] with the default parameters.

Acknowledgements

The research was generously funded by Wellcome in the form of a Senior Investigator Award (110126/Z/15/Z) and Centre Award (203128/Z/16/Z) to KEK, and a Norwegian Centre of Excellence grant (grants 2233250) and a grant from Nasjonalföreningen for folkhelsen (Project 16216) to DG. The proteomics was performed at the Biological Mass Spectrometry Facility in the Faculty of Biology, Medicine and Health (University of Manchester) with the assistance of Stacey Warwood and Ronan O'Cualain. Imaging was performed at the Bioimaging Facility in the Faculty of Biology, Medicine and Health (University of Manchester). Some of the illustrations were created with Biorender.com.

Author contributions

JC and KEK conceived the project. JC performed experiments and interpreted data. AP and RG performed experiments, and YL performed electron microscopy analyses. DG provided reagents and data interpretation. All authors co-wrote the manuscript.

Competing interests

The authors declare no competing interests.

Figure legends

Figure 1

A. Fluorescent images of tail tendon incubated with Cy3-colI for 5 days, showing presence of collagen-I within the cells, and fibril-like fluorescence signals outside of cells. Hoescht stain was used to locate cells within the tendon. Area surrounded by yellow box expanded on the right, and cells with Cy3-colI present intracellularly pointed out by yellow triangles. Area surrounded by grey box expanded on the right, and fibril-like fluorescence signals indicated with white arrows. Scale bar = 50 μm. Representative of N=3.

B. Fluorescent image series of fibroblasts incubated with 5 µg/mL Cy3-colI for 1 hr, trypsinised and replated in fresh media, and incubated for 72 hrs. Labels on top denotes the fluorescence channel corresponding to proteins detected. Representative of N>3. Scale bar = 20 μm.

C. Fluorescent image series of Cy3-colI incubated at different concentrations for 72 hrs, either cell-free (left panel), or with fibroblasts (right panel).

D. Zoom-in (red box in Figure 1C) of Cy3-positive fibrils assembled by fibroblasts when incubated with 0.1 µg/mL Cy3-colI.

E. Flow cytometry imaging of fibroblasts incubated with 5 µg/mL Cy3-labelled (left) or Cy5-labelled (right) collagen-I for 1 hr, showing that collagen-I is taken up by cells and held in vesicular structures. Images acquired using ImageStream at 40x magnification. Scale bar = 10 μm BF – brightfield channel, Cy3 – Cy3 channel, Cy5 – Cy5 channel, BF/Cy3 or BF/Cy5 – merged image of BF and Cy3 or BF and Cy5 respectively. Representative of >500 cells images collected per condition.

F. Representative dot plots from flow cytometry analysis representing Cy3 gates used in control and fibroblasts incubated with 1 µg/mL Cy3-labelled collagen (Cy3-colI) for 18 hrs. Representative of N>3.

G. Bar chart showing a progressive increase of percentage of fluorescent cells incubated with 1.5 µg/mL Cy3-colI over time (left), and an increase of percentage fluorescent cells incubated with increasing concentration of Cy3-colIfor 1 hr (right), suggesting a non-linear time-dependent and dose-dependent uptake pattern. N=3.

Figure 2

A. Scatter plot showing Dyngo4a (Dyng), an endocytosis inhibitor, treatment for 1 hr inhibits over 50% of Cy3-colI uptake in fibroblasts. Bars show mean ± s.e.m of N=6. ****p<0.0001.

B. Western blot analysis of conditioned media taken from fibroblasts treated with DMSO (ctrl) or Dyng (Dyng) for 72 h, showing a decrease in collagen-I secretion. Top: probed with collagen-I antibody (Col-I), bottom: counterstained with Ponceau (Pon) as control. Representative of N=3.

C. Fluorescent images of collagen-I (red) counterstained with DAPI (blue) in fibroblasts treated with DMSO (top) or Dyng (bottom) for 72 hrs. Scale bar = 20 μm.

D. qPCR analysis comparing col1a1 mRNA levels in control fibroblasts (DMSO) and Dyng-treated fibroblasts (Dyng), showing a decrease in collagen-I transcripts. Bars showing mean± s.e.m of N=4. ***p=0.003.

E. Percentage Cy3-colI taken up by synchronised fibroblasts over 48 hrs. Left: raw values of % Cy3-positive over time. Meta2d analysis indicates a circadian rhythm of periodicity of 23.8 hrs. Right: fluctuation of Cy3-positive cells corrected to running average (average of 12 hrs). Meta2d analysis indicates a circadian rhythm of periodicity of 23.8 hrs. Bars show mean ± s.e.m of N=3 per time point.

Figure 3

A. Electron microcopy images of fibroblasts plated on Aclar and grown for a week before fixation and imaging. Ctrl culture has numerous collagen-I fibrils, as pointed out by arrows. Yellow arrow points to a fibripositor, and green box is expanded to the left bottom corner, showing the distinct D-banding pattern of collagen-I fibril when observed with electron microscopy. VPSko clones all have fewer and thinner fibrils present in the culture (pointed out by red arrows). Representative of N=3. Scale bar = 0.5 μm.

B. Fluorescence images of collagen-I (red) and DAPI counterstain in ctrl and VPSko fibroblasts. Yellow arrows indicating collagen fibres, and white arrows pointing to collagen-I presence in intracellular vesicles. Representative of N>6. Scale bar = 25 μm.

C. Matrix deposition by ctrl or VPSko cells, after one week of culture. Left: decellularized matrix mass. N>5, * p=0.03. Right: hydroxyproline content presented as a ratio between ctrl and VPSko cells. N=5, ***p=0.0004.

D. Matrix deposition by ctrl or VPSoe cells, after one week of culture. Left: decellularized matrix mass. N=5. Right: hydroxyproline content presented as a ratio between ctrl and VPSoe cells. N=4.

E. Fluorescence images of collagen-I (red) and DAPI counterstain in ctrl and VPSoe fibroblasts. Representative of N>6. Scale bar = 20 μm.

F. Relative collagen fibre count in synchronised ctrl (black) and VPSoe (pink) fibroblasts, corrected to the number of fibres in ctrl cultures at start of time course. Fibres scored by two independent investigators. Bars show mean± s.e.m. of N=2 with 6 technical repeats at each time point.

G. Western blot analysis of conditioned media taken from ctrl and VPSoe after 72 hrs in culture. Top: probed with collage-I antibody, bottom: counterstained with Ponceau as control. Representative of N=3.

Figure 4

A. Schematic of the split-GFP detection system. GFP1-10 barrel is introduced into VPS33b (VPS-barrel), and GFP11 to Col1a1 (Col1a1-GFP11). If the two tagged proteins co-localize (e.g. in a vesicle), a GFP signal will be emitted.

B. Brightfield (top) and fluorescence (middle) images of fibroblasts expressing both VPS-barrel and Col1a1-GFP11 constructs. Green box is expanded to the bottom, to highlight the punctate fluorescence signals indicating co-localization within intracellular vesicles, as well as fibril-like structures suggestive of fibril assembly sites. Scale bar = 20 μm

C. Fluorescence images of VIPAS (green), collagen-I (red) and DAPI counterstain in fibroblasts. Representative of N=3. Green box is expanded to the right (flipped 90°) to show VIPAS co-localization with collagen-I. Scale bar = 25 μm

D. Fluorescence (left) and merged (right) images of fibroblasts expressing VPS-barrel incubated with conditioned media containing Col1a1-GFP11 for 24hr. Scale bar = 25 μm.

E. Bar chart comparing the percentage of cells that have taken up 5 µg/mL Cy5-colI after 1 hr incubation between control (ctrl), VPS33b-knockout (VPSko) and VPS33b-overexpressing (VPSoe) cells, corrected to control. N>10.

F. Fluorescence images of cells of different levels of VPS33b expression, fed with Cy5-colI and cultured for 72 hrs. Cultures were counterstained with DAPI. Bottom panel are zoomed-in images of the fibrils produced by the fibroblasts. Representative of N=2.

Figure 5

A. Top 25 Functional Annotation of proteins detected in biotin-enriched samples when compared to non-enriched samples based on p-values. Y-axis denotes the GO term, X-axis denotes –log (P value).

B. Heatmap representation of spectral counting of collagens detected in biotin-enriched surface proteins from control (ctrl), VPS33b-knockout (VPSko), and VPS33b-overexpressing (VPSoe) fibroblasts. Scale denotes quantitative value as normalized to total spectra, as determined by Scaffold analyses.

C. Heatmap representation of spectral counting of integrins detected in biotin-enriched surface proteins from control (ctrl), VPS33b-knockout (VPSko), and VPS33b-overexpressing (VPSoe) fibroblasts. Scale denotes quantitative value as normalized to total spectra, as determined by Scaffold analyses.

D. Western blot anlaysis of integrin-α11 levels in control (ctrl), VPS33b-overexpressing (VPSoe), VPS33b-knockout (VPSko) cells. Top: probed with integrin-α11 antibody, bottom: reprobed with GAPDH antibody. Representative of N=3.

E. qPCR analysis of *Itga11* transcript levels in ctrl compared to VPSko fibroblasts (left), and ctrl compared to VPSoe fibroblasts (right). N>3, ****p<0.0001, *p= 0.0226

F. Immunofluorescence images of ctrl and VPSoe fibroblasts treated either with control siRNA (scr) or siRNA again Itga11 (siItga11), after 72 hrs incubation; collagen-I (red) and DAPI (blue) counterstained. Representative of N=3. Scale bar = 25 μm.

Figure 6

Schematic showing how the endosomal system might direct collagen from different sources (endogenous and exogenous) to a site on the plasma membrane for fibril assembly. Grey, de novo synthesised collagen. Red, collagen that has been captured at the plasma membrane. Procollagen is shown with N- and C-propeptides (circle and hexagon, respectively).

Supplementary Figure 1

A. Fluorescent images of tail tendon incubated with fluorescently-tagged collagen-I for 5 days – Cy3-colI was added for the first 3 days, with 5FAM-labelled collange-I (FAM-colI) added in the last two days. Images show presence of collagen-I within the cells, and fibril-like fluorescence signals outside of cells. Hoescht stain was used to locate cells within the tendon. Area surrounded by yellow box expanded on the right highlighting a cell with only Cy3-colI present intracellularly. Area surrounded by grey boxes expanded on the right, highlighting fibril-like fluorescence signals that are either FAM-colI positive only, or have co-localization of both Cy3-colI and FAM-colI. Representative of N=2.

B. Representative dot plots from flow cytometry analysis representing Cy5 gates used in control and fibroblasts incubated with 1 µg/mL Cy5-labelled collagen (Cy5-colI) for 18 hrs. Representative of N>3.

C. Bar chart showing a progressive increase of % of fluorescent cells incubated with 1.5 µg/mL Cy5-colI over time (left), and an increase of % fluorescent cells incubated with increasing concentration of Cy5-colI for 1 hr (right), suggesting a non-linear time-dependent and dose-dependent uptake pattern. N=3.

Supplementary Figure 2

A. Alamar Blue assay showing that prolonged treatment of 20 μM Dyngo4a (Dyng) does not inhibit fibroblast proliferation.

B. Percentage of Cy3-coII taken up by synchronised cells, corrected to the maximum percentage uptake of the time course (pink, bars show mean ± s.e.m of N=3 per time point), compared to the percentage collagen fibre count over time, corrected to the maximum percentage fibril count of the time course (black, fibres scored by two independent investigators. Bars show mean± s.e.m. of N=2 with 6 technical repeats at each time point). Data presented here in maximum percentage fibril count over time (black) are taken from the control as in Figure 5F, presented in a different way.

Supplementary Figure 3

A. Western blot analysis of VPS33b knock-out (VPSko) clones compared to control (ctrl) fibroblasts. Top: probed with VPS33b antibody, bottom: probed with GAPDH antibody. Representative of N=3.

B. qPCR analysis of VPS33b expression in the 3 selected clones. *** p=0.0002, ** p=0.0039, * p=0.0163

C. Alamar blue analysis of proliferation rates of ctrl fibroblasts and VPSko fibroblasts. Representative of N=3.

D. Western blot analysis of VPS33b protein levels in control (ctrl) and VPS33b over-expressing (VPSoe) cells. Top panel probed with VPS33b antibody, bottom panel re-probed with vinculin antibody. Representative of N=4.

E. qPCR analysis of VPS33b expression in ctrl and VPSoe cells. N=4, **** p<0.0001.

F. Single parameter histograms of Flow cytometry analysis on ctrl (left) and VPSoe (right) fibroblasts, showing a shift in increase of Cy3 fluorescence and thus expression of VPSoe vector. Representative of N>4.

G. Alamar blue analysis of proliferation rates of ctrl fibroblasts and VPSoe fibroblasts. Representative of N=3.

H. MetaCycle analyses of the fibril counts showed a rhythmicity of circa 23 h in ctrl fibroblasts compared with circa 28 hrs in VPSoe fibroblasts.

I. Western blot analysis of conditioned media taken from ctrl and VPSoe treated either with siRNA scrambled control (scr) or siRNA against *Vps33b* (siVPS), and cultured for 72 hrs. Top: probed with collage-I antibody, bottom: counterstained with Ponceau as control. Representative of N=2.

Supplementary Figure 4

A. Fibroblasts expressing BFP-tagged VPS33b. Left: BFP tagged on the N-terminal end of VPS33b (VPSnBFP), Right: BFP tagged on the C-terminal end (VPScBFP). Images taken in Airy mode. Representative of N>4. Scale bar = 10 μm.

B. Quantification of average number of fibrils per cell in control Dendra-coII expressing 3T3 cells (ctrl) and Dendra-coII expressing 3T3 overexpressing VPScBFP (VPScBFP). >500 cells quantified per condition. N=12. *p =0.048.

C. Measurement of average fibril length in arbitrary units (A.U.) in control Dendra-coII expressing 3T3 cells (ctrl) and Dendra-coII expressing 3T3 overexpressing VPScBFP (VPScBFP). >500 cells quantified per condition. N=12.

D. Image of Dendra-colI in 3T3 fibroblasts. Image taken in Airy mode. Yellow arrows highlighting fibril structures at cell periphery. Representative of N>5. Scale bar = 10 μm.

E. Bar chart comparing the percentage of cells that have taken up 5 µg/mL Cy3-colI after 1 hr incubation between control (ctrl), VPS33b-knockout (VPSko) and VPScBFP overexpressing (VPSoe) cells, corrected to control. N>10

F. Cy3-fed ctrl or VPSoe fibroblasts after 72 hrs incubation. Scale bar = 20 μm.

Supplementary Figure 5

A. Spectral counts of Plod3 and VPS33b as detected by Mass Spectrometry, scale bar represents quantitative value as normalized to total spectra. Gene names of proteins detected shown here.

B. Western blot analysis of total lysates taking from control (ctrl), VPS33b-overexpressing (VPSoe), VPScBFP-overexpressing (VPScBFP), VPS33b-knockout (VPSko), probed with ITGA11 and reprobed with β-tubulin or vinculin as a loading control.

C. qPCR analysis of *Itga11* mRNA expression in ctrl fibroblasts treated either with scrambled control (scr) or siRNA against ITGA11 (siITGa11), collected after 96 hrs. N=3, $^{**}P$=0.0091.

D. qPCR analysis of *Itga11* mRNA expression in VPSoe fibroblasts treated either with scrambled control (scr) or siRNA against ITGA11 (siITGa11), collected after 96 hrs. N=3, $^{****}P$<0.0001.

E. Bar chart comparing the percentage of cells that have taken up 5 µg/mL Cy5-colI after 1 hr incubation between fibroblasts treated with scrambled control (ctrl) or siRNA against ITGA11 (siITGa11), corrected to scr. N=3. $^{**}p$=0.0062.

Supplementary Table 1

Report from Scaffold Viewer on the Quantitative Value (Normalized Total Spectra) detected of each protein in each sample.

Supplementary Table 2

Specific spectral counts of various proteins as detected by Mass Spectrometry, presented in quantitative value as normalized to total spectra. Gene names of proteins detected shown here.

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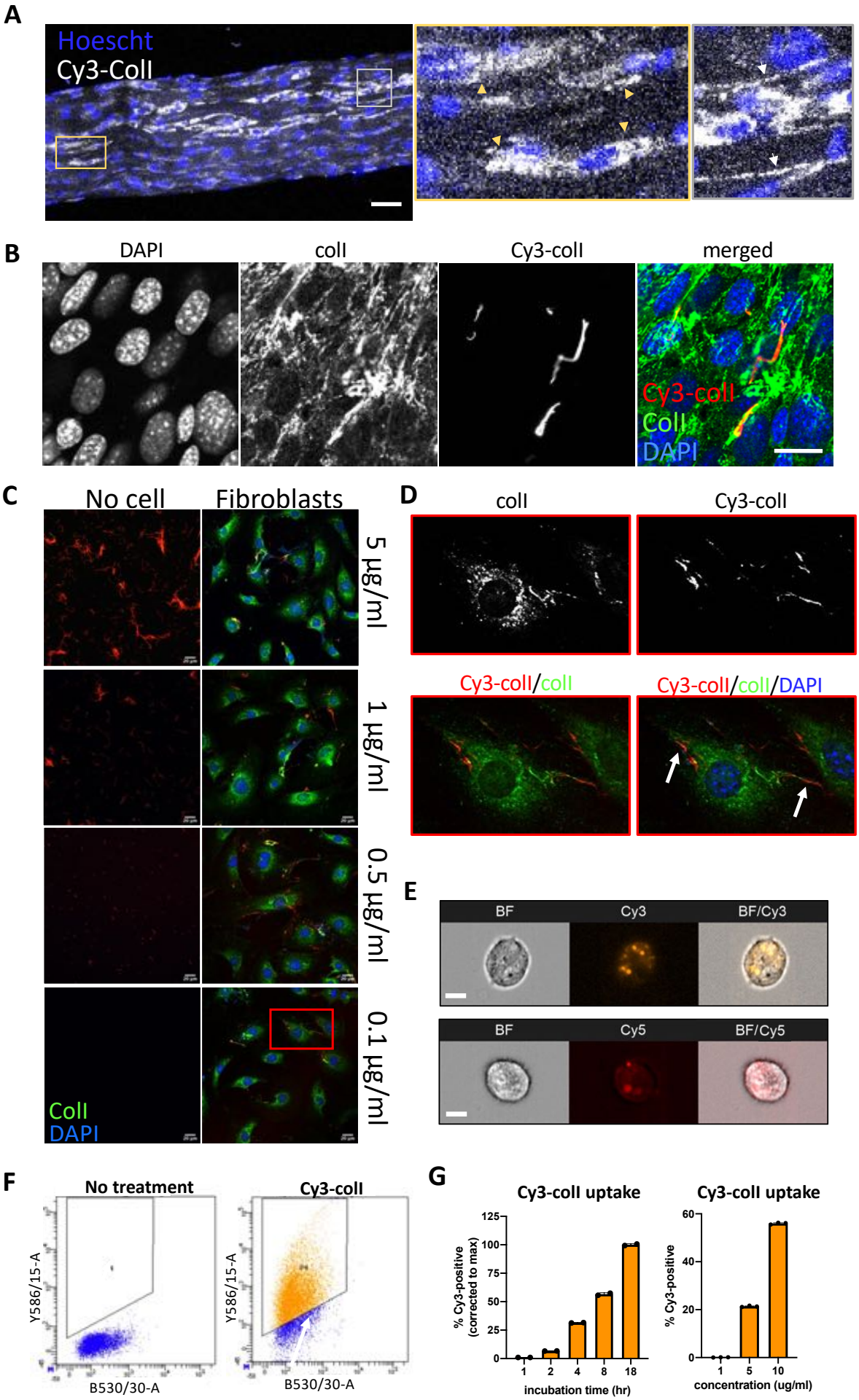
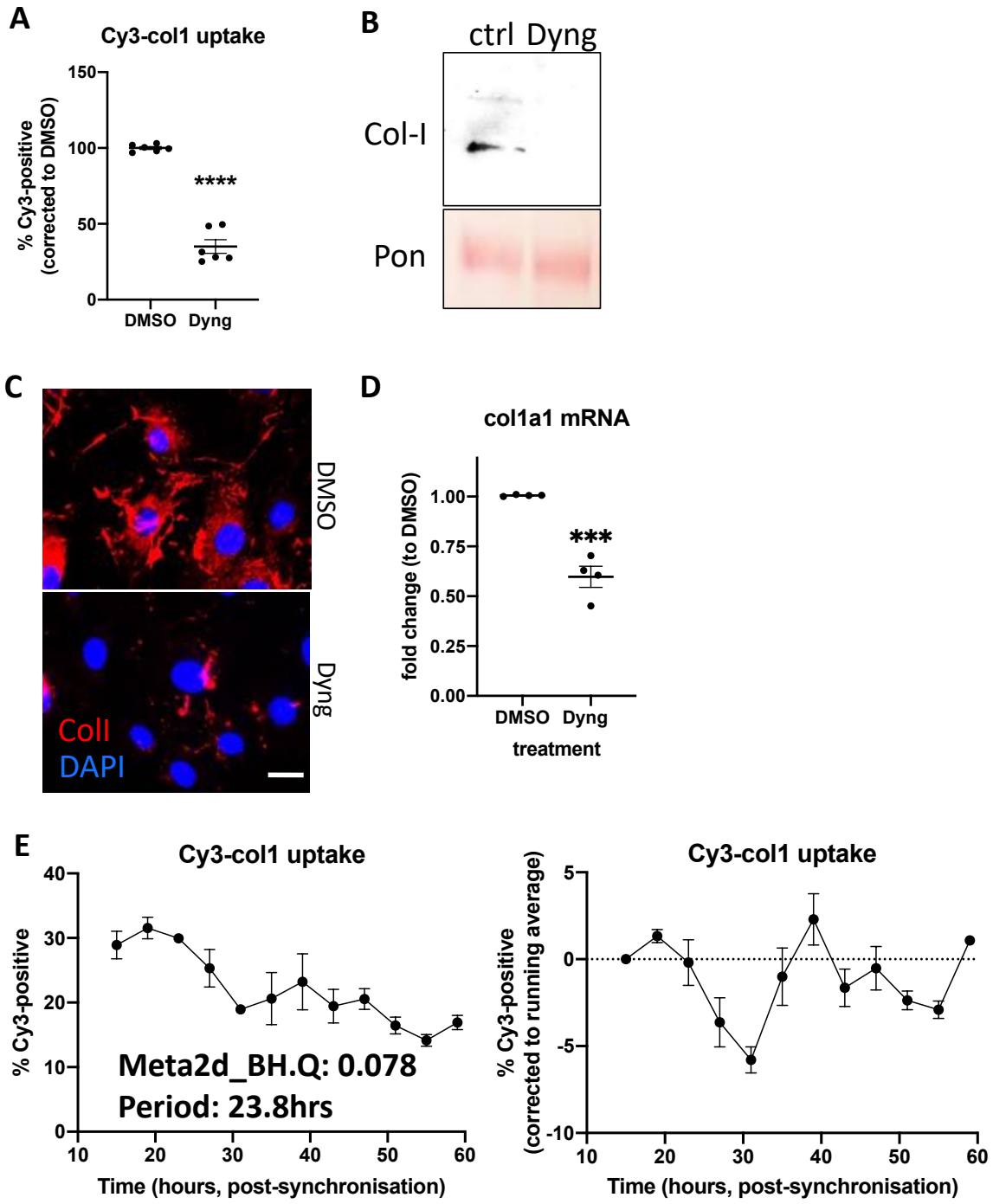
Chang et al. Figure 1



Chang et al. Figure 2



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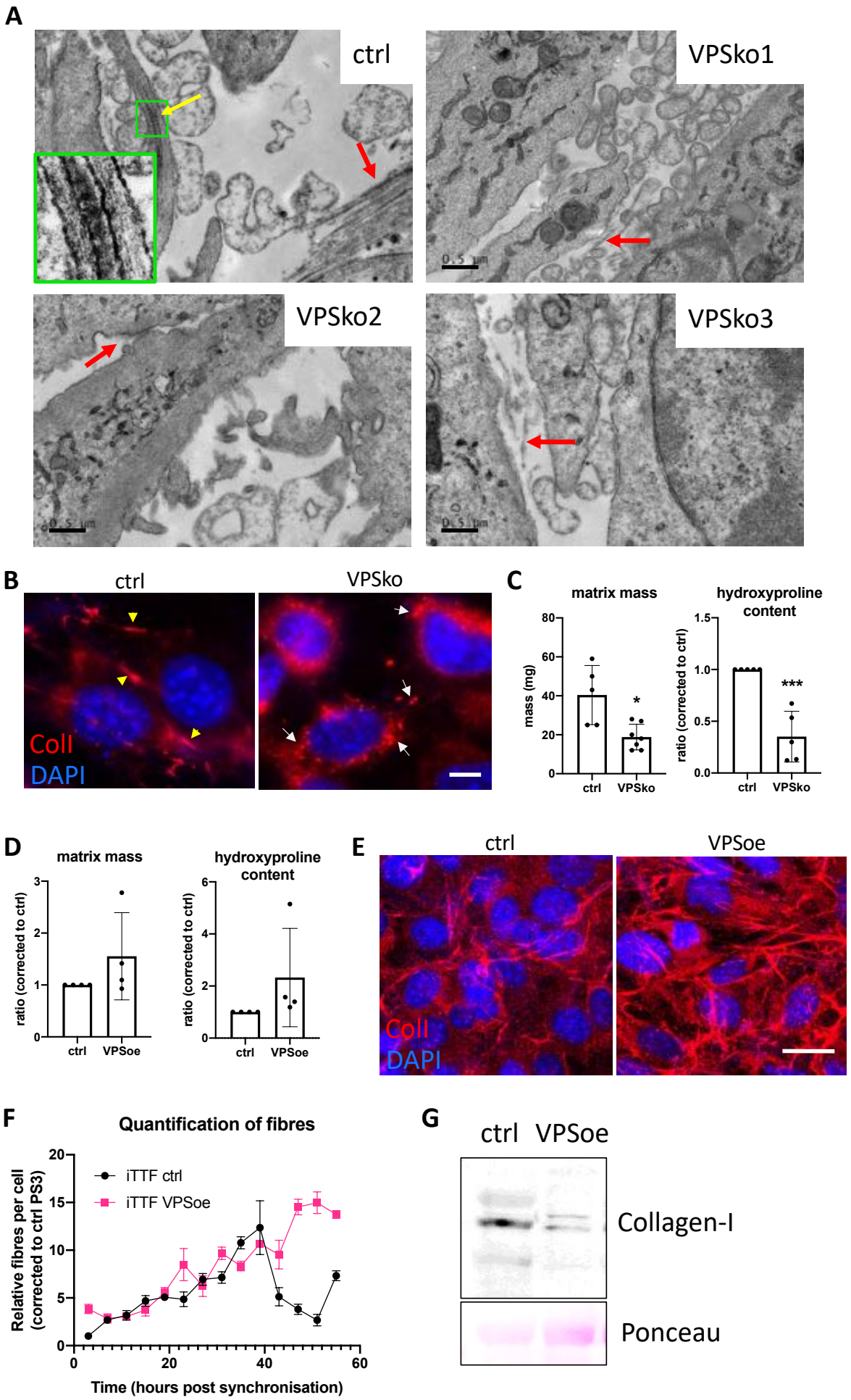

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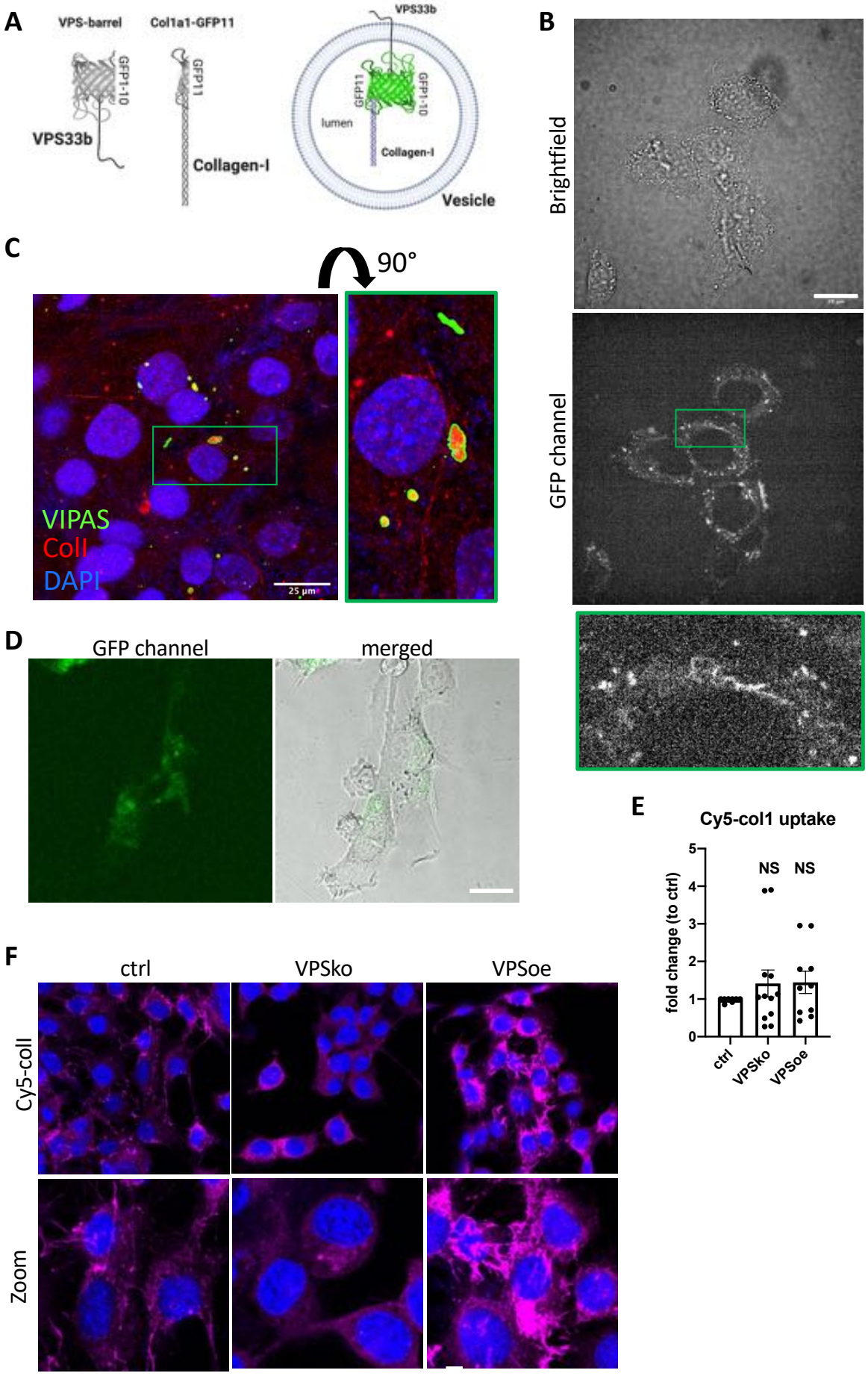

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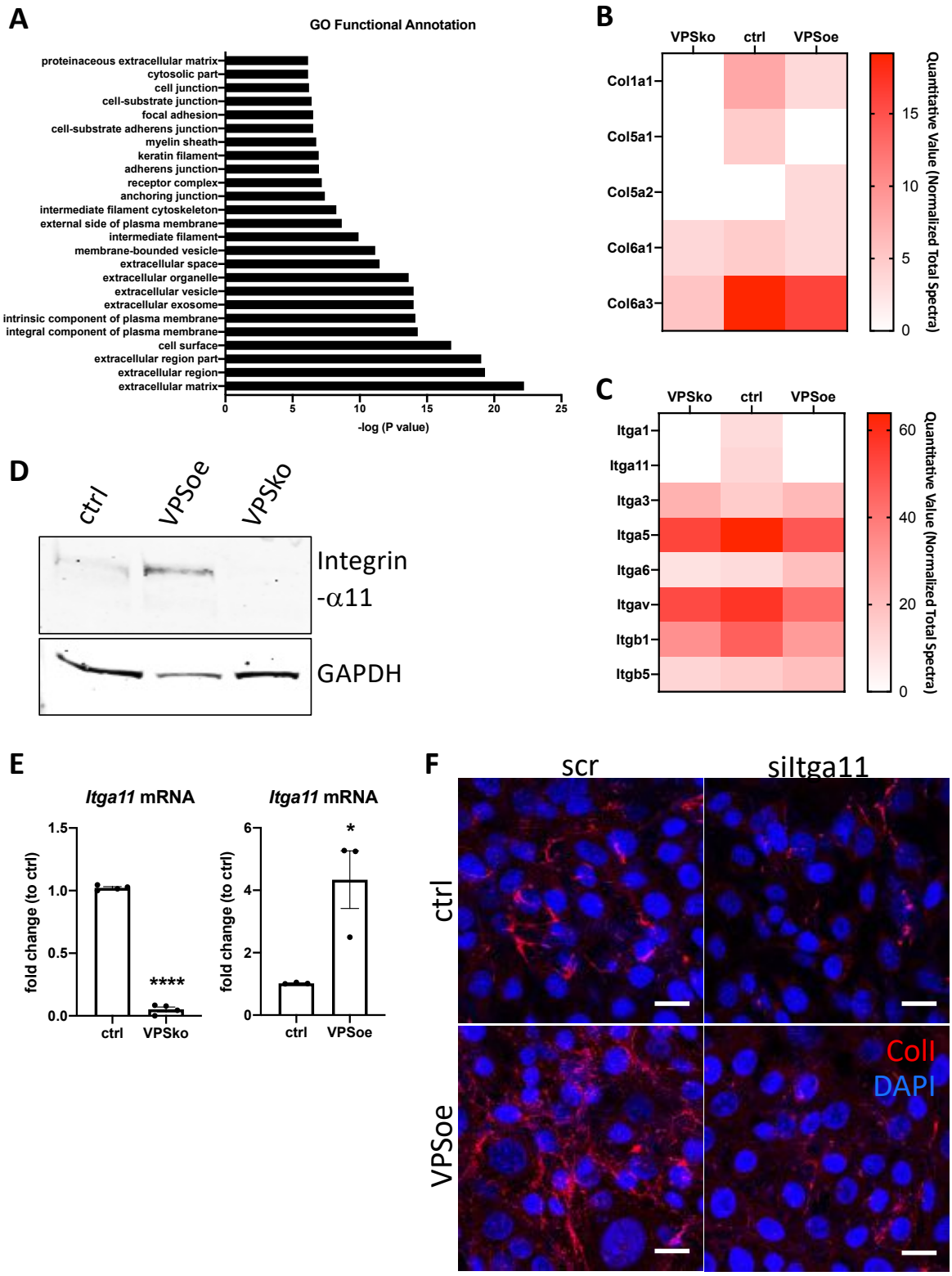

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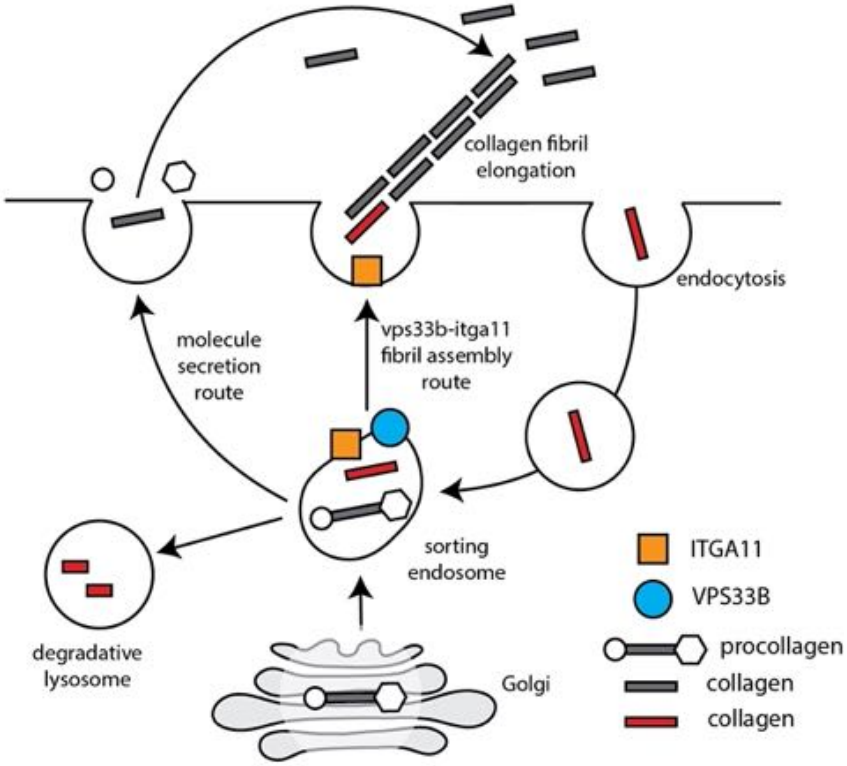
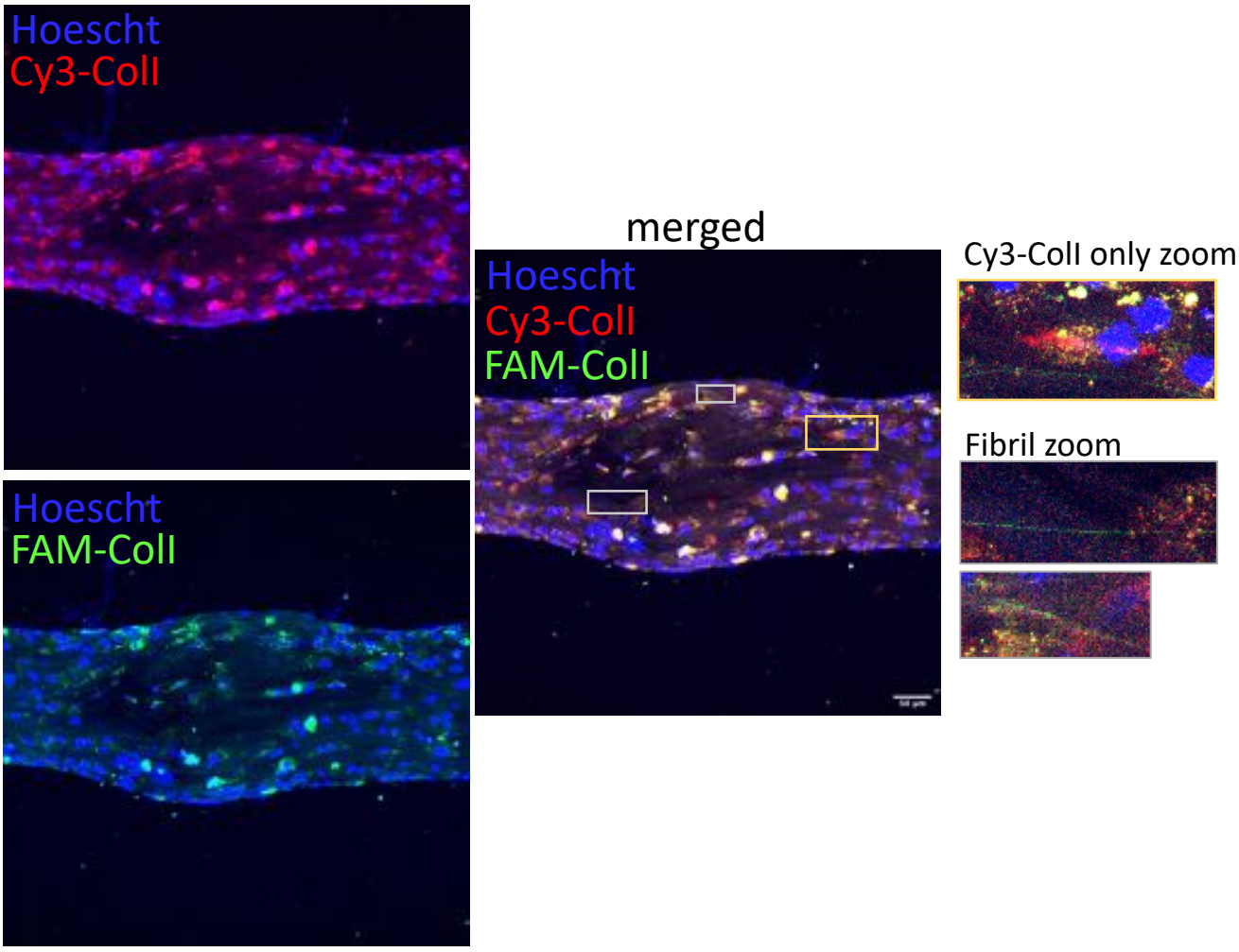


Chang et al., Supplementary figure 1

A



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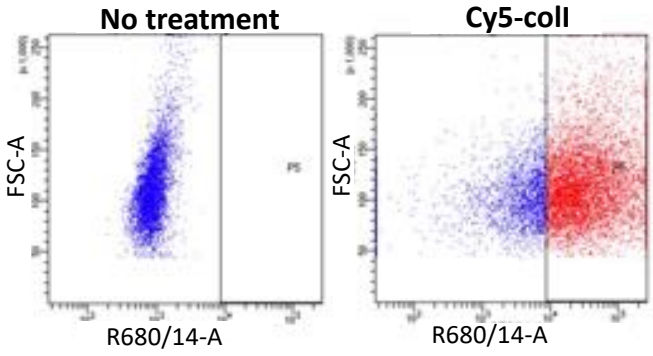

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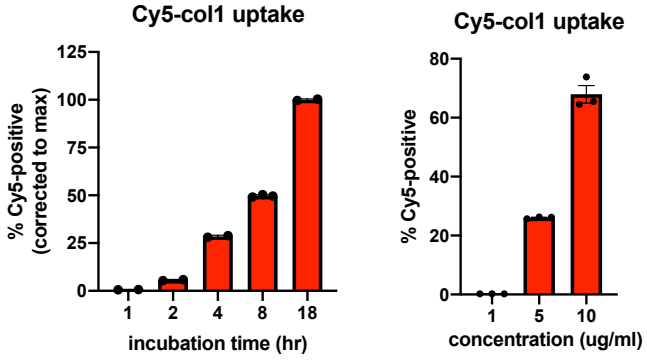
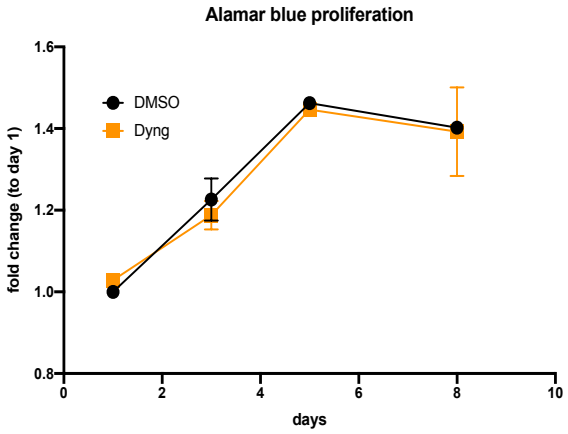


Chang et al., Supplementary figure 2

A



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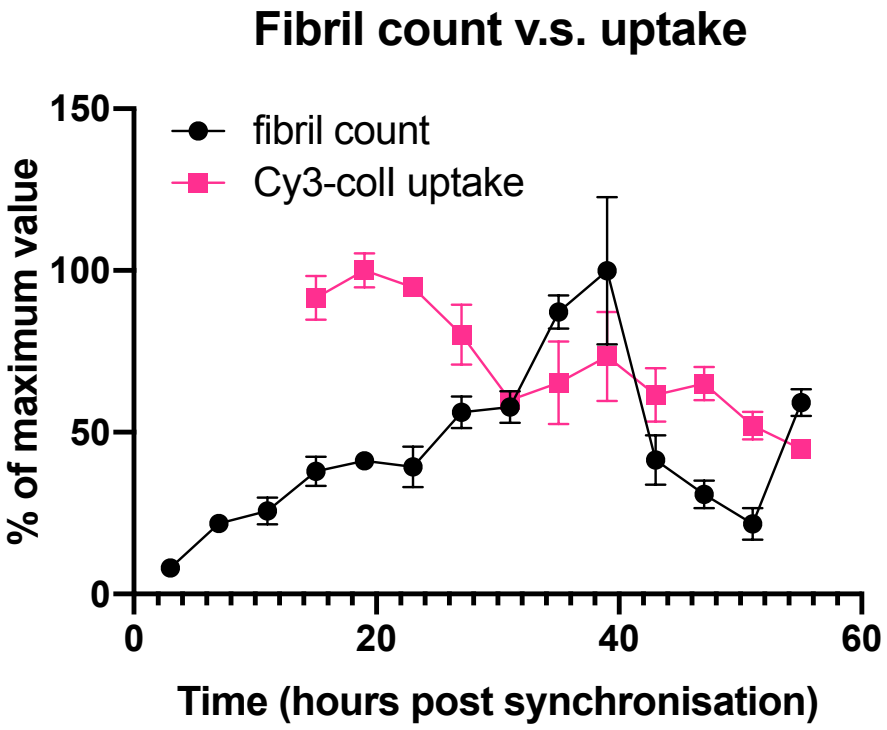

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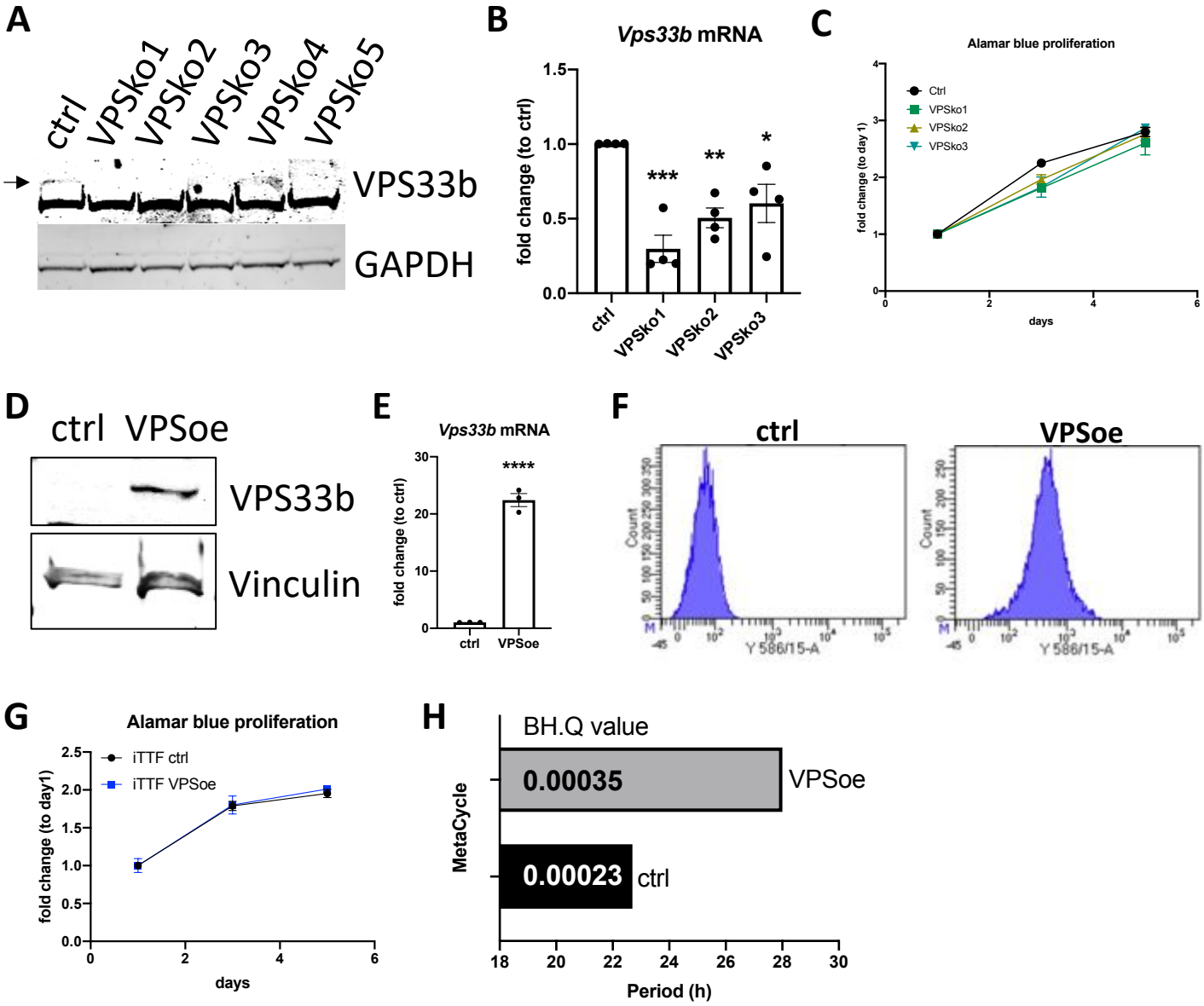

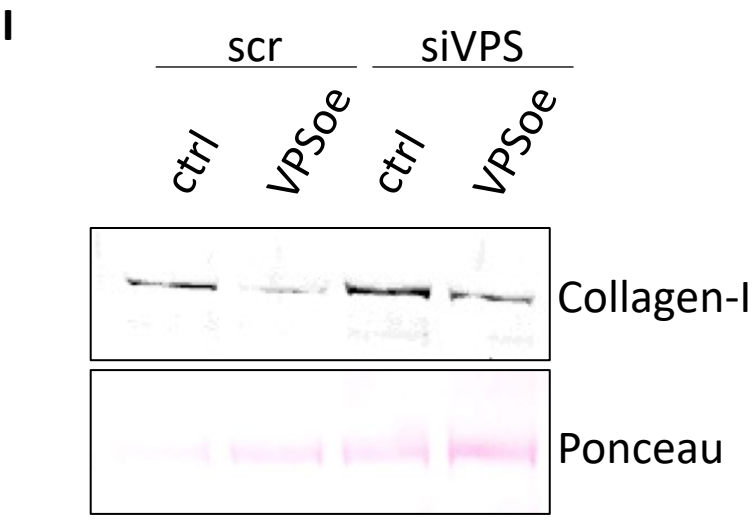

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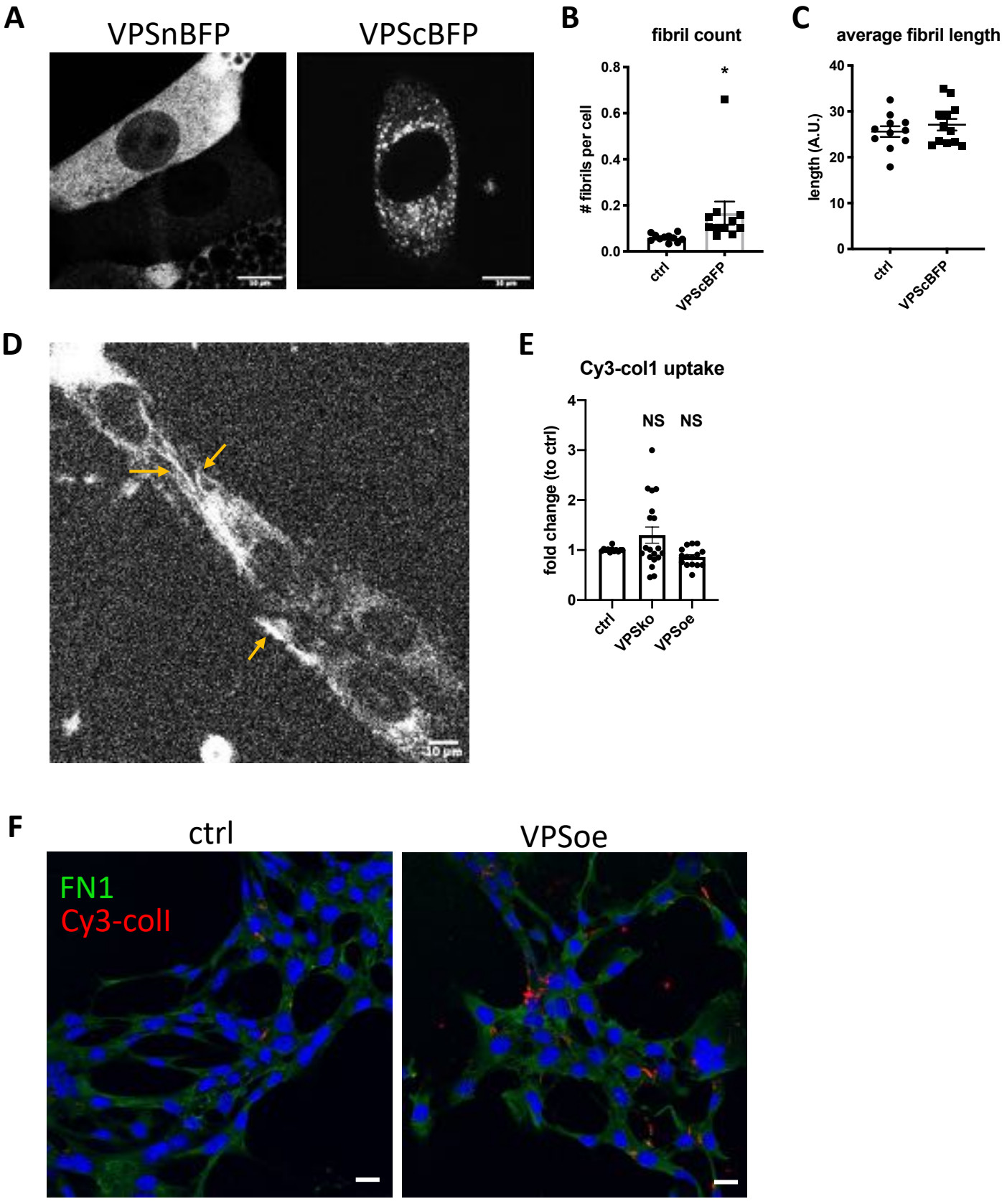

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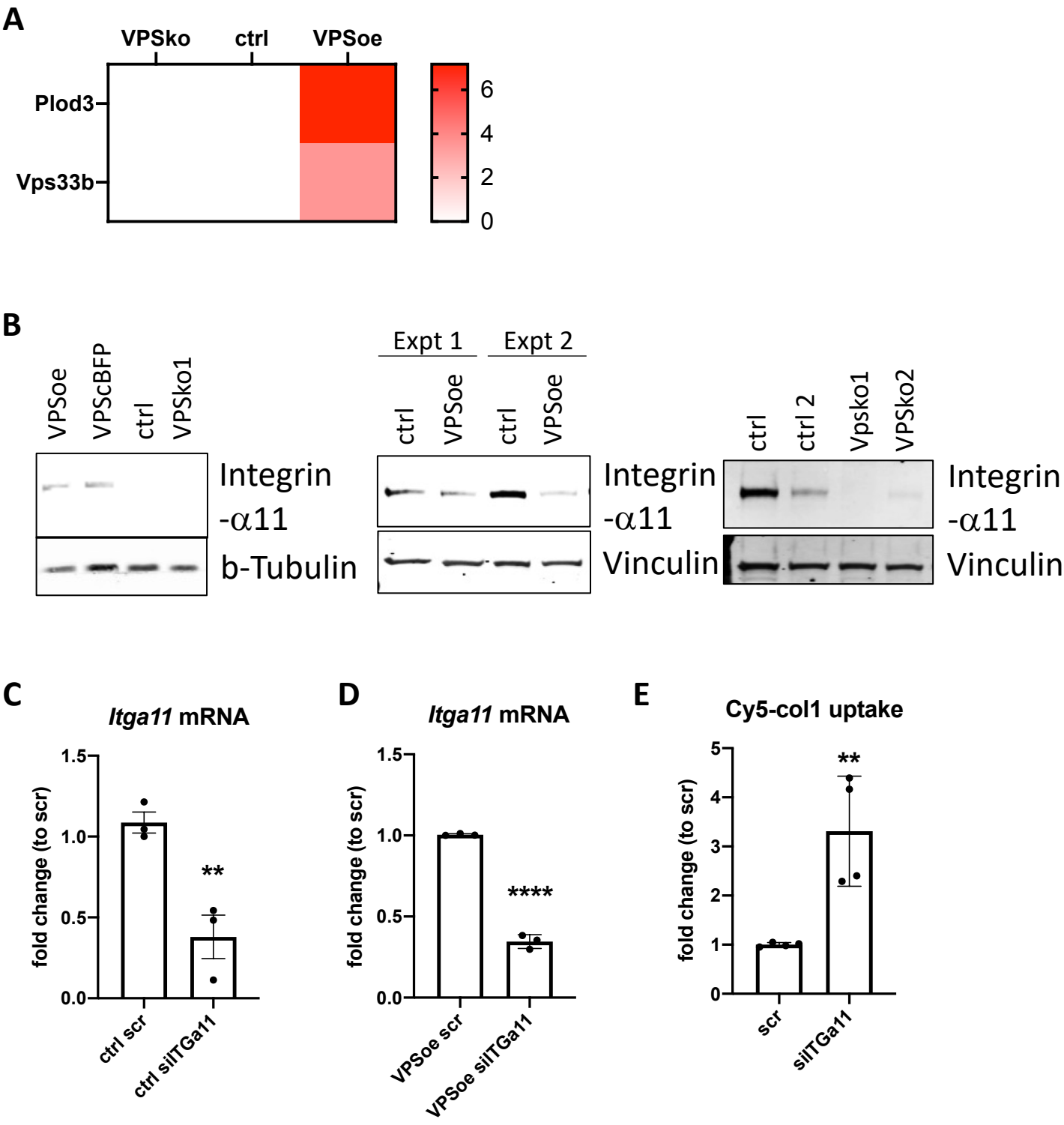

	VPSko	ctrl	VPSoe
Plod3	0	0	7.1579
Vps33b	0	0	3.5789
Col1a1	0	7.9893	3.5789
Col5a1	0	4.7936	0
Col5a2	0	0	3.5789
Col6a1	3.6831	4.7936	3.5789
Col6a3	5.5246	19.174	16.105
Itga1	0	11.185	0
Itga11	0	12.783	0
Itga3	23.94	15.979	21.474
Itga5	53.405	63.914	48.316
Itga6	9.2077	11.185	19.684
Itgav	51.563	57.523	42.947
Itgb1	33.148	46.338	30.421
Itgb5	12.891	15.979	19.684

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
1200007D18Rik protein OS=Mus musculus GN=Ergic1 PE=1 SV=1	Q4FK22 (+2)	Ergic1	33 kDa	5.5246	4.7936	7.1579	0.81665	3.8675	TRUE
14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1	P62259 (+1)	Ywhae	29 kDa	9.2077	4.7936	3.5789	6.9416	6.8755	TRUE
14-3-3 protein gamma subtype OS=Mus musculus GN=Ywhag PE=1 SV=1	A8IP69 (+1)	Ywhag	28 kDa	9.2077	0	7.1579	0	3.4377	TRUE
14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1	P63101	Ywhaz	28 kDa	9.2077	9.5872	8.9474	4.8999	6.0161	TRUE
2-oxoglutarate dehydrogenase, mitochondrial OS=Mus musculus GN=Ogdh PE=1 SV=3	Q60597	Ogdh	116 kDa	0	3.1957	8.9474	7.7582	8.1647	TRUE
26S proteasome non-ATPase regulatory subunit 5 OS=Mus musculus GN=Psmd5 PE=1 SV=4	Q8BJY1	Psmd5	56 kDa	3.6831	3.1957	3.5789	3.6749	3.4377	TRUE
26S proteasome non-ATPase regulatory subunit 9 OS=Mus musculus GN=Psmd9 PE=1 SV=1	Q9CR00 (+1)	Psmd9	25 kDa	5.5246	4.7936	7.1579	2.45	2.5783	TRUE
26S proteasome regulatory subunit 10B OS=Mus musculus GN=Psmc6 PE=1 SV=1	P62334 (+1)	Psmc6	44 kDa	5.5246	3.1957	5.3684	4.8999	3.8675	TRUE
26S proteasome regulatory subunit 6A OS=Mus musculus GN=Psmc3 PE=1 SV=1	B7ZCF1	Psmc3	50 kDa	7.3662	4.7936	7.1579	5.7166	4.7269	TRUE
26S proteasome regulatory subunit 7 OS=Mus musculus GN=Psmc2 PE=1 SV=1	Q8BVQ9	Psmc2	53 kDa	3.6831	3.1957	5.3684	4.8999	4.2972	TRUE
40S ribosomal protein S12 OS=Mus musculus GN=Rps12-ps3 PE=1 SV=1	Q6ZWZ6	Rps12-ps3	15 kDa	3.6831	6.3914	5.3684	4.4916	3.4377	TRUE
40S ribosomal protein S13 OS=Mus musculus GN=Rps13 PE=1 SV=2	P62301 (+2)	Rps13	17 kDa	14.732	14.381	16.105	6.5332	3.008	TRUE
40S ribosomal protein S15a OS=Mus musculus GN=Rps15a PE=1 SV=2	P62245 (+1)	Rps15a	15 kDa	9.2077	4.7936	7.1579	4.0833	4.2972	TRUE
40S ribosomal protein S17 OS=Mus musculus GN=Rps17 PE=1 SV=2	P63276 (+2)	Rps17	16 kDa	5.5246	0	0	3.6749	4.7269	TRUE
40S ribosomal protein S20 OS=Mus musculus GN=Rps20 PE=1 SV=1	P60867 (+1)	Rps20	13 kDa	3.6831	0	5.3684	2.0416	2.5783	TRUE
40S ribosomal protein S21 OS=Mus musculus GN=mCG_6739 PE=2 SV=1	Q8C1L7 (+1)	mCG_6739	9 kDa	5.5246	4.7936	0	1.225	0	TRUE
40S ribosomal protein S25 OS=Mus musculus GN=Rps25 PE=1 SV=1	A0A1L1SQA8 (+2)	Rps25	10 kDa	9.2077	7.9893	10.737	1.6333	2.5783	TRUE
40S ribosomal protein S27 OS=Mus musculus GN=Rps27 PE=1 SV=3	Q6ZWU9	Rps27	9 kDa	14.732	11.185	8.9474	2.45	2.5783	TRUE
40S ribosomal protein S27-like OS=Mus musculus GN=Rps27l PE=1 SV=3	Q6ZWY3	Rps27l	9 kDa	0	7.9893	0	0	0	TRUE
40S ribosomal protein S28 (Fragment) OS=Mus musculus GN=Rps28 PE=1 SV=1	G3UYV7 (+2)	Rps28	6 kDa	5.5246	4.7936	5.3684	1.6333	2.1486	TRUE
40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1	P62908 (+1)	Rps3	27 kDa	25.782	15.979	28.632	12.25	12.892	TRUE
40S ribosomal protein S3a OS=Mus musculus GN=Rps3a1 PE=2 SV=1	Q9D1S3	Rps3a1	30 kDa	18.415	14.381	17.895	6.9416	9.0241	TRUE
40S ribosomal protein S4, X isoform OS=Mus musculus GN=Rps4x PE=1 SV=2	P62702 (+2)	Rps4x	30 kDa	12.891	12.783	12.526	7.7582	8.1647	TRUE
40S ribosomal protein S5 OS=Mus musculus GN=Rps5 PE=1 SV=1	Q91V55	Rps5	23 kDa	3.6831	6.3914	5.3684	3.6749	3.4377	TRUE
40S ribosomal protein S7 OS=Mus musculus GN=Gm9493 PE=3 SV=1	F6SVV1 (+2)	Gm9493	22 kDa	11.049	4.7936	7.1579	3.2666	3.4377	TRUE
40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=2	P62242 (+1)	Rps8	24 kDa	9.2077	4.7936	8.9474	6.9416	8.1647	TRUE
45 kDa calcium-binding protein OS=Mus musculus GN=Sdf4 PE=1 SV=1	Q61112	Sdf4	42 kDa	5.5246	6.3914	3.5789	0	0	TRUE
4F2 cell-surface antigen heavy chain OS=Mus musculus GN=Slc3a2 PE=1 SV=1	P10852	Slc3a2	58 kDa	36.831	31.957	28.632	6.9416	4.2972	TRUE
5'-3' exoribonuclease 2 OS=Mus musculus GN=Xrn2 PE=1 SV=1	Q9DBR1	Xrn2	109 kDa	3.6831	0	3.5789	3.6749	3.008	TRUE
5'-nucleotidase domain-containing 2 OS=Mus musculus GN=Nt5dc2 PE=1 SV=1	Q91X76	Nt5dc2	46 kDa	0	0	3.5789	3.6749	3.4377	TRUE
60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1	P63038	Hspd1	61 kDa	42.356	41.544	50.105	17.558	19.337	TRUE
60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3	P14869 (+1)	Rplp0	34 kDa	18.415	17.576	14.316	6.1249	7.3052	TRUE
60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3	P99027	Rplp2	12 kDa	9.2077	7.9893	8.9474	3.6749	3.008	TRUE
60S ribosomal protein L12 OS=Mus musculus GN=Rpl12 PE=1 SV=2	P35979 (+1)	Rpl12	18 kDa	5.5246	7.9893	7.1579	3.6749	5.1566	TRUE
60S ribosomal protein L17 OS=Mus musculus GN=Rpl17 PE=1 SV=1	Q6ZWZ7 (+2)	Rpl17	21 kDa	9.2077	7.9893	8.9474	2.45	3.008	TRUE
60S ribosomal protein L21 OS=Mus musculus GN=Rpl21 PE=1 SV=3	O09167 (+1)	Rpl21	19 kDa	7.3662	3.1957	0	2.0416	2.5783	TRUE
60S ribosomal protein L22 OS=Mus musculus GN=Rpl22 PE=1 SV=2	P67984 (+1)	Rpl22	15 kDa	5.5246	3.1957	5.3684	3.2666	3.8675	TRUE
60S ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=1 SV=1	P62830	Rpl23	15 kDa	5.5246	3.1957	0	2.45	2.5783	TRUE
60S ribosomal protein L26 OS=Mus musculus GN=Rpl26 PE=1 SV=1	P61255 (+1)	Rpl26	17 kDa	3.6831	3.1957	5.3684	2.8583	3.4377	TRUE
60S ribosomal protein L27 OS=Mus musculus GN=Rpl27 PE=1 SV=2	P61358 (+1)	Rpl27	16 kDa	3.6831	4.7936	5.3684	2.0416	2.1486	TRUE
60S ribosomal protein L30 OS=Mus musculus GN=Rpl30 PE=1 SV=2	P62889 (+1)	Rpl30	13 kDa	11.049	4.7936	3.5789	2.45	3.008	TRUE
60S ribosomal protein L34 OS=Mus musculus GN=Rpl34 PE=1 SV=2	Q9D1R9	Rpl34	13 kDa	3.6831	0	0	0.81665	0	TRUE
60S ribosomal protein L35a OS=Mus musculus GN=Rpl35a PE=1 SV=2	O55142 (+3)	Rpl35a	13 kDa	5.5246	3.1957	5.3684	1.6333	0.85944	TRUE
60S ribosomal protein L5 OS=Mus musculus GN=Rpl5 PE=1 SV=3	P47962 (+1)	Rpl5	34 kDa	12.891	9.5872	12.526	11.841	14.181	TRUE
60S ribosomal protein L9 (Fragment) OS=Mus musculus GN=Rpl9 PE=1 SV=1	A0A0G2JES3 (+2)	Rpl9	22 kDa	3.6831	0	3.5789	3.2666	3.4377	TRUE
78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3	P20029 (+1)	Hspa5	72 kDa	51.563	57.523	53.684	28.175	29.651	TRUE
A kinase (PRKA) anchor protein 8 OS=Mus musculus GN=Akap8 PE=1 SV=1	Q059U9 (+1)	Akap8	76 kDa	9.2077	4.7936	5.3684	1.225	1.2892	TRUE
Abl interactor 1 OS=Mus musculus GN=Abi1 PE=1 SV=1	B7ZCU0 (+2)	Abi1	52 kDa	5.5246	4.7936	0	1.6333	0.85944	TRUE
Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1	Q8QZT1	Acat1	45 kDa	5.5246	0	5.3684	4.0833	5.5863	TRUE
Acetyl-CoA carboxylase 1 OS=Mus musculus GN=Acaca PE=1 SV=1	Q5SWU9	Acaca	265 kDa	167.58	135.82	166.42	7.7582	6.0161	TRUE
Acid sphingomyelinase-like phosphodiesterase 3b OS=Mus musculus GN=Smpdl3b PE=1 SV=1	P58242 (+1)	Smpdl3b	52 kDa	0	4.7936	0	1.225	0	TRUE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Aconitate hydratase, mitochondrial OS=Mus musculus GN=Aco2 PE=1 SV=1	Q99KI0	Aco2	85 kDa	9.2077	12.783	14.316	10.208	12.462	TRUE
Actin-related protein 2/3 complex subunit 5 OS=Mus musculus GN=Arpc5 PE=2 SV=1	Q3TKM9 (+1)	Arpc5	16 kDa	0	3.1957	0	1.6333	0	TRUE
Actin-related protein 2/3 complex subunit OS=Mus musculus GN=Arpc1b PE=2 SV=1	Q3TCE7 (+3)	Arpc1b	41 kDa	7.3662	4.7936	5.3684	6.1249	4.7269	TRUE
Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1	P68033 (+2)	Actc1	42 kDa	40.514	44.74	50.105	45.324	38.245	TRUE
Actin, beta OS=Mus musculus GN=Actb PE=2 SV=1	B2RRX1 (+5)	Actb	42 kDa	51.563	63.914	69.789	67.782	67.896	TRUE
Acyl-coenzyme A thioesterase 9, mitochondrial OS=Mus musculus GN=Acot9 PE=1 SV=1	Q9R0X4	Acot9	51 kDa	0	3.1957	3.5789	2.8583	4.2972	TRUE
Adenosylhomocysteinase OS=Mus musculus GN=Ahcy PE=1 SV=3	P50247 (+2)	Ahcy	48 kDa	5.5246	4.7936	10.737	9.3915	9.8835	TRUE
Adenylyl cyclase-associated protein 1 OS=Mus musculus GN=Cap1 PE=1 SV=4	P40124 (+1)	Cap1	52 kDa	0	11.185	5.3684	10.208	9.0241	TRUE
ADP-ribosylation factor 3 OS=Mus musculus GN=Arf3 PE=2 SV=2	P61205 (+2)	Arf3	21 kDa	0	4.7936	3.5789	4.8999	4.7269	TRUE
ADP-ribosylation factor 4 OS=Mus musculus GN=Arf4 PE=1 SV=2	P61750 (+1)	Arf4	20 kDa	5.5246	3.1957	3.5789	5.3082	5.1566	TRUE
ADP-ribosylation factor GTPase-activating protein 3 OS=Mus musculus GN=Arfgap3 PE=1 SV=1	A0A0R4J0T8 (+1)	Arfgap3	58 kDa	0	0	3.5789	3.2666	4.2972	TRUE
ADP-ribosylation factor-like protein 1 (Fragment) OS=Mus musculus GN=Arl1 PE=1 SV=1	F8WIB1 (+2)	Arl1	16 kDa	0	3.1957	0	2.45	1.7189	TRUE
ADP/ATP translocase 1 OS=Mus musculus GN=Slc25a4 PE=1 SV=4	P48962 (+1)	Slc25a4	33 kDa	40.514	31.957	39.368	10.616	12.892	TRUE
ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=3	P51881 (+1)	Slc25a5	33 kDa	53.405	39.947	46.526	11.025	12.892	TRUE
AHNAK nucleoprotein (desmoyokin) OS=Mus musculus GN=Ahnak PE=1 SV=1	E9Q616	Ahnak	604 kDa	44.197	39.947	37.579	39.199	36.526	TRUE
Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1	P47738 (+3)	Aldh2	57 kDa	7.3662	4.7936	8.9474	8.1665	8.1647	TRUE
Alkaline phosphatase OS=Mus musculus GN=Alpl PE=2 SV=1	B7XGA6 (+1)	Alpl	57 kDa	0	6.3914	0	0	0	TRUE
Alpha glucosidase 2 alpha neutral subunit OS=Mus musculus GN=Ganab PE=2 SV=1	A1A4T2	Ganab	109 kDa	0	15.979	17.895	15.108	16.759	TRUE
Alpha v integrin OS=Mus musculus GN=Itgav PE=2 SV=1	A0A0F7IQ06 (+1)	Itgav	115 kDa	51.563	57.523	42.947	7.3499	6.4458	TRUE
Alpha-1,3/1,6-mannosyltransferase ALG2 OS=Mus musculus GN=Alg2 PE=1 SV=2	Q9DBE8	Alg2	47 kDa	0	0	3.5789	0	0	TRUE
Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=1 SV=1	Q7TPR4	Actn1	103 kDa	0	17.576	0	17.15	13.321	TRUE
Alpha-actinin-4 OS=Mus musculus GN=Actn4 PE=1 SV=1	P57780 (+1)	Actn4	105 kDa	0	15.979	5.3684	14.7	10.743	TRUE
Alpha-crystallin B chain OS=Mus musculus GN=Cryab PE=1 SV=2	P23927 (+1)	Cryab	20 kDa	3.6831	0	0	0	0	TRUE
Alpha-globin OS=Mus musculus GN=Hbat1 PE=3 SV=1	A8DUV3 (+6)	Hbat1	15 kDa	5.5246	0	5.3684	0	0	TRUE
Amine oxidase (Fragment) OS=Mus musculus GN=Maoa PE=2 SV=1	Q3TPD9 (+3)	Maoa	59 kDa	0	3.1957	5.3684	4.0833	6.8755	TRUE
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Mus musculus GN=A	P31230 (+1)	Aimp1	34 kDa	9.2077	4.7936	3.5789	5.7166	6.4458	TRUE
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Mus musculus GN=A	Q8R010	Aimp2	35 kDa	0	3.1957	0	1.225	1.2892	TRUE
Angiopoietin-related protein 2 OS=Mus musculus GN=Angptl2 PE=2 SV=2	Q9R045	Angptl2	57 kDa	12.891	6.3914	8.9474	1.225	0	TRUE
Ankyrin repeat domain-containing protein 17 OS=Mus musculus GN=Ankrd17 PE=1 SV=1	A0A0G2JDZ9 (+1)	Ankrd17	264 kDa	23.94	22.37	25.053	2.0416	2.1486	TRUE
Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2	P07356 (+1)	Anxa2	39 kDa	34.989	39.947	44.737	11.433	13.321	TRUE
Annexin A3 OS=Mus musculus GN=Anxa3 PE=1 SV=4	O35639 (+2)	Anxa3	36 kDa	0	0	8.9474	11.025	8.5944	TRUE
Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1	P48036	Anxa5	36 kDa	11.049	14.381	23.263	10.616	12.032	TRUE
Annexin OS=Mus musculus GN=Anxa1 PE=2 SV=1	B7STB7 (+2)	Anxa1	39 kDa	14.732	15.979	25.053	14.7	12.032	TRUE
Anthrax toxin receptor 1 OS=Mus musculus GN=Antxr1 PE=1 SV=2	Q9CZ52	Antxr1	62 kDa	0	9.5872	0	0	0	TRUE
Antigen peptide transporter 2 OS=Mus musculus GN=Tap2 PE=1 SV=1	P36371 (+4)	Tap2	77 kDa	0	3.1957	0	2.45	0	TRUE
Antigen-presenting glycoprotein CD1d1 OS=Mus musculus GN=Cd1d1 PE=1 SV=1	A0A0R4J090 (+2)	Cd1d1	39 kDa	0	3.1957	3.5789	0	0	TRUE
Apoa1 protein OS=Mus musculus GN=Apoa1 PE=2 SV=1	Q58EV2	Apoa1	23 kDa	3.6831	0	0	0	0	TRUE
Apolipoprotein B-100 OS=Mus musculus GN=Apob PE=1 SV=1	E9Q414	Apob	509 kDa	5.5246	0	0	0	0	TRUE
Arf-GAP domain and FG repeat-containing protein 1 OS=Mus musculus GN=Agfg1 PE=1 SV=1	A0A087WNV1 (+3)	Agfg1	54 kDa	3.6831	3.1957	3.5789	1.6333	2.1486	TRUE
Arginine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Rars PE=1 SV=2	Q9D0I9	Rars	76 kDa	16.574	11.185	7.1579	7.7582	9.8835	TRUE
Aspartate aminotransferase, mitochondrial OS=Mus musculus GN=Got2 PE=1 SV=1	P05202	Got2	47 kDa	20.257	14.381	16.105	11.433	13.321	TRUE
Aspartyl aminopeptidase OS=Mus musculus GN=Dnpep PE=1 SV=1	Q3TVK3 (+3)	Dnpep	52 kDa	9.2077	12.783	10.737	4.8999	4.2972	TRUE
Ataxin-10 OS=Mus musculus GN=Atxn10 PE=1 SV=2	P28658 (+1)	Atxn10	54 kDa	7.3662	4.7936	8.9474	5.3082	4.2972	TRUE
Ataxin-2-like protein OS=Mus musculus GN=Atxn2l PE=1 SV=1	Q3TGG2	Atxn2l	105 kDa	3.6831	3.1957	3.5789	3.6749	1.7189	TRUE
ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 PE=1 SV=1	Q03265	Atp5a1	60 kDa	23.94	25.566	39.368	18.375	16.329	TRUE
ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2	P56480	Atp5b	56 kDa	22.099	35.153	35.789	15.925	17.618	TRUE
ATP synthase subunit d, mitochondrial (Fragment) OS=Mus musculus GN=Atp5h PE=1 SV=1	B1ASE2 (+2)	Atp5h	16 kDa	0	4.7936	0	0.81665	1.2892	TRUE
ATP synthase subunit epsilon, mitochondrial OS=Mus musculus GN=Atp5e PE=1 SV=2	P56382 (+2)	Atp5e	6 kDa	0	3.1957	3.5789	0	0	TRUE
ATP synthase subunit gamma OS=Mus musculus GN=Atp5c1 PE=1 SV=1	A2AKU9 (+3)	Atp5c1	33 kDa	7.3662	7.9893	12.526	3.2666	3.8675	TRUE
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 OS=Mus musculus	Q5I0W0 (+1)	Atp5f1	29 kDa	0	3.1957	3.5789	0.81665	1.2892	TRUE
ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit, isoform CRA_c OS=Mus	Q4FK74 (+2)	Atp5d	18 kDa	3.6831	4.7936	5.3684	1.6333	2.1486	TRUE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
ATP-binding cassette sub-family F member 2 OS=Mus musculus GN=Abcf2 PE=1 SV=1	Q99LE6	Abcf2	72 kDa	5.5246	0	0	4.4916	5.5863	TRUE
ATP-binding cassette, sub-family C (CFTR/MRP), member 1 OS=Mus musculus GN=Abcc1 PE=1 SV=	A5D6P3 (+1)	Abcc1	171 kDa	7.3662	12.783	19.684	2.45	4.2972	TRUE
ATP-dependent RNA helicase DDX1 OS=Mus musculus GN=Ddx1 PE=1 SV=1	Q91VR5	Ddx1	83 kDa	5.5246	12.783	14.316	6.9416	5.5863	TRUE
ATPase family AAA domain-containing protein 3 OS=Mus musculus GN=Atad3 PE=1 SV=1	Q925I1	Atad3	67 kDa	0	0	3.5789	0.81665	1.2892	TRUE
B-cell CLL/lymphoma 9-like protein OS=Mus musculus GN=Bcl9l PE=1 SV=1	Q67FY2	Bcl9l	157 kDa	0	0	3.5789	0	0	TRUE
Basic leucine zipper and W2 domain-containing protein 2 OS=Mus musculus molossinus GN=Bzw2	Q2L4X1 (+1)	Bzw2	48 kDa	0	0	3.5789	2.45	2.5783	TRUE
Basigin (Fragment) OS=Mus musculus GN=Bsg PE=2 SV=1	O55107	Bsg	30 kDa	14.732	14.381	16.105	2.8583	3.8675	TRUE
BCL2-associated athanogene 3 OS=Mus musculus GN=Bag3 PE=2 SV=1	A6H663 (+2)	Bag3	62 kDa	9.2077	0	12.526	1.6333	1.2892	TRUE
BCL2/adenovirus E1B 19 kDa protein-interacting protein 3 OS=Mus musculus GN=Bnip3 PE=1 SV=	A0A1B0GT26 (+1)	Bnip3	19 kDa	3.6831	0	3.5789	0	0	TRUE
Beta-2-microglobulin OS=Mus musculus GN=B2m PE=2 SV=1	Q9D239	B2m	14 kDa	7.3662	7.9893	5.3684	0.81665	0	TRUE
Beta-globin OS=Mus musculus GN=Hbbt1 PE=3 SV=1	A8DUN2	Hbbt1	16 kDa	3.6831	3.1957	3.5789	0	0	TRUE
Bifunctional glutamate/proline--tRNA ligase OS=Mus musculus GN=Eprs PE=1 SV=4	Q8CGC7	Eprs	170 kDa	20.257	15.979	19.684	22.458	18.478	TRUE
Biglycan OS=Mus musculus GN=Bgn PE=1 SV=1	P28653 (+1)	Bgn	42 kDa	0	3.1957	0	2.45	2.1486	TRUE
Bone marrow stromal antigen 2 OS=Mus musculus GN=Bst2 PE=1 SV=1	Q8R2Q8	Bst2	19 kDa	3.6831	6.3914	0	1.225	0	TRUE
Bone morphogenetic protein receptor type-2 OS=Mus musculus GN=Bmpr2 PE=1 SV=1	O35607	Bmpr2	115 kDa	0	0	3.5789	0	0	TRUE
Brain acid soluble protein 1 OS=Mus musculus GN=Basp1 PE=1 SV=3	Q91XV3	Basp1	22 kDa	3.6831	0	3.5789	3.2666	2.5783	TRUE
Branched-chain-amino-acid aminotransferase, cytosolic OS=Mus musculus GN=Bcat1 PE=1 SV=2	P24288 (+2)	Bcat1	43 kDa	3.6831	0	0	3.2666	3.008	TRUE
CAD protein OS=Mus musculus GN=Cad PE=1 SV=1	B2RQC6 (+1)	Cad	243 kDa	16.574	6.3914	7.1579	13.475	16.329	TRUE
Cadherin-11 OS=Mus musculus GN=Cdh11 PE=1 SV=1	P55288 (+1)	Cdh11	88 kDa	3.6831	25.566	8.9474	1.225	0	TRUE
Cadherin-2 OS=Mus musculus GN=Cdh2 PE=1 SV=1	D3YYT0 (+3)	Cdh2	94 kDa	0	7.9893	0	0.81665	0	TRUE
Calcium homeostasis modulator protein 2 OS=Mus musculus GN=Calhm2 PE=1 SV=1	D3Z2E8 (+2)	Calhm2	36 kDa	0	3.1957	0	0	0	TRUE
Calcium-binding mitochondrial carrier protein Aralar1 OS=Mus musculus GN=Slc25a12 PE=1 SV=	Q8BH59	Slc25a12	75 kDa	14.732	12.783	16.105	4.8999	6.0161	TRUE
Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Mus musculus GN=Slc25a24 PE=1 SV	Q8BMD8	Slc25a24	53 kDa	12.891	7.9893	10.737	2.0416	3.4377	TRUE
Caldesmon 1 OS=Mus musculus GN=Cald1 PE=1 SV=1	Q8VCQ8	Cald1	60 kDa	0	14.381	10.737	17.15	13.321	TRUE
Calmodulin-1 OS=Mus musculus GN=Calm1 PE=1 SV=1	Q3UKW2	Calm1	22 kDa	3.6831	3.1957	3.5789	2.45	2.1486	TRUE
Calnexin OS=Mus musculus GN=Canx PE=1 SV=1	P35564 (+1)	Canx	67 kDa	5.5246	11.185	12.526	12.25	13.751	TRUE
cAMP-dependent protein kinase catalytic subunit alpha OS=Mus musculus GN=Prkaca PE=1 SV=	P05132	Prkaca	41 kDa	3.6831	0	7.1579	2.0416	3.4377	TRUE
Cancer-related nucleoside-triphosphatase homolog OS=Mus musculus GN=Ntpcr PE=1 SV=1	D3Z2W9	Ntpcr	17 kDa	3.6831	0	0	0	0	TRUE
Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a OS=Mus musculus GN=Capzb	A2AMW0 (+1)	Capzb	29 kDa	5.5246	9.5872	16.105	8.9832	10.743	TRUE
Caprin-1 OS=Mus musculus GN=Caprin1 PE=1 SV=2	Q60865	Caprin1	78 kDa	7.3662	4.7936	5.3684	2.0416	2.1486	TRUE
Carboxylic ester hydrolase OS=Mus musculus GN=Ces1g PE=1 SV=1	Q3UW56 (+1)	Ces1g	63 kDa	0	7.9893	3.5789	4.0833	2.1486	TRUE
Carnitine O-palmitoyltransferase 1, liver isoform OS=Mus musculus GN=Cpt1a PE=1 SV=4	P97742 (+2)	Cpt1a	88 kDa	0	0	3.5789	0	2.1486	TRUE
Casein kinase II subunit alpha OS=Mus musculus GN=Csnk2a1 PE=1 SV=2	Q60737 (+1)	Csnk2a1	45 kDa	3.6831	3.1957	3.5789	3.2666	2.1486	TRUE
Catenin alpha-1 OS=Mus musculus GN=Ctnna1 PE=1 SV=1	P26231 (+1)	Ctnna1	100 kDa	23.94	46.338	28.632	4.4916	3.008	TRUE
Catenin beta-1 OS=Mus musculus GN=Ctnnb1 PE=1 SV=1	Q02248 (+1)	Ctnnb1	85 kDa	23.94	31.957	17.895	4.4916	2.1486	TRUE
Catenin delta-1 OS=Mus musculus GN=Ctnnd1 PE=1 SV=2	P30999	Ctnnd1	105 kDa	29.465	43.142	39.368	9.7998	5.5863	TRUE
Caveolae-associated protein 1 OS=Mus musculus GN=Cavin1 PE=1 SV=1	O54724	Cavin1	44 kDa	0	7.9893	0	5.7166	5.1566	TRUE
Caveolin-1 OS=Mus musculus GN=Cav1 PE=1 SV=1	P49817	Cav1	21 kDa	0	3.1957	0	0.81665	1.2892	TRUE
CCR4-NOT transcription complex subunit 4 OS=Mus musculus GN=Cnot4 PE=1 SV=1	E9QA19 (+1)	Cnot4	71 kDa	7.3662	7.9893	3.5789	0	0	TRUE
CD109 antigen OS=Mus musculus GN=Cd109 PE=1 SV=1	A6MDD3 (+1)	Cd109	162 kDa	18.415	11.185	17.895	0	2.1486	TRUE
CD166 antigen OS=Mus musculus GN=Alcam PE=1 SV=1	E9Q3Q6 (+3)	Alcam	64 kDa	20.257	0	10.737	0	0	TRUE
CD34 antigen, isoform CRA_b OS=Mus musculus GN=Cd34 PE=2 SV=1	Q543B6 (+1)	Cd34	41 kDa	5.5246	4.7936	3.5789	1.225	0.85944	TRUE
CD44 antigen OS=Mus musculus GN=Cd44 PE=1 SV=1	A2APM1 (+3)	Cd44	72 kDa	12.891	15.979	7.1579	3.2666	3.008	TRUE
CD63 antigen OS=Mus musculus GN=Cd63 PE=1 SV=2	P41731 (+3)	Cd63	26 kDa	0	4.7936	0	1.6333	1.7189	TRUE
CD97 antigen OS=Mus musculus GN=Cd97 PE=1 SV=2	Q9Z0M6	Cd97	90 kDa	0	7.9893	3.5789	1.225	0.85944	TRUE
Cdc42 effector protein 1 OS=Mus musculus GN=Cdc42ep1 PE=1 SV=1	Q91W92	Cdc42ep1	43 kDa	5.5246	7.9893	8.9474	1.6333	1.7189	TRUE
Cell surface glycoprotein MUC18 OS=Mus musculus GN=Mcam PE=1 SV=1	Q8R2Y2	Mcam	72 kDa	3.6831	0	0	0	0	TRUE
Cell surface hyaluronidase OS=Mus musculus GN=Tmem2 PE=1 SV=1	Q5FWI3	Tmem2	154 kDa	7.3662	14.381	3.5789	0	0	TRUE
Charged multivesicular body protein 1a OS=Mus musculus GN=Chmp1a PE=1 SV=1	Q921W0	Chmp1a	22 kDa	3.6831	0	3.5789	0	0	TRUE
Choline transporter-like protein 2 OS=Mus musculus GN=Slc44a2 PE=1 SV=2	Q8BY89	Slc44a2	80 kDa	0	6.3914	3.5789	1.6333	1.2892	TRUE
Chondroitin sulfate proteoglycan 4 OS=Mus musculus GN=Cspg4 PE=1 SV=3	Q8VHY0	Cspg4	252 kDa	51.563	60.719	17.895	1.225	0	TRUE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Citrate synthase, mitochondrial OS=Mus musculus GN=Cs PE=1 SV=1	Q9CZU6	Cs	52 kDa	9.2077	12.783	16.105	2.8583	3.008	TRUE
Clathrin interactor 1 OS=Mus musculus GN=Clint1 PE=1 SV=1	Q5SUH6 (+1)	Clint1	70 kDa	11.049	11.185	12.526	3.6749	3.8675	TRUE
Collagen alpha-1(I) chain OS=Mus musculus GN=Col1a1 PE=1 SV=4	P11087	Col1a1	138 kDa	0	7.9893	3.5789	10.616	3.8675	TRUE
Collagen alpha-1(VI) chain OS=Mus musculus GN=Col6a1 PE=1 SV=1	Q04857	Col6a1	108 kDa	3.6831	4.7936	3.5789	4.4916	3.4377	TRUE
Collagen alpha-2(V) chain OS=Mus musculus GN=Col5a2 PE=1 SV=1	Q3U962	Col5a2	145 kDa	0	0	3.5789	2.0416	1.2892	TRUE
Collagen, type V, alpha 1 OS=Mus musculus GN=Col5a1 PE=1 SV=1	B1AWB9 (+1)	Col5a1	184 kDa	0	4.7936	0	4.0833	0	TRUE
Collagen, type VI, alpha 3 OS=Mus musculus GN=Col6a3 PE=1 SV=2	E9PWQ3	Col6a3	354 kDa	5.5246	19.174	16.105	11.841	12.032	TRUE
Complement C3 OS=Mus musculus GN=C3 PE=1 SV=3	P01027	C3	186 kDa	7.3662	6.3914	7.1579	1.6333	3.4377	TRUE
Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Mus musculus GN	Q8R5L1	C1qbp	31 kDa	3.6831	0	0	1.6333	2.1486	TRUE
Complement component 4B (Childo blood group) OS=Mus musculus GN=C4b PE=2 SV=1	B2RWX2 (+2)	C4b	193 kDa	3.6831	0	0	0	0	TRUE
Constitutive coactivator of PPAR-gamma-like protein 1 OS=Mus musculus GN=FAM120A PE=1 SV	Q6A0A9	FAM120A	122 kDa	7.3662	7.9893	8.9474	5.7166	6.4458	TRUE
COP9 signalosome complex subunit 5 OS=Mus musculus GN=Cops5 PE=1 SV=3	O35864	Cops5	38 kDa	3.6831	3.1957	3.5789	2.0416	1.7189	TRUE
CTP synthase 1 OS=Mus musculus GN=Ctps1 PE=1 SV=2	P70698	Ctps1	67 kDa	14.732	14.381	10.737	6.9416	7.3052	TRUE
CUB and Sushi multiple domains 2 OS=Mus musculus GN=Csmd2 PE=1 SV=2	V9GX34	Csmd2	392 kDa	3.6831	0	0	0	0	TRUE
Cullin-associated NEDD8-dissociated protein 1 OS=Mus musculus GN=Cand1 PE=1 SV=2	Q6ZQ38	Cand1	136 kDa	11.049	22.37	21.474	15.108	12.892	TRUE
Cyclin-dependent kinase 1 OS=Mus musculus GN=Cdk1 PE=1 SV=3	P11440 (+1)	Cdk1	34 kDa	9.2077	19.174	17.895	9.3915	8.5944	TRUE
Cystatin-B OS=Mus musculus GN=Cstb PE=1 SV=1	Q62426	Cstb	11 kDa	5.5246	0	7.1579	1.225	1.2892	TRUE
Cytochrome b-c1 complex subunit 2, mitochondrial OS=Mus musculus GN=Uqcrc2 PE=1 SV=1	Q9DB77	Uqcrc2	48 kDa	11.049	12.783	14.316	5.3082	7.3052	TRUE
Cytochrome c oxidase subunit 5A, mitochondrial OS=Mus musculus GN=Cox5a PE=1 SV=2	P12787	Cox5a	16 kDa	0	4.7936	3.5789	2.0416	0.85944	TRUE
Cytochrome c oxidase subunit IV isoform 1 OS=Mus musculus GN=Cox4i1 PE=1 SV=1	A2RSV8 (+1)	Cox4i1	20 kDa	0	3.1957	3.5789	2.8583	2.1486	TRUE
Cytochrome c, somatic OS=Mus musculus GN=Cycs PE=1 SV=2	P62897 (+1)	Cycs	12 kDa	3.6831	6.3914	3.5789	4.8999	1.7189	TRUE
Cytochrome c1, heme protein, mitochondrial OS=Mus musculus GN=Cyc1 PE=1 SV=1	Q9D0M3	Cyc1	35 kDa	3.6831	6.3914	8.9474	1.225	3.008	TRUE
Cytokine receptor-like factor 1 OS=Mus musculus GN=Crlf1 PE=1 SV=1	Q9JM58	Crlf1	47 kDa	0	3.1957	0	0	0	TRUE
Cytoplasmic FMR1-interacting protein 1 OS=Mus musculus GN=Cyfip1 PE=1 SV=1	Q7TMB8	Cyfip1	145 kDa	3.6831	4.7936	3.5789	4.4916	3.4377	TRUE
Cytoskeleton-associated protein 4 OS=Mus musculus GN=Ckap4 PE=1 SV=2	Q8BMK4	Ckap4	64 kDa	22.099	27.164	28.632	8.9832	6.4458	TRUE
Cytoskeleton-associated protein 5 OS=Mus musculus GN=Ckap5 PE=1 SV=1	Z4YL78	Ckap5	219 kDa	0	0	3.5789	5.3082	3.4377	TRUE
Cytosolic phospholipase A2 OS=Mus musculus GN=Pla2g4a PE=1 SV=1	P47713 (+2)	Pla2g4a	85 kDa	0	4.7936	0	8.1665	3.8675	TRUE
D-3-phosphoglycerate dehydrogenase OS=Mus musculus GN=Phgdh PE=1 SV=3	Q61753	Phgdh	57 kDa	16.574	11.185	10.737	10.208	10.743	TRUE
Ddx3x protein OS=Mus musculus GN=Ddx3x PE=2 SV=1	B7ZWF1 (+3)	Ddx3x	73 kDa	14.732	12.783	12.526	9.3915	9.4538	TRUE
DEAD (Asp-Glu-Ala-Asp) box polypeptide 17, isoform CRA_a OS=Mus musculus GN=Ddx17 PE=1 S	Q3U741 (+1)	Ddx17	73 kDa	9.2077	6.3914	0	6.1249	6.4458	TRUE
DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 OS=Mus musculus GN=Ddx5 PE=2 SV=1	A1L333 (+4)	Ddx5	69 kDa	12.891	9.5872	10.737	7.7582	7.3052	TRUE
Death domain-containing membrane protein NRADD OS=Mus musculus GN=Nradd PE=1 SV=1	Q8CJ26	Nradd	25 kDa	7.3662	4.7936	3.5789	0	0	TRUE
Desmoglein 1 beta OS=Mus musculus GN=Dsg1b PE=2 SV=1	B2RQH0 (+1)	Dsg1b	114 kDa	9.2077	7.9893	0	0	0	TRUE
Desmoplakin OS=Mus musculus GN=Dsp PE=1 SV=1	E9Q557	Dsp	333 kDa	49.722	36.751	19.684	0	0	TRUE
Destrin OS=Mus musculus GN=Dstn PE=1 SV=1	Q4FK36 (+1)	Dstn	19 kDa	5.5246	9.5872	7.1579	6.5332	5.5863	TRUE
Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus musculus GN=Dld PE=1 SV=2	O08749	Dld	54 kDa	3.6831	3.1957	7.1579	4.4916	5.5863	TRUE
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, r	Q8BMF4	Dlat	68 kDa	0	7.9893	5.3684	3.6749	3.8675	TRUE
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase cor	Q9D2G2	Dlst	49 kDa	0	4.7936	7.1579	2.0416	2.5783	TRUE
Disabled homolog 2 OS=Mus musculus GN=Dab2 PE=1 SV=1	A0A0R4J104 (+2)	Dab2	82 kDa	0	0	3.5789	3.2666	5.1566	TRUE
Discoidin domain-containing receptor 2 OS=Mus musculus GN=Ddr2 PE=1 SV=2	Q62371	Ddr2	96 kDa	0	3.1957	0	1.225	0	TRUE
Discoidin, CUB and LCCL domain-containing protein 2 OS=Mus musculus GN=Dcbld2 PE=1 SV=1	Q91ZV3	Dcbld2	84 kDa	3.6831	6.3914	10.737	0	0	TRUE
Disintegrin and metalloproteinase domain-containing protein 10 OS=Mus musculus GN=Adam10	O35598	Adam10	84 kDa	0	0	3.5789	0	2.1486	TRUE
Disintegrin and metalloproteinase domain-containing protein 9 OS=Mus musculus GN=Adam9 PE	A0A140LHU0 (+2)	Adam9	94 kDa	0	3.1957	0	2.0416	1.7189	TRUE
DNA helicase OS=Mus musculus GN=Mcm3 PE=2 SV=1	Q3ULD6	Mcm3	92 kDa	12.891	6.3914	5.3684	6.1249	7.7349	TRUE
DnaJ homolog subfamily A member 1 OS=Mus musculus GN=Dnaja1 PE=1 SV=1	P63037 (+1)	Dnaja1	45 kDa	11.049	4.7936	10.737	7.3499	3.4377	TRUE
DnaJ homolog subfamily A member 3, mitochondrial OS=Mus musculus GN=Dnaja3 PE=1 SV=1	Q99M87	Dnaja3	52 kDa	0	4.7936	0	0	0	TRUE
DnaJ homolog subfamily B member 11 OS=Mus musculus GN=Dnajb11 PE=1 SV=1	Q99KV1	Dnajb11	41 kDa	5.5246	7.9893	8.9474	1.225	1.2892	TRUE
DnaJ homolog subfamily B member 2 OS=Mus musculus GN=Dnajb2 PE=1 SV=3	Q9QYI5	Dnajb2	36 kDa	5.5246	0	0	0	0	TRUE
DnaJ homolog subfamily B member 6 OS=Mus musculus GN=Dnajb6 PE=1 SV=4	O54946	Dnajb6	40 kDa	12.891	9.5872	16.105	0	1.2892	TRUE
DnaJ homolog subfamily C member 7 OS=Mus musculus GN=Dnajc7 PE=1 SV=2	Q9QYI3	Dnajc7	56 kDa	0	0	3.5789	2.0416	2.5783	TRUE
Dolichol-phosphate mannosyltransferase subunit 1 OS=Mus musculus GN=Dpm1 PE=1 SV=1	O70152	Dpm1	29 kDa	7.3662	4.7936	8.9474	1.225	0.85944	TRUE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Mus musculus	O54734 (+2)	Ddost	49 kDa	0	3.1957	0	2.45	2.1486	TRUE
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Mus musculus GN=I	Q3U900 (+3)	Rpn1	69 kDa	5.5246	15.979	10.737	13.066	11.602	TRUE
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Mus musculus	P46978 (+5)	Stt3a	81 kDa	0	4.7936	3.5789	3.2666	2.1486	TRUE
Dynamin-2 OS=Mus musculus GN=Dnm2 PE=1 SV=2	F8WIV5 (+4)	Dnm2	98 kDa	0	4.7936	0	2.8583	3.008	TRUE
Dystroglycan 1 OS=Mus musculus GN=Dag1 PE=1 SV=1	Q544G5 (+2)	Dag1	97 kDa	9.2077	6.3914	5.3684	0	0	TRUE
E3 SUMO-protein ligase RanBP2 OS=Mus musculus GN=Ranbp2 PE=1 SV=2	Q9ERU9	Ranbp2	341 kDa	5.5246	0	0	1.6333	0	TRUE
E3 ubiquitin-protein ligase DTX3L OS=Mus musculus GN=Dtx3l PE=1 SV=1	Q3UIR3	Dtx3l	83 kDa	0	3.1957	0	2.8583	0	TRUE
E3 ubiquitin-protein ligase RNF213 OS=Mus musculus GN=Rnf213 PE=1 SV=1	A0A171EBL2 (+1)	Rnf213	585 kDa	0	22.37	0	31.441	1.2892	TRUE
E3 ubiquitin-protein ligase XIAP OS=Mus musculus GN=Xiap PE=1 SV=2	Q60989	Xiap	56 kDa	0	4.7936	3.5789	0	0	TRUE
Ectonucleotide pyrophosphatase/phosphodiesterase 1, isoform CRA_a OS=Mus musculus GN=Enp	A0A0R4J1Q7 (+2)	Enpp1	103 kDa	5.5246	4.7936	7.1579	0	0	TRUE
eIF-2-alpha kinase activator GCN1 OS=Mus musculus GN=Gcn1 PE=1 SV=1	E9PVA8	Gcn1	293 kDa	14.732	7.9893	16.105	7.7582	6.4458	TRUE
ELAV-like protein 1 OS=Mus musculus GN=Elavl1 PE=1 SV=2	P70372 (+2)	Elavl1	36 kDa	3.6831	4.7936	3.5789	1.6333	2.1486	TRUE
Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3	P10126 (+2)	Eef1a1	50 kDa	75.503	51.132	84.105	50.224	65.317	TRUE
Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=1	A0A0R4J1E2	Eef1d	73 kDa	12.891	11.185	19.684	5.3082	4.7269	TRUE
Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tufm PE=1 SV=1	Q8BFR5	Tufm	50 kDa	0	3.1957	7.1579	5.7166	8.1647	TRUE
Elongin-B OS=Mus musculus GN=Elob PE=1 SV=1	P62869	Elob	13 kDa	12.891	9.5872	8.9474	3.2666	2.1486	TRUE
Embigin OS=Mus musculus GN=Emb PE=1 SV=2	P21995 (+3)	Emb	37 kDa	5.5246	3.1957	5.3684	0	0	TRUE
Emerin OS=Mus musculus GN=Emd PE=4 SV=1	A2AM95 (+1)	Emd	29 kDa	7.3662	4.7936	12.526	3.6749	3.4377	TRUE
Endoglin OS=Mus musculus GN=Eng PE=1 SV=1	Q3UAM9 (+1)	Eng	70 kDa	0	6.3914	0	0	0	TRUE
Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	P08113 (+3)	Hsp90b1	92 kDa	18.415	33.555	39.368	28.175	28.361	TRUE
Endosialin (Fragment) OS=Mus musculus GN=Cd248 PE=2 SV=1	A0A172Q386 (+1)	Cd248	72 kDa	3.6831	3.1957	3.5789	0	0	TRUE
Enoyl-CoA delta isomerase 1, mitochondrial OS=Mus musculus GN=Eci1 PE=1 SV=2	P42125 (+1)	Eci1	32 kDa	0	0	3.5789	0.81665	2.5783	TRUE
Envelope protein OS=Mus musculus PE=4 SV=1	A0A0A0U6W1		70 kDa	34.989	30.359	0	0	0	TRUE
Ephrin type-A receptor 2 OS=Mus musculus GN=Epha2 PE=1 SV=3	Q03145	Epha2	109 kDa	12.891	11.185	17.895	2.0416	2.1486	TRUE
Ephrin type-B receptor 4 OS=Mus musculus GN=Ephb4 PE=1 SV=2	P54761 (+2)	Ephb4	109 kDa	9.2077	9.5872	7.1579	0	0	TRUE
Ephrin-B1 OS=Mus musculus GN=Efnb1 PE=1 SV=1	P52795 (+1)	Efnb1	38 kDa	7.3662	3.1957	7.1579	0	0	TRUE
Epidermal growth factor receptor OS=Mus musculus GN=Egfr PE=1 SV=1	Q01279 (+1)	Egfr	135 kDa	0	17.576	7.1579	0	0	TRUE
Equilibrative nucleoside transporter 1 OS=Mus musculus GN=Slc29a1 PE=1 SV=3	Q9JIM1	Slc29a1	50 kDa	3.6831	0	0	0	0	TRUE
Erythrocyte band 7 integral membrane protein OS=Mus musculus GN=Stom PE=1 SV=3	P54116	Stom	31 kDa	0	0	3.5789	2.0416	2.1486	TRUE
Eukaryotic translation elongation factor 1 gamma OS=Mus musculus GN=Eef1g PE=1 SV=1	Q4FZK2 (+1)	Eef1g	50 kDa	12.891	14.381	17.895	11.841	14.61	TRUE
Eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked OS=Mus musculus G	Q3TML6 (+2)	Eif2s3x	51 kDa	7.3662	4.7936	5.3684	7.3499	6.8755	TRUE
Eukaryotic translation initiation factor 3 subunit A OS=Mus musculus GN=Eif3a PE=1 SV=5	P23116	Eif3a	162 kDa	5.5246	6.3914	8.9474	8.9832	7.7349	TRUE
Eukaryotic translation initiation factor 3 subunit E OS=Mus musculus GN=Eif3e PE=1 SV=1	P60229 (+1)	Eif3e	52 kDa	3.6831	6.3914	5.3684	4.4916	3.8675	TRUE
Eukaryotic translation initiation factor 3 subunit L OS=Mus musculus GN=Eif3l PE=1 SV=1	Q8QZY1	Eif3l	67 kDa	0	4.7936	7.1579	4.4916	4.7269	TRUE
Eukaryotic translation initiation factor 4, gamma 2 OS=Mus musculus GN=Eif4g2 PE=2 SV=1	A0JNY7 (+2)	Eif4g2	102 kDa	11.049	7.9893	12.526	2.45	2.5783	TRUE
Eukaryotic translation initiation factor 4E member 2 OS=Mus musculus GN=Eif4e2 PE=1 SV=1	Q0P688 (+1)	Eif4e2	28 kDa	7.3662	4.7936	10.737	0.81665	1.2892	TRUE
Exportin-1 OS=Mus musculus GN=Xpo1 PE=1 SV=1	Q6P5F9	Xpo1	123 kDa	3.6831	3.1957	5.3684	4.8999	7.3052	TRUE
Exportin-2 OS=Mus musculus GN=Cse1l PE=1 SV=1	Q9ERK4	Cse1l	110 kDa	9.2077	6.3914	3.5789	7.7582	6.8755	TRUE
F-actin-capping protein subunit alpha-1 OS=Mus musculus GN=Capza1 PE=1 SV=4	P47753 (+2)	Capza1	33 kDa	0	4.7936	5.3684	3.2666	2.5783	TRUE
F-actin-capping protein subunit alpha-2 OS=Mus musculus GN=Capza2 PE=1 SV=3	P47754 (+2)	Capza2	33 kDa	5.5246	4.7936	5.3684	4.4916	2.1486	TRUE
F-box-like/WD repeat-containing protein TBL1X OS=Mus musculus GN=Tbl1x PE=1 SV=2	Q9QXE7	Tbl1x	57 kDa	7.3662	3.1957	7.1579	0	3.4377	TRUE
Family with sequence similarity 171, member A1 OS=Mus musculus GN=Fam171a1 PE=1 SV=1	A2ATK9	Fam171a1	98 kDa	14.732	7.9893	7.1579	0	0	TRUE
Fascin OS=Mus musculus GN=Fscn1 PE=1 SV=4	Q61553	Fscn1	55 kDa	9.2077	9.5872	10.737	10.616	14.61	TRUE
FAT atypical cadherin 1 OS=Mus musculus GN=Fat1 PE=1 SV=1	F2Z4A3	Fat1	506 kDa	47.88	67.11	42.947	0	0	TRUE
Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2	P19096	Fasn	272 kDa	14.732	17.576	30.421	23.275	30.51	TRUE
Fatty acyl-CoA reductase 1 OS=Mus musculus GN=Far1 PE=1 SV=1	Q922J9	Far1	59 kDa	3.6831	4.7936	5.3684	1.6333	2.5783	TRUE
FERM domain-containing protein 4A OS=Mus musculus GN=Frmd4a PE=1 SV=1	H3BIZ7 (+1)	Frmd4a	115 kDa	5.5246	0	0	0	0	TRUE
FERM, ARHGEF and pleckstrin domain-containing protein 1 OS=Mus musculus GN=Farp1 PE=1 SV	F8VPU2	Farp1	119 kDa	9.2077	7.9893	14.316	5.3082	6.0161	TRUE
Ferritin heavy chain OS=Mus musculus GN=Fth1 PE=1 SV=2	P09528	Fth1	21 kDa	3.6831	3.1957	5.3684	0	0.85944	TRUE
Fibroblast growth factor receptor OS=Mus musculus GN=Fgfr2 PE=2 SV=1	A1YYN6 (+2)	Fgfr2	92 kDa	0	4.7936	0	0	0	TRUE
Fibronectin OS=Mus musculus GN=Fn1 PE=1 SV=1	Q3UHL6	Fn1	260 kDa	3.6831	11.185	5.3684	3.6749	1.7189	TRUE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Fibulin-1 OS=Mus musculus GN=Fbln1 PE=2 SV=1	Q3TWK8	Fbln1	78 kDa	0	3.1957	0	0	0	TRUE
Fibulin-2 OS=Mus musculus GN=Fbln2 PE=1 SV=2	P37889 (+1)	Fbln2	132 kDa	12.891	17.576	17.895	2.8583	4.2972	TRUE
Filamin A-interacting protein 1-like OS=Mus musculus GN=Filip1l PE=1 SV=2	Q6P6L0	Filip1l	130 kDa	0	0	3.5789	2.8583	2.5783	TRUE
Filamin-A OS=Mus musculus GN=Flna PE=1 SV=5	Q8BTM8	Flna	281 kDa	82.87	116.64	105.58	84.932	83.795	TRUE
Filamin-B OS=Mus musculus GN=Flnb PE=1 SV=3	Q80X90	Flnb	278 kDa	46.039	49.534	51.895	51.449	64.028	TRUE
Fractalkine OS=Mus musculus GN=Cx3cl1 PE=1 SV=3	O35188 (+1)	Cx3cl1	42 kDa	0	4.7936	7.1579	1.6333	1.7189	TRUE
Fragile X mental retardation syndrome-related protein 1 OS=Mus musculus GN=Fxr1 PE=1 SV=2	Q61584	Fxr1	76 kDa	7.3662	3.1957	5.3684	2.8583	2.5783	TRUE
Galectin (Fragment) OS=Mus musculus GN=Lgals3 PE=2 SV=1	Q3V471 (+1)	Lgals3	20 kDa	3.6831	4.7936	5.3684	2.8583	3.8675	TRUE
Galectin OS=Mus musculus GN=Lgals8 PE=1 SV=1	Q542M5 (+1)	Lgals8	36 kDa	0	3.1957	0	0.81665	0	TRUE
Galectin OS=Mus musculus GN=Lgals9 PE=1 SV=1	B1AQR8 (+1)	Lgals9	40 kDa	11.049	17.576	7.1579	2.8583	0.85944	TRUE
Galectin-1 OS=Mus musculus GN=Lgals1 PE=1 SV=3	P16045	Lgals1	15 kDa	22.099	15.979	12.526	20.416	24.064	TRUE
General transcription factor II-I OS=Mus musculus GN=Gtf2i PE=1 SV=1	G3UYD0 (+1)	Gtf2i	103 kDa	7.3662	0	8.9474	1.6333	2.1486	TRUE
GLI-Kruppel family member GLI3 OS=Mus musculus GN=Gli3 PE=2 SV=1	B2RUG4 (+1)	Gli3	172 kDa	7.3662	3.1957	5.3684	0	0.85944	TRUE
Glucosidase 2 subunit beta OS=Mus musculus GN=Prkcsh PE=1 SV=1	O08795 (+1)	Prkcsh	59 kDa	0	9.5872	14.316	5.3082	6.8755	TRUE
Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus GN=Glud1 PE=1 SV=1	P26443	Glud1	61 kDa	11.049	14.381	26.842	10.616	13.321	TRUE
Glutamate--cysteine ligase regulatory subunit OS=Mus musculus GN=Gclm PE=1 SV=1	O09172 (+2)	Gclm	31 kDa	0	0	5.3684	2.0416	1.2892	TRUE
Glutamine--tRNA ligase OS=Mus musculus GN=Qars PE=1 SV=2	D3Z158 (+1)	Qars	85 kDa	0	4.7936	3.5789	4.0833	5.1566	TRUE
Glutathione S-transferase P 1 OS=Mus musculus GN=Gstp1 PE=1 SV=2	P19157	Gstp1	24 kDa	3.6831	0	7.1579	4.8999	5.5863	TRUE
Glycerol-3-phosphate dehydrogenase OS=Mus musculus GN=Gpd2 PE=1 SV=1	A2AQR0 (+1)	Gpd2	83 kDa	7.3662	4.7936	3.5789	4.4916	3.8675	TRUE
Glypican 1, isoform CRA_c OS=Mus musculus GN=Gpc1 PE=1 SV=1	Q3U379 (+1)	Gpc1	61 kDa	0	0	5.3684	0	0	TRUE
Glypican-4 OS=Mus musculus GN=Gpc4 PE=1 SV=2	P51655	Gpc4	63 kDa	9.2077	12.783	7.1579	0.81665	0	TRUE
GRB10-interacting GYF protein 1 OS=Mus musculus GN=Gigyf1 PE=1 SV=2	Q99MR1	Gigyf1	116 kDa	14.732	7.9893	14.316	0	0	TRUE
GRB10-interacting GYF protein 2 OS=Mus musculus GN=Gigyf2 PE=1 SV=1	G3UYG6 (+1)	Gigyf2	149 kDa	18.415	12.783	19.684	2.0416	1.7189	TRUE
GTP-binding nuclear protein Ran OS=Mus musculus GN=Ran PE=2 SV=1	Q3ULW0	Ran	24 kDa	7.3662	4.7936	10.737	7.7582	8.5944	TRUE
GTP-binding protein SAR1a OS=Mus musculus GN=Sar1a PE=1 SV=1	Q99JZ4	Sar1a	22 kDa	0	3.1957	3.5789	1.6333	1.7189	TRUE
Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Mus musculus GN=Gnai2 PE=1 SV=5	P08752	Gnai2	40 kDa	0	4.7936	0	3.2666	3.008	TRUE
H-2 class I histocompatibility antigen, D-B alpha chain OS=Mus musculus GN=H2-D1 PE=1 SV=2	P01899 (+2)	H2-D1	41 kDa	38.672	51.132	10.737	8.1665	2.1486	TRUE
Heat shock protein 1 (Chaperonin 10) OS=Mus musculus GN=Hspe1 PE=1 SV=1	Q4KL76 (+1)	Hspe1	11 kDa	7.3662	6.3914	14.316	3.6749	2.5783	TRUE
Heat shock protein beta-1 OS=Mus musculus GN=Hspb1 PE=1 SV=3	P14602 (+1)	Hspb1	23 kDa	0	3.1957	3.5789	0	0	TRUE
Heat shock protein beta-6 OS=Mus musculus GN=Hspb6 PE=1 SV=1	Q5EBG6	Hspb6	18 kDa	0	3.1957	0	0	0	TRUE
Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4	P07901 (+1)	Hsp90aa1	85 kDa	33.148	30.359	41.158	36.749	49.847	TRUE
Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=3	P11499 (+1)	Hsp90ab1	83 kDa	53.405	46.338	62.632	54.716	69.185	TRUE
Helicase-like transcription factor OS=Mus musculus GN=Hltf PE=1 SV=1	Q6PCN7	Hltf	113 kDa	0	0	5.3684	0	0	TRUE
Hepatocyte growth factor OS=Mus musculus GN=Hgf PE=1 SV=1	Q08048 (+1)	Hgf	83 kDa	0	3.1957	0	0	0	TRUE
Heterogeneous nuclear ribonucleoprotein A/B OS=Mus musculus GN=Hnrnpab PE=1 SV=1	Q20BD0 (+2)	Hnrnpab	36 kDa	7.3662	7.9893	10.737	3.6749	3.8675	TRUE
Heterogeneous nuclear ribonucleoprotein A0 OS=Mus musculus GN=Hnrnpa0 PE=1 SV=1	Q9CX86	Hnrnpa0	31 kDa	0	0	3.5789	2.0416	1.7189	TRUE
Heterogeneous nuclear ribonucleoprotein F OS=Mus musculus GN=Hnrnpf PE=1 SV=3	Q9Z2X1	Hnrnpf	46 kDa	9.2077	4.7936	3.5789	4.4916	6.4458	TRUE
Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnph1 PE=1 SV=3	O35737 (+2)	Hnrnph1	49 kDa	9.2077	9.5872	8.9474	2.45	4.2972	TRUE
Heterogeneous nuclear ribonucleoprotein Q OS=Mus musculus GN=Syncrip PE=1 SV=1	A0A0R4J259	Syncrip	63 kDa	5.5246	6.3914	3.5789	6.1249	4.7269	TRUE
Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Mus musculus GN=Hnrnpa2b1 PE=1 SV=2	O88569	Hnrnpa2b1	37 kDa	5.5246	3.1957	3.5789	3.2666	3.008	TRUE
Hexokinase-2 OS=Mus musculus GN=Hk2 PE=1 SV=1	O08528	Hk2	103 kDa	5.5246	0	0	4.8999	6.0161	TRUE
High affinity copper uptake protein 1 OS=Mus musculus GN=Slc31a1 PE=1 SV=1	A8Y5P1 (+2)	Slc31a1	14 kDa	0	3.1957	0	0	0	TRUE
High mobility group protein B1 OS=Mus musculus GN=Hmgb1 PE=1 SV=2	P63158 (+1)	Hmgb1	25 kDa	9.2077	6.3914	17.895	16.741	21.056	TRUE
High mobility group protein B2 OS=Mus musculus GN=Hmgb2 PE=1 SV=3	P30681	Hmgb2	24 kDa	12.891	0	8.9474	12.25	16.329	TRUE
Histidine ammonia-lyase OS=Mus musculus GN=Hal PE=1 SV=1	B2RXW1 (+2)	Hal	72 kDa	0	3.1957	0	0	0	TRUE
Histidine triad nucleotide-binding protein 1 OS=Mus musculus GN=Hint1 PE=1 SV=3	P70349	Hint1	14 kDa	0	0	3.5789	2.0416	1.2892	TRUE
Histone acetyltransferase p300 OS=Mus musculus GN=Ep300 PE=1 SV=2	B2RWS6	Ep300	263 kDa	3.6831	3.1957	3.5789	0	0	TRUE
Histone deacetylase 1 OS=Mus musculus GN=Hdac1 PE=1 SV=1	O09106 (+1)	Hdac1	55 kDa	3.6831	3.1957	0	1.6333	2.5783	TRUE
Histone deacetylase 6 (Fragment) OS=Mus musculus GN=Hdac6 PE=1 SV=1	A0A1B0GX25 (+3)	Hdac6	110 kDa	3.6831	0	3.5789	2.0416	2.1486	TRUE
Histone H2A OS=Mus musculus GN=Hist2h2aa1 PE=2 SV=1	B2RWH3 (+4)	Hist2h2aa1	14 kDa	5.5246	3.1957	5.3684	0	0	TRUE
Histone H2B type 2-B OS=Mus musculus GN=Hist2h2bb PE=1 SV=3	Q64525	Hist2h2bb	14 kDa	5.5246	4.7936	7.1579	0	0	TRUE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Histone H4 OS=Mus musculus GN=Hist2h4 PE=1 SV=1	B2RTM0 (+1)	Hist2h4	11 kDa	5.5246	0	3.5789	0	0.85944	TRUE
Histone-binding protein RBBP7 OS=Mus musculus GN=Rbbp7 PE=1 SV=1	A2AFJ1 (+1)	Rbbp7	47 kDa	7.3662	7.9893	5.3684	4.0833	4.7269	TRUE
Hsc70-interacting protein OS=Mus musculus GN=St13 PE=1 SV=1	F8WJK8 (+2)	St13	41 kDa	9.2077	7.9893	8.9474	4.4916	5.5863	TRUE
Hypoxanthine-guanine phosphoribosyltransferase OS=Mus musculus GN=Hprt1 PE=1 SV=3	P00493 (+1)	Hprt1	25 kDa	0	3.1957	5.3684	3.2666	3.8675	TRUE
Immunoglobulin superfamily member 3 OS=Mus musculus GN=Igsf3 PE=1 SV=1	A0A0A6YX40 (+1)	Igsf3	137 kDa	3.6831	4.7936	8.9474	0	0	TRUE
Immunoglobulin superfamily member 8 OS=Mus musculus GN=Igsf8 PE=1 SV=1	A0A0R4J117 (+1)	Igsf8	65 kDa	7.3662	7.9893	3.5789	1.225	0	TRUE
Importin subunit alpha-1 OS=Mus musculus GN=Kpna2 PE=1 SV=2	P52293 (+1)	Kpna2	58 kDa	0	7.9893	3.5789	4.0833	3.4377	TRUE
Importin subunit beta-1 OS=Mus musculus GN=Kpnb1 PE=1 SV=2	P70168 (+2)	Kpnb1	97 kDa	5.5246	9.5872	7.1579	10.208	6.8755	TRUE
Importin-4 OS=Mus musculus GN=Ipo4 PE=1 SV=1	Q8VI75	Ipo4	119 kDa	0	3.1957	5.3684	2.8583	2.5783	TRUE
Importin-5 OS=Mus musculus GN=Ipo5 PE=1 SV=3	Q8BKC5	Ipo5	124 kDa	14.732	14.381	21.474	14.7	15.9	TRUE
Inactive tyrosine-protein kinase 7 OS=Mus musculus GN=Ptk7 PE=1 SV=1	Q8BKG3	Ptk7	118 kDa	62.613	54.327	46.526	3.6749	3.8675	TRUE
Inositol-1-monophosphatase OS=Mus musculus GN=Impa1 PE=2 SV=1	Q3U5R8 (+2)	Impa1	30 kDa	9.2077	6.3914	7.1579	1.225	2.5783	TRUE
Insulin receptor-related protein OS=Mus musculus GN=Insrr PE=1 SV=2	Q9WTL4	Insrr	145 kDa	3.6831	0	0	0	0	TRUE
Insulin-like growth factor 1 receptor OS=Mus musculus GN=Igf1r PE=1 SV=3	Q60751	Igf1r	156 kDa	5.5246	15.979	8.9474	0	0	TRUE
Insulin-like growth factor 2 mRNA-binding protein 2 OS=Mus musculus GN=Igf2bp2 PE=1 SV=1	Q5SF07	Igf2bp2	66 kDa	0	3.1957	0	2.0416	2.5783	TRUE
Insulin-like growth factor 2 mRNA-binding protein 3 OS=Mus musculus GN=Igf2bp3 PE=1 SV=1	Q9CPN8	Igf2bp3	64 kDa	7.3662	4.7936	3.5789	4.8999	5.5863	TRUE
Insulin-like growth factor 2 receptor OS=Mus musculus GN=Igf2r PE=2 SV=1	B9EKB8 (+1)	Igf2r	274 kDa	9.2077	4.7936	3.5789	5.3082	6.0161	TRUE
Integrin alpha-1 OS=Mus musculus GN=Itga1 PE=1 SV=2	Q3V3R4	Itga1	131 kDa	0	11.185	0	0.81665	0	TRUE
Integrin alpha-11 OS=Mus musculus GN=Itga11 PE=1 SV=1	A0A0B4J1F0 (+1)	Itga11	133 kDa	0	12.783	0	0	0	TRUE
Integrin alpha-3 OS=Mus musculus GN=Itga3 PE=1 SV=1	Q62470	Itga3	117 kDa	23.94	15.979	21.474	2.45	3.8675	TRUE
Integrin alpha-5 OS=Mus musculus GN=Itga5 PE=1 SV=3	P11688 (+1)	Itga5	115 kDa	53.405	63.914	48.316	5.3082	5.1566	TRUE
Integrin beta OS=Mus musculus GN=Itgb5 PE=1 SV=1	Q6PE70	Itgb5	88 kDa	12.891	15.979	19.684	1.6333	2.5783	TRUE
Integrin beta-1 OS=Mus musculus GN=Itgb1 PE=1 SV=1	P09055	Itgb1	88 kDa	33.148	46.338	30.421	8.5749	9.8835	TRUE
Inter alpha-trypsin inhibitor, heavy chain 4 OS=Mus musculus GN=Itih4 PE=1 SV=2	A6X935 (+2)	Itih4	105 kDa	5.5246	0	0	0	0	TRUE
Inter-alpha trypsin inhibitor, heavy chain 2 OS=Mus musculus GN=Itih2 PE=1 SV=1	G3X977 (+2)	Itih2	106 kDa	7.3662	4.7936	7.1579	0	0	TRUE
Interferon-activable protein 204 OS=Mus musculus GN=Ifi204 PE=1 SV=1	E9QKL6 (+1)	Ifi204	69 kDa	3.6831	4.7936	0	7.3499	4.2972	TRUE
Interferon-activable protein 205-B OS=Mus musculus GN=Mnda PE=1 SV=1	P0DOV1	Mnda	47 kDa	7.3662	11.185	7.1579	6.5332	4.7269	TRUE
Interferon-induced protein with tetratricopeptide repeats 1 OS=Mus musculus GN=Ifit1 PE=1 SV	Q64282 (+1)	Ifit1	54 kDa	0	6.3914	0	4.8999	0	TRUE
Interferon-induced transmembrane protein 3 OS=Mus musculus GN=Ifitm3 PE=1 SV=1	Q9CQW9	Ifitm3	15 kDa	3.6831	6.3914	0	2.0416	1.7189	TRUE
Interferon-stimulated gene 20 kDa protein OS=Mus musculus GN=Isg20 PE=1 SV=1	Q9JL16	Isg20	33 kDa	0	6.3914	0	0	0	TRUE
Interleukin-1 receptor accessory protein OS=Mus musculus GN=Il1rap PE=1 SV=1	Q61730	Il1rap	66 kDa	3.6831	9.5872	5.3684	0	0	TRUE
Interleukin-6 receptor subunit beta OS=Mus musculus GN=Il6st PE=1 SV=1	V9GX00	Il6st	95 kDa	0	6.3914	0	0.81665	0.85944	TRUE
Irgm1 OS=Mus musculus GN=OTTMUSPWKG00059374 PE=4 SV=1	A0A1G5SJJ3 (+5)	OTTMUSPWKG	47 kDa	0	3.1957	0	1.6333	0	TRUE
Isochorismatase domain-containing protein 1 OS=Mus musculus GN=Isoc1 PE=1 SV=1	Q91V64	Isoc1	32 kDa	3.6831	0	3.5789	0.81665	0	TRUE
Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Mus musculus GN=Idh3b PE=1 SV=1	Q91VA7	Idh3b	42 kDa	0	4.7936	5.3684	4.4916	3.8675	TRUE
Isoleucine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Iars PE=1 SV=2	Q8BU30	Iars	144 kDa	20.257	19.174	16.105	14.7	14.181	TRUE
Junction plakoglobin OS=Mus musculus GN=Jup PE=1 SV=3	Q02257	Jup	82 kDa	22.099	23.968	16.105	2.0416	2.1486	TRUE
Keratin 16 OS=Mus musculus GN=Krt16 PE=1 SV=1	Q3SYP5 (+4)	Krt16	52 kDa	75.503	33.555	44.737	2.45	2.1486	TRUE
Keratin 19 OS=Mus musculus GN=Krt19 PE=1 SV=1	B1AQ78 (+1)	Krt19	45 kDa	33.148	17.576	0	0	0	TRUE
Keratin 5 OS=Mus musculus GN=Krt5 PE=1 SV=2	Q32P04 (+1)	Krt5	62 kDa	73.662	60.719	41.158	2.8583	3.8675	TRUE
Keratin 77 OS=Mus musculus GN=Krt77 PE=2 SV=1	Q08EK4 (+2)	Krt77	61 kDa	49.722	62.317	17.895	0	0	TRUE
Keratin 83 OS=Mus musculus GN=Krt83 PE=1 SV=1	E9Q1Y9	Krt83	53 kDa	23.94	0	0	0	0	TRUE
Keratin 90 OS=Mus musculus GN=Krt90 PE=1 SV=1	E9Q1Z0 (+1)	Krt90	58 kDa	36.831	31.957	23.263	0	0	TRUE
Keratin Kb40 OS=Mus musculus GN=Krt78 PE=2 SV=1	Q6IFT3	Krt78	85 kDa	14.732	12.783	12.526	1.6333	2.5783	TRUE
Keratin, type I cuticular Ha3-II OS=Mus musculus GN=Krt33b PE=1 SV=2	Q61897	Krt33b	46 kDa	27.623	0	0	0	0	TRUE
Keratin, type I cuticular Ha5 OS=Mus musculus GN=Krt35 PE=1 SV=1	Q497I4	Krt35	51 kDa	14.732	0	0	0	0	TRUE
Keratin, type I cytoskeletal 10 OS=Mus musculus GN=Krt10 PE=1 SV=1	A2A513	Krt10	57 kDa	134.43	145.41	82.316	3.2666	6.4458	TRUE
Keratin, type I cytoskeletal 14 OS=Mus musculus GN=Krt14 PE=1 SV=2	Q61781	Krt14	53 kDa	93.919	46.338	51.895	4.0833	4.2972	TRUE
Keratin, type I cytoskeletal 17 OS=Mus musculus GN=Krt17 PE=1 SV=3	Q9QWL7	Krt17	48 kDa	77.345	35.153	51.895	3.6749	5.5863	TRUE
Keratin, type I cytoskeletal 42 OS=Mus musculus GN=Krt42 PE=1 SV=1	Q6IFX2	Krt42	50 kDa	77.345	39.947	41.158	0	0	TRUE
Keratin, type II cuticular Hb2 OS=Mus musculus GN=Krt82 PE=1 SV=2	Q99M74	Krt82	57 kDa	11.049	0	0	0	0	TRUE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Keratin, type II cuticular Hb5 OS=Mus musculus GN=Krt85 PE=1 SV=2	Q9Z2T6	Krt85	56 kDa	34.989	12.783	0	0	0	TRUE
Keratin, type II cytoskeletal 1 OS=Mus musculus GN=Krt1 PE=1 SV=4	P04104	Krt1	66 kDa	55.246	68.708	23.263	2.8583	3.4377	TRUE
Keratin, type II cytoskeletal 2 epidermal OS=Mus musculus GN=Krt2 PE=1 SV=1	Q3TTY5	Krt2	71 kDa	49.722	55.925	44.737	2.45	3.008	TRUE
Keratin, type II cytoskeletal 2 oral OS=Mus musculus GN=Krt76 PE=1 SV=1	Q3UV17	Krt76	63 kDa	36.831	28.762	0	0	0	TRUE
Keratin, type II cytoskeletal 6A OS=Mus musculus GN=Krt6a PE=1 SV=3	P50446	Krt6a	59 kDa	77.345	59.121	46.526	2.0416	5.5863	TRUE
Keratin, type II cytoskeletal 73 OS=Mus musculus GN=Krt73 PE=1 SV=1	Q6NXH9	Krt73	59 kDa	51.563	60.719	0	0	0	TRUE
Kin of IRRE-like protein 1 OS=Mus musculus GN=Kirrel1 PE=1 SV=1	Q80W68	Kirrel1	87 kDa	3.6831	3.1957	3.5789	0.81665	0.85944	TRUE
KN motif and ankyrin repeat domain-containing protein 2 OS=Mus musculus GN=Kank2 PE=1 SV=	Q8BX02	Kank2	90 kDa	9.2077	7.9893	5.3684	1.6333	2.1486	TRUE
L-lactate dehydrogenase OS=Mus musculus GN=Ldha PE=1 SV=1	A0A1B0GSX0 (+2)	Ldha	40 kDa	22.099	25.566	25.053	18.783	21.056	TRUE
La-related protein 4 OS=Mus musculus GN=Larp4 PE=1 SV=1	E9Q066 (+3)	Larp4	80 kDa	3.6831	0	0	1.225	1.2892	TRUE
Laminin receptor (Fragment) OS=Mus musculus GN=Rpsa PE=2 SV=1	B2CY77 (+1)	Rpsa	33 kDa	11.049	11.185	14.316	6.5332	5.5863	TRUE
Large proline-rich protein BAG6 OS=Mus musculus GN=Bag6 PE=1 SV=1	Q9Z1R2	Bag6	121 kDa	3.6831	0	3.5789	3.6749	2.1486	TRUE
Latent-transforming growth factor beta-binding protein 1 OS=Mus musculus GN=Ltbp1 PE=1 SV=	Q8CG19	Ltbp1	187 kDa	5.5246	4.7936	3.5789	1.225	2.1486	TRUE
Leucine-rich repeats and immunoglobulin-like domains protein 1 OS=Mus musculus GN=Lrig1 PE=	P70193	Lrig1	119 kDa	12.891	6.3914	7.1579	0	0	TRUE
Leucyl-cystinyl aminopeptidase OS=Mus musculus GN=Lnpep PE=1 SV=1	Q8C129	Lnpep	117 kDa	9.2077	3.1957	3.5789	2.8583	3.008	TRUE
LIM domain only 7 OS=Mus musculus GN=Lmo7 PE=1 SV=1	E9PYF4	Lmo7	193 kDa	31.306	15.979	21.474	1.225	0.85944	TRUE
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex	P53395 (+1)	Dbt	53 kDa	0	9.5872	3.5789	0	0	TRUE
Liprin-beta-1 OS=Mus musculus GN=Ppfibp1 PE=1 SV=3	Q8C8U0	Ppfibp1	109 kDa	5.5246	7.9893	10.737	6.1249	3.8675	TRUE
Long-chain-specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acadl PE=1 SV	A0A0R4J083	Acadl	48 kDa	0	4.7936	0	3.6749	3.008	TRUE
Low density lipoprotein receptor-related protein 1 OS=Mus musculus GN=Lrp1 PE=1 SV=1	A0A0R4J0I9 (+1)	Lrp1	505 kDa	16.574	39.947	34	22.458	29.221	TRUE
Low-density lipoprotein receptor OS=Mus musculus GN=Ldlr PE=1 SV=2	P35951 (+2)	Ldlr	95 kDa	0	3.1957	0	0	1.2892	TRUE
Low-density lipoprotein receptor-related protein 6 OS=Mus musculus GN=Lrp6 PE=1 SV=1	O88572	Lrp6	180 kDa	0	3.1957	0	0	0	TRUE
Lymphocyte antigen 75 OS=Mus musculus GN=Ly75 PE=1 SV=2	Q60767	Ly75	197 kDa	29.465	25.566	34	2.45	3.8675	TRUE
Lysine--tRNA ligase OS=Mus musculus GN=Kars PE=1 SV=1	Q3TIV6 (+2)	Kars	68 kDa	9.2077	9.5872	12.526	6.5332	6.4458	TRUE
Macrophage colony-stimulating factor 1 OS=Mus musculus GN=Csf1 PE=1 SV=2	P07141 (+1)	Csf1	61 kDa	0	4.7936	0	0	1.2892	TRUE
Macrophage migration inhibitory factor OS=Mus musculus GN=Mif PE=1 SV=2	P34884 (+1)	Mif	13 kDa	3.6831	11.185	14.316	4.8999	2.5783	TRUE
Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Mdh1 PE=1 SV=3	P14152	Mdh1	37 kDa	3.6831	0	3.5789	3.2666	3.4377	TRUE
Malate dehydrogenase, mitochondrial OS=Mus musculus GN=Mdh2 PE=1 SV=3	P08249	Mdh2	36 kDa	5.5246	9.5872	10.737	10.208	11.173	TRUE
Mannose receptor, C type 2 OS=Mus musculus GN=Mrc2 PE=2 SV=1	Q14AX9 (+1)	Mrc2	167 kDa	16.574	25.566	23.263	4.8999	4.7269	TRUE
Matrix remodeling-associated protein 8 OS=Mus musculus GN=Mxra8 PE=1 SV=1	Q9DBV4	Mxra8	50 kDa	11.049	11.185	14.316	0	1.2892	TRUE
MCG1050220 OS=Mus musculus GN=Raver1 PE=2 SV=1	A0A158RFV1 (+1)	Raver1	79 kDa	7.3662	7.9893	10.737	0.81665	0	TRUE
MCG116671 OS=Mus musculus GN=Gm11361 PE=3 SV=1	A0A1Y7VKY1 (+3)	Gm11361	18 kDa	11.049	7.9893	10.737	2.8583	3.4377	TRUE
MCG123443 OS=Mus musculus GN=Rps16 PE=1 SV=1	A4FUS1 (+3)	Rps16	16 kDa	16.574	9.5872	16.105	4.0833	4.2972	TRUE
MCG124046 OS=Mus musculus GN=Prss1 PE=1 SV=1	Q9Z1R9	Prss1	26 kDa	5.5246	6.3914	3.5789	0	0	TRUE
MCG133388, isoform CRA_n OS=Mus musculus GN=Pcdhgb6 PE=1 SV=1	Q91XX4	Pcdhgb6	101 kDa	5.5246	9.5872	3.5789	0	0	TRUE
MCG13615, isoform CRA_a OS=Mus musculus GN=Rpl38 PE=1 SV=1	Q52KP0 (+1)	Rpl38	8 kDa	3.6831	4.7936	3.5789	0.81665	0.85944	TRUE
MCG16669, isoform CRA_b OS=Mus musculus GN=Tardbp PE=1 SV=1	Q544R5 (+1)	Tardbp	45 kDa	0	3.1957	3.5789	2.8583	2.5783	TRUE
MCG16976, isoform CRA_c OS=Mus musculus GN=Rpl22l1 PE=2 SV=1	Q0VBA4 (+1)	Rpl22l1	14 kDa	5.5246	0	0	0	0	TRUE
MCG17786, isoform CRA_a OS=Mus musculus GN=Rfc3 PE=1 SV=1	Q3TKD1 (+1)	Rfc3	41 kDa	0	0	3.5789	0.81665	0	TRUE
MCG2244 OS=Mus musculus GN=Zfp703 PE=2 SV=1	F6M3K1 (+1)	Zfp703	59 kDa	3.6831	0	3.5789	0	0	TRUE
MCG2960, isoform CRA_b OS=Mus musculus GN=Steap2 PE=1 SV=1	B2RX33 (+1)	Steap2	56 kDa	12.891	9.5872	7.1579	0.81665	0	TRUE
MCG5400 OS=Mus musculus GN=Myl12a PE=1 SV=1	Q6ZWQ9	Myl12a	20 kDa	11.049	15.979	12.526	4.8999	6.8755	TRUE
MCG68069 OS=Mus musculus GN=Npm1 PE=1 SV=1	Q5SQB7 (+1)	Npm1	33 kDa	0	3.1957	5.3684	4.8999	3.8675	TRUE
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acadm PE=	P45952 (+1)	Acadm	46 kDa	0	0	3.5789	1.225	2.1486	TRUE
Membrane-associated progesterone receptor component 1 OS=Mus musculus GN=Pgrmc1 PE=1	O55022 (+2)	Pgrmc1	22 kDa	0	4.7936	0	0.81665	1.2892	TRUE
Metal transporter CNNM4 OS=Mus musculus GN=Cnnm4 PE=1 SV=2	Q69ZF7	Cnnm4	87 kDa	0	4.7936	5.3684	0	0	TRUE
Metalloreductase STEAP4 OS=Mus musculus GN=Steap4 PE=1 SV=1	Q923B6	Steap4	53 kDa	5.5246	4.7936	3.5789	0	0	TRUE
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Mus musculus GN=Mccc1 PE=	Q99MR8	Mccc1	79 kDa	57.088	44.74	39.368	0	0	TRUE
Methylcrotonoyl-Coenzyme A carboxylase 2 (Beta) OS=Mus musculus GN=Mccc2 PE=1 SV=1	B2RUK5 (+1)	Mccc2	61 kDa	29.465	20.772	25.053	0	1.7189	TRUE
MICOS complex subunit MIC13 OS=Mus musculus GN=Mic13 PE=1 SV=1	Q8R404	Mic13	13 kDa	3.6831	0	0	0	0	TRUE
Microtubule-associated protein 1B OS=Mus musculus GN=Map1b PE=2 SV=1	B2RQQ5 (+1)	Map1b	270 kDa	7.3662	3.1957	0	5.3082	9.8835	TRUE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Mitochondrial carrier homolog 2 OS=Mus musculus GN=Mtch2 PE=1 SV=1	Q791V5	Mtch2	33 kDa	5.5246	7.9893	7.1579	2.45	2.1486	TRUE
Mitochondrial dicarboxylate carrier OS=Mus musculus GN=Slc25a10 PE=1 SV=2	Q9QZD8	Slc25a10	32 kDa	3.6831	6.3914	7.1579	1.225	0	TRUE
Mitochondrial fission regulator 1-like OS=Mus musculus GN=Mtfr1l PE=1 SV=1	Q9CWE0	Mtfr1l	32 kDa	3.6831	3.1957	0	0	0	TRUE
Mitochondrial import inner membrane translocase subunit Tim23 OS=Mus musculus GN=Timm23	Q9WTQ8	Timm23	22 kDa	7.3662	6.3914	3.5789	1.225	1.2892	TRUE
MKIAA0051 protein (Fragment) OS=Mus musculus GN=Iqgap1 PE=2 SV=1	Q6ZQK2 (+1)	Iqgap1	191 kDa	7.3662	17.576	7.1579	17.966	14.181	TRUE
MKIAA0106 protein (Fragment) OS=Mus musculus GN=Prdx6 PE=2 SV=1	Q6A0D0 (+1)	Prdx6	25 kDa	0	0	7.1579	6.1249	5.5863	TRUE
MKIAA0791 protein (Fragment) OS=Mus musculus GN=Nup155 PE=2 SV=1	Q6ZQ45	Nup155	159 kDa	0	0	3.5789	3.6749	3.008	TRUE
MKIAA4115 protein (Fragment) OS=Mus musculus GN=G3bp1 PE=2 SV=1	Q571F9	G3bp1	56 kDa	7.3662	6.3914	10.737	6.5332	6.0161	TRUE
Moesin OS=Mus musculus GN=Msn PE=1 SV=3	P26041	Msn	68 kDa	12.891	25.566	32.211	23.683	20.197	TRUE
Monocarboxylate transporter 1 OS=Mus musculus GN=Slc16a1 PE=1 SV=1	P53986 (+2)	Slc16a1	53 kDa	12.891	11.185	10.737	2.0416	3.008	TRUE
Monocarboxylate transporter 4 OS=Mus musculus GN=Slc16a3 PE=1 SV=1	P57787 (+2)	Slc16a3	50 kDa	20.257	22.37	14.316	1.6333	1.7189	TRUE
Mutant fibrillin-1 OS=Mus musculus GN=Fbn1 PE=2 SV=1	O88840 (+1)	Fbn1	418 kDa	3.6831	0	3.5789	0	1.7189	TRUE
Myoferlin OS=Mus musculus GN=Myof PE=1 SV=2	Q69ZN7	Myof	233 kDa	3.6831	17.576	25.053	21.641	22.345	TRUE
Myosin light polypeptide 6 OS=Mus musculus GN=Myl6 PE=1 SV=1	A0A1W2P6F6 (+3)	Myl6	17 kDa	14.732	12.783	8.9474	4.8999	4.7269	TRUE
Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4	Q8VDD5	Myh9	226 kDa	51.563	89.48	75.158	77.582	62.309	TRUE
N-acetylated alpha-linked acidic dipeptidase 2 OS=Mus musculus GN=Naalad2 PE=2 SV=1	Q32MS9 (+2)	Naalad2	83 kDa	49.722	49.534	50.105	6.5332	3.8675	TRUE
N-myc downstream regulated gene 1 OS=Mus musculus GN=Ndrg1 PE=2 SV=1	B7ZWC0 (+3)	Ndrg1	43 kDa	0	0	5.3684	1.6333	5.1566	TRUE
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13 OS=Mus musculus GN=Ndufa1	Q9ERS2	Ndufa13	17 kDa	3.6831	3.1957	3.5789	1.225	0.85944	TRUE
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Mus muscul	A0A0R3P9C8 (+1)	Ndufa9	42 kDa	3.6831	3.1957	0	1.6333	1.2892	TRUE
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Mus musculus GN=Nd	Q9DCT2	Ndufs3	30 kDa	0	6.3914	0	0	0	TRUE
Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Mus musculus G	P70670	Naca	220 kDa	0	3.1957	3.5789	3.2666	4.7269	TRUE
Natriuretic peptide receptor 3 OS=Mus musculus GN=Npr3 PE=2 SV=1	Q7TMG7	Npr3	60 kDa	14.732	14.381	8.9474	1.225	0	TRUE
Nckap1 protein (Fragment) OS=Mus musculus GN=Nckap1 PE=2 SV=1	A1L0U6 (+2)	Nckap1	129 kDa	3.6831	3.1957	3.5789	2.8583	0.85944	TRUE
Neural cell adhesion molecule 1 OS=Mus musculus GN=Ncam1 PE=1 SV=3	P13595	Ncam1	119 kDa	51.563	65.512	44.737	3.6749	3.4377	TRUE
Neurogenic locus notch homolog protein 2 OS=Mus musculus GN=Notch2 PE=1 SV=1	G5E8J0	Notch2	266 kDa	36.831	39.947	48.316	3.2666	3.8675	TRUE
Neuropilin-2 OS=Mus musculus GN=Nrp2 PE=1 SV=2	O35375 (+1)	Nrp2	105 kDa	12.891	4.7936	8.9474	0	0	TRUE
NIN1/RPN12 binding protein 1 homolog (S. cerevisiae) OS=Mus musculus GN=Nob1 PE=2 SV=1	Q148S3 (+1)	Nob1	45 kDa	0	0	5.3684	1.225	0.85944	TRUE
Nuclear factor 1 (Fragment) OS=Mus musculus GN=Nfix PE=1 SV=1	D3YZ00 (+3)	Nfix	53 kDa	3.6831	3.1957	3.5789	0.81665	0	TRUE
Nuclear migration protein nudC OS=Mus musculus GN=Nudc PE=1 SV=1	O35685	Nudc	38 kDa	3.6831	3.1957	3.5789	3.6749	3.8675	TRUE
Nuclear pore complex protein Nup214 OS=Mus musculus GN=Nup214 PE=1 SV=2	Q80U93	Nup214	213 kDa	23.94	4.7936	5.3684	0	0	TRUE
Nuclear pore complex protein Nup93 OS=Mus musculus GN=Nup93 PE=1 SV=1	Q8BJ71	Nup93	93 kDa	11.049	0	0	2.0416	2.1486	TRUE
Nuclear pore complex protein Nup98-Nup96 OS=Mus musculus GN=Nup98 PE=1 SV=2	Q6PFD9	Nup98	197 kDa	12.891	6.3914	0	0	0	TRUE
Nuclear receptor corepressor 2 OS=Mus musculus GN=Ncor2 PE=1 SV=1	F8VQL9	Ncor2	273 kDa	0	0	3.5789	0	0	TRUE
Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	P62960 (+3)	Ybx1	36 kDa	11.049	9.5872	10.737	8.1665	6.4458	TRUE
Nucleoporin 88, isoform CRA_b OS=Mus musculus GN=Nup88 PE=2 SV=1	Q5QNU0 (+1)	Nup88	84 kDa	0	0	5.3684	0	0	TRUE
Nucleoside diphosphate kinase OS=Mus musculus GN=Gm20390 PE=3 SV=1	E9PZF0	Gm20390	30 kDa	9.2077	12.783	17.895	11.841	13.751	TRUE
Oncostatin-M-specific receptor subunit beta OS=Mus musculus GN=Osmr PE=1 SV=1	O70458	Osmr	110 kDa	5.5246	9.5872	10.737	1.225	0	TRUE
Ornithine aminotransferase, mitochondrial OS=Mus musculus GN=Oat PE=1 SV=1	P29758 (+1)	Oat	48 kDa	3.6831	12.783	17.895	8.1665	7.7349	TRUE
OTU domain-containing protein 4 OS=Mus musculus GN=Otud4 PE=1 SV=1	A0A0R4J260 (+1)	Otud4	123 kDa	5.5246	0	3.5789	0	0	TRUE
Palladin isoform OS=Mus musculus GN=Palld PE=2 SV=1	K0BWC3	Palld	108 kDa	16.574	12.783	16.105	8.1665	6.8755	TRUE
Pdk3 protein OS=Mus musculus GN=Pdk3 PE=1 SV=1	Q4FJR4 (+1)	Pdk3	48 kDa	3.6831	0	3.5789	1.225	1.7189	TRUE
Pentraxin-related protein PTX3 OS=Mus musculus GN=Ptx3 PE=1 SV=2	P48759	Ptx3	42 kDa	5.5246	3.1957	3.5789	0	0	TRUE
Peptidyl-prolyl cis-trans isomerase B OS=Mus musculus GN=Ppib PE=1 SV=2	P24369 (+1)	Ppib	24 kDa	12.891	7.9893	10.737	6.9416	6.0161	TRUE
Peptidyl-prolyl cis-trans isomerase C OS=Mus musculus GN=Ppic PE=1 SV=1	P30412 (+1)	Ppic	23 kDa	7.3662	3.1957	3.5789	2.45	2.5783	TRUE
Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Mus musculus GN=Fkbp1a PE=1 SV=2	P26883	Fkbp1a	12 kDa	3.6831	3.1957	5.3684	4.8999	4.7269	TRUE
Peroxidasin homolog OS=Mus musculus GN=Pxdn PE=1 SV=1	A0A1W2P6L9 (+1)	Pxdn	144 kDa	0	6.3914	0	1.6333	2.1486	TRUE
Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1	P35700	Prdx1	22 kDa	16.574	20.772	23.263	7.7582	10.743	TRUE
Peroxiredoxin-2 OS=Mus musculus GN=Prdx2 PE=1 SV=3	Q61171	Prdx2	22 kDa	7.3662	6.3914	7.1579	5.7166	6.0161	TRUE
Peroxiredoxin-4 OS=Mus musculus GN=Prdx4 PE=1 SV=1	O08807	Prdx4	31 kDa	12.891	15.979	14.316	7.7582	9.4538	TRUE
Peroxisomal targeting signal 1 receptor OS=Mus musculus GN=Pex5 PE=1 SV=1	D3Z600 (+1)	Pex5	70 kDa	0	0	3.5789	0.81665	0.85944	TRUE
PH domain leucine-rich repeat-containing protein phosphatase 1 OS=Mus musculus GN=Phlpp1 P	Q8CHE4	Phlpp1	182 kDa	0	0	3.5789	0	0	TRUE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Phenylalanine--tRNA ligase alpha subunit OS=Mus musculus GN=Farsa PE=1 SV=1	E9PWY9 (+1)	Farsa	57 kDa	12.891	0	10.737	2.0416	2.5783	TRUE
Phosphatidate cytidylyltransferase, mitochondrial OS=Mus musculus GN=Tamm41 PE=1 SV=1	G5E881 (+1)	Tamm41	38 kDa	11.049	4.7936	5.3684	0	0	TRUE
Phosphatidylethanolamine-binding protein 1 OS=Mus musculus GN=Pebp1 PE=1 SV=3	P70296 (+2)	Pebp1	21 kDa	3.6831	4.7936	5.3684	5.3082	6.4458	TRUE
Phosphatidylinositide phosphatase SAC1 OS=Mus musculus GN=Sacm1l PE=1 SV=1	Q9EP69	Sacm1l	67 kDa	0	3.1957	0	2.8583	3.4377	TRUE
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Mus musculus GN=Pck2 PE=1 SV=1	A0A0R4J0G0 (+1)	Pck2	73 kDa	7.3662	11.185	14.316	7.7582	7.3052	TRUE
Phosphoglycerate mutase OS=Mus musculus GN=Pgam1 PE=1 SV=1	Q3U7Z6 (+1)	Pgam1	29 kDa	5.5246	9.5872	16.105	12.25	9.8835	TRUE
Phosphomevalonate kinase OS=Mus musculus GN=Pmvk PE=1 SV=1	D3YXP6 (+2)	Pmvk	18 kDa	3.6831	0	0	1.225	1.2892	TRUE
Phosphoribosyl pyrophosphate synthetase 1-like 3 OS=Mus musculus GN=Prps1l3 PE=3 SV=1	G3UXL2 (+2)	Prps1l3	35 kDa	5.5246	0	3.5789	4.0833	5.5863	TRUE
Plakophilin-1 OS=Mus musculus GN=Pkp1 PE=1 SV=1	P97350	Pkp1	81 kDa	11.049	4.7936	7.1579	0	0	TRUE
Plasminogen activator inhibitor 1 OS=Mus musculus GN=Serpine1 PE=1 SV=1	G5E899	Serpine1	45 kDa	23.94	25.566	17.895	0.81665	1.2892	TRUE
Plasminogen activator inhibitor 1 RNA-binding protein OS=Mus musculus GN=Serbp1 PE=1 SV=2	Q9CY58	Serbp1	45 kDa	0	9.5872	0	10.208	7.7349	TRUE
Plasminogen activator inhibitor 2, macrophage OS=Mus musculus GN=Serpinb2 PE=1 SV=1	P12388 (+1)	Serpinb2	46 kDa	0	3.1957	0	3.2666	0.85944	TRUE
Plastin-3 (Fragment) OS=Mus musculus GN=Pls3 PE=1 SV=1	A0A1C7CYV0 (+2)	Pls3	71 kDa	11.049	15.979	19.684	13.883	9.4538	TRUE
Platelet-derived growth factor receptor beta OS=Mus musculus GN=Pdgfrb PE=1 SV=1	E9QN12 (+2)	Pdgfrb	123 kDa	7.3662	14.381	8.9474	2.45	1.7189	TRUE
Pleckstrin homology-like domain family B member 1 OS=Mus musculus GN=Phldb1 PE=1 SV=1	Q6PDH0	Phldb1	150 kDa	5.5246	3.1957	8.9474	1.6333	0.85944	TRUE
Pleckstrin homology-like domain family B member 2 OS=Mus musculus GN=Phldb2 PE=1 SV=2	Q8K1N2	Phldb2	141 kDa	7.3662	9.5872	3.5789	1.225	0.85944	TRUE
Plectin OS=Mus musculus GN=Plec PE=1 SV=3	Q9QXS1	Plec	534 kDa	0	7.9893	8.9474	2.8583	2.1486	TRUE
Plexin-A1 OS=Mus musculus GN=Plxna1 PE=1 SV=1	P70206	Plxna1	211 kDa	29.465	31.957	34	1.225	1.2892	TRUE
Plexin-B2 OS=Mus musculus GN=Plxnb2 PE=1 SV=1	B2RXS4	Plxnb2	206 kDa	44.197	51.132	50.105	5.3082	5.5863	TRUE
Poly [ADP-ribose] polymerase 2 OS=Mus musculus GN=Parp2 PE=1 SV=3	O88554	Parp2	63 kDa	0	4.7936	5.3684	0.81665	1.2892	TRUE
Poly [ADP-ribose] polymerase OS=Mus musculus GN=Parp1 PE=2 SV=1	Q3TM68 (+2)	Parp1	113 kDa	0	0	3.5789	2.45	2.5783	TRUE
Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1	P60335	Pcbp1	37 kDa	11.049	6.3914	5.3684	6.5332	8.5944	TRUE
Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 PE=1 SV=1	Q61990	Pcbp2	38 kDa	7.3662	7.9893	10.737	5.3082	7.7349	TRUE
Polyadenylate-binding protein 1 OS=Mus musculus GN=Pabpc1 PE=1 SV=2	P29341 (+1)	Pabpc1	71 kDa	31.306	30.359	35.789	11.841	12.032	TRUE
Prelamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2	P48678	Lmna	74 kDa	14.732	11.185	16.105	15.108	13.321	TRUE
Presequence protease, mitochondrial OS=Mus musculus GN=Pitrm1 PE=1 SV=1	Q8K411	Pitrm1	117 kDa	0	6.3914	8.9474	8.1665	6.8755	TRUE
Procollagen C-endopeptidase enhancer protein OS=Mus musculus GN=Pcolce PE=1 SV=1	Q3UIP2 (+1)	Pcolce	50 kDa	5.5246	6.3914	0	3.2666	3.4377	TRUE
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Mus musculus GN=Plod3 PE=1 SV=1	Q9R0E1	Plod3	85 kDa	0	0	7.1579	4.0833	4.7269	TRUE
Profilin-2 OS=Mus musculus GN=Pfn2 PE=1 SV=3	Q9JJV2	Pfn2	15 kDa	3.6831	0	5.3684	0.81665	0	TRUE
Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1	P67778	Phb	30 kDa	11.049	9.5872	10.737	3.6749	3.8675	TRUE
Prohibitin-2 OS=Mus musculus GN=Phb2 PE=1 SV=1	O35129 (+1)	Phb2	33 kDa	12.891	15.979	17.895	4.4916	5.5863	TRUE
Prolyl 4-hydroxylase subunit alpha-1 OS=Mus musculus GN=P4ha1 PE=1 SV=2	Q60715	P4ha1	61 kDa	5.5246	14.381	12.526	9.3915	9.8835	TRUE
Propionyl-CoA carboxylase beta chain, mitochondrial OS=Mus musculus GN=Pccb PE=1 SV=2	Q99MN9	Pccb	58 kDa	18.415	19.174	21.474	0	0	TRUE
Propionyl-Coenzyme A carboxylase, alpha polypeptide, isoform CRA_b OS=Mus musculus GN=Pcc	Q3UGC8 (+1)	Pcca	80 kDa	66.296	52.729	51.895	1.225	2.1486	TRUE
Prostacyclin synthase OS=Mus musculus GN=Ptgis PE=1 SV=1	O35074	Ptgis	57 kDa	0	7.9893	5.3684	6.9416	4.7269	TRUE
Prostaglandin F2 receptor negative regulator OS=Mus musculus GN=Ptgfrn PE=1 SV=2	Q9WV91	Ptgfrn	99 kDa	16.574	15.979	10.737	0	0.85944	TRUE
Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 13 OS=Mus musculus GN=Psmd13 P	B2RT97 (+1)	Psmd13	43 kDa	5.5246	6.3914	5.3684	5.3082	6.4458	TRUE
Proteasome activator complex subunit 1 (Fragment) OS=Mus musculus GN=Psme1 PE=1 SV=1	G3UXZ5 (+2)	Psme1	27 kDa	0	3.1957	5.3684	3.2666	0	TRUE
Proteasome subunit alpha type (Fragment) OS=Mus musculus GN=Psma4 PE=2 SV=1	Q3TL95 (+1)	Psma4	28 kDa	5.5246	4.7936	8.9474	3.6749	3.4377	TRUE
Proteasome subunit alpha type OS=Mus musculus GN=Psma1 PE=1 SV=1	Q3TS44 (+1)	Psma1	30 kDa	3.6831	6.3914	5.3684	4.0833	5.1566	TRUE
Proteasome subunit alpha type OS=Mus musculus GN=Psma3 PE=2 SV=1	Q9DCD8	Psma3	28 kDa	5.5246	4.7936	3.5789	2.0416	2.5783	TRUE
Proteasome subunit alpha type OS=Mus musculus GN=Psma7 PE=2 SV=1	Q3TN31 (+2)	Psma7	28 kDa	11.049	9.5872	7.1579	4.8999	5.1566	TRUE
Proteasome subunit alpha type-6 OS=Mus musculus GN=Psma6 PE=1 SV=1	Q9QUM9	Psma6	27 kDa	3.6831	6.3914	5.3684	4.0833	4.7269	TRUE
Proteasome subunit beta type-2 OS=Mus musculus GN=Psmb2 PE=1 SV=1	Q9R1P3	Psmb2	23 kDa	0	4.7936	0	2.0416	1.7189	TRUE
Proteasome subunit beta type-4 OS=Mus musculus GN=Psmb4 PE=1 SV=1	P99026	Psmb4	29 kDa	0	0	5.3684	2.8583	4.2972	TRUE
Proteasome subunit beta type-5 OS=Mus musculus GN=Psmb5 PE=1 SV=3	O55234	Psmb5	29 kDa	0	9.5872	5.3684	2.8583	6.4458	TRUE
Proteasome subunit beta type-6 OS=Mus musculus GN=Psmb6 PE=1 SV=3	Q60692	Psmb6	25 kDa	3.6831	3.1957	3.5789	2.0416	1.7189	TRUE
Proteasome subunit beta type-7 OS=Mus musculus GN=Psmb7 PE=1 SV=1	P70195 (+1)	Psmb7	30 kDa	0	4.7936	0	4.0833	3.8675	TRUE
Protein argonaute-2 OS=Mus musculus GN=Ago2 PE=1 SV=3	Q8CJG0	Ago2	97 kDa	11.049	12.783	10.737	3.2666	3.8675	TRUE
Protein CIP2A OS=Mus musculus GN=Kiaa1524 PE=1 SV=3	Q8BWY9	Kiaa1524	102 kDa	0	0	7.1579	0	0	TRUE
Protein CYR61 OS=Mus musculus GN=Cyr61 PE=1 SV=1	P18406 (+1)	Cyr61	42 kDa	31.306	9.5872	12.526	2.8583	2.1486	TRUE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Protein diaphanous homolog 1 OS=Mus musculus GN=Diaph1 PE=1 SV=1	E9PV41 (+1)	Diaph1	140 kDa	12.891	11.185	5.3684	0	0	TRUE
Protein disulfide-isomerase A3 OS=Mus musculus GN=Pdia3 PE=1 SV=2	P27773	Pdia3	57 kDa	29.465	39.947	37.579	28.991	24.924	TRUE
Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=2 SV=1	Q3UBY9	P4hb	57 kDa	27.623	33.555	41.158	22.458	20.197	TRUE
Protein FAM171A2 OS=Mus musculus GN=Fam171a2 PE=1 SV=1	A2A699	Fam171a2	87 kDa	0	6.3914	8.9474	0	0	TRUE
Protein FAM234A OS=Mus musculus GN=Fam234a PE=1 SV=1	Q8C0Z1	Fam234a	61 kDa	0	7.9893	5.3684	0	0	TRUE
Protein FAM83H OS=Mus musculus GN=Fam83h PE=1 SV=1	Q148V8	Fam83h	131 kDa	12.891	0	14.316	0	0	TRUE
Protein FAM98A OS=Mus musculus GN=Fam98a PE=1 SV=1	Q3TJZ6	Fam98a	55 kDa	0	3.1957	0	1.6333	1.2892	TRUE
Protein furry homolog OS=Mus musculus GN=Fry PE=1 SV=1	E9Q8I9	Fry	339 kDa	3.6831	0	3.5789	0	0	TRUE
Protein lin-7 homolog C OS=Mus musculus GN=Lin7c PE=1 SV=2	O88952 (+2)	Lin7c	22 kDa	0	3.1957	0	0	0.85944	TRUE
Protein misato homolog 1 OS=Mus musculus GN=Msto1 PE=1 SV=1	Q2YDW2	Msto1	61 kDa	0	0	3.5789	2.45	1.2892	TRUE
Protein MON2 homolog OS=Mus musculus GN=Mon2 PE=1 SV=2	Q80TL7	Mon2	189 kDa	0	3.1957	0	2.0416	0	TRUE
Protein PRRC2B OS=Mus musculus GN=Prrc2b PE=1 SV=1	F8WHT3	Prrc2b	243 kDa	18.415	7.9893	3.5789	1.225	0.85944	TRUE
Protein PRRC2C OS=Mus musculus GN=Prrc2c PE=1 SV=1	A0A0A0MQ79 (+2)	Prrc2c	311 kDa	5.5246	6.3914	0	3.6749	3.008	TRUE
Protein quaking OS=Mus musculus GN=Qki PE=1 SV=1	Q9QYS9	Qki	38 kDa	3.6831	0	0	0	0	TRUE
Protein RCC2 OS=Mus musculus GN=Rcc2 PE=1 SV=1	Q8BK67	Rcc2	56 kDa	9.2077	7.9893	14.316	8.1665	10.313	TRUE
Protein S100-A14 OS=Mus musculus GN=S100a14 PE=1 SV=1	Q9D2Q8	S100a14	12 kDa	3.6831	3.1957	3.5789	0	0	TRUE
Protein S100-A6 OS=Mus musculus GN=S100a6 PE=1 SV=3	P14069 (+1)	S100a6	10 kDa	0	0	3.5789	0	0	TRUE
Protein SMG7 OS=Mus musculus GN=Smg7 PE=2 SV=1	Q5RJH6	Smg7	127 kDa	3.6831	7.9893	5.3684	0	0	TRUE
Protein transport protein sec16 OS=Mus musculus GN=Sec16a PE=1 SV=1	A2AIX1 (+1)	Sec16a	256 kDa	7.3662	3.1957	7.1579	2.0416	0.85944	TRUE
Protein transport protein Sec61 subunit alpha isoform 1 OS=Mus musculus GN=Sec61a1 PE=1 SV	P61620 (+1)	Sec61a1	52 kDa	3.6831	4.7936	7.1579	3.2666	3.4377	TRUE
Protein transport protein Sec61 subunit beta OS=Mus musculus GN=Sec61b PE=1 SV=3	Q9CQS8	Sec61b	10 kDa	3.6831	3.1957	3.5789	1.225	1.2892	TRUE
Protein-glutamine gamma-glutamyltransferase K OS=Mus musculus GN=Tgm1 PE=1 SV=1	A0A0R4J293 (+1)	Tgm1	90 kDa	0	4.7936	0	0	0	TRUE
Protein-lysine 6-oxidase OS=Mus musculus GN=Lox PE=1 SV=1	P28301 (+3)	Lox	47 kDa	7.3662	6.3914	8.9474	2.45	2.5783	TRUE
Protein/nucleic acid deglycase DJ-1 OS=Mus musculus GN=Park7 PE=1 SV=1	Q99LX0	Park7	20 kDa	12.891	11.185	21.474	4.4916	2.5783	TRUE
Prothymosin alpha OS=Mus musculus GN=Ptma PE=1 SV=2	P26350 (+5)	Ptma	12 kDa	5.5246	4.7936	7.1579	5.3082	4.7269	TRUE
Protocadherin 7 OS=Mus musculus GN=Pcdh7 PE=1 SV=2	E9Q2S0	Pcdh7	136 kDa	7.3662	9.5872	0	0	0	TRUE
Protocadherin Fat 4 OS=Mus musculus GN=Fat4 PE=1 SV=2	Q2PZL6	Fat4	540 kDa	18.415	35.153	12.526	0	0	TRUE
Protocadherin gamma C3 OS=Mus musculus GN=Pcdhgc3 PE=1 SV=1	Q91XX1	Pcdhgc3	101 kDa	7.3662	7.9893	0	0	0	TRUE
Pumilio homolog 2 OS=Mus musculus GN=Pum2 PE=1 SV=1	Q3UR91	Pum2	114 kDa	9.2077	0	10.737	0	0	TRUE
Puromycin-sensitive aminopeptidase OS=Mus musculus GN=Npepps PE=1 SV=2	Q11011	Npepps	103 kDa	14.732	3.1957	0	4.8999	6.4458	TRUE
Putative envelope protein OS=Mus musculus GN=env PE=4 SV=1	G4V4Z0	env	70 kDa	31.306	28.762	25.053	2.0416	1.2892	TRUE
Pyruvate carboxylase OS=Mus musculus GN=Pcx PE=1 SV=1	E9QPD7 (+3)	Pcx	130 kDa	27.623	36.751	37.579	0	0	TRUE
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Mus musculus GN=Pdhb	Q9D051	Pdhb	39 kDa	3.6831	4.7936	8.9474	3.6749	5.5863	TRUE
Pyruvate dehydrogenase protein X component, mitochondrial OS=Mus musculus GN=Pdhx PE=1 S	Q8BKZ9	Pdhx	54 kDa	0	3.1957	0	1.6333	0	TRUE
Ran GTPase-activating protein 1 OS=Mus musculus GN=Rangap1 PE=1 SV=2	P46061 (+2)	Rangap1	64 kDa	3.6831	0	0	2.45	2.1486	TRUE
Ran-specific GTPase-activating protein OS=Mus musculus GN=Ranbp1 PE=1 SV=2	P34022	Ranbp1	24 kDa	0	3.1957	3.5789	2.45	2.1486	TRUE
Ras-related protein Rab-11B OS=Mus musculus GN=Rab11b PE=1 SV=3	P46638 (+1)	Rab11b	24 kDa	3.6831	0	0	2.45	3.008	TRUE
Ras-related protein Rab-2A OS=Mus musculus GN=Rab2a PE=1 SV=1	P53994 (+1)	Rab2a	24 kDa	0	4.7936	0	4.4916	6.0161	TRUE
Ras-related protein Rab-5C OS=Mus musculus GN=Rab5c PE=1 SV=2	P35278 (+2)	Rab5c	23 kDa	0	3.1957	0	1.225	1.7189	TRUE
Receptor of activated protein C kinase 1 OS=Mus musculus GN=Rack1 PE=1 SV=3	P68040	Rack1	35 kDa	12.891	14.381	17.895	9.7998	13.321	TRUE
Receptor tyrosine-protein kinase erbB-2 OS=Mus musculus GN=Erbb2 PE=1 SV=3	P70424	Erbb2	139 kDa	3.6831	4.7936	5.3684	0	0	TRUE
Receptor-interacting serine/threonine-protein kinase 1 OS=Mus musculus GN=Ripk1 PE=1 SV=1	Q60855	Ripk1	75 kDa	0	3.1957	5.3684	1.6333	1.7189	TRUE
Receptor-type tyrosine-protein phosphatase kappa OS=Mus musculus GN=Ptprk PE=1 SV=1	A0A1W2P7Y1 (+1)	Ptprk	166 kDa	14.732	44.74	30.421	3.2666	3.4377	TRUE
Receptor-type tyrosine-protein phosphatase mu OS=Mus musculus GN=Ptprm PE=1 SV=2	P28828 (+1)	Ptprm	164 kDa	5.5246	12.783	5.3684	0	0	TRUE
Receptor-type tyrosine-protein phosphatase S OS=Mus musculus GN=Ptprs PE=1 SV=1	B0V2N1	Ptprs	212 kDa	9.2077	3.1957	12.526	0	1.2892	TRUE
Recombining binding protein suppressor of hairless (Drosophila), isoform CRA_b OS=Mus musculu	A0A0J9YTV5 (+4)	Rbpj	57 kDa	3.6831	3.1957	5.3684	3.2666	3.4377	TRUE
Replication protein A subunit OS=Mus musculus GN=Rpa1 PE=2 SV=1	Q3U8B3 (+2)	Rpa1	71 kDa	0	0	5.3684	3.6749	5.5863	TRUE
Reticulocalbin-1 OS=Mus musculus GN=Rcn1 PE=1 SV=1	Q05186	Rcn1	38 kDa	3.6831	9.5872	3.5789	3.2666	1.7189	TRUE
Reticulocalbin-3 OS=Mus musculus GN=Rcn3 PE=1 SV=1	Q8BH97	Rcn3	38 kDa	5.5246	12.783	7.1579	3.2666	3.4377	TRUE
Retinol dehydrogenase 13 OS=Mus musculus GN=Rdh13 PE=1 SV=1	Q8CEE7	Rdh13	36 kDa	0	4.7936	0	0	0	TRUE
Rho guanine nucleotide exchange factor 2 OS=Mus musculus GN=Arhgef2 PE=1 SV=1	H3BJ40 (+2)	Arhgef2	110 kDa	0	0	5.3684	5.3082	4.2972	TRUE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Ribosomal protein 10 OS=Mus musculus GN=RP23-436K3.4-001 PE=4 SV=1	A2AM97 (+1)	RP23-436K3	25 kDa	7.3662	4.7936	5.3684	8.1665	7.3052	TRUE
Ribosomal protein L23A, pseudogene 3 OS=Mus musculus GN=Rpl23a-ps3 PE=3 SV=1	A0A140T8M7 (+4)	Rpl23a-ps3	18 kDa	3.6831	0	3.5789	1.6333	2.1486	TRUE
Ribosomal protein OS=Mus musculus GN=Rpl10a PE=2 SV=1	Q3U561 (+1)	Rpl10a	25 kDa	11.049	11.185	7.1579	2.8583	2.1486	TRUE
Ribosomal protein S14 OS=Mus musculus GN=rps14 PE=3 SV=1	O70569 (+1)	rps14	16 kDa	9.2077	7.9893	10.737	6.5332	7.7349	TRUE
Ribosome-binding protein 1 OS=Mus musculus GN=Rrbp1 PE=1 SV=1	A2AVJ7 (+1)	Rrbp1	158 kDa	7.3662	11.185	12.526	9.7998	6.0161	TRUE
RIKEN cDNA 2610206B13, isoform CRA_b OS=Mus musculus GN=Rnf219 PE=1 SV=1	G3X8V5 (+1)	Rnf219	80 kDa	5.5246	4.7936	5.3684	0	0	TRUE
RNA binding protein fox-1 homolog 2 OS=Mus musculus GN=Rbfox2 PE=1 SV=2	Q8BP71	Rbfox2	47 kDa	7.3662	6.3914	8.9474	0	0	TRUE
RNA-binding protein 14 OS=Mus musculus GN=Rbm14 PE=1 SV=1	Q8C2Q3	Rbm14	69 kDa	0	3.1957	0	0	0	TRUE
RNA-binding protein 3 OS=Mus musculus GN=Rbm3 PE=1 SV=1	O89086 (+1)	Rbm3	17 kDa	3.6831	0	0	2.8583	5.5863	TRUE
Rpl11 protein OS=Mus musculus GN=Rpl11 PE=2 SV=1	Q8VC94 (+1)	Rpl11	19 kDa	3.6831	6.3914	7.1579	2.45	2.5783	TRUE
Rps19 protein (Fragment) OS=Mus musculus GN=Rps19 PE=2 SV=1	Q5M9P3 (+1)	Rps19	17 kDa	9.2077	12.783	10.737	4.0833	3.8675	TRUE
S-adenosylhomocysteine hydrolase-like protein 1 OS=Mus musculus GN=Ahcyl1 PE=1 SV=1	Q80SW1	Ahcyl1	59 kDa	0	3.1957	7.1579	6.9416	7.3052	TRUE
S-methyl-5'-thioadenosine phosphorylase OS=Mus musculus GN=Mtap PE=1 SV=1	Q9CQ65	Mtap	31 kDa	9.2077	7.9893	10.737	4.0833	3.4377	TRUE
Sarcoglycan, delta (Dystrophin-associated glycoprotein), isoform CRA_b OS=Mus musculus GN=S	Q8C8D9	Sgcd	18 kDa	0	3.1957	3.5789	0	0	TRUE
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus GN=Atp2a2 PE=1 SV=2	O55143 (+1)	Atp2a2	115 kDa	7.3662	11.185	5.3684	11.841	9.8835	TRUE
Scr3 OS=Mus musculus GN=Rbms2 PE=2 SV=1	Q9WTS9	Rbms2	38 kDa	0	3.1957	0	0.81665	1.2892	TRUE
Semaphorin-3A OS=Mus musculus GN=Sema3a PE=1 SV=2	O08665	Sema3a	89 kDa	16.574	11.185	3.5789	0	0	TRUE
Semaphorin-3C OS=Mus musculus GN=Sema3c PE=1 SV=2	Q62181	Sema3c	85 kDa	12.891	6.3914	0	0	0	TRUE
Septin-11 OS=Mus musculus GN=Sept11 PE=1 SV=1	A0A0J9YTY0 (+2)	Sept11	49 kDa	5.5246	17.576	14.316	7.3499	7.7349	TRUE
Septin-2 OS=Mus musculus GN=Sept2 PE=1 SV=2	P42208	Sept2	42 kDa	0	6.3914	5.3684	4.8999	4.7269	TRUE
Serine (or cysteine) peptidase inhibitor, clade B, member 6a OS=Mus musculus GN=Serpinb6a PE	F8WIV2 (+3)	Serpinb6a	45 kDa	25.782	22.37	26.842	9.7998	9.8835	TRUE
Serine hydroxymethyltransferase OS=Mus musculus GN=Shmt2 PE=1 SV=1	Q9CZN7	Shmt2	56 kDa	11.049	17.576	23.263	10.208	12.462	TRUE
Serine/threonine kinase receptor associated protein OS=Mus musculus GN=Strap PE=1 SV=1	B2RUC7 (+1)	Strap	38 kDa	5.5246	6.3914	8.9474	4.8999	6.0161	TRUE
Serine/threonine-protein kinase Nek6 OS=Mus musculus GN=Nek6 PE=1 SV=1	Q9ES70	Nek6	36 kDa	7.3662	6.3914	5.3684	1.6333	1.2892	TRUE
Serine/threonine-protein kinase SIK3 OS=Mus musculus GN=Sik3 PE=1 SV=1	E9PU87	Sik3	151 kDa	12.891	6.3914	12.526	0	0	TRUE
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit OS=Mus musculus GN=Ppp	Q99PC9	Ppp2r5d	69 kDa	0	0	3.5789	2.0416	1.2892	TRUE
Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3	P07724 (+1)	Alb	69 kDa	3.6831	4.7936	5.3684	0	0.85944	TRUE
SH3 and PX domains 2B OS=Mus musculus GN=Sh3pxd2b PE=2 SV=1	B9EJ37	Sh3pxd2b	102 kDa	0	0	3.5789	1.6333	2.1486	TRUE
SH3 domain-binding protein 4 OS=Mus musculus GN=Sh3bp4 PE=1 SV=1	Q921I6	Sh3bp4	108 kDa	0	0	3.5789	0	0	TRUE
SHC-transforming protein 1 OS=Mus musculus GN=Shc1 PE=1 SV=3	P98083	Shc1	63 kDa	0	3.1957	0	2.8583	2.5783	TRUE
Sideroflexin-1 OS=Mus musculus GN=Sfxn1 PE=1 SV=3	Q99JR1	Sfxn1	36 kDa	5.5246	0	5.3684	1.6333	3.008	TRUE
Sideroflexin-3 OS=Mus musculus GN=Sfxn3 PE=1 SV=1	Q91V61	Sfxn3	35 kDa	5.5246	6.3914	8.9474	1.225	1.7189	TRUE
Signal peptidase complex subunit 2 OS=Mus musculus GN=Spcs2 PE=1 SV=1	A0A140LHG8 (+2)	Spcs2	28 kDa	0	3.1957	3.5789	2.0416	0.85944	TRUE
Signal transducer and activator of transcription OS=Mus musculus GN=Stat1 PE=1 SV=1	A0A087WSP5 (+3)	Stat1	88 kDa	0	3.1957	0	7.3499	0	TRUE
Signal-induced proliferation-associated 1-like protein 2 OS=Mus musculus GN=Sipa1l2 PE=1 SV=1	A0A1D5RLY9 (+2)	Sipa1l2	187 kDa	5.5246	0	0	0	0	TRUE
Smooth muscle LIM protein OS=Mus musculus GN=Csrp2 PE=2 SV=1	Q71V27	Csrp2	21 kDa	0	3.1957	3.5789	4.0833	3.4377	TRUE
Sodium channel beta2 subunit OS=Mus musculus GN=Scn2b PE=1 SV=1	Q1MXF8 (+1)	Scn2b	24 kDa	3.6831	0	0	0	0	TRUE
Sodium-coupled neutral amino acid transporter 4 OS=Mus musculus GN=Slc38a4 PE=1 SV=1	Q8R1S9	Slc38a4	60 kDa	3.6831	0	0	0	0	TRUE
Sodium/potassium-transporting ATPase subunit alpha-1 OS=Mus musculus GN=Atp1a1 PE=1 SV=	Q8VDN2	Atp1a1	113 kDa	66.296	63.914	53.684	9.7998	9.8835	TRUE
Sodium/potassium-transporting ATPase subunit beta-3 OS=Mus musculus GN=Atp1b3 PE=1 SV=1	P97370 (+1)	Atp1b3	32 kDa	12.891	9.5872	7.1579	1.6333	2.5783	TRUE
Sorting nexin OS=Mus musculus GN=Snx9 PE=2 SV=1	Q3U1P2 (+1)	Snx9	67 kDa	0	0	3.5789	2.8583	3.8675	TRUE
Spermatogenesis-associated protein 5 OS=Mus musculus GN=Spata5 PE=1 SV=1	A0A0G2JFY0 (+2)	Spata5	91 kDa	7.3662	6.3914	10.737	0.81665	0	TRUE
Spermatogenesis-associated serine-rich protein 2 OS=Mus musculus GN=Spats2 PE=1 SV=1	Q8K1N4	Spats2	59 kDa	3.6831	3.1957	0	1.6333	2.5783	TRUE
Splicing factor, proline- and glutamine-rich OS=Mus musculus GN=Sfpq PE=1 SV=1	Q8VIJ6	Sfpq	75 kDa	5.5246	4.7936	8.9474	3.2666	2.1486	TRUE
Sterol O-acyltransferase 1 OS=Mus musculus GN=Soat1 PE=1 SV=2	Q61263	Soat1	64 kDa	0	0	3.5789	2.0416	1.2892	TRUE
Stress-70 protein, mitochondrial OS=Mus musculus GN=Hspa9 PE=1 SV=3	P38647	Hspa9	73 kDa	20.257	19.174	21.474	20.416	19.767	TRUE
Stress-induced-phosphoprotein 1 OS=Mus musculus GN=Stip1 PE=1 SV=1	Q60864	Stip1	63 kDa	7.3662	11.185	12.526	15.108	12.462	TRUE
Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Mus musculus GN=Oxct1 P	Q9D0K2	Oxct1	56 kDa	0	0	5.3684	5.7166	4.7269	TRUE
Synaptosomal-associated protein 47 OS=Mus musculus GN=Snap47 PE=1 SV=1	Q8R570	Snap47	47 kDa	5.5246	9.5872	7.1579	0.81665	0	TRUE
Syndecan-1 OS=Mus musculus GN=Sdc1 PE=1 SV=1	P18828 (+1)	Sdc1	33 kDa	3.6831	0	0	0.81665	0.85944	TRUE
T-complex protein 1 subunit alpha OS=Mus musculus GN=Tcp1 PE=1 SV=3	P11983	Tcp1	60 kDa	23.94	11.185	14.316	11.433	11.173	TRUE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
T-complex protein 1 subunit beta OS=Mus musculus GN=Cct2 PE=1 SV=4	P80314 (+1)	Cct2	57 kDa	11.049	11.185	12.526	8.5749	9.8835	TRUE
T-complex protein 1 subunit delta OS=Mus musculus GN=Cct4 PE=1 SV=3	P80315 (+2)	Cct4	58 kDa	12.891	7.9893	16.105	11.841	15.47	TRUE
T-complex protein 1 subunit epsilon OS=Mus musculus GN=Cct5 PE=1 SV=1	P80316	Cct5	60 kDa	16.574	19.174	17.895	13.475	12.462	TRUE
T-complex protein 1 subunit eta OS=Mus musculus GN=Cct7 PE=1 SV=1	P80313 (+3)	Cct7	60 kDa	11.049	9.5872	7.1579	8.1665	10.743	TRUE
T-complex protein 1 subunit gamma OS=Mus musculus GN=Cct3 PE=1 SV=1	P80318 (+1)	Cct3	61 kDa	16.574	17.576	17.895	11.841	14.61	TRUE
T-complex protein 1 subunit theta OS=Mus musculus GN=Cct8 PE=1 SV=3	P42932 (+2)	Cct8	60 kDa	20.257	19.174	19.684	20.825	17.618	TRUE
T-complex protein 1 subunit zeta OS=Mus musculus GN=Cct6a PE=1 SV=3	P80317 (+2)	Cct6a	58 kDa	18.415	12.783	17.895	8.5749	9.0241	TRUE
Tenascin OS=Mus musculus GN=Tnc PE=1 SV=1	Q80YX1	Tnc	232 kDa	14.732	11.185	12.526	0	0	TRUE
Thimet oligopeptidase OS=Mus musculus GN=Thop1 PE=1 SV=1	A0A0R4IZY0 (+1)	Thop1	78 kDa	0	3.1957	3.5789	4.8999	2.5783	TRUE
Thioredoxin domain-containing protein 12 OS=Mus musculus GN=Txndc12 PE=1 SV=1	Q9CQU0	Txndc12	19 kDa	11.049	9.5872	12.526	0	0	TRUE
Thioredoxin OS=Mus musculus GN=Txn PE=1 SV=3	P10639	Txn	12 kDa	5.5246	4.7936	7.1579	3.2666	6.8755	TRUE
Thioredoxin-dependent peroxide reductase, mitochondrial OS=Mus musculus GN=Prdx3 PE=1 SV=	P20108 (+1)	Prdx3	28 kDa	0	0	3.5789	2.0416	2.1486	TRUE
Thrombospondin-1 OS=Mus musculus GN=Thbs1 PE=1 SV=1	P35441 (+1)	Thbs1	130 kDa	12.891	23.968	8.9474	8.1665	6.0161	TRUE
Tissue factor OS=Mus musculus GN=F3 PE=1 SV=1	A0A0R4J088 (+1)	F3	33 kDa	0	4.7936	0	1.6333	0	TRUE
Toll-like receptor 2 OS=Mus musculus GN=Tlr2 PE=1 SV=1	G3X8Y8 (+1)	Tlr2	89 kDa	3.6831	11.185	3.5789	0	0	TRUE
Tpm2 protein OS=Mus musculus GN=Tpm2 PE=2 SV=1	Q6PJ18	Tpm2	33 kDa	0	17.576	0	4.8999	4.2972	TRUE
Tpm3 protein OS=Mus musculus GN=Tpm3 PE=2 SV=1	Q58E70	Tpm3	29 kDa	0	0	8.9474	6.9416	6.0161	TRUE
Transcription factor 12 (Fragment) OS=Mus musculus GN=Tcf12 PE=1 SV=1	V9GXC3	Tcf12	55 kDa	7.3662	4.7936	0	0	0	TRUE
Transcriptional activator protein Pur-beta OS=Mus musculus GN=Purb PE=1 SV=3	O35295	Purb	34 kDa	0	0	3.5789	2.0416	2.5783	TRUE
Transferrin receptor, isoform CRA_a OS=Mus musculus GN=Tfrc PE=1 SV=1	Q542D9 (+1)	Tfrc	86 kDa	29.465	22.37	25.053	2.45	4.2972	TRUE
Transforming growth factor beta receptor type 3 OS=Mus musculus GN=Tgfbr3 PE=1 SV=1	A0A0R4J097	Tgfbr3	94 kDa	11.049	17.576	12.526	0.81665	0	TRUE
Transgelin OS=Mus musculus GN=Tagln PE=1 SV=3	P37804	Tagln	23 kDa	0	11.185	3.5789	5.7166	3.4377	TRUE
Transgelin-2 OS=Mus musculus GN=Tagln2 PE=1 SV=4	Q9WVA4	Tagln2	22 kDa	16.574	6.3914	12.526	6.9416	7.3052	TRUE
Transitional endoplasmic reticulum ATPase OS=Mus musculus GN=Vcp PE=1 SV=4	Q01853	Vcp	89 kDa	14.732	11.185	21.474	17.966	18.478	TRUE
Translationally-controlled tumor protein OS=Mus musculus GN=Tpt1 PE=1 SV=1	P63028	Tpt1	19 kDa	0	0	7.1579	3.6749	6.0161	TRUE
Transmembrane protein 33 OS=Mus musculus GN=Tmem33 PE=1 SV=1	A0A0R4J1Z3 (+1)	Tmem33	28 kDa	3.6831	4.7936	3.5789	1.225	0.85944	TRUE
Tricarboxylate transport protein, mitochondrial OS=Mus musculus GN=Slc25a1 PE=1 SV=1	Q8JZU2	Slc25a1	34 kDa	3.6831	0	5.3684	1.6333	0.85944	TRUE
Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1	Q8BMS1	Hadha	83 kDa	11.049	12.783	14.316	2.8583	3.8675	TRUE
Trifunctional enzyme subunit beta, mitochondrial OS=Mus musculus GN=Hadhb PE=1 SV=1	Q99JY0	Hadhb	51 kDa	12.891	11.185	8.9474	1.225	2.5783	TRUE
Trinucleotide repeat-containing gene 6B protein OS=Mus musculus GN=Tnrc6b PE=1 SV=2	Q8BKI2	Tnrc6b	192 kDa	9.2077	3.1957	12.526	0	0	TRUE
Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=4	P17751	Tpi1	32 kDa	31.306	23.968	30.421	20.008	18.908	TRUE
tRNA-splicing ligase RtcB homolog OS=Mus musculus GN=Rtcb PE=2 SV=1	Q3TJ01 (+1)	Rtcb	55 kDa	3.6831	11.185	7.1579	6.9416	4.2972	TRUE
Trophoblast glycoprotein OS=Mus musculus GN=Tpbg PE=1 SV=3	Q9Z0L0	Tpbg	46 kDa	3.6831	4.7936	3.5789	0	0.85944	TRUE
Tropomyosin 1, alpha OS=Mus musculus GN=Tpm1 PE=2 SV=1	Q564G1	Tpm1	33 kDa	5.5246	23.968	10.737	6.1249	5.1566	TRUE
Tropomyosin alpha-4 chain OS=Mus musculus GN=Tpm4 PE=1 SV=3	Q6IRU2	Tpm4	28 kDa	11.049	11.185	10.737	3.2666	4.2972	TRUE
Try10-like trypsinogen OS=Mus musculus GN=Gm5409 PE=2 SV=1	Q7M754	Gm5409	27 kDa	9.2077	4.7936	5.3684	0	0	TRUE
Tubulin alpha chain (Fragment) OS=Mus musculus GN=Tuba4a PE=1 SV=1	A0A0A0MQA5 (+1)	Tuba4a	53 kDa	64.454	0	0	37.158	36.956	TRUE
Tubulin alpha-1B chain OS=Mus musculus GN=Tuba1b PE=1 SV=2	P05213	Tuba1b	50 kDa	71.82	0	0	0	0	TRUE
Tubulin alpha-1C chain OS=Mus musculus GN=Tuba1c PE=1 SV=1	P68373 (+1)	Tuba1c	50 kDa	66.296	60.719	71.579	36.341	35.237	TRUE
Tubulin beta chain OS=Mus musculus GN=Tubb6 PE=1 SV=1	Q3UMM1 (+1)	Tubb6	50 kDa	73.662	51.132	57.263	23.275	22.345	TRUE
Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1	Q7TMM9	Tubb2a	50 kDa	97.602	70.306	94.842	37.158	39.964	TRUE
Tubulin beta-4B chain OS=Mus musculus GN=Tubb4b PE=1 SV=1	P68372	Tubb4b	50 kDa	101.29	71.904	107.37	38.791	43.831	TRUE
Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1	P99024	Tubb5	50 kDa	112.33	83.089	119.89	43.691	45.98	TRUE
Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide (	A2A5N2 (+1)	Ywhab	28 kDa	7.3662	7.9893	5.3684	4.4916	5.1566	TRUE
Tyrosine-protein kinase receptor OS=Mus musculus GN=Insr PE=2 SV=1	M4TKR7 (+1)	Insr	157 kDa	0	0	7.1579	0	0	TRUE
Tyrosine-protein kinase receptor UFO OS=Mus musculus GN=Axl PE=1 SV=2	Q00993 (+1)	Axl	98 kDa	5.5246	7.9893	5.3684	1.225	0	TRUE
Tyrosine-protein kinase transmembrane receptor ROR2 OS=Mus musculus GN=Ror2 PE=1 SV=1	E9PUN5 (+1)	Ror2	104 kDa	3.6831	7.9893	7.1579	0	0	TRUE
Ubiquitin carboxyl-terminal hydrolase 4 OS=Mus musculus GN=Usp4 PE=1 SV=1	A0A0A6YW28 (+3)	Usp4	104 kDa	5.5246	6.3914	14.316	3.6749	2.1486	TRUE
Ubiquitin-40S ribosomal protein S27a OS=Mus musculus GN=Rps27a PE=1 SV=2	P62983 (+1)	Rps27a	18 kDa	22.099	20.772	10.737	12.658	14.61	TRUE
Ubiquitin-associated protein 2 OS=Mus musculus GN=Ubap2 PE=1 SV=1	A2AMY5 (+1)	Ubap2	118 kDa	11.049	12.783	8.9474	3.2666	3.8675	TRUE
Ubiquitin-associated protein 2-like OS=Mus musculus GN=Ubap2l PE=1 SV=1	Q80X50	Ubap2l	117 kDa	38.672	41.544	39.368	8.5749	6.8755	TRUE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Ubiquitin-like modifier-activating enzyme 6 OS=Mus musculus GN=Uba6 PE=1 SV=1	Q8C7R4	Uba6	118 kDa	0	0	5.3684	5.7166	4.2972	TRUE
Ubiquitin-protein ligase E3C OS=Mus musculus GN=Ube3c PE=1 SV=2	Q80U95	Ube3c	124 kDa	11.049	3.1957	5.3684	0.81665	0	TRUE
UDP-glucose 6-dehydrogenase OS=Mus musculus GN=Ugdh PE=1 SV=1	O70475 (+2)	Ugdh	55 kDa	11.049	3.1957	8.9474	9.3915	9.0241	TRUE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Anp32b PE=2 SV=1	Q3UW32 (+1)	Anp32b	28 kDa	3.6831	3.1957	0	3.2666	2.5783	TRUE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Cbfb PE=2 SV=1	Q3UYR3	Cbfb	16 kDa	3.6831	0	0	0.81665	0	TRUE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Farsb PE=2 SV=1	Q3TG12 (+1)	Farsb	66 kDa	7.3662	4.7936	3.5789	4.8999	2.5783	TRUE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Slc25a11 PE=2 SV=1	Q9CTC7	Slc25a11	28 kDa	0	3.1957	0	2.0416	1.7189	TRUE
Uncharacterized protein OS=Mus musculus GN=2210010C04Rik PE=2 SV=1	Q9D7Y7	2210010C04Rik	26 kDa	9.2077	4.7936	8.9474	0	1.2892	TRUE
Uncharacterized protein OS=Mus musculus GN=Ahsa1 PE=2 SV=1	Q3TL79 (+1)	Ahsa1	38 kDa	5.5246	0	0	2.8583	3.8675	TRUE
Uncharacterized protein OS=Mus musculus GN=Atp5o PE=2 SV=1	Q3TF25 (+1)	Atp5o	23 kDa	3.6831	9.5872	7.1579	2.0416	2.1486	TRUE
Uncharacterized protein OS=Mus musculus GN=Csde1 PE=1 SV=1	Q3U1S6 (+1)	Csde1	89 kDa	9.2077	4.7936	5.3684	8.5749	10.743	TRUE
Uncharacterized protein OS=Mus musculus GN=Dars PE=2 SV=1	Q3TF87 (+1)	Dars	57 kDa	9.2077	11.185	5.3684	6.9416	4.7269	TRUE
Uncharacterized protein OS=Mus musculus GN=Dnaja2 PE=2 SV=1	Q3TFF0 (+1)	Dnaja2	46 kDa	9.2077	7.9893	7.1579	5.3082	4.7269	TRUE
Uncharacterized protein OS=Mus musculus GN=Eif4enif1 PE=2 SV=1	Q8BY82	Eif4enif1	105 kDa	0	6.3914	8.9474	0	0	TRUE
Uncharacterized protein OS=Mus musculus GN=Emilin1 PE=2 SV=1	Q3U254 (+1)	Emilin1	108 kDa	16.574	11.185	12.526	0	0	TRUE
Uncharacterized protein OS=Mus musculus GN=Emilin2 PE=2 SV=1	Q3TBC8 (+5)	Emilin2	117 kDa	7.3662	0	3.5789	0	0	TRUE
Uncharacterized protein OS=Mus musculus GN=G3bp2 PE=2 SV=1	Q3U931 (+1)	G3bp2	51 kDa	0	3.1957	5.3684	2.0416	3.008	TRUE
Uncharacterized protein OS=Mus musculus GN=H2-K1 PE=2 SV=1	Q3TVI9	H2-K1	41 kDa	18.415	23.968	5.3684	4.4916	1.7189	TRUE
Uncharacterized protein OS=Mus musculus GN=Hars PE=2 SV=1	Q3UDH1	Hars	57 kDa	5.5246	0	3.5789	5.7166	3.8675	TRUE
Uncharacterized protein OS=Mus musculus GN=Hnrnpa1 PE=2 SV=1	Q3TIK8	Hnrnpa1	34 kDa	7.3662	6.3914	3.5789	3.2666	4.2972	TRUE
Uncharacterized protein OS=Mus musculus GN=Hnrnpm PE=2 SV=1	A0A1S6GWJ8 (+3)	Hnrnpm	86 kDa	62.613	51.132	76.947	9.3915	10.313	TRUE
Uncharacterized protein OS=Mus musculus GN=Hnrnpu PE=2 SV=1	Q3TVV6 (+4)	Hnrnpu	88 kDa	5.5246	0	5.3684	5.3082	6.0161	TRUE
Uncharacterized protein OS=Mus musculus GN=Hspa8 PE=2 SV=1	Q3UBA6	Hspa8	71 kDa	104.97	63.914	93.053	35.524	36.096	TRUE
Uncharacterized protein OS=Mus musculus GN=Itga6 PE=2 SV=1	Q8CC06	Itga6	120 kDa	9.2077	11.185	19.684	0	3.008	TRUE
Uncharacterized protein OS=Mus musculus GN=Lrpap1 PE=2 SV=1	A0A1S6GWI9 (+6)	Lrpap1	44 kDa	0	7.9893	7.1579	0.81665	0.85944	TRUE
Uncharacterized protein OS=Mus musculus GN=Maged1 PE=2 SV=1	Q3UIL5 (+2)	Maged1	86 kDa	9.2077	7.9893	12.526	1.6333	3.008	TRUE
Uncharacterized protein OS=Mus musculus GN=Mmp14 PE=2 SV=1	Q3U2T0	Mmp14	66 kDa	9.2077	9.5872	10.737	0	0	TRUE
Uncharacterized protein OS=Mus musculus GN=Ncl PE=2 SV=1	Q8CD23	Ncl	77 kDa	20.257	15.979	17.895	14.291	14.61	TRUE
Uncharacterized protein OS=Mus musculus GN=Ncoa2 PE=2 SV=1	Q8BN74	Ncoa2	95 kDa	5.5246	0	0	0	0	TRUE
Uncharacterized protein OS=Mus musculus GN=Ndufs1 PE=2 SV=1	Q3TIU7 (+1)	Ndufs1	80 kDa	0	6.3914	0	3.6749	2.5783	TRUE
Uncharacterized protein OS=Mus musculus GN=Nono PE=2 SV=1	Q3UM20 (+2)	Nono	55 kDa	9.2077	7.9893	12.526	3.6749	6.4458	TRUE
Uncharacterized protein OS=Mus musculus GN=P4ha2 PE=2 SV=1	Q5SX74	P4ha2	61 kDa	5.5246	11.185	12.526	7.7582	6.4458	TRUE
Uncharacterized protein OS=Mus musculus GN=Pdia6 PE=2 SV=1	Q3TJL8 (+1)	Pdia6	49 kDa	22.099	15.979	25.053	8.5749	8.5944	TRUE
Uncharacterized protein OS=Mus musculus GN=Ppp1r13l PE=1 SV=1	Q3TCU2 (+1)	Ppp1r13l	89 kDa	7.3662	6.3914	7.1579	0	0	TRUE
Uncharacterized protein OS=Mus musculus GN=Ppp2r1a PE=2 SV=1	Q8C2E1	Ppp2r1a	65 kDa	9.2077	6.3914	8.9474	6.1249	7.7349	TRUE
Uncharacterized protein OS=Mus musculus GN=Prkar1a PE=2 SV=1	Q3TYK4 (+1)	Prkar1a	57 kDa	5.5246	0	7.1579	3.2666	3.8675	TRUE
Uncharacterized protein OS=Mus musculus GN=Prmt1 PE=1 SV=1	Q3UIG8 (+4)	Prmt1	41 kDa	11.049	7.9893	7.1579	6.5332	8.5944	TRUE
Uncharacterized protein OS=Mus musculus GN=Psmd11 PE=2 SV=1	Q3UWW9 (+3)	Psmd11	47 kDa	0	0	5.3684	3.6749	4.2972	TRUE
Uncharacterized protein OS=Mus musculus GN=Pum1 PE=2 SV=1	Q3TQ21 (+1)	Pum1	127 kDa	14.732	17.576	17.895	1.6333	2.1486	TRUE
Uncharacterized protein OS=Mus musculus GN=Pvr PE=2 SV=1	Q8BVF6 (+2)	Pvr	45 kDa	9.2077	4.7936	5.3684	0	0.85944	TRUE
Uncharacterized protein OS=Mus musculus GN=Rbm39 PE=2 SV=1	Q3U313 (+2)	Rbm39	59 kDa	5.5246	4.7936	0	2.45	3.008	TRUE
Uncharacterized protein OS=Mus musculus GN=Rcn2 PE=2 SV=1	Q3TE95 (+1)	Rcn2	41 kDa	5.5246	9.5872	12.526	1.225	1.2892	TRUE
Uncharacterized protein OS=Mus musculus GN=Rpl14 PE=2 SV=1	Q9CWK0	Rpl14	26 kDa	3.6831	3.1957	0	2.8583	2.1486	TRUE
Uncharacterized protein OS=Mus musculus GN=Rpl24 PE=2 SV=1	Q3UW40 (+1)	Rpl24	18 kDa	3.6831	3.1957	3.5789	4.0833	3.008	TRUE
Uncharacterized protein OS=Mus musculus GN=Serpinh1 PE=2 SV=1	Q3TWG9	Serpinh1	47 kDa	60.771	63.914	62.632	18.375	16.329	TRUE
Uncharacterized protein OS=Mus musculus GN=Slc25a3 PE=2 SV=1	Q3THU8 (+1)	Slc25a3	40 kDa	11.049	11.185	16.105	6.5332	6.4458	TRUE
Uncharacterized protein OS=Mus musculus GN=Slc7a5 PE=2 SV=1	Q3UQM7 (+1)	Slc7a5	56 kDa	11.049	7.9893	7.1579	2.45	2.1486	TRUE
Uncharacterized protein OS=Mus musculus GN=Sqor PE=2 SV=1	Q3UDS4 (+1)	Sqor	50 kDa	29.465	17.576	21.474	3.6749	5.1566	TRUE
Uncharacterized protein OS=Mus musculus GN=Steap1 PE=2 SV=1	Q3UNB9 (+2)	Steap1	39 kDa	9.2077	6.3914	5.3684	0	0	TRUE
Uncharacterized protein OS=Mus musculus GN=Tpp2 PE=2 SV=1	Q3TW28	Tpp2	138 kDa	3.6831	11.185	5.3684	10.208	9.8835	TRUE
Uncharacterized protein OS=Mus musculus GN=Trap1 PE=2 SV=1	Q3UPJ8 (+2)	Trap1	80 kDa	18.415	14.381	21.474	7.7582	9.0241	TRUE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Uncharacterized protein OS=Mus musculus GN=Txndc5 PE=1 SV=1	Q3TEE8 (+1)	Txndc5	46 kDa	18.415	17.576	19.684	6.1249	9.0241	TRUE
Uncharacterized protein OS=Mus musculus GN=Unc5b PE=2 SV=1	Q3TYW6 (+1)	Unc5b	104 kDa	0	17.576	10.737	0	0	TRUE
Uncharacterized protein OS=Mus musculus GN=Uqcrc1 PE=2 SV=1	Q3TIC8 (+1)	Uqcrc1	53 kDa	0	4.7936	8.9474	6.5332	5.5863	TRUE
Uncharacterized protein OS=Mus musculus PE=2 SV=1	Q8CBU3		38 kDa	5.5246	4.7936	0	2.0416	2.1486	TRUE
Uridine 5'-monophosphate synthase OS=Mus musculus GN=Umps PE=1 SV=3	P13439 (+1)	Umps	52 kDa	0	0	7.1579	2.8583	3.008	TRUE
V-crk sarcoma virus CT10 oncogene homolog (Avian)-like OS=Mus musculus GN=Crkl PE=1 SV=1	A2RS58 (+1)	Crkl	34 kDa	5.5246	4.7936	7.1579	0.81665	1.2892	TRUE
Vacuolar protein sorting-associated protein 33B OS=Mus musculus GN=Vps33b PE=1 SV=1	P59016	Vps33b	71 kDa	0	0	3.5789	0	6.0161	TRUE
Vacuolar protein sorting-associated protein 35 OS=Mus musculus GN=Vps35 PE=2 SV=1	Q3TJ43 (+2)	Vps35	92 kDa	0	3.1957	0	4.0833	2.5783	TRUE
Valyl-tRNA synthetase 2, isoform CRA_b OS=Mus musculus GN=Vars PE=1 SV=1	Q790I0 (+1)	Vars	140 kDa	14.732	11.185	10.737	14.291	12.892	TRUE
Vascular cell adhesion molecule 1 OS=Mus musculus GN=Vcam1 PE=2 SV=1	Q8K0X1	Vcam1	81 kDa	31.306	30.359	23.263	3.2666	1.2892	TRUE
Vasorin OS=Mus musculus GN=Vasn PE=2 SV=2	Q9CZT5	Vasn	72 kDa	11.049	12.783	8.9474	0	0	TRUE
Versican core protein OS=Mus musculus GN=Vcan PE=1 SV=1	E9PYH0	Vcan	367 kDa	12.891	11.185	10.737	1.6333	0.85944	TRUE
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acadvl PE	P50544	Acadvl	71 kDa	0	3.1957	0	2.8583	3.008	TRUE
Very-long-chain 3-oxoacyl-CoA reductase OS=Mus musculus GN=Hsd17b12 PE=1 SV=1	O70503 (+1)	Hsd17b12	35 kDa	5.5246	4.7936	3.5789	6.5332	5.1566	TRUE
Very-long-chain enoyl-CoA reductase OS=Mus musculus GN=Tecr PE=1 SV=1	Q9CY27	Tecr	36 kDa	9.2077	12.783	10.737	1.6333	3.8675	TRUE
Vesicle-associated membrane protein-associated protein A OS=Mus musculus GN=Vapa PE=1 SV	Q9WV55	Vapa	28 kDa	9.2077	3.1957	5.3684	3.6749	3.8675	TRUE
Vimentin OS=Mus musculus GN=Vim PE=1 SV=3	P20152 (+2)	Vim	54 kDa	11.049	15.979	5.3684	2.8583	1.2892	TRUE
Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4	Q64727	Vcl	117 kDa	0	19.174	12.526	18.783	14.181	TRUE
Voltage-dependent anion-selective channel protein 2 OS=Mus musculus GN=Vdac2 PE=1 SV=2	Q60930	Vdac2	32 kDa	5.5246	3.1957	7.1579	3.6749	6.4458	TRUE
WD repeat-containing protein 5 OS=Mus musculus GN=Wdr5 PE=1 SV=1	P61965 (+1)	Wdr5	37 kDa	5.5246	4.7936	0	1.225	0	TRUE
X-ray repair cross-complementing protein 6 OS=Mus musculus GN=Xrcc6 PE=1 SV=1	A0A0R4J187 (+1)	Xrcc6	69 kDa	0	0	7.1579	1.225	1.7189	TRUE
Y-box-binding protein 3 OS=Mus musculus GN=Ybx3 PE=1 SV=2	Q9JKB3	Ybx3	39 kDa	7.3662	6.3914	8.9474	6.9416	6.0161	TRUE
YTH domain family 1, isoform CRA_a OS=Mus musculus GN=Ythdf1 PE=1 SV=1	A2AWN8 (+1)	Ythdf1	64 kDa	9.2077	0	5.3684	2.0416	2.1486	TRUE
YTH domain-containing family protein 2 OS=Mus musculus GN=Ythdf2 PE=1 SV=1	Q91YT7	Ythdf2	62 kDa	11.049	0	0	2.45	3.008	TRUE
YTH domain-containing family protein 3 OS=Mus musculus GN=Ythdf3 PE=1 SV=2	Q8BYK6	Ythdf3	64 kDa	9.2077	0	3.5789	3.2666	3.008	TRUE
Zinc finger protein ZFPM2 OS=Mus musculus GN=Zfpm2 PE=1 SV=2	Q8CCH7	Zfpm2	128 kDa	5.5246	3.1957	7.1579	0	0	TRUE
Zinc transporter ZIP10 OS=Mus musculus GN=Slc39a10 PE=1 SV=1	Q6P5F6	Slc39a10	94 kDa	9.2077	4.7936	7.1579	0	0	TRUE
Zyx protein OS=Mus musculus GN=Zyx PE=1 SV=1	Q7TQE2	Zyx	57 kDa	0	4.7936	3.5789	7.7582	4.7269	TRUE
[F-actin]-monooxygenase MICAL1 OS=Mus musculus GN=Mical1 PE=1 SV=1	Q8VDP3	Mical1	117 kDa	0	0	0	2.0416	1.7189	FALSE
[Protein ADP-ribosylarginine] hydrolase OS=Mus musculus GN=Adprh PE=1 SV=1	P54923 (+1)	Adprh	40 kDa	0	0	0	1.225	0	FALSE
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial OS=Mus muscul	Q8BFP9 (+1)	Pdk1	49 kDa	0	0	0	0	1.7189	FALSE
1-acyl-sn-glycerol-3-phosphate acyltransferase delta OS=Mus musculus GN=Agpat4 PE=1 SV=1	Q8K4X7	Agpat4	44 kDa	0	0	0	0.81665	1.2892	FALSE
1-acyl-sn-glycerol-3-phosphate acyltransferase OS=Mus musculus GN=Agpat1 PE=1 SV=1	A0A0R4J263 (+1)	Agpat1	32 kDa	0	0	0	0	0.85944	FALSE
1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase OS=Mus musculus GN=Adi1 PE=1 SV=1	Q99JT9	Adi1	22 kDa	0	0	0	0	0.85944	FALSE
1,4-alpha-glucan-branching enzyme OS=Mus musculus GN=Gbe1 PE=1 SV=1	G3UW30 (+1)	Gbe1	76 kDa	0	0	0	0	0.85944	FALSE
116 kDa U5 small nuclear ribonucleoprotein component OS=Mus musculus GN=Eftud2 PE=1 SV=1	A2AH85 (+4)	Eftud2	109 kDa	0	0	0	1.225	2.5783	FALSE
130kDa Protein 4.1B MEF cell isoform OS=Mus musculus GN=Epb41l3 PE=1 SV=1	A7YY80	Epb41l3	98 kDa	5.5246	3.1957	5.3684	11.433	12.892	FALSE
14 kDa phosphohistidine phosphatase OS=Mus musculus GN=Phpt1 PE=1 SV=1	Q9DAK9	Phpt1	14 kDa	0	0	0	1.225	3.008	FALSE
14-3-3 protein eta OS=Mus musculus GN=Ywhah PE=1 SV=2	P68510	Ywhah	28 kDa	0	0	0	2.0416	2.5783	FALSE
17beta-hydroxysteroid dehydrogenase type 10/short chain L-3-hydroxyacyl-CoA dehydrogenase	Q99N15	Hsd17b10	27 kDa	3.6831	0	0	4.4916	3.8675	FALSE
182 kDa tankyrase-1-binding protein OS=Mus musculus GN=Tnks1bp1 PE=1 SV=2	P58871	Tnks1bp1	182 kDa	3.6831	3.1957	3.5789	10.208	10.743	FALSE
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial OS=Mus musculus GN=Gcat PE=1 SV=	O88986	Gcat	45 kDa	0	0	0	0.81665	2.1486	FALSE
2-aminoethanethiol dioxygenase OS=Mus musculus GN=Ado PE=1 SV=2	Q6PDY2	Ado	28 kDa	0	0	0	0.81665	0	FALSE
2-iminobutanoate/2-iminopropanoate deaminase OS=Mus musculus GN=Rida PE=1 SV=3	P52760	Rida	14 kDa	0	0	0	1.6333	0.85944	FALSE
2'-5'-oligoadenylate synthase 1A OS=Mus musculus GN=Oas1a PE=1 SV=2	P11928	Oas1a	42 kDa	0	0	0	2.45	0	FALSE
2'-deoxynucleoside 5'-phosphate N-hydrolase 1 OS=Mus musculus GN=Dnph1 PE=1 SV=2	Q80VJ3	Dnph1	19 kDa	0	0	0	0	1.2892	FALSE
2',5'-phosphodiesterase 12 OS=Mus musculus GN=Pde12 PE=1 SV=2	Q3TIU4	Pde12	68 kDa	0	0	0	1.225	0.85944	FALSE
26S proteasome non-ATPase regulatory subunit 1 OS=Mus musculus GN=Psmd1 PE=1 SV=1	Q3TXS7	Psmd1	106 kDa	0	0	0	5.3082	3.8675	FALSE
26S proteasome non-ATPase regulatory subunit 12 OS=Mus musculus GN=Psmd12 PE=1 SV=1	B1AT36 (+2)	Psmd12	51 kDa	0	0	0	2.45	3.008	FALSE
26S proteasome non-ATPase regulatory subunit 14 OS=Mus musculus GN=Psmd14 PE=1 SV=2	O35593 (+1)	Psmd14	35 kDa	0	0	0	1.6333	1.7189	FALSE
26S proteasome non-ATPase regulatory subunit 3 OS=Mus musculus GN=Psmd3 PE=1 SV=3	P14685	Psmd3	61 kDa	0	0	0	6.1249	5.5863	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
26S proteasome non-ATPase regulatory subunit 4 OS=Mus musculus GN=Psmd4 PE=1 SV=1	O35226 (+1)	Psmd4	41 kDa	0	0	0	2.45	2.5783	FALSE
26S proteasome non-ATPase regulatory subunit 6 OS=Mus musculus GN=Psmd6 PE=1 SV=1	Q99JI4	Psmd6	46 kDa	0	0	0	3.2666	3.4377	FALSE
26S proteasome non-ATPase regulatory subunit 8 OS=Mus musculus GN=Psmd8 PE=1 SV=2	Q9CX56	Psmd8	40 kDa	0	0	0	3.2666	3.8675	FALSE
26S proteasome regulatory subunit 4 OS=Mus musculus GN=Psmc1 PE=1 SV=1	P62192 (+1)	Psmc1	49 kDa	0	0	0	4.0833	3.8675	FALSE
28S ribosomal protein S22, mitochondrial OS=Mus musculus GN=Mrps22 PE=1 SV=1	Q9CXW2	Mrps22	41 kDa	0	0	0	0.81665	1.2892	FALSE
28S ribosomal protein S29, mitochondrial OS=Mus musculus GN=Dap3 PE=1 SV=1	Q9ER88	Dap3	45 kDa	0	0	0	1.225	1.2892	FALSE
28S ribosomal protein S30, mitochondrial OS=Mus musculus GN=Mrps30 PE=1 SV=1	Q9D0G0	Mrps30	50 kDa	0	0	0	0.81665	0	FALSE
28S ribosomal protein S34, mitochondrial OS=Mus musculus GN=Mrps34 PE=1 SV=1	Q9JIK9	Mrps34	26 kDa	0	0	0	0.81665	0.85944	FALSE
3-alpha-hydroxysteroid dehydrogenase type 1 OS=Mus musculus GN=Akr1c14 PE=1 SV=1	Q91WT7	Akr1c14	37 kDa	0	0	0	1.225	0	FALSE
3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase OS=Mus musculus GN=Ebp PE=1 SV=3	P70245	Ebp	26 kDa	0	0	0	0.81665	0	FALSE
3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Mus musculus GN=Hibadh PE=1 SV=1	Q99L13	Hibadh	35 kDa	0	0	0	2.45	3.008	FALSE
3-ketoacyl-CoA thiolase A, peroxisomal OS=Mus musculus GN=Acaa1a PE=1 SV=1	Q921H8	Acaa1a	44 kDa	0	0	0	5.3082	6.4458	FALSE
3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN=Acaa2 PE=1 SV=3	Q8BWT1	Acaa2	42 kDa	0	0	0	3.2666	3.8675	FALSE
39S ribosomal protein L3, mitochondrial OS=Mus musculus GN=Mrpl3 PE=1 SV=1	D3Z456 (+2)	Mrpl3	34 kDa	0	0	0	0.81665	0	FALSE
39S ribosomal protein L37, mitochondrial OS=Mus musculus GN=Mrpl37 PE=1 SV=1	Q921S7	Mrpl37	48 kDa	0	0	0	0.81665	0	FALSE
40S ribosomal protein S10 OS=Mus musculus GN=Rps10 PE=1 SV=1	P63325 (+1)	Rps10	19 kDa	0	0	0	1.6333	1.2892	FALSE
40S ribosomal protein S15 OS=Mus musculus GN=Rps15 PE=1 SV=1	D3YTQ9 (+2)	Rps15	14 kDa	0	0	0	1.6333	1.2892	FALSE
40S ribosomal protein S2 OS=Mus musculus GN=Rps2 PE=1 SV=3	P25444 (+3)	Rps2	31 kDa	3.6831	3.1957	3.5789	7.7582	7.7349	FALSE
40S ribosomal protein S23 OS=Mus musculus GN=Rps23 PE=1 SV=3	P62267 (+3)	Rps23	16 kDa	0	0	0	1.225	1.2892	FALSE
40S ribosomal protein S24 OS=Mus musculus GN=Rps24 PE=1 SV=1	A0A286YEB7 (+7)	Rps24	14 kDa	0	0	0	1.225	2.1486	FALSE
40S ribosomal protein S26 OS=Mus musculus GN=Rps26 PE=1 SV=3	P62855 (+1)	Rps26	13 kDa	0	0	0	0	1.2892	FALSE
40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1	P62754 (+2)	Rps6	29 kDa	0	0	0	7.3499	6.4458	FALSE
40S ribosomal protein S9 OS=Mus musculus GN=Rps9 PE=1 SV=3	Q6ZWN5	Rps9	23 kDa	0	0	0	5.3082	5.5863	FALSE
5'-3' exoribonuclease 1 OS=Mus musculus GN=Xrn1 PE=1 SV=1	A0A087WQN7 (+2)	Xrn1	194 kDa	0	0	0	1.225	0.85944	FALSE
5'-AMP-activated protein kinase subunit gamma-1 OS=Mus musculus GN=Prkag1 PE=1 SV=2	O54950 (+1)	Prkag1	38 kDa	0	0	0	1.6333	2.1486	FALSE
55 kDa erythrocyte membrane protein OS=Mus musculus GN=Mpp1 PE=1 SV=1	A2AN84 (+3)	Mpp1	51 kDa	0	0	0	1.225	2.1486	FALSE
6-phosphogluconate dehydrogenase, decarboxylating OS=Mus musculus GN=Pgd PE=2 SV=1	Q91V28 (+1)	Pgd	53 kDa	0	0	0	8.9832	9.0241	FALSE
6-phosphogluconolactonase OS=Mus musculus GN=Pgls PE=1 SV=1	Q9CQ60	Pgls	27 kDa	0	0	0	1.225	1.2892	FALSE
60 kDa SS-A/Ro ribonucleoprotein OS=Mus musculus GN=Trove2 PE=1 SV=1	O08848 (+3)	Trove2	60 kDa	0	0	0	0.81665	0.85944	FALSE
60S ribosomal export protein NMD3 OS=Mus musculus GN=Nmd3 PE=1 SV=1	Q99L48	Nmd3	58 kDa	0	0	0	2.0416	1.7189	FALSE
60S ribosomal protein L13 OS=Mus musculus GN=Rpl13 PE=1 SV=3	P47963	Rpl13	24 kDa	0	0	0	2.45	3.4377	FALSE
60S ribosomal protein L13a OS=Mus musculus GN=Rpl13a PE=1 SV=4	P19253 (+1)	Rpl13a	23 kDa	0	0	0	2.0416	3.4377	FALSE
60S ribosomal protein L18 OS=Mus musculus GN=Rpl18 PE=1 SV=3	P35980 (+2)	Rpl18	22 kDa	0	0	0	5.7166	5.1566	FALSE
60S ribosomal protein L18a OS=Mus musculus GN=Rpl18a PE=1 SV=1	A0A1D5RLW5 (+1)	Rpl18a	17 kDa	0	0	0	4.0833	4.2972	FALSE
60S ribosomal protein L27a OS=Mus musculus GN=Rpl27a PE=1 SV=5	P14115	Rpl27a	17 kDa	0	0	0	2.8583	2.1486	FALSE
60S ribosomal protein L29 OS=Mus musculus GN=Rpl29 PE=1 SV=2	P47915 (+1)	Rpl29	18 kDa	0	0	0	0	1.7189	FALSE
60S ribosomal protein L3 OS=Mus musculus GN=Rpl3 PE=1 SV=3	P27659 (+2)	Rpl3	46 kDa	0	4.7936	3.5789	12.25	12.032	FALSE
60S ribosomal protein L31 OS=Mus musculus GN=Rpl31 PE=1 SV=1	A0A0A6YX26 (+3)	Rpl31	15 kDa	0	0	0	1.6333	1.7189	FALSE
60S ribosomal protein L32 OS=Mus musculus GN=Rpl32 PE=1 SV=2	P62911 (+1)	Rpl32	16 kDa	0	0	0	1.6333	3.008	FALSE
60S ribosomal protein L35 OS=Mus musculus GN=Rpl35 PE=1 SV=1	Q6ZWV7	Rpl35	15 kDa	0	0	0	1.6333	1.2892	FALSE
60S ribosomal protein L36 OS=Mus musculus GN=Rpl36 PE=1 SV=1	Q6ZWZ4	Rpl36	12 kDa	0	0	0	1.225	1.2892	FALSE
60S ribosomal protein L36a OS=Mus musculus GN=Rpl36a PE=1 SV=2	P83882 (+1)	Rpl36a	12 kDa	0	0	0	1.6333	1.2892	FALSE
60S ribosomal protein L6 OS=Mus musculus GN=Rpl6 PE=1 SV=3	P47911 (+1)	Rpl6	34 kDa	0	0	0	6.5332	7.3052	FALSE
60S ribosomal protein L7 OS=Mus musculus GN=Rpl7 PE=1 SV=2	P14148 (+2)	Rpl7	31 kDa	0	3.1957	0	4.8999	6.4458	FALSE
60S ribosomal protein L8 OS=Mus musculus GN=Rpl8 PE=1 SV=2	P62918 (+1)	Rpl8	28 kDa	0	0	0	5.7166	4.2972	FALSE
7-dehydrocholesterol reductase OS=Mus musculus GN=Dhcr7 PE=1 SV=1	A0A140LIT2 (+2)	Dhcr7	54 kDa	0	0	0	1.225	0.85944	FALSE
7-methylguanosine phosphate-specific 5'-nucleotidase OS=Mus musculus GN=Nt5c3b PE=1 SV=3	Q3UFY7	Nt5c3b	34 kDa	0	0	0	1.6333	0	FALSE
A kinase (PRKA) anchor protein (Gravin) 12 OS=Mus musculus GN=Akap12 PE=2 SV=1	B2RRE0 (+1)	Akap12	181 kDa	0	0	0	1.225	0	FALSE
A-kinase anchor protein 1, mitochondrial OS=Mus musculus GN=Akap1 PE=1 SV=4	O08715	Akap1	92 kDa	0	0	0	0.81665	0	FALSE
Abce1 protein (Fragment) OS=Mus musculus GN=Abce1 PE=2 SV=1	Q6NXX7	Abce1	65 kDa	0	0	0	1.6333	3.4377	FALSE
Acetoacetyl-CoA synthetase OS=Mus musculus GN=Aacs PE=1 SV=1	Q9D2R0	Aacs	75 kDa	0	0	0	3.6749	4.2972	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Acetolactate synthase-like protein OS=Mus musculus GN=Ilvbl PE=1 SV=1	Q8BU33	Ilvbl	68 kDa	0	0	0	1.6333	0	FALSE
Acetyl-CoA acetyltransferase, cytosolic OS=Mus musculus GN=Acat2 PE=1 SV=2	Q8CAY6	Acat2	41 kDa	0	0	0	3.2666	4.2972	FALSE
Acetyl-coenzyme A transporter 1 OS=Mus musculus GN=Slc33a1 PE=1 SV=1	Q99J27	Slc33a1	61 kDa	0	0	0	0	0.85944	FALSE
Acid phosphatase 1, soluble OS=Mus musculus GN=Acp1 PE=2 SV=1	Q4VAI2 (+1)	Acp1	18 kDa	0	0	0	1.225	1.7189	FALSE
Acidic leucine-rich nuclear phosphoprotein 32 family member A (Fragment) OS=Mus musculus GN	D3YYE1 (+2)	Anp32a	23 kDa	0	0	0	0	1.7189	FALSE
Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Mus musculus GN=Anp32e PE	P97822 (+1)	Anp32e	30 kDa	0	0	0	2.8583	2.5783	FALSE
Actin-like 6A, isoform CRA_a OS=Mus musculus GN=Actl6a PE=1 SV=1	Q505L1 (+1)	Actl6a	47 kDa	0	0	0	0.81665	1.2892	FALSE
Actin-related protein 10 OS=Mus musculus GN=Actr10 PE=1 SV=2	Q9QZB7	Actr10	46 kDa	0	0	0	1.6333	0.85944	FALSE
Actin-related protein 2 OS=Mus musculus GN=Actr2 PE=1 SV=1	P61161 (+1)	Actr2	45 kDa	0	0	0	6.9416	6.4458	FALSE
Actin-related protein 2/3 complex subunit 3 OS=Mus musculus GN=Arpc3 PE=1 SV=1	H7BWZ3 (+1)	Arpc3	20 kDa	0	0	0	0.81665	0	FALSE
Actin-related protein 2/3 complex subunit 4 OS=Mus musculus GN=Arpc4 PE=1 SV=3	P59999 (+2)	Arpc4	20 kDa	0	0	0	1.6333	1.7189	FALSE
Activated RNA polymerase II transcriptional coactivator p15 OS=Mus musculus GN=Sub1 PE=1 S	P11031	Sub1	14 kDa	0	0	0	0.81665	3.008	FALSE
Activating signal cointegrator 1 complex subunit 3 OS=Mus musculus GN=Ascc3 PE=1 SV=1	E9PZJ8	Ascc3	251 kDa	0	0	0	1.225	0	FALSE
Acyl-CoA dehydrogenase family member 9, mitochondrial OS=Mus musculus GN=Acad9 PE=1 SV=	Q8JZN5	Acad9	69 kDa	0	0	0	1.225	3.4377	FALSE
Acyl-CoA synthetase family member 2, mitochondrial OS=Mus musculus GN=Acsf2 PE=1 SV=1	Q8VCW8	Acsf2	68 kDa	0	0	0	3.6749	3.4377	FALSE
Acyl-CoA synthetase long-chain family member 5, isoform CRA_b OS=Mus musculus GN=Acsl5 PE	Q3UC67 (+2)	Acsl5	76 kDa	0	0	0	2.0416	1.7189	FALSE
Acyl-Coenzyme A binding domain containing 3, isoform CRA_b OS=Mus musculus GN=Acbd3 PE=1	A0A0R4J079 (+2)	Acbd3	60 kDa	0	0	0	1.6333	1.7189	FALSE
Acyl-Coenzyme A binding domain containing 6 OS=Mus musculus GN=Acbd6 PE=2 SV=1	Q14BV7 (+1)	Acbd6	31 kDa	0	0	0	0.81665	0	FALSE
Acylamino-acid-releasing enzyme OS=Mus musculus GN=Apeh PE=1 SV=3	Q8R146	Apeh	82 kDa	0	0	0	1.6333	3.008	FALSE
Acylglycerol kinase, mitochondrial OS=Mus musculus GN=Agk PE=1 SV=1	Q9ESW4	Agk	47 kDa	0	0	0	0.81665	0.85944	FALSE
Adapter molecule crk OS=Mus musculus GN=Crk PE=1 SV=2	Q5ND50	Crk	29 kDa	0	0	0	2.8583	2.1486	FALSE
Adenine phosphoribosyltransferase OS=Mus musculus GN=Aprt PE=1 SV=2	P08030	Aprt	20 kDa	0	0	0	2.8583	3.8675	FALSE
Adenosine kinase OS=Mus musculus GN=Adk PE=1 SV=2	P55264	Adk	40 kDa	0	0	0	3.2666	4.7269	FALSE
Adenylate kinase 2, mitochondrial OS=Mus musculus GN=Ak2 PE=1 SV=5	Q9WTP6	Ak2	26 kDa	0	0	0	0.81665	1.7189	FALSE
Adenylate kinase isoenzyme 1 OS=Mus musculus GN=Ak1 PE=1 SV=1	Q9R0Y5	Ak1	22 kDa	0	0	0	2.8583	1.2892	FALSE
Adenylosuccinate lyase OS=Mus musculus GN=Adsl PE=1 SV=2	P54822 (+1)	Adsl	55 kDa	0	0	0	2.45	3.008	FALSE
Adenylosuccinate synthetase isozyme 2 OS=Mus musculus GN=Adss PE=1 SV=1	B9EIE9 (+1)	Adss	50 kDa	0	0	0	4.0833	3.8675	FALSE
Adenylyl cyclase-associated protein 2 OS=Mus musculus GN=Cap2 PE=1 SV=1	Q9CYT6	Cap2	53 kDa	0	0	0	0.81665	1.2892	FALSE
Adipocyte enhancer-binding protein 1 OS=Mus musculus GN=Aebp1 PE=1 SV=1	Q640N1	Aebp1	128 kDa	0	0	0	1.6333	1.7189	FALSE
ADP-dependent glucokinase OS=Mus musculus GN=Adpgk PE=1 SV=1	A0A1L1SSF2 (+3)	Adpgk	54 kDa	0	0	0	1.225	1.2892	FALSE
ADP-ribose pyrophosphatase, mitochondrial OS=Mus musculus GN=Nudt9 PE=1 SV=1	Q8BVU5	Nudt9	39 kDa	0	0	0	1.6333	0.85944	FALSE
ADP-ribosylation factor 5 OS=Mus musculus GN=Arf5 PE=1 SV=2	P84084	Arf5	21 kDa	0	0	0	5.3082	5.5863	FALSE
ADP-ribosylation factor 6 OS=Mus musculus GN=Arf6 PE=1 SV=2	P62331 (+1)	Arf6	20 kDa	0	0	0	0.81665	0.85944	FALSE
ADP-ribosylation factor GTPase activating protein 1, isoform CRA_d (Fragment) OS=Mus musculu	Q05DE0 (+2)	Arfgap1	43 kDa	0	0	0	2.45	2.1486	FALSE
ADP-ribosylation factor GTPase-activating protein 2 OS=Mus musculus GN=Arfgap2 PE=1 SV=1	Q99K28	Arfgap2	57 kDa	0	0	0	2.0416	3.008	FALSE
ADP-ribosylation factor-binding protein GGA1 OS=Mus musculus GN=Gga1 PE=1 SV=1	Q8R0H9	Gga1	70 kDa	0	0	0	1.225	0.85944	FALSE
ADP-ribosylation factor-interacting protein 1 OS=Mus musculus GN=Arfip1 PE=1 SV=1	G5E8V9	Arfip1	42 kDa	0	0	0	2.8583	2.1486	FALSE
ADP-ribosylation factor-like protein 8B OS=Mus musculus GN=Arl8b PE=1 SV=1	Q9CQW2 (+1)	Arl8b	22 kDa	0	0	0	2.0416	2.1486	FALSE
ADP-sugar pyrophosphatase OS=Mus musculus GN=Nudt5 PE=1 SV=1	Q9JKX6	Nudt5	24 kDa	0	0	0	2.45	1.7189	FALSE
Afadin OS=Mus musculus GN=Afdn PE=1 SV=1	E9Q9C3 (+1)	Afdn	207 kDa	0	0	0	2.45	2.1486	FALSE
Aflatoxin B1 aldehyde reductase member 2 OS=Mus musculus GN=Akr7a2 PE=1 SV=3	Q8CG76	Akr7a2	41 kDa	0	0	0	1.225	0.85944	FALSE
AH receptor-interacting protein OS=Mus musculus GN=Aip PE=1 SV=1	O08915	Aip	38 kDa	0	0	0	1.6333	2.1486	FALSE
AHNAK nucleoprotein 2 (Fragment) OS=Mus musculus GN=Ahnak2 PE=1 SV=1	F7DBB3	Ahnak2	166 kDa	0	0	0	1.6333	2.1486	FALSE
Aladin OS=Mus musculus GN=Aaas PE=1 SV=1	P58742 (+2)	Aaas	59 kDa	0	0	0	1.225	1.7189	FALSE
Alanine aminotransferase 2 OS=Mus musculus GN=Gpt2 PE=1 SV=1	Q8BGT5	Gpt2	58 kDa	0	0	0	0.81665	0.85944	FALSE
Alanyl-tRNA editing protein Aarsd1 OS=Mus musculus GN=Aarsd1 PE=1 SV=2	Q3THG9	Aarsd1	45 kDa	0	0	0	0.81665	1.7189	FALSE
Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=2	P00329 (+1)	Adh1	40 kDa	0	0	0	0	0.85944	FALSE
Alcohol dehydrogenase class-3 OS=Mus musculus GN=Adh5 PE=1 SV=3	P28474 (+1)	Adh5	40 kDa	0	0	0	3.2666	4.2972	FALSE
Aldehyde dehydrogenase family 16 member A1 OS=Mus musculus GN=Aldh16a1 PE=1 SV=2	Q571I9	Aldh16a1	85 kDa	0	0	0	2.45	1.2892	FALSE
Aldehyde dehydrogenase OS=Mus musculus GN=Aldh3a2 PE=3 SV=1	Q99PH3 (+1)	Aldh3a2	54 kDa	0	0	0	2.45	0.85944	FALSE
Aldehyde reductase OS=Mus musculus GN=Akr1a1 PE=1 SV=1	Q540D7 (+1)	Akr1a1	37 kDa	0	0	0	4.4916	3.8675	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Aldhehyde dehydrogenase family 5, subfamily A1 OS=Mus musculus GN=Aldh5a1 PE=1 SV=1	B2RS41 (+1)	Aldh5a1	56 kDa	0	0	0	0.81665	1.7189	FALSE
Aldo-keto reductase family 1, member B3 (Aldose reductase) OS=Mus musculus GN=Akr1b3 PE=2	Q5U415	Akr1b3	36 kDa	0	0	0	2.45	2.1486	FALSE
Aldose reductase-related protein 2 OS=Mus musculus GN=Akr1b8 PE=1 SV=2	P45377	Akr1b8	36 kDa	0	0	0	2.0416	1.7189	FALSE
Alkylglycerone-phosphate synthase OS=Mus musculus GN=Agps PE=1 SV=1	A2AL50 (+1)	Agps	74 kDa	0	0	0	3.6749	4.7269	FALSE
Alpha-1,4 glucan phosphorylase OS=Mus musculus GN=Pygb PE=2 SV=1	Q3TFQ8 (+2)	Pygb	97 kDa	0	0	0	7.7582	4.2972	FALSE
Alpha-adducin OS=Mus musculus GN=Add1 PE=1 SV=2	Q9QYC0	Add1	81 kDa	0	0	0	1.225	0.85944	FALSE
Alpha-aminoadipic semialdehyde dehydrogenase OS=Mus musculus GN=Aldh7a1 PE=1 SV=4	Q9DBF1	Aldh7a1	59 kDa	0	0	0	4.4916	3.4377	FALSE
Alpha-centractin OS=Mus musculus GN=Actr1a PE=1 SV=1	P61164	Actr1a	43 kDa	0	0	0	1.225	2.5783	FALSE
Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3	P17182 (+1)	Eno1	47 kDa	23.94	22.37	32.211	38.383	39.534	FALSE
Alpha-ketoglutarate-dependent dioxygenase FTO OS=Mus musculus GN=Fto PE=1 SV=1	Q8BGW1	Fto	58 kDa	0	0	0	0	0.85944	FALSE
Alpha-mannosidase 2 OS=Mus musculus GN=Man2a1 PE=1 SV=2	P27046	Man2a1	132 kDa	0	0	0	4.4916	5.1566	FALSE
Alpha-methylacyl-CoA racemase OS=Mus musculus GN=Amacr PE=1 SV=4	O09174 (+1)	Amacr	42 kDa	0	0	0	0.81665	0	FALSE
Alpha-parvin OS=Mus musculus GN=Parva PE=1 SV=1	Q3UF75 (+1)	Parva	38 kDa	0	0	0	2.45	1.2892	FALSE
Alpha-soluble NSF attachment protein OS=Mus musculus GN=Napa PE=1 SV=1	Q9DB05	Napa	33 kDa	0	0	0	0.81665	0	FALSE
Amino acid transporter OS=Mus musculus GN=Slc1a5 PE=2 SV=1	Q3UFR4 (+2)	Slc1a5	58 kDa	0	0	0	1.225	0	FALSE
Aminopeptidase B OS=Mus musculus GN=Rnpep PE=1 SV=2	Q8VCT3	Rnpep	72 kDa	0	0	0	1.6333	1.7189	FALSE
AMP deaminase OS=Mus musculus GN=Ampd2 PE=1 SV=1	A2AE27 (+1)	Ampd2	95 kDa	0	0	0	1.6333	2.1486	FALSE
AMP deaminase OS=Mus musculus GN=Ampd3 PE=1 SV=1	A0A1L1SRX2 (+1)	Ampd3	90 kDa	0	0	0	3.2666	0.85944	FALSE
Amylo-1,6-glucosidase, 4-alpha-glucanotransferase OS=Mus musculus GN=Agl PE=1 SV=1	F8VPN4	Agl	174 kDa	0	0	0	0	1.2892	FALSE
Amyloid beta (A4) protein-binding, family B, member 1 interacting protein OS=Mus musculus GN	B1AYC9 (+1)	Apbb1ip	74 kDa	0	0	0	1.225	0	FALSE
Amyloid-beta A4 precursor protein-binding family B member 2 OS=Mus musculus GN=Apbb2 PE=	E9PWH3 (+3)	Apbb2	81 kDa	0	0	0	0.81665	0.85944	FALSE
Amyloid-beta A4 protein OS=Mus musculus GN=App PE=1 SV=3	P12023 (+2)	App	87 kDa	0	0	0	0.81665	0	FALSE
AN1-type zinc finger protein 5 OS=Mus musculus GN=Zfand5 PE=1 SV=1	O88878	Zfand5	23 kDa	0	0	0	0	1.2892	FALSE
AN1-type zinc finger protein 6 OS=Mus musculus GN=Zfand6 PE=1 SV=1	Q9DCH6	Zfand6	24 kDa	0	0	0	1.225	1.7189	FALSE
Anamorsin OS=Mus musculus GN=Ciapin1 PE=1 SV=2	F8WIK0 (+1)	Ciapin1	33 kDa	0	0	0	0	0.85944	FALSE
Anaphase promoting complex subunit 2 OS=Mus musculus GN=Anapc2 PE=2 SV=1	Q3U430 (+2)	Anapc2	95 kDa	0	0	0	1.225	0	FALSE
Anaphase-promoting complex subunit 7 OS=Mus musculus GN=Anapc7 PE=1 SV=3	Q9WVM3	Anapc7	63 kDa	0	0	0	0.81665	0	FALSE
Angio-associated migratory protein OS=Mus musculus GN=Aamp PE=1 SV=1	J3QN89 (+3)	Aamp	47 kDa	0	0	0	0	0.85944	FALSE
Anillin OS=Mus musculus GN=Anln PE=1 SV=2	Q8K298	Anln	123 kDa	0	0	0	3.2666	4.2972	FALSE
Anion exchange protein OS=Mus musculus GN=Slc4a7 PE=2 SV=1	U3RF68	Slc4a7	135 kDa	0	0	0	1.225	1.2892	FALSE
Ankycorbin OS=Mus musculus GN=Rai14 PE=1 SV=1	Q9EP71	Rai14	109 kDa	0	0	0	1.6333	0.85944	FALSE
Ankyrin repeat and FYVE domain containing 1 OS=Mus musculus GN=Ankfy1 PE=2 SV=1	B7ZP20 (+1)	Ankfy1	129 kDa	0	0	0	2.8583	1.2892	FALSE
Annexin A11 OS=Mus musculus GN=Anxa11 PE=1 SV=2	P97384	Anxa11	54 kDa	0	0	0	0	1.2892	FALSE
Annexin A4 OS=Mus musculus GN=Anxa4 PE=1 SV=4	P97429 (+1)	Anxa4	36 kDa	3.6831	0	3.5789	5.7166	5.1566	FALSE
Annexin OS=Mus musculus GN=Anxa6 PE=1 SV=1	F8WIT2	Anxa6	75 kDa	0	9.5872	0	17.558	10.743	FALSE
Annexin OS=Mus musculus GN=Anxa7 PE=2 SV=1	Q922A2	Anxa7	50 kDa	0	0	0	3.2666	2.5783	FALSE
Anoctamin-6 OS=Mus musculus GN=Ano6 PE=1 SV=1	Q6P9J9	Ano6	106 kDa	0	0	0	1.6333	0.85944	FALSE
AP complex subunit beta OS=Mus musculus GN=Ap1b1 PE=2 SV=1	Q8CC13	Ap1b1	105 kDa	0	0	0	4.0833	3.8675	FALSE
AP complex subunit beta OS=Mus musculus GN=Ap2b1 PE=2 SV=1	Q5SWR1 (+1)	Ap2b1	106 kDa	0	4.7936	0	4.8999	5.5863	FALSE
AP-1 complex subunit mu-1 OS=Mus musculus GN=Ap1m1 PE=1 SV=3	P35585 (+1)	Ap1m1	49 kDa	0	0	0	2.0416	2.1486	FALSE
AP-2 complex subunit alpha-1 OS=Mus musculus GN=Ap2a1 PE=1 SV=1	P17426	Ap2a1	108 kDa	0	0	0	5.7166	3.008	FALSE
AP-2 complex subunit alpha-2 OS=Mus musculus GN=Ap2a2 PE=1 SV=2	P17427 (+2)	Ap2a2	104 kDa	0	3.1957	3.5789	5.3082	5.1566	FALSE
AP-2 complex subunit mu OS=Mus musculus GN=Ap2m1 PE=1 SV=1	P84091 (+3)	Ap2m1	50 kDa	0	0	0	3.2666	4.7269	FALSE
AP-3 complex subunit beta-1 OS=Mus musculus GN=Ap3b1 PE=1 SV=2	Q9Z1T1	Ap3b1	123 kDa	0	0	0	3.2666	3.008	FALSE
AP-3 complex subunit delta-1 OS=Mus musculus GN=Ap3d1 PE=1 SV=1	O54774	Ap3d1	135 kDa	0	0	0	2.45	1.7189	FALSE
AP-3 complex subunit mu-1 OS=Mus musculus GN=Ap3m1 PE=1 SV=1	Q9JKC8	Ap3m1	47 kDa	0	0	0	2.45	2.1486	FALSE
AP2-associated protein kinase 1 OS=Mus musculus GN=Aak1 PE=1 SV=2	Q3UHJ0	Aak1	103 kDa	0	0	0	1.6333	1.2892	FALSE
Apoptosis inhibitor 5 OS=Mus musculus GN=Api5 PE=1 SV=2	O35841	Api5	57 kDa	0	0	0	3.2666	3.8675	FALSE
Apoptosis regulator BAX (Fragment) OS=Mus musculus GN=Bax PE=1 SV=1	A0A1B0GTA4 (+6)	Bax	20 kDa	0	0	0	0.81665	0.85944	FALSE
Apoptosis-inducing factor 1, mitochondrial OS=Mus musculus GN=Aifm1 PE=1 SV=1	Q9Z0X1	Aifm1	67 kDa	0	0	0	3.6749	4.7269	FALSE
ARF GTPase-activating protein GIT2 OS=Mus musculus GN=Git2 PE=1 SV=2	Q9JLQ2	Git2	79 kDa	0	0	0	1.225	0	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1 OS=Mus musculus G	E9QN63 (+3)	Asap1	127 kDa	0	0	0	1.225	0	FALSE
Argininosuccinate lyase OS=Mus musculus GN=Asl PE=1 SV=1	Q91YI0	Asl	52 kDa	0	0	0	0.81665	0	FALSE
Arginyl-tRNA--protein transferase 1 OS=Mus musculus GN=Ate1 PE=1 SV=1	A0A1L1SQ41 (+2)	Ate1	64 kDa	0	0	0	0.81665	0	FALSE
Arp2/3 complex 34 kDa subunit (Fragment) OS=Mus musculus GN=Arpc2 PE=2 SV=1	Q3UA52 (+1)	Arpc2	43 kDa	0	0	0	4.0833	4.2972	FALSE
Arpin OS=Mus musculus GN=Arpin PE=1 SV=1	Q9D0A3	Arpin	25 kDa	0	0	0	2.45	2.1486	FALSE
Aryl hydrocarbon receptor nuclear translocator OS=Mus musculus GN=Arnt PE=1 SV=2	E9QLT6 (+3)	Arnt	85 kDa	0	0	0	0	0.85944	FALSE
Arylamine N-acetyltransferase 2 OS=Mus musculus GN=Nat2 PE=1 SV=1	P50295 (+2)	Nat2	34 kDa	0	0	0	0.81665	0	FALSE
Arylsulfatase B OS=Mus musculus GN=Arsb PE=1 SV=1	A0A0R4J138	Arsb	60 kDa	0	0	0	1.6333	1.7189	FALSE
Asparagine synthetase [glutamine-hydrolyzing] OS=Mus musculus GN=Asns PE=1 SV=3	Q61024	Asns	64 kDa	3.6831	6.3914	3.5789	8.9832	11.602	FALSE
Asparagine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Nars PE=1 SV=2	Q8BP47	Nars	64 kDa	0	0	0	11.841	8.1647	FALSE
Aspartate aminotransferase, cytoplasmic OS=Mus musculus GN=Got1 PE=1 SV=3	P05201	Got1	46 kDa	0	0	0	4.4916	6.8755	FALSE
Aspartyl/asparaginyl beta-hydroxylase OS=Mus musculus GN=Asph PE=1 SV=1	A2AL85 (+3)	Asph	81 kDa	0	0	0	2.8583	3.008	FALSE
Aspartylglucosaminidase OS=Mus musculus GN=Aga PE=1 SV=1	A2RSS6 (+1)	Aga	37 kDa	0	0	0	1.225	1.7189	FALSE
Ataxin-2 OS=Mus musculus GN=Atxn2 PE=1 SV=1	O70305	Atxn2	136 kDa	0	0	0	2.45	3.4377	FALSE
Atlastin-3 OS=Mus musculus GN=Atl3 PE=1 SV=1	Q91YH5	Atl3	61 kDa	0	0	0	4.0833	3.008	FALSE
ATP-binding cassette sub-family F member 1 OS=Mus musculus GN=Abcf1 PE=1 SV=1	Q6P542	Abcf1	95 kDa	0	0	0	5.7166	6.8755	FALSE
ATP-binding cassette sub-family F member 3 OS=Mus musculus GN=Abcf3 PE=1 SV=1	Q8K268	Abcf3	80 kDa	0	0	0	0	1.7189	FALSE
ATP-binding cassette, sub-family B (MDR/TAP), member 1B OS=Mus musculus GN=Abcb1b PE=1 S	B2RUR3 (+1)	Abcb1b	141 kDa	0	0	0	0	0.85944	FALSE
ATP-binding cassette, sub-family C (CFTR/MRP), member 4 OS=Mus musculus GN=Abcc4 PE=1 SV	E9Q236 (+1)	Abcc4	149 kDa	0	0	0	0	1.7189	FALSE
ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1	Q3V117	Acly	121 kDa	0	0	7.1579	8.5749	11.602	FALSE
ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Mus musculus GN=Naxd PE=1 SV=1	J3QMM7 (+2)	Naxd	35 kDa	0	0	0	0	1.7189	FALSE
ATP-dependent 6-phosphofructokinase, liver type OS=Mus musculus GN=Pfkl PE=1 SV=4	P12382	Pfkl	85 kDa	5.5246	3.1957	5.3684	8.1665	9.8835	FALSE
ATP-dependent 6-phosphofructokinase, muscle type OS=Mus musculus GN=Pfkm PE=1 SV=3	P47857	Pfkm	85 kDa	0	0	0	4.0833	6.4458	FALSE
ATP-dependent 6-phosphofructokinase, platelet type OS=Mus musculus GN=Pfkp PE=1 SV=1	Q9WUA3	Pfkp	85 kDa	0	0	0	4.4916	7.3052	FALSE
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial OS=Mus musculus GN=	Q6P8N8 (+1)	Clpx	67 kDa	0	0	0	0.81665	3.4377	FALSE
ATP-dependent DNA helicase OS=Mus musculus GN=Recql PE=1 SV=1	E9Q3N0 (+2)	Recql	71 kDa	0	0	0	0.81665	0	FALSE
ATP-dependent RNA helicase A OS=Mus musculus GN=Dhx9 PE=1 SV=2	O70133	Dhx9	149 kDa	0	0	0	0	0.85944	FALSE
ATP-dependent RNA helicase DDX19A OS=Mus musculus GN=Ddx19a PE=1 SV=2	Q61655	Ddx19a	54 kDa	0	0	0	3.6749	4.2972	FALSE
ATP-dependent RNA helicase DDX42 OS=Mus musculus GN=Ddx42 PE=1 SV=3	Q810A7	Ddx42	102 kDa	0	0	0	1.225	0	FALSE
ATP-dependent RNA helicase DHX29 OS=Mus musculus GN=Dhx29 PE=1 SV=1	Q6PGC1	Dhx29	154 kDa	0	0	0	1.225	0.85944	FALSE
ATP-dependent RNA helicase DHX36 OS=Mus musculus GN=Dhx36 PE=1 SV=2	Q8VHK9	Dhx36	114 kDa	0	0	0	1.225	1.2892	FALSE
ATP-dependent zinc metalloprotease YME1L1 OS=Mus musculus GN=Yme1l1 PE=1 SV=1	O88967	Yme1l1	80 kDa	0	0	0	1.6333	0.85944	FALSE
ATPase Asna1 OS=Mus musculus GN=Asna1 PE=1 SV=2	O54984	Asna1	39 kDa	0	0	0	1.225	2.1486	FALSE
ATPase inhibitor, mitochondrial OS=Mus musculus GN=Atpif1 PE=1 SV=2	O35143	Atpif1	12 kDa	0	0	0	1.225	1.7189	FALSE
ATPase WRNIP1 OS=Mus musculus GN=Wrnip1 PE=1 SV=2	Q91XU0	Wrnip1	72 kDa	0	0	0	0	1.2892	FALSE
BAG family molecular chaperone regulator 2 OS=Mus musculus GN=Bag2 PE=1 SV=1	Q91YN9	Bag2	23 kDa	0	0	0	0.81665	0	FALSE
Band 4.1-like protein 1 OS=Mus musculus GN=Epb41l1 PE=1 SV=1	A2AUK5 (+2)	Epb41l1	98 kDa	0	0	0	1.6333	2.1486	FALSE
Basement membrane-specific heparan sulfate proteoglycan core protein OS=Mus musculus GN=H	E9PZ16	Hspg2	470 kDa	0	0	0	2.45	5.1566	FALSE
Beta-1,3-glucosyltransferase OS=Mus musculus GN=B3glct PE=1 SV=3	Q8BHT6	B3glct	55 kDa	0	0	0	0.81665	1.2892	FALSE
Beta-1,4-galactosyltransferase 5 OS=Mus musculus GN=B4galt5 PE=2 SV=2	Q9JMK0 (+1)	B4galt5	45 kDa	0	0	0	0	0.85944	FALSE
Beta-centractin OS=Mus musculus GN=Actr1b PE=1 SV=1	Q8R5C5	Actr1b	42 kDa	0	0	0	0	2.5783	FALSE
Beta-enolase OS=Mus musculus GN=Eno3 PE=1 SV=3	P21550	Eno3	47 kDa	0	0	0	20.825	16.759	FALSE
Beta-galactosidase OS=Mus musculus PE=2 SV=1	Q8C847		85 kDa	0	0	0	2.0416	1.2892	FALSE
Beta-glucuronidase OS=Mus musculus GN=Gusb PE=2 SV=1	Q3TW82	Gusb	74 kDa	0	0	0	1.225	3.4377	FALSE
Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1 OS=Mus musculus GN=Papss1 PE	Q60967	Papss1	71 kDa	0	0	0	2.0416	2.5783	FALSE
Bifunctional polynucleotide phosphatase/kinase OS=Mus musculus GN=Pnkp PE=1 SV=1	G5E8N7 (+1)	Pnkp	57 kDa	0	0	0	0.81665	0	FALSE
Bifunctional purine biosynthesis protein PURH OS=Mus musculus GN=Atic PE=1 SV=2	Q9CWJ9	Atic	64 kDa	0	0	0	10.208	11.173	FALSE
Biliverdin reductase A OS=Mus musculus GN=Blvra PE=1 SV=1	Q9CY64	Blvra	34 kDa	0	0	0	2.45	1.2892	FALSE
Biliverdin reductase B (Flavin reductase (NADPH)) OS=Mus musculus GN=Blvrb PE=1 SV=1	Q3U6G1 (+1)	Blvrb	22 kDa	0	0	0	2.8583	3.008	FALSE
Bin1 protein OS=Mus musculus GN=Bin1 PE=1 SV=1	Q6P1B9	Bin1	53 kDa	0	0	0	1.225	2.1486	FALSE
Bisphosphate 3'-nucleotidase 1, isoform CRA_a OS=Mus musculus GN=Bpnt1 PE=2 SV=1	Q3U449	Bpnt1	33 kDa	0	0	0	1.6333	0.85944	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Bleomycin hydrolase OS=Mus musculus GN=Blmh PE=1 SV=1	Q8R016	Blmh	53 kDa	0	0	0	1.6333	2.5783	FALSE
Brain cDNA, clone MNCb-1208, similar to Mus musculus mitogen activated protein kinase kinase	Q9JJE1	Map2k1	43 kDa	0	0	0	3.2666	2.5783	FALSE
Branched-chain-amino-acid aminotransferase OS=Mus musculus GN=Bcat2 PE=1 SV=1	A0A1B0GX27 (+3)	Bcat2	43 kDa	0	0	0	2.45	1.7189	FALSE
BRCA2 and CDKN1A-interacting protein OS=Mus musculus GN=Bccip PE=1 SV=1	Q9CWI3	Bccip	36 kDa	0	0	0	0.81665	0	FALSE
BRI3-binding protein OS=Mus musculus GN=Bri3bp PE=1 SV=1	Q8BXV2	Bri3bp	28 kDa	0	0	0	1.225	0.85944	FALSE
BRISC and BRCA1-A complex member 2 OS=Mus musculus GN=Babam2 PE=1 SV=3	D3Z7P0 (+1)	Babam2	44 kDa	0	0	0	1.6333	0.85944	FALSE
BRISC complex subunit Abraxas 2 OS=Mus musculus GN=Abraxas2 PE=1 SV=1	Q3TCJ1 (+1)	Abraxas2	47 kDa	0	0	0	1.225	0	FALSE
Bromodomain and WD repeat domain containing 2, isoform CRA_a OS=Mus musculus GN=Wdr11	G5E8J3 (+1)	Wdr11	136 kDa	0	0	0	1.225	0	FALSE
BUB3-interacting and GLEBS motif-containing protein ZNF207 OS=Mus musculus GN=Znf207 PE=1	Q9JMD0	Znf207	53 kDa	0	0	0	1.225	0.85944	FALSE
C-1-tetrahydrofolate synthase, cytoplasmic OS=Mus musculus GN=Mthfd1 PE=1 SV=4	Q922D8	Mthfd1	101 kDa	0	0	0	7.7582	7.7349	FALSE
C-Jun-amino-terminal kinase-interacting protein 3 OS=Mus musculus GN=Mapk8ip3 PE=1 SV=1	E9Q6B6 (+5)	Mapk8ip3	143 kDa	0	0	0	1.225	1.2892	FALSE
C-terminal-binding protein 1 OS=Mus musculus GN=Ctbp1 PE=1 SV=1	A0A0J9YU62 (+2)	Ctbp1	47 kDa	0	0	0	1.225	1.7189	FALSE
C-terminal-binding protein 2 OS=Mus musculus GN=Ctbp2 PE=1 SV=2	P56546 (+3)	Ctbp2	49 kDa	0	0	0	1.225	1.7189	FALSE
C230096C10Rik protein OS=Mus musculus GN=Emc1 PE=2 SV=1	A1L2Z3 (+2)	Emc1	112 kDa	0	0	0	1.6333	2.5783	FALSE
Calcium load-activated calcium channel (Fragment) OS=Mus musculus GN=Tmco1 PE=1 SV=1	A0A0A6YVS2 (+2)	Tmco1	22 kDa	0	0	0	0.81665	0	FALSE
Calcium uniporter protein, mitochondrial OS=Mus musculus GN=Mcu PE=1 SV=2	Q3UMR5	Mcu	40 kDa	0	0	0	0	1.2892	FALSE
Calcium uptake protein 2, mitochondrial OS=Mus musculus GN=Micu2 PE=1 SV=2	Q8CD10	Micu2	49 kDa	0	0	0	0.81665	0.85944	FALSE
Calcium/calmodulin-dependent protein kinase I OS=Mus musculus GN=Camk1 PE=1 SV=1	Q3UY68 (+2)	Camk1	42 kDa	0	0	0	0.81665	0	FALSE
Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Mus musculus GN=Camk2	E9Q1V9 (+1)	Camk2d	55 kDa	0	0	0	2.0416	2.1486	FALSE
Calcium/calmodulin-dependent protein kinase type II subunit gamma OS=Mus musculus GN=Cam	Q923T9	Camk2g	60 kDa	0	0	0	1.6333	3.4377	FALSE
Calcyclin-binding protein OS=Mus musculus GN=Cacybp PE=1 SV=1	Q9CXW3	Cacybp	27 kDa	0	0	0	6.1249	4.7269	FALSE
Calpain small subunit 1 OS=Mus musculus GN=Capns1 PE=1 SV=1	O88456	Capns1	28 kDa	0	0	0	2.45	3.008	FALSE
Calpain-1 catalytic subunit OS=Mus musculus GN=Capn1 PE=1 SV=1	O35350 (+4)	Capn1	82 kDa	0	0	0	4.4916	6.0161	FALSE
Calpain-2 catalytic subunit OS=Mus musculus GN=Capn2 PE=1 SV=4	O08529	Capn2	80 kDa	3.6831	3.1957	3.5789	7.7582	5.5863	FALSE
Calpastatin OS=Mus musculus GN=Cast PE=1 SV=1	Q8CE80	Cast	81 kDa	0	0	0	5.7166	4.7269	FALSE
Calponin OS=Mus musculus GN=Cnn1 PE=2 SV=1	B2RSH3 (+1)	Cnn1	33 kDa	0	0	0	2.45	0	FALSE
Calponin-2 OS=Mus musculus GN=Cnn2 PE=1 SV=1	Q08093 (+1)	Cnn2	33 kDa	0	6.3914	0	12.25	9.0241	FALSE
Calponin-3 OS=Mus musculus GN=Cnn3 PE=1 SV=1	Q9DAW9	Cnn3	36 kDa	3.6831	0	3.5789	7.7582	6.4458	FALSE
Calreticulin OS=Mus musculus GN=Calr PE=1 SV=1	B2MWM9 (+1)	Calr	48 kDa	9.2077	6.3914	8.9474	17.15	17.618	FALSE
Calumenin OS=Mus musculus GN=Calu PE=1 SV=1	O35887 (+1)	Calu	37 kDa	5.5246	6.3914	7.1579	13.475	10.313	FALSE
Calumenin OS=Mus musculus GN=Calu PE=1 SV=1	Q6XLQ8	Calu	37 kDa	0	0	0	11.841	9.0241	FALSE
cAMP-dependent protein kinase catalytic subunit beta OS=Mus musculus GN=Prkacb PE=1 SV=2	P68181	Prkacb	41 kDa	0	0	0	2.45	2.5783	FALSE
cAMP-dependent protein kinase type II-beta regulatory subunit OS=Mus musculus GN=Prkar2b	P31324	Prkar2b	46 kDa	0	0	0	3.6749	4.2972	FALSE
CAP-Gly domain-containing linker protein 1 OS=Mus musculus GN=Clip1 PE=1 SV=1	D3Z2Z1 (+2)	Clip1	160 kDa	0	0	0	1.6333	2.1486	FALSE
CAP-Gly domain-containing linker protein 2 OS=Mus musculus GN=Clip2 PE=1 SV=2	Q9Z0H8	Clip2	116 kDa	0	0	0	0.81665	2.5783	FALSE
Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1 OS=Mus musculus GN=Cmtr1 PE=1 SV=	Q9DBC3	Cmtr1	96 kDa	0	0	0	6.1249	4.2972	FALSE
Capping protein (Actin filament), gelsolin-like OS=Mus musculus GN=Capg PE=1 SV=1	Q99LB4	Capg	39 kDa	0	0	0	4.8999	5.1566	FALSE
Carbonic anhydrase 13 OS=Mus musculus GN=Ca13 PE=1 SV=1	Q9D6N1	Ca13	30 kDa	0	0	0	1.6333	1.7189	FALSE
Carbonyl reductase [NADPH] 2 OS=Mus musculus GN=Cbr2 PE=1 SV=1	P08074 (+1)	Cbr2	26 kDa	0	0	0	2.45	0	FALSE
Carbonyl reductase 1 OS=Mus musculus GN=Cbr1 PE=1 SV=1	B2RXY7 (+1)	Cbr1	31 kDa	0	0	0	1.225	0	FALSE
Carboxypeptidase Q OS=Mus musculus GN=Cpq PE=1 SV=1	Q9WVJ3	Cpq	52 kDa	0	0	0	0.81665	0.85944	FALSE
Carnitine O-palmitoyltransferase 2, mitochondrial OS=Mus musculus GN=Cpt2 PE=1 SV=2	P52825 (+1)	Cpt2	74 kDa	0	0	0	1.6333	1.7189	FALSE
Casein kinase I isoform alpha OS=Mus musculus GN=Csnk1a1 PE=1 SV=1	E9PWB2 (+2)	Csnk1a1	43 kDa	0	0	0	2.45	1.7189	FALSE
Casein kinase II subunit alpha' OS=Mus musculus GN=Csnk2a2 PE=1 SV=1	O54833 (+1)	Csnk2a2	41 kDa	0	0	0	1.6333	2.1486	FALSE
Casein kinase II subunit beta OS=Mus musculus GN=Csnk2b PE=2 SV=1	N0E4C0 (+1)	Csnk2b	25 kDa	0	0	0	0	1.2892	FALSE
Cask protein OS=Mus musculus GN=Cask PE=2 SV=1	B7ZP42 (+2)	Cask	104 kDa	0	0	0	1.225	0	FALSE
Caspase 6 OS=Mus musculus GN=Casp6 PE=2 SV=1	Q99M47	Casp6	32 kDa	0	0	0	2.45	3.8675	FALSE
Caspase-2 OS=Mus musculus GN=Casp2 PE=1 SV=1	D6RFN6 (+1)	Casp2	38 kDa	0	0	0	0.81665	0	FALSE
Caspase-3 OS=Mus musculus GN=Casp3 PE=1 SV=1	P70677	Casp3	31 kDa	0	0	0	3.6749	4.2972	FALSE
Catalase OS=Mus musculus GN=Cat PE=1 SV=4	P24270 (+1)	Cat	60 kDa	0	0	0	5.3082	4.2972	FALSE
Catechol O-methyltransferase OS=Mus musculus GN=Comt PE=1 SV=2	O88587	Comt	29 kDa	0	0	0	1.6333	0.85944	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Cathepsin B OS=Mus musculus GN=Ctsb PE=1 SV=2	P10605 (+2)	Ctsb	37 kDa	3.6831	0	0	7.7582	10.743	FALSE
Cathepsin D OS=Mus musculus GN=Ctsd PE=1 SV=2	F8WIR1 (+8)	Ctsd	44 kDa	0	0	0	2.8583	1.7189	FALSE
Cathepsin L1 OS=Mus musculus GN=Ctsl PE=1 SV=2	P06797 (+2)	Ctsl	38 kDa	0	0	0	2.8583	3.008	FALSE
Cathepsin Z, isoform CRA_b OS=Mus musculus GN=Ctsz PE=1 SV=1	Q545I6 (+2)	Ctsz	34 kDa	0	0	0	3.2666	2.5783	FALSE
Cation-dependent mannose-6-phosphate receptor OS=Mus musculus GN=M6pr PE=1 SV=1	P24668 (+2)	M6pr	31 kDa	0	0	0	1.225	0.85944	FALSE
Caveolae-associated protein 2 OS=Mus musculus GN=Cavin2 PE=1 SV=3	Q63918	Cavin2	47 kDa	0	0	0	0.81665	0	FALSE
CBP-interacting protein 3 OS=Mus musculus GN=Exosc8 PE=1 SV=1	Q546F8 (+3)	Exosc8	30 kDa	0	0	0	0	0.85944	FALSE
CCA tRNA nucleotidyltransferase 1, mitochondrial OS=Mus musculus GN=Trnt1 PE=1 SV=1	Q8K1J6	Trnt1	50 kDa	0	0	0	2.45	4.2972	FALSE
Ccdc102a protein (Fragment) OS=Mus musculus GN=Ccdc102a PE=2 SV=1	A4FUJ5 (+2)	Ccdc102a	53 kDa	0	0	0	0.81665	0.85944	FALSE
CCR4-NOT transcription complex subunit 1 OS=Mus musculus GN=Cnot1 PE=1 SV=2	Q6ZQ08	Cnot1	267 kDa	0	0	0	3.6749	3.8675	FALSE
CD2-associated protein OS=Mus musculus GN=Cd2ap PE=1 SV=3	Q9JLQ0	Cd2ap	70 kDa	0	0	0	1.225	1.2892	FALSE
CD81 antigen OS=Mus musculus GN=Cd81 PE=1 SV=2	P35762 (+1)	Cd81	26 kDa	0	0	0	1.6333	3.008	FALSE
CD9 antigen OS=Mus musculus GN=Cd9 PE=1 SV=2	P40240	Cd9	25 kDa	0	0	0	2.45	1.7189	FALSE
CDC16 cell division cycle 16 homolog (S. cerevisiae), isoform CRA_e OS=Mus musculus GN=Cdc16	Q3TI84 (+1)	Cdc16	71 kDa	0	0	0	1.225	1.2892	FALSE
Cdc42 effector protein 3 OS=Mus musculus GN=Cdc42ep3 PE=1 SV=1	Q9CQC5	Cdc42ep3	28 kDa	0	0	0	0.81665	0.85944	FALSE
Cdc42-interacting protein 4 OS=Mus musculus GN=Trip10 PE=1 SV=2	Q8CJ53	Trip10	68 kDa	0	0	0	1.6333	1.2892	FALSE
CDKN2A-interacting protein OS=Mus musculus GN=Cdkn2aip PE=1 SV=1	Q8BI72	Cdkn2aip	60 kDa	0	0	0	1.225	1.2892	FALSE
CDW13/WDR61 OS=Mus musculus GN=Wdr61 PE=1 SV=1	A0MNP4 (+1)	Wdr61	34 kDa	0	0	0	0	2.1486	FALSE
Cell cycle and apoptosis regulator protein 2 OS=Mus musculus GN=Ccar2 PE=1 SV=2	Q8VDP4	Ccar2	103 kDa	0	0	0	1.225	3.008	FALSE
Cell division control protein 42 homolog OS=Mus musculus GN=Cdc42 PE=1 SV=2	P60766	Cdc42	21 kDa	0	0	0	3.2666	3.8675	FALSE
Cellular nucleic acid-binding protein OS=Mus musculus GN=Cnbp PE=1 SV=2	P53996 (+2)	Cnbp	20 kDa	0	0	0	3.2666	3.8675	FALSE
Cellular retinoic acid-binding protein 1 OS=Mus musculus GN=Crabp1 PE=1 SV=2	P62965	Crabp1	16 kDa	0	0	0	4.4916	5.1566	FALSE
Cellular retinoic acid-binding protein 2 OS=Mus musculus GN=Crabp2 PE=2 SV=2	P22935	Crabp2	16 kDa	0	0	0	1.225	1.2892	FALSE
Cellular tumor antigen p53 OS=Mus musculus GN=Trp53 PE=3 SV=1	A0A158SIS7 (+6)	Trp53	43 kDa	0	0	0	4.0833	4.2972	FALSE
Centrosomal protein of 170 kDa OS=Mus musculus GN=Cep170 PE=1 SV=1	H7BX26 (+1)	Cep170	174 kDa	0	0	0	2.0416	2.5783	FALSE
Ceramide synthase 6 OS=Mus musculus GN=Cers6 PE=1 SV=1	Q8C172	Cers6	45 kDa	0	0	0	0.81665	0	FALSE
cGMP-dependent protein kinase 1 OS=Mus musculus GN=Prkg1 PE=1 SV=1	P0C605 (+1)	Prkg1	76 kDa	0	0	0	0.81665	0	FALSE
Chloride channel CLIC-like 1, isoform CRA_a OS=Mus musculus GN=Clcc1 PE=1 SV=1	A2AEM2 (+1)	Clcc1	61 kDa	0	0	0	2.0416	1.7189	FALSE
Chloride channel protein OS=Mus musculus GN=Clcn5 PE=2 SV=1	Q3UL16 (+1)	Clcn5	83 kDa	0	0	0	0	1.2892	FALSE
Chloride intracellular channel protein OS=Mus musculus GN=Clic1 PE=1 SV=1	Q542F1 (+1)	Clic1	27 kDa	0	0	0	5.3082	5.1566	FALSE
Chloride intracellular channel protein OS=Mus musculus GN=Clic4 PE=1 SV=1	Q543N5 (+1)	Clic4	29 kDa	0	0	0	4.4916	4.7269	FALSE
Choline transporter-like protein 1 OS=Mus musculus GN=Slc44a1 PE=1 SV=3	Q6X893	Slc44a1	73 kDa	0	0	0	0.81665	0.85944	FALSE
Choline-phosphate cytidylyltransferase A OS=Mus musculus GN=Pcyt1a PE=1 SV=1	P49586	Pcyt1a	42 kDa	0	0	0	1.225	1.2892	FALSE
Chromatin assembly factor 1 subunit A OS=Mus musculus GN=Chaf1a PE=1 SV=1	Q9QWF0	Chaf1a	102 kDa	0	0	0	0.81665	1.7189	FALSE
Chromobox protein homolog 3 OS=Mus musculus GN=Cbx3 PE=1 SV=2	P23198 (+1)	Cbx3	21 kDa	0	0	0	2.45	3.4377	FALSE
Chromodomain-helicase-DNA-binding protein 8 OS=Mus musculus GN=Chd8 PE=1 SV=1	Q09XV5	Chd8	291 kDa	0	0	0	0	1.7189	FALSE
Chromosome-associated kinesin KIF4 OS=Mus musculus GN=Kif4 PE=1 SV=3	P33174	Kif4	140 kDa	0	0	0	1.6333	2.5783	FALSE
Citramalyl-CoA lyase, mitochondrial OS=Mus musculus GN=Clybl PE=1 SV=2	Q8R4N0	Clybl	38 kDa	0	0	0	0	1.2892	FALSE
Clathrin light chain OS=Mus musculus GN=Clta PE=1 SV=1	B1AWD9	Clta	27 kDa	0	0	0	0	0.85944	FALSE
Cleavage and polyadenylation specificity factor subunit 5 OS=Mus musculus GN=Nudt21 PE=1 SV	Q9CQF3 (+1)	Nudt21	26 kDa	0	0	0	0.81665	0.85944	FALSE
Cleavage and polyadenylation specificity factor subunit 7 OS=Mus musculus GN=Cpsf7 PE=1 SV=	Q8BTV2	Cpsf7	52 kDa	0	0	0	0.81665	0	FALSE
Cleavage and polyadenylation-specificity factor subunit 6 OS=Mus musculus GN=Cpsf6 PE=1 SV=	H3BJ30 (+2)	Cpsf6	59 kDa	0	0	0	0.81665	2.1486	FALSE
Cleavage stimulation factor subunit 1 OS=Mus musculus GN=Cstf1 PE=1 SV=1	Q99LC2	Cstf1	48 kDa	0	0	0	1.6333	1.2892	FALSE
Cleft lip and palate transmembrane protein 1 homolog OS=Mus musculus GN=Clptm1 PE=1 SV=1	Q8VBZ3	Clptm1	75 kDa	0	0	0	3.2666	3.008	FALSE
CLIP-associating protein 1 OS=Mus musculus GN=Clasp1 PE=1 SV=2	A0A087WNW8 (+13)	Clasp1	163 kDa	0	0	0	4.8999	2.5783	FALSE
CLIP-associating protein 2 OS=Mus musculus GN=Clasp2 PE=1 SV=1	E9Q8N5 (+3)	Clasp2	141 kDa	0	0	0	2.8583	1.7189	FALSE
Clustered mitochondria protein homolog OS=Mus musculus GN=Cluh PE=1 SV=1	A0A0R4J140	Cluh	152 kDa	0	0	0	2.8583	3.8675	FALSE
CMP-sialic acid transporter OS=Mus musculus GN=Slc35a1 PE=1 SV=2	Q61420	Slc35a1	36 kDa	0	0	0	0.81665	0	FALSE
Coatomer subunit alpha OS=Mus musculus GN=Copa PE=1 SV=2	Q8CIE6	Copa	138 kDa	3.6831	0	0	16.741	13.321	FALSE
Coatomer subunit beta OS=Mus musculus GN=Copb1 PE=1 SV=1	Q9JIF7	Copb1	107 kDa	0	0	0	5.3082	5.1566	FALSE
Coatomer subunit beta' OS=Mus musculus GN=Copb2 PE=1 SV=2	O55029	Copb2	102 kDa	0	4.7936	3.5789	8.5749	10.313	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Coatomer subunit delta OS=Mus musculus GN=Arcn1 PE=1 SV=2	Q5XJY5	Arcn1	57 kDa	0	0	0	6.9416	6.4458	FALSE
Coatomer subunit epsilon OS=Mus musculus GN=Cope PE=1 SV=3	O89079 (+1)	Cope	35 kDa	0	0	0	1.6333	1.2892	FALSE
Coatomer subunit gamma-1 OS=Mus musculus GN=Copg1 PE=1 SV=1	Q9QZE5	Copg1	98 kDa	0	0	3.5789	7.3499	4.7269	FALSE
Coatomer subunit gamma-2 OS=Mus musculus GN=Copg2 PE=1 SV=1	Q9QXK3	Copg2	98 kDa	0	0	0	1.6333	0	FALSE
Cofilin-1 OS=Mus musculus GN=Cfl1 PE=1 SV=1	F8WGL3 (+2)	Cfl1	25 kDa	0	4.7936	0	9.3915	7.7349	FALSE
Cofilin-2 OS=Mus musculus GN=Cfl2 PE=1 SV=1	P45591 (+1)	Cfl2	19 kDa	0	0	0	1.6333	1.7189	FALSE
Coiled-coil domain containing 25 OS=Mus musculus GN=Ccdc25 PE=1 SV=1	A0PK78 (+1)	Ccdc25	24 kDa	0	0	0	1.225	0.85944	FALSE
Coiled-coil domain containing 47 OS=Mus musculus GN=Ccdc47 PE=2 SV=1	Q0VBU4 (+1)	Ccdc47	56 kDa	0	0	0	2.8583	2.5783	FALSE
Coiled-coil-helix-coiled-coil-helix domain-containing protein 2 OS=Mus musculus GN=Chchd2 PE=2	Q9D1L0	Chchd2	16 kDa	0	0	0	0.81665	1.2892	FALSE
Col3a1 protein (Fragment) OS=Mus musculus GN=Col3a1 PE=2 SV=1	Q8K173	Col3a1	115 kDa	0	0	0	2.45	1.7189	FALSE
Collagen alpha-1(XII) chain OS=Mus musculus GN=Col12a1 PE=2 SV=3	Q60847	Col12a1	340 kDa	0	0	0	2.45	0	FALSE
Collagen alpha-2(I) chain OS=Mus musculus GN=Col1a2 PE=1 SV=2	Q01149 (+1)	Col1a2	130 kDa	0	0	0	3.2666	0	FALSE
Collagen alpha-2(VI) chain OS=Mus musculus GN=Col6a2 PE=1 SV=3	Q02788	Col6a2	110 kDa	0	0	0	0.81665	0	FALSE
Collagen triple helix repeat containing 1 OS=Mus musculus GN=Cthrc1 PE=2 SV=1	A2RRY6 (+1)	Cthrc1	26 kDa	0	0	0	0.81665	0	FALSE
Collagen type IV alpha-3-binding protein OS=Mus musculus GN=Col4a3bp PE=1 SV=1	Q9EQG9	Col4a3bp	71 kDa	0	0	0	0.81665	2.5783	FALSE
Collectin-12 OS=Mus musculus GN=Colec12 PE=1 SV=1	Q8K4Q8	Colec12	81 kDa	0	0	0	0.81665	0	FALSE
Complex I intermediate-associated protein 30, mitochondrial OS=Mus musculus GN=Ndufaf1 PE=	A0A0R4J081 (+2)	Ndufaf1	38 kDa	0	0	0	1.225	1.2892	FALSE
Condensin complex subunit 1 OS=Mus musculus GN=Ncapd2 PE=1 SV=1	A0A0R4J0H7	Ncapd2	156 kDa	0	0	0	4.4916	3.8675	FALSE
Condensin complex subunit 2 OS=Mus musculus GN=Ncaph PE=1 SV=1	Q8C156	Ncaph	82 kDa	0	0	0	4.4916	4.2972	FALSE
Conserved oligomeric Golgi complex subunit 3 OS=Mus musculus GN=Cog3 PE=1 SV=3	Q8CI04	Cog3	93 kDa	0	0	0	0.81665	0	FALSE
COP9 signalosome complex subunit 1 OS=Mus musculus GN=Gps1 PE=1 SV=1	G3UXW9	Gps1	59 kDa	0	0	0	2.0416	2.1486	FALSE
COP9 signalosome complex subunit 2 OS=Mus musculus GN=Cops2 PE=1 SV=1	P61202 (+1)	Cops2	52 kDa	0	0	0	4.4916	4.2972	FALSE
COP9 signalosome complex subunit 3 OS=Mus musculus GN=Cops3 PE=1 SV=3	O88543 (+1)	Cops3	48 kDa	0	0	0	4.0833	3.008	FALSE
COP9 signalosome complex subunit 4 OS=Mus musculus GN=Cops4 PE=1 SV=1	O88544 (+1)	Cops4	46 kDa	0	0	0	2.8583	1.2892	FALSE
COP9 signalosome complex subunit 6 OS=Mus musculus GN=Cops6 PE=1 SV=1	O88545 (+1)	Cops6	36 kDa	0	0	0	2.0416	3.008	FALSE
COP9 signalosome complex subunit 7a OS=Mus musculus GN=Cops7a PE=1 SV=2	Q9CZ04	Cops7a	30 kDa	0	0	0	0.81665	0	FALSE
COP9 signalosome complex subunit 8 OS=Mus musculus GN=Cops8 PE=1 SV=1	Q8VBV7	Cops8	23 kDa	0	0	0	0.81665	0.85944	FALSE
Copine-1 OS=Mus musculus GN=Cpne1 PE=1 SV=1	Q8C166	Cpne1	59 kDa	0	0	0	2.8583	2.1486	FALSE
Copine-2 OS=Mus musculus GN=Cpne2 PE=1 SV=1	A0A0R4J1D0 (+1)	Cpne2	61 kDa	0	0	0	1.6333	1.2892	FALSE
Copine-3 OS=Mus musculus GN=Cpne3 PE=1 SV=2	Q8BT60	Cpne3	60 kDa	0	0	0	2.0416	3.008	FALSE
Copper transport protein ATOX1 OS=Mus musculus GN=Atox1 PE=1 SV=1	O08997	Atox1	7 kDa	0	0	0	0.81665	0	FALSE
Cordon-bleu protein-like 1 OS=Mus musculus GN=Cobll1 PE=1 SV=2	Q3UMF0	Cobll1	137 kDa	0	0	0	2.0416	4.2972	FALSE
Coronin OS=Mus musculus GN=Coro1b PE=1 SV=1	A2RS22 (+1)	Coro1b	54 kDa	0	0	0	2.45	3.008	FALSE
Coronin OS=Mus musculus GN=Coro1c PE=1 SV=1	Q499X7 (+2)	Coro1c	53 kDa	0	0	0	3.2666	2.5783	FALSE
Cotl1 protein OS=Mus musculus GN=Cotl1 PE=1 SV=1	Q544F6 (+1)	Cotl1	16 kDa	0	0	0	2.45	1.7189	FALSE
Craniofacial development protein 1 OS=Mus musculus GN=Cfdp1 PE=1 SV=1	O88271	Cfdp1	33 kDa	0	0	0	1.225	2.1486	FALSE
Crip2 protein OS=Mus musculus GN=Crip2 PE=1 SV=1	Q4FJU3 (+1)	Crip2	23 kDa	0	0	0	0	0.85944	FALSE
CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae), isoform CRA_a OS=M	A0A0R4J0I4 (+1)	Chtf18	108 kDa	0	0	0	0.81665	0	FALSE
CTP synthase 2 OS=Mus musculus GN=Ctps2 PE=1 SV=1	P70303	Ctps2	66 kDa	0	0	0	2.45	4.7269	FALSE
CTTNBP2 N-terminal-like protein OS=Mus musculus GN=Cttnbp2nl PE=1 SV=1	Q99LJ0	Cttnbp2nl	70 kDa	0	0	0	1.225	1.2892	FALSE
CUGBP Elav-like family member 1 OS=Mus musculus GN=Celf1 PE=1 SV=2	P28659	Celf1	52 kDa	0	0	0	2.8583	1.2892	FALSE
Cullin 7 OS=Mus musculus GN=Cul7 PE=2 SV=1	A9C491 (+1)	Cul7	192 kDa	0	0	0	1.6333	0	FALSE
Cullin-1 OS=Mus musculus GN=Cul1 PE=1 SV=1	Q9WTX6	Cul1	90 kDa	0	0	0	3.2666	2.5783	FALSE
Cullin-4B OS=Mus musculus GN=Cul4b PE=1 SV=1	A2A432 (+1)	Cul4b	111 kDa	0	0	0	3.2666	3.4377	FALSE
Cullin-5 OS=Mus musculus GN=Cul5 PE=1 SV=1	E9PV12 (+3)	Cul5	96 kDa	0	0	0	1.6333	1.7189	FALSE
Cyclin-dependent kinase 2 OS=Mus musculus GN=Cdk2 PE=1 SV=2	P97377 (+2)	Cdk2	39 kDa	0	0	0	2.0416	3.4377	FALSE
Cyclin-dependent kinase 6 OS=Mus musculus GN=Cdk6 PE=1 SV=1	Q0VBK8 (+2)	Cdk6	37 kDa	0	0	0	0	1.2892	FALSE
Cyclin-dependent kinase 9 OS=Mus musculus GN=Cdk9 PE=1 SV=1	Q99J95	Cdk9	43 kDa	0	0	0	0	1.7189	FALSE
Cyclin-dependent kinase inhibitor 2A OS=Mus musculus GN=Cdkn2a PE=1 SV=2	P51480	Cdkn2a	18 kDa	0	0	0	1.225	0	FALSE
Cyclin-dependent-like kinase 5 OS=Mus musculus GN=Cdk5 PE=1 SV=1	P49615 (+1)	Cdk5	33 kDa	0	0	0	2.0416	1.2892	FALSE
Cyclin-G-associated kinase OS=Mus musculus GN=Gak PE=1 SV=1	A0A0R4J0F6 (+2)	Gak	144 kDa	0	0	0	0.81665	0.85944	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Cystatin-C OS=Mus musculus GN=Cst3 PE=1 SV=2	P21460 (+2)	Cst3	16 kDa	0	0	0	0.81665	0	FALSE
Cysteine and glycine-rich protein 1 OS=Mus musculus GN=Csrp1 PE=1 SV=3	P97315 (+1)	Csrp1	21 kDa	0	0	0	5.3082	4.7269	FALSE
Cysteine and histidine-rich domain-containing protein 1 OS=Mus musculus GN=Chordc1 PE=1 SV=	Q9D1P4	Chordc1	37 kDa	0	0	0	3.2666	2.5783	FALSE
Cysteine desulfurase, mitochondrial OS=Mus musculus GN=Nfs1 PE=1 SV=3	Q9Z1J3	Nfs1	51 kDa	0	0	0	1.225	0.85944	FALSE
Cysteine protease OS=Mus musculus GN=Atg4b PE=1 SV=1	A0A0R4J065	Atg4b	44 kDa	0	0	0	0.81665	0.85944	FALSE
Cysteine-rich with EGF-like domain protein 2 OS=Mus musculus GN=Creld2 PE=1 SV=1	Q9CYA0	Creld2	38 kDa	0	0	0	4.4916	4.2972	FALSE
Cytidine deaminase OS=Mus musculus GN=Cda PE=1 SV=2	P56389	Cda	16 kDa	0	0	0	0	1.2892	FALSE
Cytochrome b-5, isoform CRA_a OS=Mus musculus GN=Cyb5a PE=1 SV=1	G5E850 (+2)	Cyb5a	11 kDa	0	0	0	2.0416	2.1486	FALSE
Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Mus musculus GN=Uqcrfs1 PE=1 SV=	Q9CR68	Uqcrfs1	29 kDa	0	0	0	0	0.85944	FALSE
Cytochrome b5 type B OS=Mus musculus GN=Cyb5b PE=1 SV=1	Q9CQX2	Cyb5b	16 kDa	0	0	0	2.0416	0	FALSE
Cytochrome c oxidase subunit 2 OS=Mus musculus musculus GN=COX2 PE=3 SV=1	A0A023J6F3 (+9)	COX2	26 kDa	0	0	0	3.6749	3.008	FALSE
Cytochrome c oxidase subunit 6B1 OS=Mus musculus GN=Cox6b1 PE=1 SV=2	P56391	Cox6b1	10 kDa	0	0	0	1.225	0	FALSE
Cytochrome c-type heme lyase OS=Mus musculus GN=Hccs PE=1 SV=2	P53702 (+1)	Hccs	31 kDa	0	0	0	0	0.85944	FALSE
Cytochrome P450 20A1 OS=Mus musculus GN=Cyp20a1 PE=1 SV=1	Q8BKE6	Cyp20a1	52 kDa	0	0	0	2.0416	0.85944	FALSE
Cytoplasmic aconitase OS=Mus musculus GN=aco1 PE=3 SV=1	Q8VDC3	aco1	99 kDa	0	0	0	4.8999	3.008	FALSE
Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dync1h1 PE=1 SV=2	Q9JHU4	Dync1h1	532 kDa	11.049	14.381	17.895	28.175	34.377	FALSE
Cytoplasmic dynein 1 intermediate chain 2 OS=Mus musculus GN=Dync1i2 PE=1 SV=1	A2BFF9 (+4)	Dync1i2	71 kDa	0	0	0	2.45	2.5783	FALSE
Cytoplasmic dynein 1 light intermediate chain 2 OS=Mus musculus GN=Dync1li2 PE=1 SV=2	Q6PDL0	Dync1li2	54 kDa	0	0	0	2.45	3.8675	FALSE
Cytoplasmic protein NCK1 OS=Mus musculus GN=Nck1 PE=1 SV=1	Q8BH99 (+1)	Nck1	36 kDa	0	0	0	0	0.85944	FALSE
Cytoplasmic tRNA 2-thiolation protein 2 OS=Mus musculus GN=Ctu2 PE=1 SV=1	G3UXB4 (+1)	Ctu2	45 kDa	0	0	0	0.81665	0	FALSE
Cytoskeletal protein OS=Mus musculus GN=Utrn PE=2 SV=1	O08614	Utrn	393 kDa	0	0	0	2.0416	2.1486	FALSE
Cytosol aminopeptidase OS=Mus musculus GN=Lap3 PE=1 SV=3	Q9CPY7	Lap3	56 kDa	0	0	0	8.9832	8.5944	FALSE
Cytosolic acyl coenzyme A thioester hydrolase OS=Mus musculus GN=Acot7 PE=1 SV=1	E9PYH2 (+1)	Acot7	43 kDa	0	0	0	4.0833	4.2972	FALSE
Cytosolic Fe-S cluster assembly factor NUBP1 OS=Mus musculus GN=Nubp1 PE=1 SV=1	Q9R060	Nubp1	34 kDa	0	0	0	0.81665	0.85944	FALSE
Cytosolic Fe-S cluster assembly factor NUBP2 OS=Mus musculus GN=Nubp2 PE=1 SV=1	Q9R061	Nubp2	30 kDa	0	0	0	0	0.85944	FALSE
Cytosolic non-specific dipeptidase OS=Mus musculus GN=Cndp2 PE=1 SV=1	Q9D1A2	Cndp2	53 kDa	0	0	0	2.0416	2.5783	FALSE
Cytosolic purine 5'-nucleotidase OS=Mus musculus GN=Nt5c2 PE=1 SV=1	E9Q9M1 (+2)	Nt5c2	68 kDa	0	0	0	3.2666	3.008	FALSE
D-aminoacyl-tRNA deacylase 1 OS=Mus musculus GN=Dtd1 PE=1 SV=2	Q9DD18	Dtd1	23 kDa	0	0	0	0.81665	0	FALSE
D-dopachrome decarboxylase OS=Mus musculus GN=Ddt PE=1 SV=3	O35215 (+1)	Ddt	13 kDa	0	0	0	2.45	2.1486	FALSE
DAZ associated protein 1, isoform CRA_b OS=Mus musculus GN=Dazap1 PE=1 SV=1	Q3UGB5 (+1)	Dazap1	43 kDa	0	0	0	0.81665	1.2892	FALSE
DCC-interacting protein 13-alpha OS=Mus musculus GN=Appl1 PE=1 SV=1	Q8K3H0	Appl1	79 kDa	0	0	0	2.45	2.5783	FALSE
DDB1- and CUL4-associated factor 8 OS=Mus musculus GN=Dcaf8 PE=1 SV=1	Q8N7N5	Dcaf8	66 kDa	0	0	0	1.6333	1.2892	FALSE
Ddx58 protein (Fragment) OS=Mus musculus GN=Ddx58 PE=2 SV=1	A1L0V6 (+2)	Ddx58	106 kDa	0	0	0	9.7998	0.85944	FALSE
DEAD (Asp-Glu-Ala-Asp) box polypeptide 21 OS=Mus musculus GN=Ddx21 PE=2 SV=1	Q6PCP0 (+1)	Ddx21	94 kDa	0	0	0	2.45	2.1486	FALSE
DEAD (Asp-Glu-Ala-Asp) box polypeptide 23 OS=Mus musculus GN=Ddx23 PE=1 SV=1	D3Z0M9	Ddx23	95 kDa	0	0	0	0	0.85944	FALSE
DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 OS=Mus musculus GN=Ddx47 PE=2 SV=1	Q4VBG1 (+1)	Ddx47	51 kDa	0	0	0	0	0.85944	FALSE
DEAH (Asp-Glu-Ala-His) box polypeptide 38 OS=Mus musculus GN=Dhx38 PE=1 SV=1	Q80X98	Dhx38	141 kDa	0	0	0	0	0.85944	FALSE
Death-associated protein kinase 3 OS=Mus musculus GN=Dapk3 PE=1 SV=1	O54784 (+1)	Dapk3	51 kDa	0	0	0	0.81665	0	FALSE
Decr1 protein OS=Mus musculus GN=Decr1 PE=1 SV=1	Q4FJK0 (+1)	Decr1	36 kDa	0	0	0	0.81665	1.2892	FALSE
Dedicator of cytokinesis protein 11 OS=Mus musculus GN=Dock11 PE=1 SV=1	A2AF47	Dock11	238 kDa	0	0	0	0	1.2892	FALSE
Dedicator of cytokinesis protein 7 OS=Mus musculus GN=Dock7 PE=1 SV=2	A2A9M4 (+2)	Dock7	241 kDa	0	0	0	1.6333	3.8675	FALSE
Dehydrogenase/reductase SDR family member 1 OS=Mus musculus GN=Dhrs1 PE=1 SV=1	Q99L04	Dhrs1	34 kDa	0	0	0	2.45	3.008	FALSE
Delta-1-pyrroline-5-carboxylate synthase OS=Mus musculus GN=Aldh18a1 PE=1 SV=2	Q9Z110	Aldh18a1	87 kDa	0	3.1957	5.3684	8.1665	7.3052	FALSE
Delta-6 desaturase (Fragment) OS=Mus musculus GN=Fads2 PE=2 SV=1	F2WWK6 (+1)	Fads2	51 kDa	0	0	0	1.6333	0	FALSE
Delta-aminolevulinic acid dehydratase OS=Mus musculus GN=Alad PE=1 SV=1	P10518 (+1)	Alad	36 kDa	0	0	0	2.45	2.1486	FALSE
Delta(24)-sterol reductase OS=Mus musculus GN=Dhcr24 PE=1 SV=1	Q8VCH6	Dhcr24	60 kDa	0	0	0	0.81665	0	FALSE
Density-regulated protein OS=Mus musculus GN=Denr PE=1 SV=1	Q9CQJ6	Denr	22 kDa	0	0	0	1.6333	2.1486	FALSE
Deoxycytidine kinase OS=Mus musculus GN=Dck PE=1 SV=1	P43346 (+1)	Dck	30 kDa	0	0	0	0	0.85944	FALSE
Deoxyhypusine synthase OS=Mus musculus GN=Dhps PE=1 SV=2	Q3TXU5	Dhps	41 kDa	0	0	0	0.81665	0.85944	FALSE
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Mus musculus GN=Samhd1 PE=	F8WJE0 (+1)	Samhd1	76 kDa	0	3.1957	3.5789	4.4916	3.8675	FALSE
Deoxyuridine triphosphatase OS=Mus musculus GN=Dut PE=1 SV=1	Q9CQ43 (+1)	Dut	17 kDa	0	0	0	3.2666	3.4377	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Depdc6-001 OS=Mus musculus GN=Deptor PE=4 SV=1	B2ZRS3 (+1)	Deptor	46 kDa	0	0	0	0	0.85944	FALSE
Dephospho-CoA kinase domain-containing protein OS=Mus musculus GN=Dcakd PE=1 SV=1	Q8BHC4	Dcakd	26 kDa	0	0	0	0	0.85944	FALSE
Deubiquitinating protein VCIP135 OS=Mus musculus GN=Vcpip1 PE=1 SV=1	A0A0R4J0M9 (+1)	Vcpip1	134 kDa	0	0	0	1.225	0	FALSE
Developmentally-regulated GTP-binding protein 1 OS=Mus musculus GN=Drg1 PE=1 SV=1	P32233 (+2)	Drg1	41 kDa	0	0	0	4.0833	5.5863	FALSE
Developmentally-regulated GTP-binding protein 2 OS=Mus musculus GN=Drg2 PE=1 SV=1	Q9QXB9	Drg2	41 kDa	0	0	0	6.1249	6.0161	FALSE
Dihydrofolate reductase OS=Mus musculus GN=Dhfr PE=1 SV=3	P00375 (+1)	Dhfr	22 kDa	0	0	0	1.6333	1.7189	FALSE
Dihydroorotate dehydrogenase (quinone), mitochondrial OS=Mus musculus GN=Dhodh PE=1 SV=	O35435	Dhodh	43 kDa	0	0	0	0.81665	0.85944	FALSE
Dihydropteridine reductase OS=Mus musculus GN=Qdpr PE=1 SV=2	Q8BVI4	Qdpr	26 kDa	0	0	0	2.45	2.5783	FALSE
Dihydropyrimidinase-related protein 2 OS=Mus musculus GN=Dpysl2 PE=1 SV=2	O08553	Dpysl2	62 kDa	7.3662	4.7936	5.3684	14.7	17.618	FALSE
Dihydropyrimidinase-related protein 3 OS=Mus musculus GN=Dpysl3 PE=1 SV=1	E9PWE8	Dpysl3	74 kDa	0	0	0	8.5749	9.0241	FALSE
Dipeptidyl peptidase 3 OS=Mus musculus GN=Dpp3 PE=2 SV=1	Q3UDD5 (+3)	Dpp3	83 kDa	0	0	0	4.4916	5.1566	FALSE
Dipeptidyl peptidase 9 OS=Mus musculus GN=Dpp9 PE=1 SV=2	Q8BVG4	Dpp9	98 kDa	0	0	0	0	0.85944	FALSE
Disco-interacting protein 2 homolog B OS=Mus musculus GN=Dip2b PE=1 SV=1	Q3UH60	Dip2b	171 kDa	0	0	0	0.81665	0.85944	FALSE
Dishevelled 2, dsh homolog (Drosophila) OS=Mus musculus GN=Dvl2 PE=2 SV=1	I6L9H1 (+1)	Dvl2	79 kDa	0	0	0	1.6333	1.7189	FALSE
Disks large homolog 1 OS=Mus musculus GN=Dlg1 PE=1 SV=1	E9Q9H0 (+1)	Dlg1	101 kDa	0	0	0	1.6333	2.1486	FALSE
Disks large homolog 3 OS=Mus musculus GN=Dlg3 PE=1 SV=1	A2BEE9 (+2)	Dlg3	92 kDa	0	0	0	1.6333	0	FALSE
Disks large-associated protein 5 OS=Mus musculus GN=Dlgap5 PE=1 SV=2	Q8K4R9	Dlgap5	90 kDa	0	0	0	1.225	1.2892	FALSE
Dlk1 OS=Mus musculus GN=Dlk1 PE=2 SV=1	B4YB46 (+4)	Dlk1	33 kDa	0	0	0	0.81665	0	FALSE
DNA (cytosine-5)-methyltransferase OS=Mus musculus GN=Dnmt1 PE=2 SV=1	Q7TSJ0	Dnmt1	184 kDa	0	0	0	3.2666	4.2972	FALSE
DNA damage-binding protein 1 OS=Mus musculus GN=Ddb1 PE=1 SV=2	Q3U1J4	Ddb1	127 kDa	3.6831	0	0	8.9832	12.032	FALSE
DNA excision repair protein ERCC-6-like OS=Mus musculus GN=Ercc6l PE=1 SV=1	Q8BHK9	Ercc6l	139 kDa	0	0	0	2.45	3.4377	FALSE
DNA helicase OS=Mus musculus GN=Mcm2 PE=2 SV=1	Q3UK39	Mcm2	102 kDa	0	0	0	8.1665	8.1647	FALSE
DNA helicase OS=Mus musculus GN=Mcm4 PE=2 SV=1	Q9D077	Mcm4	97 kDa	0	0	0	3.6749	3.008	FALSE
DNA helicase OS=Mus musculus GN=Mcm5 PE=2 SV=1	Q8BQ03	Mcm5	82 kDa	5.5246	6.3914	5.3684	6.9416	7.7349	FALSE
DNA helicase OS=Mus musculus GN=Mcm7 PE=1 SV=1	Q3U4T8 (+3)	Mcm7	81 kDa	0	0	0	7.3499	6.8755	FALSE
DNA ligase 1 OS=Mus musculus GN=Lig1 PE=1 SV=2	P37913 (+1)	Lig1	102 kDa	0	0	0	3.2666	3.008	FALSE
DNA mismatch repair protein Msh2 OS=Mus musculus GN=Msh2 PE=1 SV=1	P43247 (+2)	Msh2	104 kDa	0	0	0	4.0833	4.7269	FALSE
DNA mismatch repair protein Msh6 OS=Mus musculus GN=Msh6 PE=1 SV=3	P54276 (+1)	Msh6	151 kDa	0	0	0	4.8999	5.5863	FALSE
DNA polymerase alpha catalytic subunit OS=Mus musculus GN=Pola1 PE=1 SV=2	P33609	Pola1	167 kDa	0	0	0	1.6333	1.7189	FALSE
DNA polymerase alpha subunit B OS=Mus musculus GN=Pola2 PE=1 SV=2	P33611	Pola2	66 kDa	0	0	0	0.81665	2.1486	FALSE
DNA polymerase OS=Mus musculus GN=Pold1 PE=2 SV=1	Q8C2N0 (+1)	Pold1	124 kDa	0	0	0	2.45	2.1486	FALSE
DNA primase large subunit OS=Mus musculus GN=Prim2 PE=1 SV=1	P33610 (+1)	Prim2	58 kDa	0	0	0	0	0.85944	FALSE
DNA repair protein RAD51 homolog 1 OS=Mus musculus GN=Rad51 PE=1 SV=1	Q08297	Rad51	37 kDa	0	0	0	1.6333	1.2892	FALSE
DNA repair protein Sfr1 OS=Mus musculus GN=Sfr1 PE=2 SV=1	E3WH30 (+1)	Sfr1	34 kDa	0	0	0	0.81665	0.85944	FALSE
DNA replication licensing factor MCM6 OS=Mus musculus GN=Mcm6 PE=1 SV=1	P97311 (+1)	Mcm6	93 kDa	0	0	0	9.3915	8.1647	FALSE
DNA segment, Chr 15, ERATO Doi 621, expressed, isoform CRA_a OS=Mus musculus GN=Fam91a	B6YY24 (+1)	Fam91a1	93 kDa	0	0	0	2.0416	0.85944	FALSE
DNA segment, Chr 6, Wayne State University 176, expressed, isoform CRA_a OS=Mus musculus	G3X9I1 (+2)	Fam3c	21 kDa	0	0	0	2.8583	2.1486	FALSE
DNA segment, human DXS9928E OS=Mus musculus GN=Fam50a PE=4 SV=1	A0A158SIT3 (+1)	Fam50a	40 kDa	0	0	0	1.225	0.85944	FALSE
DNA-(apurinic or apyrimidinic site) lyase OS=Mus musculus GN=Apex1 PE=1 SV=2	P28352 (+1)	Apex1	35 kDa	0	0	0	5.3082	4.7269	FALSE
DNA-directed RNA polymerase II subunit RPB2 OS=Mus musculus GN=Polr2b PE=1 SV=2	Q8CFI7	Polr2b	134 kDa	0	0	0	0.81665	0	FALSE
DNA-directed RNA polymerases I, II, and III subunit RPABC3 OS=Mus musculus GN=Polr2h PE=1 S	Q923G2	Polr2h	17 kDa	0	0	0	0.81665	0.85944	FALSE
DnaJ (Hsp40) homolog, subfamily B, member 1 OS=Mus musculus GN=Dnajb1 PE=1 SV=1	Q3TU79 (+1)	Dnajb1	38 kDa	0	0	0	2.0416	3.008	FALSE
DnaJ (Hsp40) homolog, subfamily C, member 3 OS=Mus musculus GN=Dnajc3 PE=1 SV=1	Q3UFV9 (+2)	Dnajc3	57 kDa	0	0	0	2.0416	1.7189	FALSE
DnaJ heat shock protein family (Hsp40) member C13 OS=Mus musculus GN=Dnajc13 PE=1 SV=1	G3X922	Dnajc13	254 kDa	0	0	0	3.6749	3.8675	FALSE
DnaJ homolog subfamily B member 4 OS=Mus musculus GN=Dnajb4 PE=1 SV=1	Q9D832	Dnajb4	38 kDa	0	0	0	2.45	1.7189	FALSE
DnaJ homolog subfamily C member 10 OS=Mus musculus GN=Dnajc10 PE=1 SV=2	Q9DC23	Dnajc10	91 kDa	0	0	0	3.2666	3.8675	FALSE
DnaJ homolog subfamily C member 2 OS=Mus musculus GN=Dnajc2 PE=1 SV=2	P54103	Dnajc2	72 kDa	0	0	0	2.45	3.8675	FALSE
DnaJ homolog subfamily C member 8 (Fragment) OS=Mus musculus GN=Dnajc8 PE=1 SV=1	F6TQL3	Dnajc8	28 kDa	0	0	0	0.81665	0	FALSE
DnaJ homolog subfamily C member 9 OS=Mus musculus GN=Dnajc9 PE=1 SV=2	Q91WN1	Dnajc9	30 kDa	0	0	0	1.225	3.008	FALSE
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Mus musculus	P61804	Dad1	12 kDa	0	0	0	0.81665	0	FALSE
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Mus musculus	A0A0R4J0D3 (+1)	Stt3b	93 kDa	0	0	0	3.2666	1.7189	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Double-stranded RNA-binding protein Staufen homolog 1 OS=Mus musculus GN=Stau1 PE=1 SV=	A2A5R8 (+1)	Stau1	54 kDa	0	0	0	1.225	0.85944	FALSE
Drebrin OS=Mus musculus GN=Dbn1 PE=1 SV=1	A0A0R4J1E3 (+2)	Dbn1	73 kDa	0	0	0	1.225	0.85944	FALSE
Drebrin-like protein OS=Mus musculus GN=Dbnl PE=1 SV=2	Q62418	Dbnl	49 kDa	0	0	0	4.0833	4.7269	FALSE
Dual specificity mitogen-activated protein kinase kinase 2 OS=Mus musculus GN=Map2k2 PE=1	Q63932 (+1)	Map2k2	44 kDa	0	0	0	2.0416	2.1486	FALSE
Dual specificity mitogen-activated protein kinase kinase 4 OS=Mus musculus GN=Map2k4 PE=1	P47809 (+1)	Map2k4	44 kDa	0	0	0	0	0.85944	FALSE
Dual-specificity protein phosphatase 3 OS=Mus musculus GN=Dusp3 PE=1 SV=1	B1AQF4 (+2)	Dusp3	23 kDa	0	0	0	0.81665	0.85944	FALSE
Dynactin 2 OS=Mus musculus GN=Dctn2 PE=1 SV=1	Q3TPZ5 (+1)	Dctn2	44 kDa	0	0	0	3.6749	2.5783	FALSE
Dynactin subunit 1 OS=Mus musculus GN=Dctn1 PE=1 SV=3	O08788	Dctn1	142 kDa	0	0	0	8.1665	6.4458	FALSE
Dynamin-1 OS=Mus musculus GN=Dnm1 PE=1 SV=2	P39053	Dnm1	98 kDa	0	0	0	2.45	0	FALSE
Dynamin-like 120 kDa protein, mitochondrial OS=Mus musculus GN=Opa1 PE=1 SV=1	P58281	Opa1	111 kDa	0	0	0	1.225	1.2892	FALSE
Dynein cytoplasmic 1 light intermediate chain 1 OS=Mus musculus GN=Dync1li1 PE=1 SV=1	Q3TWG5 (+1)	Dync1li1	57 kDa	0	0	0	2.8583	3.008	FALSE
Dystonin OS=Mus musculus GN=Dst PE=1 SV=2	Q91ZU6 (+1)	Dst	834 kDa	0	0	0	0.81665	0	FALSE
E-selectin ligand 1 OS=Mus musculus GN=Glg1 PE=1 SV=1	Q53WR6 (+1)	Glg1	134 kDa	3.6831	0	0	4.4916	3.8675	FALSE
E2 ubiquitin-conjugating enzyme UBE2O OS=Mus musculus GN=Ube2o PE=1 SV=3	sp|Q6ZPJ3|UBE2O_	Ube2o	141 kDa	0	0	0	2.8583	4.2972	FALSE
E3 ubiquitin-protein ligase ARIH1 OS=Mus musculus GN=Arih1 PE=1 SV=3	Q9Z1K5	Arih1	64 kDa	0	0	0	1.225	2.1486	FALSE
E3 ubiquitin-protein ligase HECTD1 OS=Mus musculus GN=Hectd1 PE=1 SV=1	F8WIE5	Hectd1	289 kDa	0	0	0	3.2666	0.85944	FALSE
E3 ubiquitin-protein ligase HUWE1 OS=Mus musculus GN=Huwe1 PE=1 SV=5	Q7TMY8	Huwe1	483 kDa	0	0	0	4.0833	8.5944	FALSE
E3 ubiquitin-protein ligase MARCH5 OS=Mus musculus GN=March5 PE=1 SV=1	A0A0R4J1H0 (+2)	March5	27 kDa	0	0	0	0.81665	0	FALSE
E3 ubiquitin-protein ligase Midline-1 OS=Mus musculus GN=Mid1 PE=1 SV=1	B1AV01 (+1)	Mid1	72 kDa	0	0	0	0.81665	0	FALSE
E3 ubiquitin-protein ligase OS=Mus musculus GN=Nedd4 PE=1 SV=1	B2RSC8 (+1)	Nedd4	103 kDa	5.5246	9.5872	5.3684	11.841	15.9	FALSE
E3 ubiquitin-protein ligase PPP1R11 OS=Mus musculus GN=Ppp1r11 PE=1 SV=1	Q8K1L5	Ppp1r11	15 kDa	0	0	0	1.225	1.7189	FALSE
E3 ubiquitin-protein ligase Praja-2 OS=Mus musculus GN=Pja2 PE=1 SV=2	Q80U04	Pja2	78 kDa	0	0	0	0	0.85944	FALSE
E3 ubiquitin-protein ligase RLIM OS=Mus musculus GN=Rlim PE=1 SV=2	Q9WTV7	Rlim	66 kDa	0	0	0	0	0.85944	FALSE
E3 ubiquitin-protein ligase RNF114 OS=Mus musculus GN=Rnf114 PE=1 SV=2	Q9ET26	Rnf114	26 kDa	0	0	0	0.81665	0.85944	FALSE
E3 ubiquitin-protein ligase TRIP12 OS=Mus musculus GN=Trip12 PE=1 SV=1	G5E870	Trip12	224 kDa	0	0	0	2.45	0.85944	FALSE
E3 ubiquitin-protein ligase UBR4 OS=Mus musculus GN=Ubr4 PE=1 SV=1	A2AN08	Ubr4	572 kDa	3.6831	4.7936	0	7.3499	9.8835	FALSE
Echinoderm microtubule-associated protein-like 1 OS=Mus musculus GN=Eml1 PE=1 SV=1	Q05BC3	Eml1	90 kDa	0	0	0	0.81665	0.85944	FALSE
Echinoderm microtubule-associated protein-like 3 OS=Mus musculus GN=Eml3 PE=1 SV=1	Q8VC03	Eml3	96 kDa	0	0	0	0	0.85944	FALSE
Echinoderm microtubule-associated protein-like 4 OS=Mus musculus GN=Eml4 PE=1 SV=1	F8WJ93 (+1)	Eml4	110 kDa	0	0	0	0.81665	2.1486	FALSE
Ectonucleotide pyrophosphatase/phosphodiesterase family member 2 OS=Mus musculus GN=Enp	G3UXY9 (+1)	Enpp2	105 kDa	0	0	0	0.81665	0.85944	FALSE
EGF domain-specific O-linked N-acetylglucosamine transferase OS=Mus musculus GN=Eogt PE=1	Q8BYW9	Eogt	61 kDa	0	0	0	0	0.85944	FALSE
EH domain-containing protein 2 OS=Mus musculus GN=Ehd2 PE=1 SV=1	Q8BH64	Ehd2	61 kDa	0	0	0	3.6749	2.5783	FALSE
EH-domain containing 1 OS=Mus musculus GN=Ehd1 PE=1 SV=2	Q80ZZ0 (+2)	Ehd1	61 kDa	0	0	3.5789	6.5332	5.5863	FALSE
EH-domain containing 4 OS=Mus musculus GN=Ehd4 PE=1 SV=1	Q3TM70 (+1)	Ehd4	61 kDa	0	0	0	1.6333	0.85944	FALSE
Eif2ak2 protein OS=Mus musculus GN=Eif2ak2 PE=2 SV=1	Q91YN2	Eif2ak2	58 kDa	0	0	0	3.2666	1.2892	FALSE
Eif2s2 protein OS=Mus musculus GN=Eif2s2 PE=1 SV=1	Q3ULL5 (+1)	Eif2s2	38 kDa	0	0	0	4.4916	5.5863	FALSE
Electron transfer flavoprotein subunit alpha, mitochondrial OS=Mus musculus GN=Etfa PE=1 SV=	Q99LC5	Etfa	35 kDa	0	0	0	3.6749	4.7269	FALSE
Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfb PE=1 SV=3	Q9DCW4	Etfb	28 kDa	0	0	0	3.6749	5.1566	FALSE
Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Mus musculus GN=	Q921G7	Etfdh	68 kDa	0	0	0	1.225	1.2892	FALSE
Elongation factor 1-beta OS=Mus musculus GN=Eef1b PE=1 SV=5	O70251	Eef1b	25 kDa	0	3.1957	0	4.0833	4.2972	FALSE
Elongation factor G, mitochondrial OS=Mus musculus GN=Gfm1 PE=1 SV=1	Q8K0D5	Gfm1	84 kDa	0	0	0	1.225	3.4377	FALSE
Elongation factor Ts, mitochondrial OS=Mus musculus GN=Tsfm PE=2 SV=1	A0A1S6GWJ9 (+2)	Tsfm	36 kDa	0	0	0	0.81665	0.85944	FALSE
Elongation factor-like GTPase 1 OS=Mus musculus GN=Efl1 PE=1 SV=1	Q8C0D5	Efl1	126 kDa	0	0	0	1.225	0.85944	FALSE
Elongator complex protein 1 OS=Mus musculus GN=Elp1 PE=1 SV=2	Q7TT37	Elp1	150 kDa	0	0	0	3.6749	3.8675	FALSE
Elongator complex protein 2 OS=Mus musculus GN=Elp2 PE=1 SV=1	Q91WG4	Elp2	93 kDa	0	0	0	2.0416	2.1486	FALSE
Elongator complex protein 3 OS=Mus musculus GN=Elp3 PE=1 SV=1	Q9CZX0	Elp3	62 kDa	0	0	0	2.45	2.5783	FALSE
Elongator complex protein 4 OS=Mus musculus GN=Elp4 PE=1 SV=2	Q9ER73	Elp4	46 kDa	0	0	0	0	0.85944	FALSE
Elongin-C OS=Mus musculus GN=Eloc PE=1 SV=1	A0A087WNT1 (+2)	Eloc	15 kDa	0	0	0	3.2666	3.008	FALSE
Endophilin-B1 OS=Mus musculus GN=Sh3glb1 PE=1 SV=1	Q9JK48	Sh3glb1	41 kDa	0	0	0	1.6333	0	FALSE
Endoplasmic reticulum aminopeptidase 1 OS=Mus musculus GN=Erap1 PE=1 SV=2	Q9EQH2	Erap1	107 kDa	0	0	0	3.2666	0	FALSE
Endoplasmic reticulum junction formation protein lunapark OS=Mus musculus GN=Lnpk PE=1 SV	Q7TQ95	Lnpk	48 kDa	0	0	0	1.225	1.7189	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Endoplasmic reticulum metallopeptidase 1 OS=Mus musculus GN=Ermp1 PE=1 SV=2	Q3UVK0	Ermp1	100 kDa	0	0	0	2.0416	1.2892	FALSE
Endoplasmic reticulum resident protein 29 OS=Mus musculus GN=Erp29 PE=1 SV=2	P57759	Erp29	29 kDa	0	0	0	0.81665	0.85944	FALSE
Endoplasmic reticulum-Golgi intermediate compartment protein 3 OS=Mus musculus GN=Ergic3	Q9CQE7	Ergic3	43 kDa	0	0	0	0.81665	0	FALSE
Engulfment and cell motility protein 2 OS=Mus musculus GN=Elmo2 PE=1 SV=1	Q8BHL5	Elmo2	84 kDa	0	0	0	0.81665	0	FALSE
Enhancer of mRNA-decapping protein 4 OS=Mus musculus GN=Edc4 PE=1 SV=2	Q3UJB9	Edc4	152 kDa	0	0	0	1.6333	3.008	FALSE
Enoyl-[acyl-carrier-protein] reductase, mitochondrial OS=Mus musculus GN=Mecr PE=1 SV=2	Q9DCS3	Mecr	40 kDa	0	0	0	0.81665	0.85944	FALSE
Enoyl-CoA delta isomerase 2, mitochondrial OS=Mus musculus GN=Eci2 PE=1 SV=2	Q9WUR2	Eci2	43 kDa	0	0	0	1.225	2.1486	FALSE
Enoyl-CoA hydratase, mitochondrial OS=Mus musculus GN=Echs1 PE=1 SV=1	Q8BH95	Echs1	31 kDa	0	0	0	2.45	2.1486	FALSE
Epidermal growth factor receptor kinase substrate 8 OS=Mus musculus GN=Eps8 PE=1 SV=2	Q08509 (+1)	Eps8	92 kDa	0	0	0	0	0.85944	FALSE
Epidermal growth factor receptor substrate 15-like 1 OS=Mus musculus GN=Eps15l1 PE=1 SV=3	Q60902	Eps15l1	99 kDa	0	0	0	1.225	0	FALSE
ER membrane protein complex subunit 3 OS=Mus musculus GN=Emc3 PE=1 SV=3	Q99KI3	Emc3	30 kDa	0	0	0	0	0.85944	FALSE
ER membrane protein complex subunit 4 OS=Mus musculus GN=Emc4 PE=1 SV=1	Q9CZX9	Emc4	20 kDa	0	0	0	0	0.85944	FALSE
Erbb2 interacting protein OS=Mus musculus GN=Erbin PE=2 SV=1	B2RUK2 (+2)	Erbin	162 kDa	0	0	0	1.225	0	FALSE
Erlin-2 OS=Mus musculus GN=Erlin2 PE=1 SV=1	Q8BFZ9	Erlin2	38 kDa	0	0	0	1.6333	1.2892	FALSE
Ero1l protein OS=Mus musculus GN=Ero1l PE=1 SV=1	Q4FK57 (+1)	Ero1l	54 kDa	0	0	0	3.2666	4.7269	FALSE
Erythrocyte protein band 4.1-like 3 isoform B OS=Mus musculus GN=Epb41l3 PE=2 SV=1	D0VYV6	Epb41l3	101 kDa	0	0	0	11.025	12.032	FALSE
ES1 protein homolog, mitochondrial OS=Mus musculus GN=D10Jhu81e PE=1 SV=1	Q9D172	D10Jhu81e	28 kDa	0	0	0	1.6333	0.85944	FALSE
Ester hydrolase C11orf54 homolog OS=Mus musculus PE=1 SV=1	Q91V76		35 kDa	0	0	0	0	0.85944	FALSE
Estradiol 17-beta-dehydrogenase 11 OS=Mus musculus GN=Hsd17b11 PE=1 SV=1	Q9EQ06	Hsd17b11	33 kDa	0	0	0	1.6333	0.85944	FALSE
Eukaryotic initiation factor 4A-I OS=Mus musculus GN=Eif4a1 PE=1 SV=1	P60843 (+3)	Eif4a1	46 kDa	7.3662	11.185	16.105	17.15	17.618	FALSE
Eukaryotic initiation factor 4A-II OS=Mus musculus GN=Eif4a2 PE=1 SV=2	P10630 (+1)	Eif4a2	46 kDa	0	0	0	5.7166	6.4458	FALSE
Eukaryotic initiation factor 4A-III OS=Mus musculus GN=Eif4a3 PE=1 SV=3	Q91VC3	Eif4a3	47 kDa	0	0	0	3.2666	3.4377	FALSE
Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Mus musculus GN=Gspt1	Q8R050	Gspt1	69 kDa	0	3.1957	0	4.8999	4.2972	FALSE
Eukaryotic translation initiation factor 1A, X-chromosomal OS=Mus musculus GN=Eif1ax PE=2 SV	Q8BMJ3	Eif1ax	16 kDa	0	0	0	1.225	0.85944	FALSE
Eukaryotic translation initiation factor 1b OS=Mus musculus GN=Eif1b PE=1 SV=2	Q9CXU9 (+3)	Eif1b	13 kDa	0	0	0	0.81665	0	FALSE
Eukaryotic translation initiation factor 2 subunit 1 OS=Mus musculus GN=Eif2s1 PE=1 SV=3	Q6ZWX6	Eif2s1	36 kDa	3.6831	3.1957	3.5789	6.1249	5.1566	FALSE
Eukaryotic translation initiation factor 2A OS=Mus musculus GN=Eif2a PE=1 SV=2	Q8BJW6	Eif2a	64 kDa	0	0	0	4.4916	3.4377	FALSE
Eukaryotic translation initiation factor 2B, subunit 1 (Alpha) OS=Mus musculus GN=Eif2b1 PE=1 S	Q3UZR8 (+1)	Eif2b1	34 kDa	0	0	0	0.81665	1.7189	FALSE
Eukaryotic translation initiation factor 2B, subunit 3 OS=Mus musculus GN=Eif2b3 PE=1 SV=1	Q3UKV0	Eif2b3	50 kDa	0	0	0	0.81665	0.85944	FALSE
Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=2 SV=1	Q8CIJ3 (+1)	Eif3b	109 kDa	7.3662	11.185	10.737	11.841	15.04	FALSE
Eukaryotic translation initiation factor 3 subunit C OS=Mus musculus GN=Eif3c PE=1 SV=1	Q8R1B4	Eif3c	106 kDa	5.5246	6.3914	7.1579	10.208	9.4538	FALSE
Eukaryotic translation initiation factor 3 subunit D OS=Mus musculus GN=Eif3d PE=1 SV=2	O70194	Eif3d	64 kDa	0	0	0	7.7582	8.1647	FALSE
Eukaryotic translation initiation factor 3 subunit F OS=Mus musculus GN=Eif3f PE=2 SV=1	Q3U8X1 (+4)	Eif3f	38 kDa	0	3.1957	0	3.2666	3.4377	FALSE
Eukaryotic translation initiation factor 3 subunit G OS=Mus musculus GN=Eif3g PE=1 SV=1	Q544H0 (+1)	Eif3g	36 kDa	0	0	0	3.2666	4.2972	FALSE
Eukaryotic translation initiation factor 3 subunit H OS=Mus musculus GN=Eif3h PE=2 SV=1	Q3THW7 (+3)	Eif3h	40 kDa	0	0	0	2.45	1.2892	FALSE
Eukaryotic translation initiation factor 3 subunit I OS=Mus musculus GN=Eif3i PE=1 SV=1	Q9QZD9	Eif3i	36 kDa	0	3.1957	3.5789	5.3082	5.5863	FALSE
Eukaryotic translation initiation factor 3 subunit J-A OS=Mus musculus GN=Eif3j1 PE=2 SV=1	Q3UGC7 (+1)	Eif3j1	29 kDa	0	0	0	1.6333	1.2892	FALSE
Eukaryotic translation initiation factor 3 subunit K OS=Mus musculus GN=Eif3k PE=1 SV=1	Q9DBZ5	Eif3k	25 kDa	0	0	0	1.6333	1.2892	FALSE
Eukaryotic translation initiation factor 3 subunit M OS=Mus musculus GN=Eif3m PE=1 SV=1	Q99JX4	Eif3m	43 kDa	0	0	0	2.0416	2.1486	FALSE
Eukaryotic translation initiation factor 4 gamma 1 OS=Mus musculus GN=Eif4g1 PE=1 SV=1	Q6NZJ6	Eif4g1	176 kDa	0	0	0	9.7998	12.462	FALSE
Eukaryotic translation initiation factor 4E OS=Mus musculus GN=Eif4e PE=1 SV=1	P63073 (+1)	Eif4e	25 kDa	0	0	0	0.81665	1.7189	FALSE
Eukaryotic translation initiation factor 5 OS=Mus musculus GN=Eif5 PE=1 SV=1	P59325 (+1)	Eif5	49 kDa	0	0	0	2.0416	2.5783	FALSE
Eukaryotic translation initiation factor 5A-1 OS=Mus musculus GN=Eif5a PE=1 SV=2	P63242	Eif5a	17 kDa	7.3662	7.9893	8.9474	9.7998	10.743	FALSE
Eukaryotic translation initiation factor 5B OS=Mus musculus GN=Eif5b PE=1 SV=2	Q05D44	Eif5b	138 kDa	0	0	0	5.3082	6.8755	FALSE
Eukaryotic translation initiation factor 6 OS=Mus musculus GN=Eif6 PE=1 SV=2	O55135 (+3)	Eif6	27 kDa	0	0	0	3.6749	3.8675	FALSE
Exopolyphosphatase PRUNE1 OS=Mus musculus GN=Prune1 PE=1 SV=1	Q8BIW1	Prune1	50 kDa	0	0	0	0	0.85944	FALSE
Exosome complex component CSL4 OS=Mus musculus GN=Exosc1 PE=1 SV=1	Q9DAA6	Exosc1	21 kDa	0	0	0	0	0.85944	FALSE
Exosome complex component RRP45 OS=Mus musculus GN=Exosc9 PE=1 SV=1	Q9JHI7	Exosc9	49 kDa	0	0	0	0.81665	0.85944	FALSE
Exosome complex exonuclease RRP44 OS=Mus musculus GN=Dis3 PE=1 SV=4	Q9CSH3	Dis3	109 kDa	0	0	0	6.1249	9.4538	FALSE
Exosome RNA helicase MTR4 OS=Mus musculus GN=Mtrex PE=1 SV=1	Q9CZU3	Mtrex	118 kDa	0	0	0	0.81665	0.85944	FALSE
Exportin-5 OS=Mus musculus GN=Xpo5 PE=1 SV=1	Q924C1	Xpo5	137 kDa	0	0	3.5789	6.5332	6.0161	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Exportin-7 OS=Mus musculus GN=Xpo7 PE=1 SV=1	E9PUW7 (+1)	Xpo7	124 kDa	0	0	0	2.8583	4.2972	FALSE
Exportin-T OS=Mus musculus GN=Xpot PE=1 SV=1	A0A1W2P7Q6 (+1)	Xpot	110 kDa	0	0	0	3.2666	2.1486	FALSE
Extended synaptotagmin-1 OS=Mus musculus GN=Esyt1 PE=1 SV=2	Q3U7R1	Esyt1	122 kDa	0	0	0	2.0416	1.7189	FALSE
Extended synaptotagmin-2 OS=Mus musculus GN=Esyt2 PE=1 SV=1	Q3TZZ7	Esyt2	94 kDa	0	0	0	1.225	0.85944	FALSE
Extracellular matrix protein OS=Mus musculus PE=4 SV=1	Q9QX30		63 kDa	0	0	0	2.0416	4.7269	FALSE
Extracellular superoxide dismutase [Cu-Zn] OS=Mus musculus GN=Sod3 PE=1 SV=1	O09164 (+1)	Sod3	27 kDa	0	0	0	0	0.85944	FALSE
Ezrin OS=Mus musculus GN=Ezr PE=1 SV=3	P26040 (+3)	Ezr	69 kDa	0	0	0	6.5332	6.4458	FALSE
F-box only protein 30 OS=Mus musculus GN=Fbxo30 PE=1 SV=2	Q8BJL1	Fbxo30	83 kDa	0	0	0	2.45	0.85944	FALSE
FACT complex subunit SSRP1 OS=Mus musculus GN=Ssrp1 PE=1 SV=2	Q08943	Ssrp1	81 kDa	0	0	0	3.6749	4.2972	FALSE
FAD-linked sulfhydryl oxidase ALR OS=Mus musculus GN=Gfer PE=1 SV=2	P56213	Gfer	23 kDa	0	0	0	0	0.85944	FALSE
Far upstream element-binding protein 1 OS=Mus musculus GN=Fubp1 PE=1 SV=1	Q3TUE1	Fubp1	67 kDa	0	0	0	4.4916	3.8675	FALSE
Far upstream element-binding protein 2 OS=Mus musculus GN=Khsrp PE=1 SV=2	Q3U0V1	Khsrp	77 kDa	3.6831	3.1957	5.3684	10.616	13.751	FALSE
FAS-associated factor 1 OS=Mus musculus GN=Faf1 PE=1 SV=2	P54731	Faf1	74 kDa	0	0	0	0.81665	0	FALSE
FAS-associated factor 2 OS=Mus musculus GN=Faf2 PE=1 SV=2	Q3TDN2	Faf2	52 kDa	0	0	0	2.0416	2.1486	FALSE
Fatty acid-binding protein, adipocyte OS=Mus musculus GN=Fabp4 PE=1 SV=3	P04117 (+1)	Fabp4	15 kDa	0	0	0	3.2666	3.4377	FALSE
Fatty acid-binding protein, epidermal OS=Mus musculus GN=Fabp5 PE=1 SV=3	Q05816 (+1)	Fabp5	15 kDa	0	0	0	11.025	17.189	FALSE
Fdps protein OS=Mus musculus GN=Fdps PE=1 SV=1	Q4FJN9 (+1)	Fdps	41 kDa	0	0	0	3.2666	0.85944	FALSE
Ferritin light chain 1 OS=Mus musculus GN=Ftl1 PE=1 SV=2	P29391 (+3)	Ftl1	21 kDa	0	0	0	0	2.5783	FALSE
Fibronectin type III domain-containing protein 3B OS=Mus musculus GN=Fndc3b PE=1 SV=1	Q6NWW9	Fndc3b	133 kDa	0	0	0	2.45	1.7189	FALSE
Filamin-binding LIM protein 1 OS=Mus musculus GN=Fblim1 PE=1 SV=2	Q71FD7	Fblim1	41 kDa	0	0	0	1.225	1.2892	FALSE
Filamin-C OS=Mus musculus GN=Flnc PE=1 SV=3	Q8VHX6	Flnc	291 kDa	22.099	22.37	23.263	37.974	38.675	FALSE
Flap endonuclease 1 OS=Mus musculus GN=Fen1 PE=2 SV=1	Q3TGH6 (+2)	Fen1	43 kDa	0	0	0	1.225	1.7189	FALSE
Focal adhesion kinase 1 OS=Mus musculus GN=Ptk2 PE=1 SV=3	P34152	Ptk2	124 kDa	0	0	0	2.0416	0.85944	FALSE
Follistatin-related protein 1 OS=Mus musculus GN=Fstl1 PE=1 SV=2	Q62356	Fstl1	35 kDa	0	0	0	3.6749	4.7269	FALSE
Forkhead box protein K1 OS=Mus musculus GN=Foxk1 PE=1 SV=2	P42128	Foxk1	75 kDa	0	0	0	0.81665	2.1486	FALSE
Four and a half LIM domains protein 1 OS=Mus musculus GN=Fhl1 PE=1 SV=1	A2AEX6 (+2)	Fhl1	35 kDa	0	0	0	3.2666	1.2892	FALSE
Four and a half LIM domains protein 2 OS=Mus musculus GN=Fhl2 PE=1 SV=1	O70433 (+1)	Fhl2	32 kDa	0	0	0	4.4916	4.2972	FALSE
Four and a half LIM domains protein 3 OS=Mus musculus GN=Fhl3 PE=1 SV=2	Q9R059	Fhl3	32 kDa	0	0	0	2.8583	3.008	FALSE
Fragile X mental retardation syndrome-related protein 2 OS=Mus musculus GN=Fxr2 PE=1 SV=1	Q6P5B5	Fxr2	74 kDa	0	0	0	2.0416	1.2892	FALSE
Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2	P05064 (+1)	Aldoa	39 kDa	16.574	17.576	14.316	25.725	23.205	FALSE
Fumarate hydratase, mitochondrial OS=Mus musculus GN=Fh PE=1 SV=3	P97807	Fh	54 kDa	0	0	0	2.8583	4.2972	FALSE
FUN14 domain-containing protein 2 OS=Mus musculus GN=Fundc2 PE=1 SV=1	Q9D6K8	Fundc2	17 kDa	0	0	0	0.81665	0	FALSE
Fusion, derived from t(1216) malignant liposarcoma (Human) OS=Mus musculus GN=Fus PE=1 SV	Q8CFQ9	Fus	53 kDa	0	0	0	2.0416	1.7189	FALSE
G1p2 protein OS=Mus musculus GN=Isg15 PE=1 SV=1	Q4FJR9 (+1)	Isg15	18 kDa	0	0	0	3.6749	0	FALSE
GA-binding protein alpha chain OS=Mus musculus GN=Gabpa PE=1 SV=2	Q00422 (+2)	Gabpa	51 kDa	0	0	0	2.45	1.2892	FALSE
Galactokinase OS=Mus musculus GN=Galk1 PE=1 SV=2	Q9R0N0	Galk1	42 kDa	0	0	0	2.8583	3.008	FALSE
Galectin-3-binding protein OS=Mus musculus GN=Lgals3bp PE=1 SV=1	Q07797	Lgals3bp	64 kDa	0	0	0	3.2666	0	FALSE
Galectin-related protein OS=Mus musculus GN=Lgalsl PE=1 SV=1	Q8VED9	Lgalsl	19 kDa	0	0	0	1.225	0	FALSE
Gasdermin-D OS=Mus musculus GN=Gsdmdc1 PE=1 SV=1	Q9D8T2	Gsdmdc1	53 kDa	0	0	0	1.225	1.7189	FALSE
Gasdermin-E OS=Mus musculus GN=Gsdme PE=1 SV=1	Q9Z2D3	Gsdme	57 kDa	0	0	0	1.6333	3.8675	FALSE
GDH/6PGL endoplasmic bifunctional protein OS=Mus musculus GN=H6pd PE=1 SV=1	A2A7A7 (+1)	H6pd	90 kDa	0	0	0	3.6749	3.008	FALSE
GDP-fucose protein O-fucosyltransferase 1 OS=Mus musculus GN=Pofut1 PE=1 SV=1	A2AMC3 (+1)	Pofut1	40 kDa	0	0	0	0	0.85944	FALSE
GDP-L-fucose synthase OS=Mus musculus GN=Tsta3 PE=1 SV=3	P23591 (+1)	Tsta3	36 kDa	0	0	0	3.2666	2.5783	FALSE
GDP-mannose 4,6 dehydratase OS=Mus musculus GN=Gmds PE=1 SV=1	Q8K0C9	Gmds	42 kDa	0	0	0	3.2666	3.008	FALSE
Gelsolin, isoform CRA_c OS=Mus musculus GN=Gsn PE=2 SV=1	Q6PAC1	Gsn	81 kDa	0	6.3914	10.737	12.658	13.321	FALSE
Gem (Nuclear organelle) associated protein 4 OS=Mus musculus GN=Gemin4 PE=2 SV=1	Q8K1K1	Gemin4	120 kDa	0	0	0	0.81665	1.2892	FALSE
Gem-associated protein 5 OS=Mus musculus GN=Gemin5 PE=1 SV=1	A2AFQ9 (+2)	Gemin5	167 kDa	0	0	0	3.6749	3.008	FALSE
General transcription factor IIF subunit 1 OS=Mus musculus GN=Gtf2f1 PE=1 SV=2	Q3THK3	Gtf2f1	57 kDa	0	0	0	2.45	3.4377	FALSE
General transcription factor IIF subunit 2 OS=Mus musculus GN=Gtf2f2 PE=1 SV=1	Q3UMJ4 (+1)	Gtf2f2	28 kDa	0	0	0	2.0416	1.7189	FALSE
General vesicular transport factor p115 OS=Mus musculus GN=Uso1 PE=1 SV=2	Q9Z1Z0	Uso1	107 kDa	0	0	0	6.9416	4.7269	FALSE
Gephyrin OS=Mus musculus GN=Gphn PE=1 SV=1	A0JNY3 (+1)	Gphn	84 kDa	0	0	0	0	0.85944	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Girdin OS=Mus musculus GN=Ccdc88a PE=1 SV=2	Q5SNZ0	Ccdc88a	216 kDa	0	0	0	0.81665	0.85944	FALSE
Glia maturation factor beta OS=Mus musculus GN=Gmfb PE=2 SV=1	A7VJ98 (+2)	Gmfb	17 kDa	0	0	0	0	0.85944	FALSE
Glt8d1 protein OS=Mus musculus GN=Glt8d1 PE=2 SV=1	Q7TNU1	Glt8d1	20 kDa	0	0	0	0	1.2892	FALSE
Glucosamine 6-phosphate N-acetyltransferase OS=Mus musculus GN=Gnpnat1 PE=1 SV=1	Q9JK38	Gnpnat1	21 kDa	0	0	0	1.6333	1.7189	FALSE
Glucose-6-phosphate 1-dehydrogenase X OS=Mus musculus GN=G6pdx PE=1 SV=3	Q00612 (+1)	G6pdx	59 kDa	0	0	0	11.025	10.743	FALSE
Glucose-6-phosphate isomerase OS=Mus musculus GN=Gpi PE=1 SV=4	P06745	Gpi	63 kDa	3.6831	3.1957	5.3684	8.5749	7.7349	FALSE
Glucosylceramidase OS=Mus musculus GN=Gba PE=1 SV=1	P17439	Gba	58 kDa	0	0	0	0.81665	0.85944	FALSE
Glutaminase kidney isoform, mitochondrial OS=Mus musculus GN=Gls PE=1 SV=1	D3Z7P3	Gls	74 kDa	0	0	0	4.0833	4.7269	FALSE
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Mus musculus GN=Gfpt1 P	P47856	Gfpt1	79 kDa	0	0	0	6.1249	5.5863	FALSE
Glutaredoxin-3 OS=Mus musculus GN=Glrx3 PE=1 SV=1	Q9CQM9	Glrx3	38 kDa	0	0	0	2.0416	3.008	FALSE
Glutaredoxin, isoform CRA_a OS=Mus musculus GN=Glrx PE=1 SV=1	Q3U6L3 (+1)	Glrx	12 kDa	0	0	0	0	1.2892	FALSE
Glutaryl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Gcdh PE=1 SV=1	A0A0A0MQ68 (+3)	Gcdh	50 kDa	0	0	0	0.81665	1.7189	FALSE
Glutathione peroxidase 1 OS=Mus musculus GN=Gpx1 PE=1 SV=2	P11352	Gpx1	22 kDa	0	0	0	0.81665	0	FALSE
Glutathione peroxidase OS=Mus musculus GN=Gpx4 PE=2 SV=2	Q3TI34 (+2)	Gpx4	20 kDa	0	0	0	0.81665	1.2892	FALSE
Glutathione peroxidase OS=Mus musculus GN=Gpx7 PE=1 SV=1	Q3TNK3 (+1)	Gpx7	21 kDa	0	0	0	1.6333	1.2892	FALSE
Glutathione S-transferase (Fragment) OS=Mus musculus GN=Gstm5 PE=1 SV=1	E9PVM7	Gstm5	26 kDa	0	0	0	1.225	1.2892	FALSE
Glutathione S-transferase Mu 1 OS=Mus musculus GN=Gstm1 PE=1 SV=2	P10649	Gstm1	26 kDa	0	0	3.5789	4.8999	5.1566	FALSE
Glutathione S-transferase Mu 2 OS=Mus musculus GN=Gstm2 PE=1 SV=2	P15626	Gstm2	26 kDa	0	0	0	2.8583	2.1486	FALSE
Glutathione S-transferase omega-1 OS=Mus musculus GN=Gsto1 PE=1 SV=2	O09131	Gsto1	27 kDa	0	0	0	2.8583	3.8675	FALSE
Glutathione S-transferase theta-1 OS=Mus musculus GN=Gstt1 PE=1 SV=4	Q64471 (+1)	Gstt1	27 kDa	0	0	0	1.6333	1.7189	FALSE
Glutathione synthetase OS=Mus musculus GN=Gss PE=1 SV=1	P51855 (+3)	Gss	52 kDa	0	0	0	0.81665	0	FALSE
Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=1	A0A0A0MQF6 (+2)	Gapdh	39 kDa	20.257	17.576	30.421	40.833	46.41	FALSE
Glycerol-3-phosphate phosphatase OS=Mus musculus GN=Pgp PE=1 SV=1	Q8CHP8	Pgp	35 kDa	0	0	0	0.81665	1.7189	FALSE
Glycine--tRNA ligase OS=Mus musculus GN=Gars PE=1 SV=1	Q9CZD3	Gars	82 kDa	0	4.7936	0	11.025	7.7349	FALSE
Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2	Q9Z1E4	Gys1	84 kDa	0	0	0	0.81665	1.2892	FALSE
Glycogen synthase kinase-3 alpha OS=Mus musculus GN=Gsk3a PE=1 SV=2	Q2NL51	Gsk3a	52 kDa	0	0	0	1.225	1.2892	FALSE
Glycogen synthase kinase-3 beta OS=Mus musculus GN=Gsk3b PE=1 SV=1	E9QAQ5 (+2)	Gsk3b	48 kDa	0	0	0	1.6333	1.7189	FALSE
Glycogenin (Fragment) OS=Mus musculus GN=Gyg PE=1 SV=1	V9GX26	Gyg	41 kDa	0	0	0	0.81665	0.85944	FALSE
Glycylpeptide N-tetradecanoyltransferase 1 OS=Mus musculus GN=Nmt1 PE=1 SV=1	O70310 (+1)	Nmt1	57 kDa	0	0	0	5.3082	4.7269	FALSE
Glycylpeptide N-tetradecanoyltransferase 2 OS=Mus musculus GN=Nmt2 PE=1 SV=1	O70311 (+1)	Nmt2	60 kDa	0	0	0	0	2.1486	FALSE
Glyoxalase domain-containing protein 4 OS=Mus musculus GN=Glod4 PE=1 SV=1	Q9CPV4	Glod4	33 kDa	0	0	0	4.4916	5.5863	FALSE
Glyoxylate reductase/hydroxypyruvate reductase OS=Mus musculus GN=Grhpr PE=1 SV=1	Q3T9Z2 (+1)	Grhpr	35 kDa	0	0	0	1.225	1.7189	FALSE
GMP reductase 1 OS=Mus musculus GN=Gmpr PE=1 SV=1	Q9DCZ1	Gmpr	37 kDa	0	0	0	0	0.85944	FALSE
GMP reductase 2 OS=Mus musculus GN=Gmpr2 PE=1 SV=2	Q99L27	Gmpr2	38 kDa	0	0	0	0	1.7189	FALSE
Golgi integral membrane protein 4 OS=Mus musculus GN=Golim4 PE=1 SV=1	D3YVW2	Golim4	80 kDa	0	0	0	1.225	0	FALSE
Golgi reassembly stacking protein 2, isoform CRA_d OS=Mus musculus GN=Gorasp2 PE=1 SV=1	A2ATI9 (+3)	Gorasp2	45 kDa	0	0	0	2.8583	3.008	FALSE
Golgi to ER traffic protein 4 homolog OS=Mus musculus GN=Get4 PE=1 SV=2	Q9D1H7	Get4	37 kDa	0	0	0	1.225	1.2892	FALSE
Golgi-associated plant pathogenesis-related protein 1 OS=Mus musculus GN=Glipr2 PE=1 SV=3	Q9CYL5	Glipr2	17 kDa	0	0	0	0.81665	0	FALSE
Golgi-specific brefeldin A-resistance factor 1 OS=Mus musculus GN=Gbf1 PE=1 SV=1	Q6DFZ1	Gbf1	207 kDa	0	0	0	1.225	1.7189	FALSE
Granulins OS=Mus musculus GN=Grn PE=1 SV=2	P28798 (+9)	Grn	63 kDa	0	0	0	2.8583	1.7189	FALSE
Growth factor receptor bound protein 2, isoform CRA_b OS=Mus musculus GN=Grb2 PE=2 SV=1	Q3U5I5 (+1)	Grb2	25 kDa	0	0	0	0.81665	1.2892	FALSE
Growth factor receptor-bound protein 10 OS=Mus musculus GN=Grb10 PE=1 SV=2	Q60760	Grb10	71 kDa	0	0	0	1.6333	0	FALSE
Growth hormone-inducible transmembrane protein OS=Mus musculus GN=Ghitm PE=1 SV=1	Q91VC9	Ghitm	37 kDa	0	0	0	1.225	0	FALSE
Grwd1 protein (Fragment) OS=Mus musculus GN=Grwd1 PE=2 SV=1	Q5XJZ3 (+2)	Grwd1	49 kDa	0	0	0	0.81665	0	FALSE
GTP-binding protein 1 OS=Mus musculus GN=Gtpbp1 PE=1 SV=2	O08582	Gtpbp1	72 kDa	0	0	0	2.0416	2.5783	FALSE
GTPase HRas OS=Mus musculus GN=Hras PE=1 SV=2	Q61411	Hras	21 kDa	0	0	0	1.225	0.85944	FALSE
GTPase-activating protein and VPS9 domain-containing protein 1 OS=Mus musculus GN=Gapvd1	Q6PAR5	Gapvd1	162 kDa	0	0	0	1.6333	0	FALSE
Guanine monphosphate synthetase OS=Mus musculus GN=Gmps PE=1 SV=1	B2RRH9 (+1)	Gmps	77 kDa	0	0	0	6.5332	8.5944	FALSE
Guanine nucleotide binding protein, alpha 11 OS=Mus musculus GN=Gna11 PE=2 SV=1	Q91X95	Gna11	42 kDa	0	0	0	1.225	1.2892	FALSE
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Mus musculus GN=Gnb1 PE	P62874 (+2)	Gnb1	37 kDa	0	0	0	4.4916	2.5783	FALSE
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Mus musculus GN=Gnb2 PE	P62880 (+1)	Gnb2	37 kDa	0	0	0	5.3082	3.4377	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Guanine nucleotide-binding protein G(k) subunit alpha OS=Mus musculus GN=Gnai3 PE=1 SV=3	Q9DC51	Gnai3	41 kDa	0	0	0	2.45	1.7189	FALSE
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Mus musculus GN=Gnas	Q6R0H7	Gnas	122 kDa	0	0	0	2.0416	2.1486	FALSE
Guanine nucleotide-binding protein subunit beta-4 OS=Mus musculus GN=Gnb4 PE=1 SV=4	P29387 (+2)	Gnb4	37 kDa	0	0	0	2.8583	0	FALSE
Guanine nucleotide-binding protein-like 1 OS=Mus musculus GN=Gnl1 PE=1 SV=4	P36916	Gnl1	69 kDa	0	0	0	3.6749	2.5783	FALSE
Guanylate-binding protein 2 OS=Mus musculus GN=Gbp2 PE=1 SV=1	Q9Z0E6	Gbp2	67 kDa	0	0	0	1.225	0	FALSE
Guanylate-binding protein 4 OS=Mus musculus GN=Gbp4 PE=1 SV=1	Q61107	Gbp4	71 kDa	0	0	0	2.45	0	FALSE
H1 histone family, member X OS=Mus musculus GN=H1fx PE=1 SV=1	Q80ZM5	H1fx	20 kDa	0	0	0	0	0.85944	FALSE
HBS1-like protein OS=Mus musculus GN=Hbs1l PE=1 SV=1	Q3TGM7 (+1)	Hbs1l	75 kDa	0	0	0	1.225	0.85944	FALSE
Heat shock 70 kDa protein 14 OS=Mus musculus GN=Hspa14 PE=1 SV=2	Q99M31	Hspa14	55 kDa	0	0	0	3.6749	4.2972	FALSE
Heat shock 70 kDa protein 1B OS=Mus musculus GN=Hspa1b PE=1 SV=3	P17879	Hspa1b	70 kDa	0	0	0	10.208	9.0241	FALSE
Heat shock 70 kDa protein 4L OS=Mus musculus GN=Hspa4l PE=1 SV=2	P48722	Hspa4l	94 kDa	0	0	0	4.8999	6.8755	FALSE
Heat shock protein 105 kDa OS=Mus musculus GN=Hsph1 PE=1 SV=2	Q61699	Hsph1	96 kDa	0	0	3.5789	11.433	13.321	FALSE
Helicase with zinc finger domain 2 OS=Mus musculus GN=Helz2 PE=1 SV=1	E9QAM5	Helz2	332 kDa	0	0	0	2.45	0	FALSE
Heme oxygenase 1 OS=Mus musculus GN=Hmox1 PE=1 SV=1	P14901 (+1)	Hmox1	33 kDa	0	0	0	0.81665	0	FALSE
Heme oxygenase 2 OS=Mus musculus GN=Hmox2 PE=1 SV=1	O70252 (+2)	Hmox2	36 kDa	0	0	0	1.6333	1.7189	FALSE
Heme-binding protein 2 OS=Mus musculus GN=Hebp2 PE=1 SV=1	Q9WU63	Hebp2	23 kDa	0	0	0	0	0.85944	FALSE
Heparan-alpha-glucosaminide N-acetyltransferase OS=Mus musculus GN=Hgsnat PE=1 SV=2	Q3UDW8	Hgsnat	73 kDa	0	0	0	0	0.85944	FALSE
Hepatocyte growth factor-regulated tyrosine kinase substrate OS=Mus musculus GN=Hgs PE=1 S	B1ATZ0 (+1)	Hgs	86 kDa	0	0	0	1.6333	2.5783	FALSE
Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2	P51859	Hdgf	26 kDa	0	0	0	4.4916	5.1566	FALSE
Hepatoma-derived growth factor-related protein 2 OS=Mus musculus GN=Hdgfl2 PE=1 SV=1	Q3UMU9	Hdgfl2	74 kDa	0	0	0	0.81665	1.7189	FALSE
Heterogeneous nuclear ribonucleoprotein A3 OS=Mus musculus GN=Hnrnpa3 PE=1 SV=1	A2AL12 (+4)	Hnrnpa3	34 kDa	0	0	0	2.8583	2.1486	FALSE
Heterogeneous nuclear ribonucleoprotein D-like OS=Mus musculus GN=Hnrnpdl PE=1 SV=1	Q9Z130	Hnrnpdl	34 kDa	0	0	0	2.0416	0	FALSE
Heterogeneous nuclear ribonucleoprotein D0 OS=Mus musculus GN=Hnrnpd PE=1 SV=2	Q60668	Hnrnpd	38 kDa	0	0	0	4.0833	5.1566	FALSE
Heterogeneous nuclear ribonucleoprotein H2 OS=Mus musculus GN=Hnrnph2 PE=1 SV=1	P70333	Hnrnph2	49 kDa	0	0	0	2.45	3.4377	FALSE
Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrnpk PE=1 SV=1	P61979 (+1)	Hnrnpk	51 kDa	9.2077	6.3914	8.9474	11.841	9.8835	FALSE
Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Mus musculus GN=Hnrnpl PE=1 SV=1	G5E924 (+1)	Hnrnpl	67 kDa	0	0	0	2.0416	0.85944	FALSE
Heterogeneous nuclear ribonucleoprotein L-like OS=Mus musculus GN=Hnrnpll PE=1 SV=3	Q921F4	Hnrnpll	64 kDa	0	0	0	2.45	3.008	FALSE
Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Mus musculus GN=Hnrnpul1 PE=1	Q8VDM6	Hnrnpul1	96 kDa	0	0	0	1.6333	1.7189	FALSE
Hexokinase 1, isoform CRA_d OS=Mus musculus GN=Hk1 PE=2 SV=1	Q6GQU1	Hk1	102 kDa	0	0	0	10.208	9.0241	FALSE
High affinity cationic amino acid transporter 1 OS=Mus musculus GN=Slc7a1 PE=1 SV=1	Q09143 (+2)	Slc7a1	67 kDa	0	0	0	0.81665	0.85944	FALSE
High density lipoprotein (HDL) binding protein, isoform CRA_d OS=Mus musculus GN=Hdlbp PE=1	Q3U4Z7 (+1)	Hdlbp	142 kDa	0	3.1957	3.5789	11.433	7.7349	FALSE
High mobility group box 3 OS=Mus musculus GN=Hmgb3 PE=1 SV=1	Q544R9 (+1)	Hmgb3	23 kDa	0	0	0	0	1.7189	FALSE
Hippocalcin-like protein 1 OS=Mus musculus GN=Hpcal1 PE=1 SV=2	P62748	Hpcal1	22 kDa	0	0	0	1.225	3.008	FALSE
HIRA-interacting protein 3 OS=Mus musculus GN=Hirip3 PE=1 SV=1	Q8BLH7	Hirip3	65 kDa	0	0	0	0	1.2892	FALSE
Histone acetyltransferase type B catalytic subunit OS=Mus musculus GN=Hat1 PE=1 SV=1	A2ATU9 (+1)	Hat1	50 kDa	0	0	0	1.225	2.5783	FALSE
Histone deacetylase OS=Mus musculus GN=Hdac2 PE=1 SV=1	A0A0R4J008 (+1)	Hdac2	55 kDa	0	0	0	0	2.1486	FALSE
Histone deacetylase OS=Mus musculus GN=Hdac7 PE=1 SV=1	E9PXW1 (+2)	Hdac7	97 kDa	0	0	0	0	0.85944	FALSE
Histone H1.2 OS=Mus musculus GN=Hist1h1c PE=1 SV=2	P15864 (+2)	Hist1h1c	21 kDa	0	0	0	2.45	3.008	FALSE
Histone H1.5 OS=Mus musculus GN=Hist1h1b PE=1 SV=2	P43276 (+1)	Hist1h1b	23 kDa	0	0	0	1.225	0.85944	FALSE
Histone PARylation factor 1 OS=Mus musculus GN=Hpf1 PE=1 SV=1	Q8CFE2	Hpf1	39 kDa	0	0	0	1.225	1.2892	FALSE
Histone-arginine methyltransferase CARM1 OS=Mus musculus GN=Carm1 PE=1 SV=2	Q9WVG6	Carm1	66 kDa	0	0	0	2.45	2.1486	FALSE
Histone-binding protein RBBP4 OS=Mus musculus GN=Rbbp4 PE=1 SV=5	Q60972	Rbbp4	48 kDa	0	0	0	2.45	0	FALSE
Histone-lysine N-methyltransferase SETD7 OS=Mus musculus GN=Setd7 PE=1 SV=2	Q8VHL1	Setd7	41 kDa	0	0	0	0	2.1486	FALSE
HIV Tat-specific factor 1 homolog OS=Mus musculus GN=Htatsf1 PE=1 SV=1	Q8BGC0	Htatsf1	86 kDa	0	0	0	0.81665	0.85944	FALSE
HN1-like protein OS=Mus musculus GN=Jpt2 PE=1 SV=1	Q3TM10 (+2)	Jpt2	20 kDa	0	0	0	1.225	1.7189	FALSE
Host cell factor 1 OS=Mus musculus GN=Hcfc1 PE=1 SV=2	Q61191	Hcfc1	210 kDa	0	0	0	2.8583	2.5783	FALSE
Hsp90 co-chaperone Cdc37 OS=Mus musculus GN=Cdc37 PE=1 SV=1	Q61081	Cdc37	45 kDa	0	0	3.5789	4.4916	4.2972	FALSE
HSPB1-associated protein 1 OS=Mus musculus GN=Hspbap1 PE=1 SV=2	Q8BK58	Hspbap1	54 kDa	0	0	0	0	1.2892	FALSE
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Mus musculus GN=Hadh PE=1 SV=2	Q61425	Hadh	34 kDa	0	0	0	1.225	2.5783	FALSE
Hydroxyacylglutathione hydrolase, mitochondrial OS=Mus musculus GN=Hagh PE=1 SV=1	A0A0R4J052 (+3)	Hagh	29 kDa	0	0	0	0.81665	0.85944	FALSE
Hydroxymethylglutaryl-CoA synthase, cytoplasmic OS=Mus musculus GN=Hmgcs1 PE=1 SV=1	Q8JZK9 (+1)	Hmgcs1	58 kDa	0	0	0	4.0833	2.1486	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Hypoxia up-regulated protein 1 OS=Mus musculus GN=Hyou1 PE=1 SV=1	Q9JKR6	Hyou1	111 kDa	0	3.1957	3.5789	9.7998	7.7349	FALSE
Immunity related GTPase family B member 6 homologue allele 2 OS=Mus musculus domesticus G	A0A1G5SLN0 (+3)	OTTMUSWSBG	47 kDa	0	0	0	2.45	0	FALSE
Immunity-related GTPase family member m3 OS=Mus musculus molossinus GN=Irgm3 PE=4 SV=1	U5NG76	Irgm3	46 kDa	0	0	0	0.81665	0	FALSE
Immunoglobulin-binding protein 1 OS=Mus musculus GN=Igbp1 PE=1 SV=1	Q61249	Igbp1	39 kDa	0	0	0	0.81665	0.85944	FALSE
Importin subunit alpha-7 OS=Mus musculus GN=Kpna6 PE=1 SV=2	O35345 (+2)	Kpna6	60 kDa	0	0	0	2.45	0.85944	FALSE
Importin-7 OS=Mus musculus GN=Ipo7 PE=1 SV=2	Q9EPL8	Ipo7	119 kDa	0	0	0	4.0833	4.7269	FALSE
Importin-9 OS=Mus musculus GN=Ipo9 PE=1 SV=1	E9QKZ2 (+1)	Ipo9	116 kDa	0	0	0	3.6749	2.1486	FALSE
Inorganic pyrophosphatase 2, mitochondrial OS=Mus musculus GN=Ppa2 PE=1 SV=1	Q91VM9	Ppa2	38 kDa	0	0	0	1.225	2.5783	FALSE
Inosine triphosphate pyrophosphatase OS=Mus musculus GN=Itpa PE=1 SV=1	Q60I30 (+1)	Itpa	22 kDa	0	0	0	3.6749	3.4377	FALSE
Inosine-5'-monophosphate dehydrogenase 2 OS=Mus musculus GN=Impdh2 PE=1 SV=2	P24547 (+2)	Impdh2	56 kDa	3.6831	0	0	10.616	9.8835	FALSE
Inosine-5'-monophosphate dehydrogenase OS=Mus musculus GN=Impdh1 PE=1 SV=2	F7DEU6 (+1)	Impdh1	58 kDa	0	0	0	0.81665	1.7189	FALSE
Inositol 1,4,5-trisphosphate receptor type 3 OS=Mus musculus GN=Itpr3 PE=1 SV=3	P70227	Itpr3	304 kDa	0	0	0	5.7166	6.8755	FALSE
Inositol polyphosphate 1-phosphatase OS=Mus musculus GN=Inpp1 PE=1 SV=2	P49442	Inpp1	43 kDa	0	0	0	0.81665	0.85944	FALSE
Inositol-1-monophosphatase OS=Mus musculus GN=Impa2 PE=2 SV=1	Q3TAU6 (+3)	Impa2	32 kDa	0	0	0	0.81665	0.85944	FALSE
Insulin-degrading enzyme OS=Mus musculus GN=Ide PE=1 SV=1	Q9JHR7	Ide	118 kDa	0	0	0	4.4916	3.8675	FALSE
Insulin-like growth factor 2 mRNA-binding protein 1 OS=Mus musculus GN=Igf2bp1 PE=1 SV=1	O88477	Igf2bp1	63 kDa	0	0	0	3.6749	3.8675	FALSE
Insulin-like growth factor binding protein 7 OS=Mus musculus GN=Igfbp7 PE=2 SV=1	A0A5E1 (+3)	Igfbp7	29 kDa	0	0	0	2.0416	1.2892	FALSE
Integrin-associated protein OS=Mus musculus GN=Cd47 PE=2 SV=1	E5Q371 (+2)	Cd47	33 kDa	0	0	0	1.225	0.85944	FALSE
Integrin-linked kinase-associated serine/threonine phosphatase 2C OS=Mus musculus GN=Ilkap P	Q8R0F6	Ilkap	43 kDa	0	0	0	0	1.2892	FALSE
Integrin-linked protein kinase OS=Mus musculus GN=Ilk PE=1 SV=2	O55222	Ilk	51 kDa	0	0	0	3.2666	3.8675	FALSE
Interferon gamma inducible protein 47 OS=Mus musculus molossinus GN=Irgd PE=4 SV=1	U5NG85	Irgd	47 kDa	0	0	0	3.2666	0	FALSE
Interferon regulatory factor 2-binding protein 2 OS=Mus musculus GN=Irf2bp2 PE=1 SV=1	E9Q1P8	Irf2bp2	59 kDa	0	0	0	2.0416	1.7189	FALSE
Interferon regulatory factor 9 OS=Mus musculus GN=Irf9 PE=1 SV=1	E9Q8M6 (+2)	Irf9	47 kDa	0	0	0	0.81665	0	FALSE
Interferon-gamma-inducible GTPase Ifgga1 protein OS=Mus musculus GN=Iigp1 PE=1 SV=1	J7NNX8 (+2)	Iigp1	48 kDa	0	0	0	2.0416	0	FALSE
Interferon-induced 35 kDa protein homolog OS=Mus musculus GN=Ifi35 PE=1 SV=3	Q9D8C4	Ifi35	32 kDa	0	0	0	0.81665	0	FALSE
Interferon-induced protein 44 OS=Mus musculus GN=Ifi44 PE=2 SV=1	Q8BV66	Ifi44	48 kDa	0	0	0	0.81665	0	FALSE
Interferon-induced protein with tetratricopeptide repeats 3 OS=Mus musculus GN=Ifit3 PE=1 SV	Q5FW82 (+1)	Ifit3	47 kDa	0	0	0	2.0416	0	FALSE
Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Mus muscul	Q9WTX2	Prkra	34 kDa	0	0	0	2.0416	1.7189	FALSE
Interleukin enhancer-binding factor 3 OS=Mus musculus GN=Ilf3 PE=1 SV=1	A0A1L1STE4 (+3)	Ilf3	97 kDa	0	0	0	0.81665	0.85944	FALSE
Intraflagellar transport protein 22 homolog OS=Mus musculus GN=Ift22 PE=1 SV=1	Q9DAI2	Ift22	21 kDa	0	0	0	0.81665	0	FALSE
Inverted formin-2 OS=Mus musculus GN=Inf2 PE=1 SV=1	Q0GNC1	Inf2	139 kDa	0	0	0	1.225	1.7189	FALSE
Iron-sulfur cluster assembly 2 homolog, mitochondrial OS=Mus musculus GN=Isca2 PE=1 SV=2	Q9DCB8	Isca2	17 kDa	0	0	0	0.81665	0	FALSE
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Mus musculus GN=Idh3a PE=1	Q9D6R2	Idh3a	40 kDa	0	3.1957	0	4.8999	4.2972	FALSE
Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial OS=Mus musculus GN=Idh3g PE	P70404 (+2)	Idh3g	43 kDa	0	0	0	3.6749	3.008	FALSE
Isocitrate dehydrogenase [NADP] cytoplasmic OS=Mus musculus GN=Idh1 PE=1 SV=2	O88844 (+2)	Idh1	47 kDa	0	0	0	4.8999	6.4458	FALSE
Isocitrate dehydrogenase [NADP], mitochondrial OS=Mus musculus GN=Idh2 PE=1 SV=3	P54071	Idh2	51 kDa	0	4.7936	10.737	11.025	14.181	FALSE
Isoleucine--tRNA ligase, mitochondrial OS=Mus musculus GN=Iars2 PE=1 SV=1	Q8BIJ6	Iars2	113 kDa	0	0	0	2.0416	2.1486	FALSE
Isopentenyl-diphosphate Delta-isomerase 1 OS=Mus musculus GN=Idi1 PE=1 SV=1	P58044	Idi1	26 kDa	0	0	0	0	1.2892	FALSE
Isovaleryl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Ivd PE=1 SV=1	Q9JHI5	Ivd	46 kDa	0	0	0	1.6333	1.7189	FALSE
IST1 homolog OS=Mus musculus GN=Ist1 PE=1 SV=1	Q9CX00	Ist1	39 kDa	0	0	0	0	0.85944	FALSE
JNK-interacting leucine zipper protein long form OS=Mus musculus GN=Spag9 PE=2 SV=1	B8X349 (+1)	Spag9	146 kDa	0	0	0	1.6333	0	FALSE
Junctional adhesion molecule A OS=Mus musculus GN=F11r PE=1 SV=2	O88792	F11r	32 kDa	0	0	0	0	0.85944	FALSE
Jupiter microtubule associated homolog 1 OS=Mus musculus GN=JPT1 PE=1 SV=3	P97825	JPT1	16 kDa	0	0	0	2.45	1.7189	FALSE
KDEL (Lys-Asp-Glu-Leu) containing 2, isoform CRA_b OS=Mus musculus GN=Kdelc2 PE=1 SV=1	G5E897 (+1)	Kdelc2	58 kDa	0	0	0	0.81665	0	FALSE
KDEL motif-containing protein 1 OS=Mus musculus GN=Kdelc1 PE=1 SV=1	Q9JHP7	Kdelc1	58 kDa	0	0	0	2.8583	2.5783	FALSE
Kelch domain containing 4, isoform CRA_a OS=Mus musculus GN=Klhdc4 PE=1 SV=1	G3X961	Klhdc4	65 kDa	0	0	0	2.8583	2.5783	FALSE
Kelch-like protein 22 OS=Mus musculus GN=Klhl22 PE=1 SV=1	H9KV05 (+1)	Klhl22	74 kDa	0	0	0	0.81665	0.85944	FALSE
Kinectin OS=Mus musculus GN=Ktn1 PE=1 SV=1	Q61595	Ktn1	153 kDa	0	0	0	3.2666	3.008	FALSE
Kinesin family member 13B OS=Mus musculus GN=Kif13b PE=1 SV=1	E9Q4K7	Kif13b	205 kDa	0	0	0	0.81665	1.2892	FALSE
Kinesin light chain 1 OS=Mus musculus GN=Klc1 PE=1 SV=1	Q8CD76	Klc1	69 kDa	0	0	0	2.0416	1.7189	FALSE
Kinesin-1 heavy chain OS=Mus musculus GN=Kif5b PE=1 SV=3	Q61768	Kif5b	110 kDa	3.6831	3.1957	0	6.5332	4.2972	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Kinesin-like protein KIF11 OS=Mus musculus GN=Kif11 PE=1 SV=1	Q6P9P6	Kif11	118 kDa	0	0	0	3.6749	3.4377	FALSE
Kinesin-like protein KIF15 OS=Mus musculus GN=Kif15 PE=1 SV=1	Q6P9L6	Kif15	160 kDa	0	0	0	0.81665	0.85944	FALSE
Kinesin-like protein KIF1B OS=Mus musculus GN=Kif1b PE=1 SV=2	Q60575	Kif1b	204 kDa	0	0	0	1.225	1.2892	FALSE
Kinesin-like protein KIF2A OS=Mus musculus GN=Kif2a PE=1 SV=2	P28740	Kif2a	80 kDa	0	0	0	4.0833	3.4377	FALSE
Kinesin-like protein OS=Mus musculus GN=Kif2c PE=2 SV=1	Q8BU22 (+1)	Kif2c	81 kDa	0	0	0	0	1.2892	FALSE
Kinesin-like protein OS=Mus musculus GN=Kifc1 PE=2 SV=1	A0A068BFR6 (+1)	Kifc1	74 kDa	0	0	0	0.81665	1.2892	FALSE
Kinetochore protein NDC80 homolog OS=Mus musculus GN=Ndc80 PE=1 SV=1	Q9D0F1	Ndc80	74 kDa	0	0	0	0	0.85944	FALSE
Kinetochore-associated protein 1 OS=Mus musculus GN=Kntc1 PE=1 SV=2	Q8C3Y4	Kntc1	250 kDa	0	0	0	1.225	0	FALSE
L-lactate dehydrogenase B chain OS=Mus musculus GN=Ldhb PE=1 SV=2	P16125	Ldhb	37 kDa	0	0	0	2.0416	0	FALSE
La-related protein 1 OS=Mus musculus GN=Larp1 PE=1 SV=3	Q6ZQ58 (+1)	Larp1	121 kDa	0	3.1957	3.5789	4.4916	4.7269	FALSE
La-related protein 7 OS=Mus musculus GN=Larp7 PE=1 SV=2	Q05CL8	Larp7	65 kDa	0	0	0	1.225	2.1486	FALSE
Lactadherin OS=Mus musculus GN=Mfge8 PE=1 SV=3	P21956	Mfge8	51 kDa	0	0	0	0.81665	0	FALSE
Lactoylglutathione lyase OS=Mus musculus GN=Glo1 PE=1 SV=1	A5GZX3 (+1)	Glo1	21 kDa	0	0	0	2.0416	1.7189	FALSE
Lamin-B receptor OS=Mus musculus GN=Lbr PE=1 SV=2	Q3U9G9	Lbr	71 kDa	0	0	0	1.225	1.2892	FALSE
Lamina-associated polypeptide 2, isoforms alpha/zeta OS=Mus musculus GN=Tmpo PE=1 SV=4	Q61033	Tmpo	75 kDa	0	0	0	0	2.1486	FALSE
Laminin subunit gamma-1 OS=Mus musculus GN=Lamc1 PE=1 SV=1	F8VQJ3	Lamc1	177 kDa	0	0	5.3684	7.7582	9.4538	FALSE
Lanosterol 14-alpha demethylase OS=Mus musculus GN=Cyp51a1 PE=1 SV=1	Q8K0C4	Cyp51a1	57 kDa	0	0	0	1.6333	0	FALSE
Lanosterol synthase OS=Mus musculus GN=Lss PE=1 SV=2	Q8BLN5	Lss	83 kDa	0	0	0	2.8583	2.1486	FALSE
Large subunit GTPase 1 homolog OS=Mus musculus GN=Lsg1 PE=1 SV=2	Q3UM18	Lsg1	73 kDa	0	0	0	0	1.2892	FALSE
Lariat debranching enzyme OS=Mus musculus GN=Dbr1 PE=1 SV=2	Q923B1	Dbr1	62 kDa	0	0	0	0.81665	0.85944	FALSE
Latexin OS=Mus musculus GN=Lxn PE=1 SV=2	P70202 (+1)	Lxn	25 kDa	0	0	0	2.8583	3.008	FALSE
Lclat1 protein OS=Mus musculus GN=Lclat1 PE=1 SV=1	B0V2Q7 (+1)	Lclat1	44 kDa	0	0	0	0	0.85944	FALSE
Leiomodin-1 OS=Mus musculus GN=Lmod1 PE=1 SV=1	F8VPR1 (+1)	Lmod1	66 kDa	0	0	0	1.6333	0	FALSE
Lethal(2) giant larvae protein homolog 1 OS=Mus musculus GN=Llgl1 PE=1 SV=1	A0A0R4J0S4 (+1)	Llgl1	116 kDa	0	0	0	1.6333	1.7189	FALSE
Leucine rich repeat containing 40, isoform CRA_a OS=Mus musculus GN=Lrrc40 PE=1 SV=1	A0A0R4J0W6 (+1)	Lrrc40	68 kDa	0	0	0	0.81665	0	FALSE
Leucine rich repeat containing 47 OS=Mus musculus GN=Lrrc47 PE=1 SV=1	B1AX98 (+2)	Lrrc47	64 kDa	0	0	0	1.6333	1.2892	FALSE
Leucine-rich PPR motif-containing protein, mitochondrial OS=Mus musculus GN=Lrpprc PE=1 SV=2	Q6PB66	Lrpprc	157 kDa	0	0	3.5789	6.9416	6.4458	FALSE
Leucine-rich repeat flightless-interacting protein 1 OS=Mus musculus GN=Lrrfip1 PE=1 SV=2	Q3UZ39	Lrrfip1	79 kDa	0	0	0	2.0416	2.5783	FALSE
Leucine-rich repeat-containing protein 58 OS=Mus musculus GN=Lrrc58 PE=2 SV=1	Q3UGP9	Lrrc58	40 kDa	0	0	0	0.81665	1.7189	FALSE
Leucine-rich repeat-containing protein 59 OS=Mus musculus GN=Lrrc59 PE=1 SV=1	Q922Q8	Lrrc59	35 kDa	3.6831	3.1957	3.5789	5.7166	6.0161	FALSE
Leucyl-tRNA synthetase OS=Mus musculus GN=Lars PE=2 SV=1	Q7TSZ3 (+1)	Lars	134 kDa	3.6831	6.3914	0	11.025	10.313	FALSE
Leukotriene A-4 hydrolase OS=Mus musculus GN=Lta4h PE=1 SV=4	P24527	Lta4h	69 kDa	0	0	0	6.1249	4.2972	FALSE
LIM and cysteine-rich domains 1 OS=Mus musculus GN=Lmcd1 PE=1 SV=1	Q3TVW6 (+1)	Lmcd1	41 kDa	0	0	0	1.6333	0	FALSE
LIM and senescent cell antigen-like-containing domain protein OS=Mus musculus GN=Lims1 PE=1	A0A0R4J005 (+3)	Lims1	38 kDa	0	0	0	4.4916	2.1486	FALSE
LIM and SH3 protein 1, isoform CRA_b OS=Mus musculus GN=Lasp1 PE=1 SV=1	Q543N3 (+1)	Lasp1	30 kDa	0	0	0	5.3082	5.1566	FALSE
LIM domain and actin-binding protein 1 OS=Mus musculus GN=Lima1 PE=1 SV=3	Q9ERG0	Lima1	84 kDa	0	0	0	2.0416	1.2892	FALSE
Lipase maturation factor 2 OS=Mus musculus GN=Lmf2 PE=1 SV=1	Q8C3X8	Lmf2	80 kDa	0	0	0	1.6333	2.1486	FALSE
Lipoma-preferred partner homolog OS=Mus musculus GN=Lpp PE=1 SV=1	Q8BFW7	Lpp	66 kDa	0	0	0	6.9416	5.1566	FALSE
Lipopolysaccharide-induced tumor necrosis factor-alpha factor homolog OS=Mus musculus GN=Lit	Q9JLJ0	Litaf	17 kDa	0	0	0	0	0.85944	FALSE
Lon protease homolog, mitochondrial OS=Mus musculus GN=Lonp1 PE=1 SV=2	Q8CGK3	Lonp1	106 kDa	0	0	0	4.4916	5.5863	FALSE
Long-chain acyl-CoA synthetase OS=Mus musculus GN=Acsl6 PE=2 SV=1	A8IP90 (+3)	Acsl6	78 kDa	0	0	0	0	0.85944	FALSE
Long-chain-fatty-acid--CoA ligase 1 OS=Mus musculus GN=Acsl1 PE=1 SV=1	D3Z041 (+1)	Acsl1	78 kDa	0	0	0	2.0416	2.1486	FALSE
Long-chain-fatty-acid--CoA ligase 3 OS=Mus musculus GN=Acsl3 PE=1 SV=2	Q9CZW4	Acsl3	80 kDa	0	0	0	0.81665	0.85944	FALSE
LRP chaperone MESD OS=Mus musculus GN=Mesd PE=1 SV=1	Q9ERE7	Mesd	25 kDa	0	0	0	0.81665	0.85944	FALSE
Luc7-like protein 3 OS=Mus musculus GN=Luc7l3 PE=1 SV=1	Q5SUF2	Luc7l3	51 kDa	0	0	0	1.6333	1.2892	FALSE
Lupus La protein homolog OS=Mus musculus GN=Ssb PE=1 SV=1	P32067 (+2)	Ssb	48 kDa	3.6831	3.1957	3.5789	5.7166	5.5863	FALSE
Lymphocyte antigen 6E (Fragment) OS=Mus musculus GN=Ly6e PE=1 SV=6	A0A087WNT2 (+6)	Ly6e	12 kDa	0	0	0	1.225	1.2892	FALSE
Lymphocyte-specific helicase OS=Mus musculus GN=Hells PE=1 SV=2	Q60848	Hells	95 kDa	0	0	0	0.81665	1.2892	FALSE
Lymphokine-activated killer T-cell-originated protein kinase OS=Mus musculus GN=Pbk PE=1 SV=	Q9JJ78	Pbk	37 kDa	0	0	0	2.45	1.7189	FALSE
Lysine-specific demethylase 3A OS=Mus musculus GN=Kdm3a PE=1 SV=1	Q6PCM1	Kdm3a	148 kDa	0	0	0	0	0.85944	FALSE
Lysophosphatidic acid phosphatase type 6 OS=Mus musculus GN=Acp6 PE=1 SV=1	Q8BP40	Acp6	48 kDa	0	0	0	1.225	1.2892	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Lysosomal alpha-glucosidase OS=Mus musculus GN=Gaa PE=1 SV=2	P70699	Gaa	106 kDa	0	0	0	2.0416	1.7189	FALSE
Lysosomal Pro-X carboxypeptidase OS=Mus musculus GN=Prcp PE=1 SV=2	Q7TMR0	Prcp	55 kDa	0	0	0	1.225	2.1486	FALSE
Lysosomal protective protein OS=Mus musculus GN=Ctsa PE=1 SV=1	P16675 (+2)	Ctsa	54 kDa	0	0	0	3.6749	2.1486	FALSE
Lysosome membrane protein 2 OS=Mus musculus GN=Scarb2 PE=1 SV=3	O35114	Scarb2	54 kDa	0	0	0	0.81665	0	FALSE
Lysosome-associated membrane glycoprotein 1 OS=Mus musculus GN=Lamp1 PE=1 SV=2	P11438 (+4)	Lamp1	44 kDa	0	0	0	2.8583	1.7189	FALSE
m7GpppX diphosphatase OS=Mus musculus GN=Dcps PE=1 SV=1	Q9DAR7	Dcps	39 kDa	0	0	0	3.6749	3.4377	FALSE
MAD2 mitotic arrest deficient-like 1 (Yeast) OS=Mus musculus GN=Mad2l1 PE=1 SV=1	Q5HZH8 (+1)	Mad2l1	24 kDa	0	0	0	0.81665	1.2892	FALSE
Maged2 protein OS=Mus musculus GN=Maged2 PE=1 SV=1	Q9ER67	Maged2	65 kDa	0	0	0	2.8583	2.1486	FALSE
Magnesium transporter protein 1 OS=Mus musculus GN=Magt1 PE=1 SV=1	A2ADH1 (+3)	Magt1	42 kDa	0	0	0	0.81665	1.7189	FALSE
Mago nashi protein OS=Mus musculus GN=Magohb PE=1 SV=1	A0A023T778 (+2)	Magohb	17 kDa	0	0	0	1.6333	1.2892	FALSE
Major facilitator superfamily domain-containing protein 10 OS=Mus musculus GN=Mfsd10 PE=1 S	Q9D2V8	Mfsd10	49 kDa	0	0	0	0.81665	0.85944	FALSE
Major vault protein OS=Mus musculus GN=Mvp PE=1 SV=1	E9Q3X0 (+2)	Mvp	97 kDa	0	0	0	4.4916	4.7269	FALSE
Malectin OS=Mus musculus GN=Mlec PE=1 SV=2	Q6ZQI3	Mlec	32 kDa	0	0	0	3.2666	3.008	FALSE
Malonyl-CoA-acyl carrier protein transacylase, mitochondrial OS=Mus musculus GN=Mcat PE=1 S	Q8R3F5	Mcat	42 kDa	0	0	0	0	0.85944	FALSE
Mammalian ependymin-related protein 1 OS=Mus musculus GN=Epdr1 PE=1 SV=1	Q99M71	Epdr1	25 kDa	0	0	0	2.0416	1.2892	FALSE
Mammalian sterile twenty 3 kinase OS=Mus musculus GN=Stk24 PE=1 SV=1	Q3U335 (+2)	Stk24	48 kDa	0	0	0	2.0416	3.4377	FALSE
Manganese-transporting ATPase 13A1 OS=Mus musculus GN=Atp13a1 PE=1 SV=2	Q9EPE9	Atp13a1	132 kDa	0	0	0	4.0833	4.7269	FALSE
Mannose-1-phosphate guanyltransferase beta OS=Mus musculus GN=Gmppb PE=1 SV=1	Q8BTZ7	Gmppb	40 kDa	0	0	0	2.0416	0.85944	FALSE
Mannose-6-phosphate isomerase OS=Mus musculus GN=Mpi PE=1 SV=1	Q3V100 (+1)	Mpi	47 kDa	0	0	0	2.0416	1.2892	FALSE
Mannosyltransferase IV(V) OS=Mus musculus GN=Alg11 PE=2 SV=1	A0A077K846 (+1)	Alg11	55 kDa	0	0	0	0.81665	0.85944	FALSE
MAP kinase-activated protein kinase 2 OS=Mus musculus GN=Mapkapk2 PE=1 SV=2	P49138 (+1)	Mapkapk2	44 kDa	0	0	0	1.6333	0	FALSE
MAP7 domain-containing protein 1 OS=Mus musculus GN=Map7d1 PE=1 SV=1	A2AJI0 (+1)	Map7d1	93 kDa	0	0	0	1.6333	1.2892	FALSE
MARCKS-related protein OS=Mus musculus GN=Marcksl1 PE=1 SV=2	P28667	Marcksl1	20 kDa	0	0	0	2.0416	3.4377	FALSE
Maspardin OS=Mus musculus GN=Spg21 PE=1 SV=1	A0A1L1SST5 (+2)	Spg21	35 kDa	0	0	0	1.225	0.85944	FALSE
MCG113697 OS=Mus musculus GN=1110005A23Rik PE=1 SV=1	B2RXM7 (+2)	1110005A23Rik	24 kDa	0	0	0	1.6333	1.2892	FALSE
MCG115964 OS=Mus musculus GN=Wdr70 PE=1 SV=1	G3X934 (+1)	Wdr70	73 kDa	0	0	0	1.225	1.7189	FALSE
MCG1196 OS=Mus musculus GN=Actr3 PE=1 SV=1	Q3ULF7 (+1)	Actr3	47 kDa	0	0	0	7.3499	4.7269	FALSE
MCG123182 OS=Mus musculus GN=Tsg101 PE=1 SV=1	Q3UCW0 (+1)	Tsg101	44 kDa	0	0	0	2.0416	1.2892	FALSE
MCG126220 OS=Mus musculus GN=Ywhaq PE=2 SV=1	A3KML3 (+3)	Ywhaq	28 kDa	0	0	0	4.0833	4.2972	FALSE
MCG127675 OS=Mus musculus GN=Ube2v2 PE=2 SV=1	Q4VBX4 (+1)	Ube2v2	16 kDa	0	0	0	2.0416	1.2892	FALSE
MCG127945, isoform CRA_a OS=Mus musculus GN=Tcerg1 PE=2 SV=1	Q3TH57 (+1)	Tcerg1	124 kDa	0	0	0	1.6333	1.7189	FALSE
MCG129075 OS=Mus musculus GN=Tmx4 PE=1 SV=1	Q0P5W2 (+1)	Tmx4	37 kDa	0	0	0	0.81665	0.85944	FALSE
MCG129810, isoform CRA_c OS=Mus musculus GN=Pdxdc1 PE=1 SV=1	A0A0R4J034	Pdxdc1	87 kDa	0	0	0	4.4916	4.7269	FALSE
MCG130899 OS=Mus musculus GN=Pcnp PE=1 SV=1	Q3UCC5 (+1)	Pcnp	19 kDa	0	0	0	1.6333	2.1486	FALSE
MCG142017, isoform CRA_a OS=Mus musculus GN=Tmtc3 PE=1 SV=1	G5E8C4 (+1)	Tmtc3	104 kDa	0	0	0	1.6333	2.1486	FALSE
MCG14259, isoform CRA_a OS=Mus musculus GN=U2af1 PE=1 SV=1	Q14C24 (+1)	U2af1	28 kDa	0	0	0	1.225	1.2892	FALSE
MCG16662 OS=Mus musculus GN=Srm PE=1 SV=1	Q543H0 (+1)	Srm	34 kDa	0	0	0	5.3082	7.7349	FALSE
MCG17262 OS=Mus musculus GN=Pdap1 PE=1 SV=1	B2RTB0 (+1)	Pdap1	21 kDa	0	0	0	2.8583	4.2972	FALSE
MCG19514, isoform CRA_a OS=Mus musculus GN=Wdr82 PE=1 SV=1	B2RXQ8 (+1)	Wdr82	35 kDa	0	0	0	1.225	2.5783	FALSE
MCG4297 OS=Mus musculus GN=Ube2n PE=1 SV=1	A2RTT4 (+1)	Ube2n	17 kDa	0	0	0	1.6333	2.1486	FALSE
MCG5603 OS=Mus musculus GN=Ndufa11 PE=1 SV=1	G5E814 (+1)	Ndufa11	15 kDa	0	0	0	0.81665	0.85944	FALSE
MCG6846, isoform CRA_c OS=Mus musculus GN=Prpsap1 PE=1 SV=1	B1AT82 (+2)	Prpsap1	42 kDa	0	0	0	2.45	3.008	FALSE
Melanoma differentiation-associated protein 5 OS=Mus musculus GN=Ifih1 PE=2 SV=1	D2CGM4 (+2)	Ifih1	116 kDa	0	0	0	2.8583	0	FALSE
Membrane magnesium transporter 1 OS=Mus musculus GN=Mmgt1 PE=1 SV=1	Q8K273	Mmgt1	15 kDa	0	0	0	0.81665	0	FALSE
Membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6), isoform CRA_b OS=Mus	Q3UN60 (+1)	Mpp6	63 kDa	0	0	0	1.225	0	FALSE
Membrane-associated phosphatidylinositol transfer protein 1 OS=Mus musculus GN=Pitpnm1 PE	O35954	Pitpnm1	135 kDa	0	0	0	0	0.85944	FALSE
Membrane-associated progesterone receptor component 2 OS=Mus musculus GN=Pgrmc2 PE=1 S	Q80UU9	Pgrmc2	23 kDa	0	0	0	1.225	2.5783	FALSE
Metalloproteinase inhibitor 3 OS=Mus musculus GN=Timp3 PE=1 SV=1	P39876 (+1)	Timp3	24 kDa	0	0	0	0.81665	0	FALSE
Metallothionein-1 OS=Mus musculus GN=Mt1 PE=1 SV=1	P02802	Mt1	6 kDa	0	0	0	0	0.85944	FALSE
Metallothionein-2 OS=Mus musculus GN=Mt2 PE=1 SV=2	P02798	Mt2	6 kDa	0	0	0	0	3.008	FALSE
Metastasis-associated protein MTA2 OS=Mus musculus GN=Mta2 PE=1 SV=1	Q9R190	Mta2	75 kDa	0	0	0	3.6749	3.008	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Metaxin OS=Mus musculus GN=Mtx1 PE=2 SV=1	Q8R5C0	Mtx1	36 kDa	0	0	0	0.81665	0	FALSE
Methionine adenosyltransferase 2 subunit beta OS=Mus musculus GN=Mat2b PE=1 SV=1	Q99LB6	Mat2b	37 kDa	0	0	0	2.0416	2.5783	FALSE
Methionine aminopeptidase 2 OS=Mus musculus GN=Metap2 PE=1 SV=1	O08663 (+1)	Metap2	53 kDa	0	0	0	1.225	0.85944	FALSE
Methionine aminopeptidase OS=Mus musculus GN=Metap1 PE=1 SV=1	Q4VAA9 (+1)	Metap1	43 kDa	0	0	0	1.225	1.7189	FALSE
Methionine sulfoxide reductase B3 OS=Mus musculus GN=Msrb3 PE=1 SV=1	A0A0R4J139 (+1)	Msrb3	20 kDa	0	0	0	1.6333	0	FALSE
Methionine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Mars PE=1 SV=1	Q68FL6	Mars	101 kDa	3.6831	4.7936	0	8.9832	7.7349	FALSE
Methylmalonyl-CoA mutase, mitochondrial OS=Mus musculus GN=Mut PE=1 SV=2	P16332 (+1)	Mut	83 kDa	0	0	0	1.225	0.85944	FALSE
Methylosome protein 50 OS=Mus musculus GN=Wdr77 PE=1 SV=1	Q99J09	Wdr77	37 kDa	0	0	0	1.225	2.1486	FALSE
Methylosome subunit pICln OS=Mus musculus GN=Clns1a PE=1 SV=1	Q61189 (+1)	Clns1a	26 kDa	0	0	0	0.81665	0.85944	FALSE
Methylthioribose-1-phosphate isomerase OS=Mus musculus GN=Mri1 PE=1 SV=1	Q9CQT1	Mri1	39 kDa	0	0	0	1.225	2.1486	FALSE
Methylthioribulose-1-phosphate dehydratase OS=Mus musculus GN=Apip PE=1 SV=1	Q9WVQ5	Apip	27 kDa	0	0	0	1.6333	0	FALSE
MFLJ00316 protein (Fragment) OS=Mus musculus GN=Gbp7 PE=2 SV=1	Q6KAN1 (+2)	Gbp7	73 kDa	0	0	0	2.0416	0	FALSE
MICAL-like protein 1 OS=Mus musculus GN=Micall1 PE=1 SV=3	Q8BGT6	Micall1	94 kDa	0	0	0	0	1.2892	FALSE
MICAL-like protein 2 OS=Mus musculus GN=Micall2 PE=1 SV=1	Q3TN34	Micall2	108 kDa	0	0	0	3.2666	5.5863	FALSE
MICOS complex subunit Mic19 OS=Mus musculus GN=Chchd3 PE=1 SV=1	Q9CRB9	Chchd3	26 kDa	0	0	0	0.81665	0	FALSE
MICOS complex subunit Mic26 OS=Mus musculus GN=Apoo PE=1 SV=2	Q9DCZ4 (+1)	Apoo	23 kDa	0	0	0	0	0.85944	FALSE
MICOS complex subunit Mic27 OS=Mus musculus GN=Apool PE=1 SV=1	Q78IK4 (+1)	Apool	29 kDa	0	0	0	1.225	1.7189	FALSE
MICOS complex subunit Mic60 OS=Mus musculus GN=Immt PE=1 SV=1	Q8CAQ8	Immt	84 kDa	3.6831	0	3.5789	6.1249	3.8675	FALSE
Microtubule-associated protein 1S OS=Mus musculus GN=Map1s PE=1 SV=2	Q8C052	Map1s	103 kDa	0	0	0	2.0416	1.2892	FALSE
Microtubule-associated protein 4 OS=Mus musculus GN=Map4 PE=1 SV=3	P27546	Map4	117 kDa	0	4.7936	3.5789	9.3915	6.8755	FALSE
Microtubule-associated protein 6 OS=Mus musculus GN=Map6 PE=1 SV=2	Q7TSJ2	Map6	96 kDa	0	0	0	0	0.85944	FALSE
Microtubule-associated protein, RP/EB family, member 1 OS=Mus musculus GN=Mapre1 PE=1 SV	Q3U4H0 (+1)	Mapre1	30 kDa	0	0	0	3.6749	3.008	FALSE
Microtubule-associated proteins 1A/1B light chain 3B OS=Mus musculus GN=Map1lc3b PE=1 SV=	Q9CQV6	Map1lc3b	15 kDa	0	0	0	0	0.85944	FALSE
Mini-chromosome maintenance complex-binding protein OS=Mus musculus GN=Mcmbp PE=1 SV=	Q8R3C0	Mcmbp	73 kDa	0	0	0	2.0416	1.7189	FALSE
Minor histocompatibility antigen H13 OS=Mus musculus GN=Hm13 PE=1 SV=1	Q9D8V0	Hm13	42 kDa	0	0	0	2.45	2.1486	FALSE
Mitochondrial 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh1l2 PE=1 SV	Q8K009	Aldh1l2	102 kDa	0	3.1957	0	10.616	6.4458	FALSE
Mitochondrial amidoxime reducing component 2 OS=Mus musculus GN=Marc2 PE=1 SV=1	Q922Q1	Marc2	38 kDa	0	0	0	1.225	1.2892	FALSE
Mitochondrial antiviral-signaling protein OS=Mus musculus GN=Mavs PE=1 SV=1	Q8VCF0	Mavs	53 kDa	0	0	0	1.225	1.2892	FALSE
Mitochondrial carnitine/acylcarnitine carrier protein OS=Mus musculus GN=Slc25a20 PE=1 SV=1	Q9Z2Z6	Slc25a20	33 kDa	0	0	0	0	0.85944	FALSE
Mitochondrial carrier homolog 1 OS=Mus musculus GN=Mtch1 PE=1 SV=1	Q791T5	Mtch1	42 kDa	0	0	0	1.225	0.85944	FALSE
Mitochondrial import inner membrane translocase subunit TIM44 OS=Mus musculus GN=Timm4	O35857 (+1)	Timm44	51 kDa	0	0	0	2.45	2.5783	FALSE
Mitochondrial import inner membrane translocase subunit TIM50 OS=Mus musculus GN=Timm5	Q9D880	Timm50	40 kDa	0	0	0	2.45	2.5783	FALSE
Mitochondrial import receptor subunit TOM34 OS=Mus musculus GN=Tomm34 PE=1 SV=1	Q9CYG7	Tomm34	34 kDa	0	0	0	3.2666	2.1486	FALSE
Mitochondrial import receptor subunit TOM40 homolog OS=Mus musculus GN=Tomm40 PE=1 SV	Q9QYA2	Tomm40	38 kDa	0	0	0	1.225	1.7189	FALSE
Mitochondrial pyruvate carrier 2 OS=Mus musculus GN=Mpc2 PE=1 SV=1	Q9D023	Mpc2	14 kDa	0	0	0	0	1.7189	FALSE
Mitochondrial Rho GTPase 1 OS=Mus musculus GN=Rhot1 PE=1 SV=1	Q8BG51	Rhot1	72 kDa	0	0	0	2.45	3.008	FALSE
Mitochondrial ribosomal protein L9 OS=Mus musculus GN=Mrpl9 PE=1 SV=1	Q14B21 (+1)	Mrpl9	30 kDa	0	0	0	0.81665	0	FALSE
Mitochondrial ribosomal protein S9, isoform CRA_b OS=Mus musculus GN=Mrps9 PE=2 SV=1	A0A1S6GWG5 (+1)	Mrps9	46 kDa	0	0	0	1.225	2.1486	FALSE
Mitogen-activated protein kinase 14 OS=Mus musculus GN=Mapk14 PE=1 SV=3	P47811	Mapk14	41 kDa	0	0	0	1.6333	0.85944	FALSE
Mitogen-activated protein kinase 3 OS=Mus musculus GN=Mapk3 PE=1 SV=5	Q63844	Mapk3	43 kDa	0	0	0	4.0833	3.4377	FALSE
Mitogen-activated protein kinase kinase kinase kinase 4 OS=Mus musculus GN=Map4k4 PE=1 S	A0A0A6YWM8	Map4k4	145 kDa	0	0	0	2.0416	0	FALSE
Mitogen-activated protein kinase kinase kinase kinase 5 OS=Mus musculus GN=Map4k5 PE=1 S	Q8BPM2	Map4k5	95 kDa	0	0	0	0.81665	0.85944	FALSE
Mitogen-activated protein kinase OS=Mus musculus GN=Mapk1 PE=2 SV=1	Q3UF82	Mapk1	41 kDa	0	0	0	4.0833	3.8675	FALSE
Mitogen-activated protein kinase OS=Mus musculus GN=Mapk9 PE=2 SV=1	Q5NCK8	Mapk9	48 kDa	0	0	0	1.6333	0	FALSE
Mitotic checkpoint protein BUB3 OS=Mus musculus GN=Bub3 PE=1 SV=1	A0A140LHA2 (+1)	Bub3	37 kDa	0	0	0	4.4916	2.5783	FALSE
Mitotic checkpoint serine/threonine-protein kinase BUB1 beta OS=Mus musculus GN=Bub1b PE=	Q9Z1S0	Bub1b	118 kDa	0	0	0	1.225	0	FALSE
Mixed lineage kinase domain-like protein OS=Mus musculus GN=Mlkl PE=1 SV=1	Q9D2Y4	Mlkl	54 kDa	0	0	0	4.8999	3.4377	FALSE
MKIAA0034 protein (Fragment) OS=Mus musculus GN=mKIAA0034 PE=4 SV=2	Q80U89	mKIAA0034	192 kDa	11.049	20.772	17.895	22.05	21.916	FALSE
MKIAA0103 protein (Fragment) OS=Mus musculus GN=Emc2 PE=1 SV=1	Q6A0D1 (+1)	Emc2	35 kDa	0	0	0	0.81665	1.2892	FALSE
MKIAA0617 protein (Fragment) OS=Mus musculus GN=mKIAA0617 PE=3 SV=1	Q6ZQ84 (+1)	mKIAA0617	91 kDa	0	0	0	5.3082	3.008	FALSE
MKIAA0790 protein (Fragment) OS=Mus musculus GN=Sash1 PE=2 SV=1	Q6ZQ46	Sash1	119 kDa	0	0	0	1.6333	2.1486	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
MKIAA1027 protein (Fragment) OS=Mus musculus GN=Tln1 PE=2 SV=4	Q80TM2	Tln1	272 kDa	7.3662	9.5872	8.9474	33.483	29.651	FALSE
MKIAA1423 protein (Fragment) OS=Mus musculus GN=mKIAA1423 PE=4 SV=3	Q80TD8	mKIAA1423	51 kDa	0	0	0	0	0.85944	FALSE
MKIAA1547 protein (Fragment) OS=Mus musculus GN=Tle3 PE=2 SV=1	Q80TC1	Tle3	96 kDa	0	0	0	0.81665	0.85944	FALSE
MKIAA1631 protein (Fragment) OS=Mus musculus GN=Mov10 PE=2 SV=1	Q69ZE2	Mov10	116 kDa	0	3.1957	3.5789	6.5332	5.1566	FALSE
MKIAA4025 protein (Fragment) OS=Mus musculus GN=Hspa4 PE=2 SV=1	Q571M2	Hspa4	103 kDa	0	4.7936	3.5789	18.783	15.04	FALSE
MKIAA4075 protein (Fragment) OS=Mus musculus GN=Chd4 PE=2 SV=1	Q5DTP7	Chd4	221 kDa	0	0	0	3.6749	2.5783	FALSE
MKIAA4106 protein (Fragment) OS=Mus musculus GN=Cul2 PE=2 SV=1	Q571A2 (+1)	Cul2	87 kDa	0	0	0	2.0416	1.2892	FALSE
MKIAA4114 protein (Fragment) OS=Mus musculus GN=Picalm PE=2 SV=1	Q570Z8	Picalm	73 kDa	0	0	0	3.2666	1.2892	FALSE
MKIAA4198 protein (Fragment) OS=Mus musculus GN=Stambp PE=2 SV=1	Q5DTH9 (+1)	Stambp	39 kDa	0	0	0	1.225	0.85944	FALSE
MKL/myocardin-like protein 1 OS=Mus musculus GN=Mkl1 PE=1 SV=1	D3YUI2 (+2)	Mkl1	93 kDa	0	0	0	0.81665	1.7189	FALSE
Mkl2 protein (Fragment) OS=Mus musculus GN=Mkl2 PE=2 SV=1	A3KMF2 (+3)	Mkl2	117 kDa	0	0	0	0.81665	0	FALSE
MOB kinase activator 1A OS=Mus musculus GN=Mob1a PE=2 SV=3	Q921Y0	Mob1a	25 kDa	0	0	0	1.225	1.2892	FALSE
Monoacylglycerol lipase ABHD12 OS=Mus musculus GN=Abhd12 PE=1 SV=2	Q99LR1	Abhd12	45 kDa	0	0	0	0.81665	0	FALSE
Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Mus musculus GN=Mthfd1l PE=	Q3V3R1	Mthfd1l	106 kDa	0	4.7936	3.5789	10.616	8.5944	FALSE
Mothers against decapentaplegic homolog (Fragment) OS=Mus musculus GN=Smad3 PE=2 SV=1	Q3V3E0 (+1)	Smad3	42 kDa	0	0	0	0	0.85944	FALSE
Mothers against decapentaplegic homolog OS=Mus musculus GN=Smad4 PE=3 SV=1	Q811W8	Smad4	60 kDa	0	0	0	1.225	0	FALSE
Motile sperm domain-containing protein 2 OS=Mus musculus GN=Mospd2 PE=1 SV=1	B1AU74 (+1)	Mospd2	60 kDa	0	0	0	1.225	0.85944	FALSE
Mpa2l protein (Fragment) OS=Mus musculus GN=Gbp6 PE=2 SV=1	Q7TMV8	Gbp6	44 kDa	0	0	0	1.225	0	FALSE
mRNA cap guanine-N7 methyltransferase OS=Mus musculus GN=Rnmt PE=1 SV=1	Q9D0L8	Rnmt	53 kDa	0	0	0	0.81665	1.7189	FALSE
Mrpl13 protein (Fragment) OS=Mus musculus GN=Mrpl13 PE=2 SV=1	Q7TMH5 (+1)	Mrpl13	20 kDa	0	0	0	0.81665	0	FALSE
Multifunctional protein ADE2 OS=Mus musculus GN=Paics PE=1 SV=4	Q9DCL9	Paics	47 kDa	0	0	0	6.5332	8.5944	FALSE
Muscleblind-like protein 2 OS=Mus musculus GN=Mbnl2 PE=2 SV=2	Q8C181	Mbnl2	40 kDa	0	0	0	1.225	0	FALSE
MYB binding protein (P160) 1a, isoform CRA_b OS=Mus musculus GN=Mybbp1a PE=1 SV=1	Q3U2W2 (+1)	Mybbp1a	152 kDa	0	0	0	4.8999	4.7269	FALSE
Myelin expression factor 2 OS=Mus musculus GN=Myef2 PE=1 SV=1	Q8C854	Myef2	63 kDa	0	0	0	1.225	1.2892	FALSE
Myeloid-derived growth factor OS=Mus musculus GN=Mydgf PE=1 SV=1	Q9CPT4	Mydgf	18 kDa	0	0	0	0.81665	0.85944	FALSE
Myosin phosphatase Rho-interacting protein OS=Mus musculus GN=Mprip PE=1 SV=1	Q5SWZ5	Mprip	257 kDa	0	0	0	2.45	1.7189	FALSE
Myosin regulatory light polypeptide 9 OS=Mus musculus GN=Myl9 PE=1 SV=3	Q9CQ19	Myl9	20 kDa	0	0	0	4.0833	0	FALSE
Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=1	Q3UH59 (+1)	Myh10	233 kDa	0	0	0	31.033	21.056	FALSE
Myotrophin OS=Mus musculus GN=Mtpn PE=1 SV=2	P62774	Mtpn	13 kDa	0	0	0	0.81665	0.85944	FALSE
Myotubularin-related protein 5 OS=Mus musculus GN=Sbf1 PE=1 SV=2	Q6ZPE2	Sbf1	209 kDa	0	0	0	0	0.85944	FALSE
Myotubularin-related protein 6 OS=Mus musculus GN=Mtmr6 PE=1 SV=1	Q8VE11	Mtmr6	71 kDa	0	0	0	0	0.85944	FALSE
Myristoylated alanine-rich C-kinase substrate OS=Mus musculus GN=Marcks PE=1 SV=2	P26645	Marcks	30 kDa	0	3.1957	0	4.0833	3.4377	FALSE
N-acetyl-D-glucosamine kinase OS=Mus musculus GN=Nagk PE=1 SV=1	Q9D997	Nagk	39 kDa	0	0	0	0.81665	0.85944	FALSE
N-acetylglucosamine-6-phosphate deacetylase OS=Mus musculus GN=Amdhd2 PE=1 SV=1	Q8JZV7	Amdhd2	44 kDa	0	0	0	0.81665	0	FALSE
N-acetylglucosamine-6-sulfatase OS=Mus musculus GN=Gns PE=1 SV=1	Q8BFR4	Gns	61 kDa	0	0	0	0.81665	2.1486	FALSE
N-alpha-acetyltransferase 10 OS=Mus musculus GN=Naa10 PE=1 SV=1	B1AUY7 (+3)	Naa10	26 kDa	0	0	0	0.81665	1.2892	FALSE
N-alpha-acetyltransferase 15, NatA auxiliary subunit OS=Mus musculus GN=Naa15 PE=1 SV=1	G3X8Y3	Naa15	101 kDa	0	0	0	4.8999	5.1566	FALSE
N-alpha-acetyltransferase 16, NatA auxiliary subunit OS=Mus musculus GN=Naa16 PE=2 SV=1	Q9DBB4	Naa16	101 kDa	0	0	0	1.6333	0	FALSE
N-alpha-acetyltransferase 35, NatC auxiliary subunit OS=Mus musculus GN=Naa35 PE=1 SV=1	Q6PHQ8	Naa35	83 kDa	0	0	0	1.225	0.85944	FALSE
N-alpha-acetyltransferase 50 OS=Mus musculus GN=Naa50 PE=1 SV=1	Q6PGB6	Naa50	19 kDa	0	0	0	1.6333	3.4377	FALSE
N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Mus musculus GN=Ntmt1 PE=1 SV=3	Q8R2U4	Ntmt1	25 kDa	0	0	0	1.225	0.85944	FALSE
N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Mus musculus GN=Ddah1 PE=1 SV=3	Q9CWS0	Ddah1	31 kDa	0	0	0	1.6333	2.1486	FALSE
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Mus musculus GN=Ddah2 PE=1 SV=1	Q99LD8	Ddah2	30 kDa	0	0	0	2.45	2.5783	FALSE
Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Mus musculus GN=Slc9a3r1 PE=1 SV=3	P70441 (+1)	Slc9a3r1	39 kDa	0	0	0	1.225	1.2892	FALSE
NACHT OS=Mus musculus GN=Nlrp2 PE=2 SV=1	Q4PLS0	Nlrp2	119 kDa	0	0	0	0	1.7189	FALSE
NAD kinase 2, mitochondrial OS=Mus musculus GN=Nadk2 PE=1 SV=1	Z4YK42	Nadk2	45 kDa	0	0	0	1.225	1.2892	FALSE
NAD-dependent malic enzyme, mitochondrial OS=Mus musculus GN=Me2 PE=1 SV=1	Q99KE1	Me2	66 kDa	0	0	0	2.0416	2.1486	FALSE
NAD(P)-dependent steroid dehydrogenase-like protein OS=Mus musculus GN=Nsdhl PE=2 SV=1	U3M993	Nsdhl	41 kDa	0	0	0	1.6333	1.2892	FALSE
NAD(P)H dehydrogenase, quinone 1 OS=Mus musculus GN=Nqo1 PE=1 SV=1	Q542Y0 (+1)	Nqo1	31 kDa	0	0	0	1.6333	5.5863	FALSE
NAD(P)H-hydrate epimerase OS=Mus musculus GN=Naxe PE=1 SV=1	Q8K4Z3	Naxe	31 kDa	0	0	0	2.0416	2.5783	FALSE
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Mus muscu	Q99LC3	Ndufa10	41 kDa	0	0	0	0.81665	0	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Mus musculus GN=Ndufa1	A0A0R4J275 (+3)	Ndufa12	18 kDa	0	0	0	0.81665	0.85944	FALSE
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial OS=Mus muscul	O09111 (+1)	Ndufb11	17 kDa	0	0	0	0.81665	0	FALSE
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Mus musculus GN=Ndufv1	D3YUM1	Ndufv1	50 kDa	0	0	0	2.45	1.2892	FALSE
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Mus musculus GN=Nd	Q91WD5	Ndufs2	53 kDa	0	0	0	1.225	0	FALSE
NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial OS=Mus musculus GN=Nd	P52503	Ndufs6	13 kDa	0	0	0	0.81665	0.85944	FALSE
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Mus musculus GN=Nd	Q9DC70	Ndufs7	25 kDa	0	0	0	0.81665	0	FALSE
NADH-cytochrome b5 reductase 1 OS=Mus musculus GN=Cyb5r1 PE=1 SV=1	Q9DB73	Cyb5r1	34 kDa	0	0	0	1.225	1.2892	FALSE
NADH-cytochrome b5 reductase 3 OS=Mus musculus GN=Cyb5r3 PE=1 SV=3	Q9DCN2	Cyb5r3	34 kDa	0	4.7936	5.3684	9.3915	12.032	FALSE
NADP-dependent malic enzyme OS=Mus musculus GN=Me1 PE=1 SV=2	P06801 (+2)	Me1	64 kDa	0	0	0	1.6333	1.7189	FALSE
NADPH--cytochrome P450 reductase OS=Mus musculus GN=Por PE=1 SV=2	P37040	Por	77 kDa	0	0	0	4.4916	7.7349	FALSE
Nardilysin, N-arginine dibasic convertase, NRD convertase 1 OS=Mus musculus GN=Nrd1 PE=1 SV	A2A9Q2 (+1)	Nrd1	141 kDa	0	0	0	6.5332	5.5863	FALSE
NECAP endocytosis associated 1 OS=Mus musculus GN=Necap1 PE=1 SV=1	Q0VB06 (+2)	Necap1	30 kDa	0	0	0	0.81665	0.85944	FALSE
NEDD8 ultimate buster 1 OS=Mus musculus GN=Nub1 PE=1 SV=1	A0A0G2JGQ4 (+2)	Nub1	73 kDa	0	0	0	1.225	0	FALSE
NEDD8-activating enzyme E1 catalytic subunit OS=Mus musculus GN=Uba3 PE=1 SV=1	Q3TL72 (+1)	Uba3	50 kDa	0	0	0	3.6749	2.5783	FALSE
NEDD8-activating enzyme E1 regulatory subunit OS=Mus musculus GN=Nae1 PE=1 SV=1	Q3UK27 (+1)	Nae1	60 kDa	0	0	0	3.6749	2.5783	FALSE
NEDD8-conjugating enzyme Ubc12 OS=Mus musculus GN=Ube2m PE=1 SV=1	P61082	Ube2m	21 kDa	0	0	0	2.0416	1.7189	FALSE
Negative elongation factor E OS=Mus musculus GN=Nelfe PE=1 SV=2	P19426 (+1)	Nelfe	43 kDa	0	0	0	1.225	0.85944	FALSE
Neurofibromin OS=Mus musculus GN=Nf1 PE=1 SV=1	Q04690	Nf1	320 kDa	0	0	0	0.81665	1.2892	FALSE
Neurolysin, mitochondrial OS=Mus musculus GN=Nln PE=1 SV=1	A0A286YD12 (+1)	Nln	78 kDa	0	0	0	2.8583	2.5783	FALSE
Neuroplastin OS=Mus musculus GN=Nptn PE=1 SV=3	P97300	Nptn	44 kDa	0	0	0	3.6749	3.4377	FALSE
Neutral amino acid transporter A OS=Mus musculus GN=Slc1a4 PE=1 SV=1	O35874 (+4)	Slc1a4	56 kDa	0	0	0	0.81665	0	FALSE
Neutrophil gelatinase-associated lipocalin OS=Mus musculus GN=Lcn2 PE=1 SV=1	P11672	Lcn2	23 kDa	0	0	0	0	1.7189	FALSE
NFU1 iron-sulfur cluster scaffold homolog, mitochondrial OS=Mus musculus GN=Nfu1 PE=1 SV=1	A0A0N4SUH8 (+1)	Nfu1	29 kDa	0	0	0	0.81665	0.85944	FALSE
NHL repeat containing 2 OS=Mus musculus GN=Nhlrc2 PE=1 SV=1	B2RR26 (+1)	Nhlrc2	78 kDa	0	0	0	1.225	1.2892	FALSE
Niban-like protein 1 OS=Mus musculus GN=Fam129b PE=1 SV=2	Q8R1F1	Fam129b	85 kDa	0	0	0	4.4916	4.2972	FALSE
Nicalin OS=Mus musculus GN=Ncln PE=1 SV=1	D3YU17 (+1)	Ncln	63 kDa	0	0	0	2.0416	2.5783	FALSE
Nicastrin OS=Mus musculus GN=Ncstn PE=1 SV=3	P57716 (+3)	Ncstn	78 kDa	0	0	0	1.225	0	FALSE
Nicotinamide phosphoribosyltransferase OS=Mus musculus GN=Nampt PE=1 SV=1	Q99KQ4	Nampt	55 kDa	0	0	0	4.0833	4.7269	FALSE
Nidogen-1 OS=Mus musculus GN=Nid1 PE=1 SV=2	P10493	Nid1	137 kDa	0	0	0	0	0.85944	FALSE
Nischarin OS=Mus musculus GN=Nisch PE=1 SV=2	Q80TM9	Nisch	175 kDa	0	0	0	3.2666	3.8675	FALSE
Nitric oxide synthase, inducible OS=Mus musculus GN=Nos2 PE=1 SV=1	P29477	Nos2	131 kDa	0	0	0	0	1.2892	FALSE
NmrA-like family domain-containing protein 1 OS=Mus musculus GN=Nmral1 PE=1 SV=1	D3YU12 (+1)	Nmral1	33 kDa	0	0	0	0.81665	0.85944	FALSE
Nodal modulator 1 OS=Mus musculus GN=Nomo1 PE=1 SV=1	Q6GQT9	Nomo1	133 kDa	0	0	0	4.8999	4.7269	FALSE
Non-SMC condensin I complex, subunit G OS=Mus musculus GN=Ncapg PE=1 SV=1	E9PWG6	Ncapg	113 kDa	0	0	0	1.6333	2.1486	FALSE
Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 PE=1 SV=3	P32020	Scp2	59 kDa	0	0	0	2.0416	0.85944	FALSE
Non-specific serine/threonine protein kinase (Fragment) OS=Mus musculus GN=Mark2 PE=2 SV=	Q571J8	Mark2	87 kDa	0	0	0	0	0.85944	FALSE
Non-specific serine/threonine protein kinase OS=Mus musculus GN=Prkaa1 PE=2 SV=1	Q3TUQ7 (+1)	Prkaa1	63 kDa	0	0	0	1.6333	2.5783	FALSE
Nsfl1c protein (Fragment) OS=Mus musculus GN=Nsfl1c PE=2 SV=1	Q3KQQ1 (+2)	Nsfl1c	41 kDa	0	0	0	5.7166	6.0161	FALSE
Nuclear autoantigenic sperm protein OS=Mus musculus GN=Nasp PE=1 SV=1	B1AU75 (+1)	Nasp	84 kDa	0	0	0	2.8583	1.7189	FALSE
Nuclear cap-binding protein subunit 1 OS=Mus musculus GN=Ncbp1 PE=1 SV=2	Q3UYV9	Ncbp1	92 kDa	0	0	0	2.45	2.5783	FALSE
Nuclear export mediator factor Nemf OS=Mus musculus GN=Nemf PE=1 SV=2	Q8CCP0	Nemf	121 kDa	0	0	0	0.81665	0	FALSE
Nuclear factor NF-kappa-B p105 subunit OS=Mus musculus GN=Nfkb1 PE=1 SV=2	P25799	Nfkb1	106 kDa	0	0	0	0	1.2892	FALSE
Nuclear fragile X mental retardation-interacting protein 2 OS=Mus musculus GN=Nufip2 PE=1 SV	Q5F2E7	Nufip2	76 kDa	0	0	0	2.0416	1.7189	FALSE
Nuclear inhibitor of protein phosphatase 1 OS=Mus musculus GN=Ppp1r8 PE=1 SV=1	A2ADR8 (+1)	Ppp1r8	38 kDa	0	0	0	0.81665	0	FALSE
Nuclear localized protein-1 isoform d (Fragment) OS=Mus musculus GN=Tcf25 PE=1 SV=1	B2ZAC8 (+1)	Tcf25	74 kDa	0	0	0	1.6333	1.7189	FALSE
Nuclear pore complex protein Nup50 OS=Mus musculus GN=Nup50 PE=1 SV=3	Q9JIH2	Nup50	49 kDa	0	0	0	0	1.2892	FALSE
Nuclear protein localization protein 4 homolog OS=Mus musculus GN=Nploc4 PE=1 SV=3	P60670 (+1)	Nploc4	68 kDa	0	0	0	3.2666	2.5783	FALSE
Nuclear transcription factor, X-box-binding-like 1 OS=Mus musculus GN=Nfxl1 PE=1 SV=1	E9Q8I7	Nfxl1	102 kDa	0	0	0	0	0.85944	FALSE
Nucleolar protein 58 OS=Mus musculus GN=Nop58 PE=1 SV=1	Q6DFW4	Nop58	60 kDa	0	0	0	1.225	0	FALSE
Nucleolysin TIAR OS=Mus musculus GN=Tial1 PE=1 SV=1	P70318 (+2)	Tial1	43 kDa	0	0	0	1.225	2.1486	FALSE
Nucleoporin NDC1 OS=Mus musculus GN=Ndc1 PE=1 SV=1	Q8VCB1	Ndc1	75 kDa	0	0	0	0.81665	0	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Nucleoporin NUP53 OS=Mus musculus GN=Nup35 PE=1 SV=2	Q8R4R6	Nup35	35 kDa	0	0	0	0.81665	0.85944	FALSE
Nucleoporin SEH1 OS=Mus musculus GN=Seh1l PE=2 SV=1	Q8R2U0	Seh1l	40 kDa	0	0	0	0	1.2892	FALSE
Nucleoredoxin OS=Mus musculus GN=Nxn PE=1 SV=1	P97346	Nxn	48 kDa	0	0	0	2.45	2.1486	FALSE
Nucleoside diphosphate kinase (Fragment) OS=Mus musculus GN=Nme4 PE=2 SV=1	Q9CS68 (+1)	Nme4	22 kDa	0	0	0	0.81665	0	FALSE
Nucleoside diphosphate kinase A OS=Mus musculus GN=Nme1 PE=1 SV=1	P15532 (+1)	Nme1	17 kDa	0	0	0	9.3915	0	FALSE
Nucleosome assembly protein 1-like 1 OS=Mus musculus GN=Nap1l1 PE=1 SV=2	P28656 (+2)	Nap1l1	45 kDa	0	0	3.5789	5.3082	6.4458	FALSE
Nucleosome assembly protein 1-like 4 OS=Mus musculus GN=Nap1l4 PE=1 SV=1	A2RSB1 (+3)	Nap1l4	43 kDa	0	0	0	3.2666	3.8675	FALSE
NudC domain containing 3, isoform CRA_a OS=Mus musculus GN=Nudcd3 PE=2 SV=1	B0FTY3 (+1)	Nudcd3	41 kDa	0	0	0	0	0.85944	FALSE
NudC domain-containing protein 1 OS=Mus musculus GN=Nudcd1 PE=1 SV=2	Q6PIP5	Nudcd1	67 kDa	0	0	0	2.8583	3.4377	FALSE
NudC domain-containing protein 2 OS=Mus musculus GN=Nudcd2 PE=1 SV=1	Q9CQ48	Nudcd2	18 kDa	0	0	0	1.225	1.2892	FALSE
O-acetyl-ADP-ribose deacetylase MACROD1 OS=Mus musculus GN=Macrod1 PE=1 SV=2	Q922B1	Macrod1	35 kDa	0	0	0	1.225	0	FALSE
Obg-like ATPase 1 OS=Mus musculus GN=Ola1 PE=1 SV=1	Q9CZ30	Ola1	45 kDa	0	0	0	4.0833	6.0161	FALSE
Obscurin-like protein 1 OS=Mus musculus GN=Obsl1 PE=1 SV=1	D3YYU8	Obsl1	198 kDa	0	0	0	2.8583	2.1486	FALSE
OCIA domain-containing protein 1 (Fragment) OS=Mus musculus GN=Ociad1 PE=1 SV=1	A0A0J9YUB6 (+1)	Ociad1	20 kDa	0	0	0	0	0.85944	FALSE
Omega-amidase NIT2 OS=Mus musculus GN=Nit2 PE=1 SV=1	Q9JHW2	Nit2	31 kDa	0	0	0	2.45	3.4377	FALSE
Osteoclast-stimulating factor 1 OS=Mus musculus GN=Ostf1 PE=1 SV=2	Q62422	Ostf1	24 kDa	0	0	0	1.6333	1.2892	FALSE
Osteopontin OS=Mus musculus GN=Spp1 PE=1 SV=1	F8WIP8 (+4)	Spp1	33 kDa	0	0	0	0.81665	0.85944	FALSE
OTTMUSWSBP00075795 OS=Mus musculus domesticus GN=OTTMUSWSBG00059279 PE=4 SV=1	A0A1G5SJA5 (+2)	OTTMUSWSBG	27 kDa	0	0	0	0.81665	0	FALSE
Oxidation resistance protein 1 OS=Mus musculus GN=Oxr1 PE=1 SV=3	Q4KMM3	Oxr1	96 kDa	0	4.7936	0	9.7998	7.3052	FALSE
Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial OS=Mus musculus GN=Cpox PE	P36552	Cpox	50 kDa	0	0	0	3.6749	3.4377	FALSE
Oxysterol-binding protein 1 OS=Mus musculus GN=Osbp PE=1 SV=3	Q3B7Z2	Osbp	89 kDa	0	0	0	0.81665	1.2892	FALSE
Oxysterol-binding protein OS=Mus musculus GN=Osbpl11 PE=1 SV=1	G5E8A0	Osbpl11	84 kDa	0	0	0	0.81665	0	FALSE
Oxysterol-binding protein-related protein 3 OS=Mus musculus GN=Osbpl3 PE=1 SV=2	Q9DBS9	Osbpl3	97 kDa	0	0	0	2.45	2.5783	FALSE
Pachytene checkpoint protein 2 homolog OS=Mus musculus GN=Trip13 PE=1 SV=1	Q3UA06	Trip13	48 kDa	0	0	0	3.2666	3.8675	FALSE
Paired mesoderm homeobox protein 1 OS=Mus musculus GN=Prrx1 PE=1 SV=1	G3UZ44 (+1)	Prrx1	23 kDa	0	0	0	0	0.85944	FALSE
Paraspeckle component 1 OS=Mus musculus GN=Pspc1 PE=1 SV=1	Q8R326	Pspc1	59 kDa	0	0	0	1.225	2.1486	FALSE
Parvin, beta OS=Mus musculus GN=Parvb PE=1 SV=1	Q3UGT9 (+1)	Parvb	42 kDa	0	0	0	0	1.7189	FALSE
Paxillin OS=Mus musculus GN=Pxn PE=1 SV=1	F8VQ28 (+1)	Pxn	65 kDa	0	0	0	1.6333	1.2892	FALSE
PC4 and SFRS1-interacting protein OS=Mus musculus GN=Psip1 PE=1 SV=1	Q99JF8	Psip1	60 kDa	0	0	0	2.0416	1.7189	FALSE
PDZ and LIM domain protein 2 OS=Mus musculus GN=Pdlim2 PE=1 SV=1	Q8R1G6	Pdlim2	38 kDa	0	0	0	0.81665	0.85944	FALSE
PDZ and LIM domain protein 4 OS=Mus musculus GN=Pdlim4 PE=1 SV=3	P70271	Pdlim4	36 kDa	0	0	0	0	0.85944	FALSE
PDZ and LIM domain protein 5 OS=Mus musculus GN=Pdlim5 PE=1 SV=4	Q8CI51	Pdlim5	63 kDa	0	4.7936	3.5789	11.433	9.8835	FALSE
PDZ and LIM domain protein 7 OS=Mus musculus GN=Pdlim7 PE=1 SV=1	Q3TJD7	Pdlim7	50 kDa	0	0	0	4.0833	3.008	FALSE
PDZ domain-containing protein GIPC1 OS=Mus musculus GN=Gipc1 PE=1 SV=1	Q9Z0G0	Gipc1	36 kDa	0	0	0	0.81665	0	FALSE
Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2	P17742 (+3)	Ppia	18 kDa	12.891	12.783	17.895	20.416	25.353	FALSE
Peptidyl-prolyl cis-trans isomerase D OS=Mus musculus GN=Ppid PE=1 SV=3	Q9CR16	Ppid	41 kDa	0	0	5.3684	6.9416	8.1647	FALSE
Peptidyl-prolyl cis-trans isomerase FKBP10 OS=Mus musculus GN=Fkbp10 PE=1 SV=2	Q61576	Fkbp10	65 kDa	0	4.7936	3.5789	8.9832	8.5944	FALSE
Peptidyl-prolyl cis-trans isomerase FKBP11 OS=Mus musculus GN=Fkbp11 PE=1 SV=1	Q9D1M7	Fkbp11	22 kDa	0	0	0	1.225	1.7189	FALSE
Peptidyl-prolyl cis-trans isomerase FKBP2 OS=Mus musculus GN=Fkbp2 PE=1 SV=1	P45878 (+1)	Fkbp2	15 kDa	0	0	0	1.225	1.2892	FALSE
Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Mus musculus GN=Fkbp4 PE=1 SV=5	P30416	Fkbp4	52 kDa	5.5246	3.1957	7.1579	13.475	15.04	FALSE
Peptidyl-prolyl cis-trans isomerase FKBP7 OS=Mus musculus GN=Fkbp7 PE=1 SV=1	O54998 (+1)	Fkbp7	25 kDa	0	0	0	0.81665	2.1486	FALSE
Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Mus musculus GN=Fkbp8 PE=1 SV=2	O35465	Fkbp8	44 kDa	0	0	0	1.225	1.2892	FALSE
Peptidyl-prolyl cis-trans isomerase FKBP9 OS=Mus musculus GN=Fkbp9 PE=1 SV=1	Q9Z247	Fkbp9	63 kDa	0	0	0	3.6749	1.7189	FALSE
Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 OS=Mus musculus GN=Pin4 PE=1 SV=1	Q9CWW6	Pin4	14 kDa	0	0	0	1.225	0.85944	FALSE
Peptidyl-prolyl cis-trans isomerase OS=Mus musculus GN=Pin1 PE=2 SV=1	Q3UTI7 (+1)	Pin1	18 kDa	0	0	0	2.0416	2.5783	FALSE
Peptidyl-prolyl cis-trans isomerase OS=Mus musculus GN=Ppih PE=1 SV=1	Q4G0C5	Ppih	19 kDa	0	0	0	0.81665	1.2892	FALSE
Peptidyl-prolyl cis-trans isomerase OS=Mus musculus GN=Ppil1 PE=1 SV=1	B9EJX8 (+2)	Ppil1	18 kDa	0	0	0	1.225	2.1486	FALSE
Peptidyl-tRNA hydrolase 2, mitochondrial OS=Mus musculus GN=Ptrh2 PE=1 SV=1	Q8R2Y8	Ptrh2	20 kDa	0	0	0	2.45	2.1486	FALSE
Peptidylprolyl isomerase OS=Mus musculus GN=Fkbp3 PE=1 SV=1	Q3UBU9 (+1)	Fkbp3	25 kDa	0	0	0	2.0416	2.5783	FALSE
Peptidylprolyl isomerase OS=Mus musculus GN=Fkbp5 PE=1 SV=1	Q4FJN2 (+1)	Fkbp5	51 kDa	0	0	0	1.6333	1.7189	FALSE
Perilipin-2 OS=Mus musculus GN=Plin2 PE=1 SV=2	P43883 (+2)	Plin2	47 kDa	0	0	0	0.81665	3.008	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Perilipin-3 OS=Mus musculus GN=Plin3 PE=1 SV=1	Q9DBG5	Plin3	47 kDa	3.6831	0	3.5789	4.8999	4.7269	FALSE
Peroxisomal acyl-coenzyme A oxidase 1 OS=Mus musculus GN=Acox1 PE=1 SV=5	Q9R0H0	Acox1	75 kDa	0	0	0	0	1.2892	FALSE
Peroxisomal carnitine O-octanoyltransferase OS=Mus musculus GN=Crot PE=1 SV=1	Q9DC50	Crot	70 kDa	0	0	0	2.0416	0.85944	FALSE
Peroxisomal multifunctional enzyme type 2 OS=Mus musculus GN=Hsd17b4 PE=1 SV=3	P51660 (+2)	Hsd17b4	79 kDa	0	3.1957	0	5.3082	5.1566	FALSE
Peroxisomal trans-2-enoyl-CoA reductase OS=Mus musculus GN=Pecr PE=1 SV=1	Q3UXD9 (+1)	Pecr	28 kDa	0	0	0	1.225	0.85944	FALSE
Pescadillo homolog OS=Mus musculus GN=Pes1 PE=1 SV=1	Q9EQ61	Pes1	68 kDa	0	0	0	0	0.85944	FALSE
Pgm2 protein (Fragment) OS=Mus musculus GN=Pgm2 PE=2 SV=1	Q66JR7 (+2)	Pgm2	64 kDa	0	0	0	8.1665	9.8835	FALSE
PHD finger protein 6 OS=Mus musculus GN=Phf6 PE=1 SV=1	E9QAG2 (+1)	Phf6	36 kDa	0	0	0	1.6333	1.7189	FALSE
PHD finger-like domain-containing protein 5A OS=Mus musculus GN=Phf5a PE=1 SV=1	P83870	Phf5a	12 kDa	0	0	0	0.81665	0.85944	FALSE
Phosducin-like protein 3 OS=Mus musculus GN=Pdcl3 PE=1 SV=1	Q8BVF2	Pdcl3	28 kDa	0	0	0	1.6333	0.85944	FALSE
Phosphatase and actin regulator 4 OS=Mus musculus GN=Phactr4 PE=1 SV=2	Q501J7	Phactr4	77 kDa	0	0	0	0.81665	0	FALSE
Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2 OS=Mus musculus GN=Inppl1 PE=1 SV=	Q6P549	Inppl1	139 kDa	0	0	0	0.81665	0	FALSE
Phosphatidylinositol 4-kinase beta OS=Mus musculus GN=Pi4kb PE=1 SV=2	Q8BKC8	Pi4kb	92 kDa	0	0	0	0	0.85944	FALSE
Phosphatidylinositol transfer protein alpha isoform OS=Mus musculus GN=Pitpna PE=1 SV=2	P53810 (+2)	Pitpna	32 kDa	0	0	0	3.2666	3.008	FALSE
Phosphatidylinositol transfer protein beta isoform OS=Mus musculus GN=Pitpnb PE=1 SV=2	P53811	Pitpnb	31 kDa	0	0	0	2.45	3.8675	FALSE
Phosphatidylserine receptor transcript variant 2 OS=Mus musculus GN=Jmjd6 PE=2 SV=1	B2WTI2 (+1)	Jmjd6	48 kDa	0	0	0	0.81665	1.2892	FALSE
Phosphoacetylglucosamine mutase OS=Mus musculus GN=Pgm3 PE=2 SV=1	Q3TFH8 (+3)	Pgm3	59 kDa	0	0	0	0.81665	1.2892	FALSE
Phosphofurin acidic cluster sorting protein 1 OS=Mus musculus GN=Pacs1 PE=1 SV=2	Q8K212	Pacs1	105 kDa	0	0	0	1.225	0.85944	FALSE
Phosphoglucomutase-2 OS=Mus musculus GN=Pgm2 PE=1 SV=1	Q7TSV4	Pgm2	69 kDa	0	0	0	2.45	2.5783	FALSE
Phosphoglycerate kinase 1 OS=Mus musculus GN=Pgk1 PE=1 SV=4	P09411	Pgk1	45 kDa	16.574	15.979	25.053	28.175	28.791	FALSE
Phosphoinositide phospholipase C (Fragment) OS=Mus musculus GN=Plcb3 PE=2 SV=1	Q571K9	Plcb3	117 kDa	0	0	0	2.0416	3.008	FALSE
Phosphoinositide phospholipase C OS=Mus musculus GN=Plcd1 PE=1 SV=1	G5DDB7 (+1)	Plcd1	89 kDa	0	0	0	1.6333	1.7189	FALSE
Phosphoinositide phospholipase C OS=Mus musculus GN=Plcg1 PE=1 SV=1	A2A4A6 (+1)	Plcg1	149 kDa	0	0	0	2.8583	1.7189	FALSE
Phospholipase A-2-activating protein OS=Mus musculus GN=Plaa PE=1 SV=4	P27612	Plaa	87 kDa	0	0	0	4.4916	6.4458	FALSE
Phospholipid scramblase OS=Mus musculus GN=Plscr3 PE=2 SV=1	Q3T9B7 (+2)	Plscr3	32 kDa	0	0	0	0	0.85944	FALSE
Phosphomannomutase OS=Mus musculus GN=Pmm2 PE=1 SV=1	Q545N8 (+1)	Pmm2	28 kDa	0	0	0	0.81665	0	FALSE
Phosphoribosylformylglycinamidine synthase OS=Mus musculus GN=Pfas PE=1 SV=1	Q5SUR0	Pfas	145 kDa	0	0	0	8.5749	9.0241	FALSE
Phosphorylated adapter RNA export protein OS=Mus musculus GN=Phax PE=1 SV=1	Q9JJT9	Phax	43 kDa	0	0	0	0	0.85944	FALSE
Phosphoserine aminotransferase OS=Mus musculus GN=Psat1 PE=2 SV=1	Q3ULZ3 (+2)	Psat1	40 kDa	0	0	3.5789	8.9832	7.7349	FALSE
Phosphoserine phosphatase OS=Mus musculus GN=Psph PE=1 SV=1	Q99LS3	Psph	25 kDa	0	0	0	1.225	0	FALSE
Pigment epithelium-derived factor OS=Mus musculus GN=Serpinf1 PE=1 SV=2	P97298	Serpinf1	46 kDa	0	0	0	1.225	0	FALSE
Pituitary tumor-transforming gene 1 protein-interacting protein OS=Mus musculus GN=Pttg1ip P	Q8R143	Pttg1ip	20 kDa	0	0	0	0.81665	0	FALSE
Plasma membrane calcium-transporting ATPase 1 OS=Mus musculus GN=Atp2b1 PE=1 SV=1	G5E829	Atp2b1	135 kDa	0	0	0	5.3082	5.1566	FALSE
Platelet-activating factor acetylhydrolase IB subunit alpha OS=Mus musculus GN=Pafah1b1 PE=1	P63005 (+3)	Pafah1b1	47 kDa	0	0	0	5.3082	4.7269	FALSE
Platelet-activating factor acetylhydrolase IB subunit beta OS=Mus musculus GN=Pafah1b2 PE=1	Q61206	Pafah1b2	26 kDa	0	0	0	1.6333	1.7189	FALSE
Platelet-activating factor acetylhydrolase, isoform 1b, alpha1 subunit, isoform CRA_a OS=Mus m	Q3TJC2 (+1)	Pafah1b3	26 kDa	0	0	0	1.225	1.2892	FALSE
Pleckstrin homology domain containing, family C (With FERM domain) member 1 OS=Mus muscu	Q3TLE2 (+1)	Fermt2	78 kDa	0	0	0	6.5332	4.7269	FALSE
Pleckstrin homology domain-containing family F member 1 OS=Mus musculus GN=Plekhf1 PE=2 S	Q3TB82	Plekhf1	31 kDa	0	0	0	0	1.2892	FALSE
Pleckstrin homology domain-containing family O member 2 OS=Mus musculus GN=Plekho2 PE=1	Q8K124	Plekho2	54 kDa	0	0	0	1.225	1.2892	FALSE
Polr1c protein OS=Mus musculus GN=Polr1c PE=2 SV=1	A1L3C2 (+1)	Polr1c	39 kDa	0	0	0	2.0416	1.7189	FALSE
Poly (ADP-ribose) glycohydrolase, isoform CRA_c OS=Mus musculus GN=Parg PE=1 SV=1	G3X8U8 (+1)	Parg	109 kDa	0	0	0	0	0.85944	FALSE
Poly [ADP-ribose] polymerase (Fragment) OS=Mus musculus GN=Parp10 PE=2 SV=1	Q3U6C0 (+2)	Parp10	102 kDa	0	0	0	0.81665	0	FALSE
Poly [ADP-ribose] polymerase 14 OS=Mus musculus GN=Parp14 PE=1 SV=3	Q2EMV9	Parp14	204 kDa	0	0	0	3.2666	0	FALSE
Poly [ADP-ribose] polymerase 9 OS=Mus musculus GN=Parp9 PE=1 SV=2	Q8CAS9	Parp9	97 kDa	0	0	0	4.0833	0	FALSE
Poly [ADP-ribose] polymerase OS=Mus musculus GN=Parp3 PE=2 SV=1	Q8BXU2 (+1)	Parp3	60 kDa	0	0	0	2.0416	1.2892	FALSE
Poly(U)-binding-splicing factor PUF60 OS=Mus musculus GN=Puf60 PE=1 SV=2	Q3UEB3	Puf60	60 kDa	0	0	0	2.0416	2.5783	FALSE
Polyadenylate-binding protein OS=Mus musculus GN=Pabpc4 PE=1 SV=1	A3KFU8 (+1)	Pabpc4	71 kDa	0	0	0	4.8999	6.0161	FALSE
Polyadenylate-binding protein-interacting protein 1 OS=Mus musculus GN=Paip1 PE=1 SV=1	Q8VE62	Paip1	46 kDa	0	0	0	0.81665	0.85944	FALSE
Polymerase delta-interacting protein 2 OS=Mus musculus GN=Poldip2 PE=1 SV=1	Q91VA6	Poldip2	42 kDa	0	0	0	1.225	0.85944	FALSE
Polypeptide N-acetylgalactosaminyltransferase (Fragment) OS=Mus musculus GN=Galnt2 PE=2 S	Q3UA32 (+2)	Galnt2	61 kDa	0	0	0	0	0.85944	FALSE
Polypyrimidine tract binding protein 1 OS=Mus musculus GN=Ptbp1 PE=2 SV=1	Q5RJV5 (+3)	Ptbp1	59 kDa	3.6831	4.7936	7.1579	7.7582	8.1647	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Polypyrimidine tract-binding protein 2 OS=Mus musculus GN=Ptbp2 PE=1 SV=2	Q91Z31	Ptbp2	57 kDa	0	0	0	1.225	1.2892	FALSE
Polypyrimidine tract-binding protein 3 OS=Mus musculus GN=Ptbp3 PE=1 SV=1	G3UXA6 (+2)	Ptbp3	60 kDa	0	0	0	2.8583	0	FALSE
Polyribonucleotide nucleotidyltransferase 1, mitochondrial OS=Mus musculus GN=Pnpt1 PE=1 SV	Q8K1R3	Pnpt1	86 kDa	0	0	0	2.45	0.85944	FALSE
Ppfia1 protein OS=Mus musculus GN=Ppfia1 PE=1 SV=1	B2RXQ2 (+2)	Ppfia1	143 kDa	0	0	0	0.81665	0	FALSE
Pqbp1 protein OS=Mus musculus GN=Pqbp1 PE=1 SV=1	A2AER7 (+1)	Pqbp1	31 kDa	0	0	0	0	0.85944	FALSE
PRA1 family protein 2 OS=Mus musculus GN=Praf2 PE=1 SV=1	Q9JIG8	Praf2	19 kDa	0	0	0	0	0.85944	FALSE
Pre-mRNA-processing factor 19 OS=Mus musculus GN=Prpf19 PE=1 SV=1	Q99KP6	Prpf19	55 kDa	0	0	0	1.225	1.7189	FALSE
Pre-mRNA-processing-splicing factor 8 OS=Mus musculus GN=Prpf8 PE=1 SV=2	Q99PV0	Prpf8	274 kDa	0	0	0	1.6333	1.2892	FALSE
Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Mus musculus GN=Dhx15 PE=1	O35286 (+2)	Dhx15	91 kDa	0	0	0	5.7166	5.5863	FALSE
Pre-rRNA-processing protein TSR1 homolog OS=Mus musculus GN=Tsr1 PE=1 SV=1	Q5SWD9	Tsr1	92 kDa	0	0	0	4.0833	4.7269	FALSE
Predicted gene 20425 OS=Mus musculus GN=Gm20425 PE=4 SV=1	E9Q035	Gm20425	108 kDa	0	0	0	3.6749	3.008	FALSE
Prefoldin subunit 2 OS=Mus musculus GN=Pfdn2 PE=1 SV=2	O70591	Pfdn2	17 kDa	0	0	0	0.81665	0.85944	FALSE
Prenylcysteine oxidase-like OS=Mus musculus GN=Pcyox1l PE=1 SV=1	Q8C7K6	Pcyox1l	55 kDa	0	0	0	0.81665	0	FALSE
Probable ATP-dependent RNA helicase DDX20 OS=Mus musculus GN=Ddx20 PE=1 SV=2	Q9JJY4	Ddx20	92 kDa	0	0	0	0	1.7189	FALSE
Probable ATP-dependent RNA helicase DDX46 OS=Mus musculus GN=Ddx46 PE=1 SV=2	Q569Z5	Ddx46	117 kDa	0	0	0	1.6333	3.8675	FALSE
Probable ATP-dependent RNA helicase DDX6 OS=Mus musculus GN=Ddx6 PE=1 SV=1	P54823	Ddx6	54 kDa	0	0	0	5.3082	4.2972	FALSE
Probable ATP-dependent RNA helicase DHX58 OS=Mus musculus GN=Dhx58 PE=1 SV=2	Q99J87	Dhx58	77 kDa	0	0	0	2.0416	0	FALSE
Probable C-mannosyltransferase DPY19L1 OS=Mus musculus GN=Dpy19l1 PE=1 SV=1	A6X919	Dpy19l1	84 kDa	0	0	0	1.225	1.2892	FALSE
Probable cytosolic iron-sulfur protein assembly protein CIAO1 OS=Mus musculus GN=Ciao1 PE=1	Q99KN2	Ciao1	38 kDa	0	0	0	1.6333	2.1486	FALSE
Probable E3 ubiquitin-protein ligase HERC4 OS=Mus musculus GN=Herc4 PE=1 SV=2	Q6PAV2	Herc4	118 kDa	0	0	0	1.225	0	FALSE
Probable RNA polymerase II nuclear localization protein SLC7A6OS OS=Mus musculus GN=Slc7a6	Q7TPE5	Slc7a6os	35 kDa	0	0	0	0.81665	1.7189	FALSE
Probable tRNA N6-adenosine threonylcarbamoyltransferase OS=Mus musculus GN=Osgep PE=2 S	Q58EU1 (+1)	Osgep	36 kDa	0	0	0	1.225	2.5783	FALSE
Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Mus musculus GN=Usp9x PE=1 SV=2	P70398 (+1)	Usp9x	291 kDa	5.5246	3.1957	8.9474	8.9832	11.173	FALSE
Probable Xaa-Pro aminopeptidase 3 OS=Mus musculus GN=Xpnpep3 PE=1 SV=1	B7ZMP1	Xpnpep3	57 kDa	0	0	0	0.81665	0.85944	FALSE
Processing of 1, ribonuclease P/MRP family, (S. cerevisiae) OS=Mus musculus GN=Pop1 PE=1 SV=	Q8K205 (+1)	Pop1	117 kDa	0	0	0	0	0.85944	FALSE
Procollagen galactosyltransferase 1 OS=Mus musculus GN=Colgalt1 PE=1 SV=2	Q8K297	Colgalt1	71 kDa	0	0	3.5789	4.0833	4.2972	FALSE
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Mus musculus GN=Plod1 PE=1 SV=1	Q9R0E2	Plod1	84 kDa	0	0	0	4.0833	2.5783	FALSE
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 OS=Mus musculus GN=Plod2 PE=1 SV=1	E9Q718 (+2)	Plod2	87 kDa	0	0	0	2.0416	3.8675	FALSE
Profilin-1 OS=Mus musculus GN=Pfn1 PE=1 SV=2	P62962 (+1)	Pfn1	15 kDa	7.3662	7.9893	8.9474	12.658	11.602	FALSE
Programmed cell death 2, isoform CRA_b OS=Mus musculus GN=Pdcd2 PE=1 SV=1	A0A0R4J0N5 (+1)	Pdcd2	38 kDa	0	0	0	0	0.85944	FALSE
Programmed cell death 6-interacting protein OS=Mus musculus GN=Pdcd6ip PE=1 SV=3	Q9WU78	Pdcd6ip	96 kDa	3.6831	0	3.5789	6.1249	5.5863	FALSE
Programmed cell death protein 10 OS=Mus musculus GN=Pdcd10 PE=1 SV=1	Q8VE70	Pdcd10	25 kDa	0	0	0	0.81665	0.85944	FALSE
Programmed cell death protein 4 OS=Mus musculus GN=Pdcd4 PE=1 SV=1	Q61823	Pdcd4	52 kDa	0	0	0	0.81665	0.85944	FALSE
Prolactin regulatory element binding, isoform CRA_b OS=Mus musculus GN=Preb PE=1 SV=1	D3Z3S1 (+2)	Preb	38 kDa	0	0	0	1.225	1.2892	FALSE
Proliferating cell nuclear antigen OS=Mus musculus GN=Pcna PE=1 SV=2	P17918 (+2)	Pcna	29 kDa	0	0	0	4.8999	7.3052	FALSE
Proliferation-associated protein 2G4 OS=Mus musculus GN=Pa2g4 PE=1 SV=3	P50580 (+1)	Pa2g4	44 kDa	0	0	3.5789	8.9832	10.743	FALSE
Prolyl 3-hydroxylase 1 OS=Mus musculus GN=P3h1 PE=1 SV=1	A6PW84 (+1)	P3h1	84 kDa	0	0	0	3.2666	1.2892	FALSE
Prostaglandin G/H synthase 1 OS=Mus musculus GN=Ptgs1 PE=1 SV=1	P22437 (+1)	Ptgs1	69 kDa	0	0	0	1.6333	1.7189	FALSE
Prostaglandin G/H synthase 2 OS=Mus musculus GN=Ptgs2 PE=1 SV=1	Q05769 (+1)	Ptgs2	69 kDa	0	0	0	4.0833	2.5783	FALSE
Prostaglandin reductase 1 OS=Mus musculus GN=Ptgr1 PE=1 SV=2	Q91YR9	Ptgr1	36 kDa	0	0	0	4.0833	3.008	FALSE
Proteasomal ubiquitin receptor ADRM1 OS=Mus musculus GN=Adrm1 PE=1 SV=2	Q9JKV1	Adrm1	42 kDa	0	0	0	1.225	1.2892	FALSE
Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 7 OS=Mus musculus GN=Psmd7 PE=	A1L3B8 (+1)	Psmd7	37 kDa	0	0	0	3.2666	3.008	FALSE
Proteasome activator complex subunit 3 OS=Mus musculus GN=Psme3 PE=1 SV=1	P61290 (+1)	Psme3	30 kDa	0	0	0	2.0416	1.7189	FALSE
Proteasome activator complex subunit 4 OS=Mus musculus GN=Psme4 PE=1 SV=1	Q5SSW2	Psme4	211 kDa	0	0	0	2.0416	1.2892	FALSE
Proteasome assembly chaperone 1 OS=Mus musculus GN=Psmg1 PE=1 SV=1	D3Z795 (+1)	Psmg1	31 kDa	0	0	0	2.0416	3.4377	FALSE
Proteasome assembly chaperone 3 OS=Mus musculus GN=Psmg3 PE=1 SV=1	Q9CZH3	Psmg3	13 kDa	0	0	0	0.81665	0.85944	FALSE
Proteasome subunit alpha type OS=Mus musculus GN=Psma5 PE=2 SV=1	Q3TUI9 (+3)	Psma5	26 kDa	0	0	3.5789	3.6749	4.2972	FALSE
Proteasome subunit alpha type-2 OS=Mus musculus GN=Psma2 PE=1 SV=3	P49722 (+2)	Psma2	26 kDa	0	0	0	2.0416	3.008	FALSE
Proteasome subunit beta type OS=Mus musculus GN=Psmb3 PE=1 SV=1	Q545G0 (+1)	Psmb3	23 kDa	0	0	0	2.45	2.5783	FALSE
Proteasome subunit beta type OS=Mus musculus GN=Psmb8 PE=2 SV=1	A0A068BIT8 (+1)	Psmb8	30 kDa	0	0	0	3.2666	0	FALSE
Proteasome subunit beta type-1 OS=Mus musculus GN=Psmb1 PE=1 SV=1	O09061 (+1)	Psmb1	26 kDa	0	0	0	3.6749	4.2972	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Proteasome subunit beta type-10 OS=Mus musculus GN=Psmb10 PE=1 SV=1	O35955 (+1)	Psmb10	29 kDa	0	0	0	1.225	0	FALSE
Proteasome-associated protein ECM29 homolog OS=Mus musculus GN=Ecm29 PE=1 SV=3	Q6PDI5	Ecm29	204 kDa	0	0	0	3.2666	2.1486	FALSE
Protein 4.1G OS=Mus musculus GN=Epb41l2 PE=2 SV=1	Q80UE3	Epb41l2	110 kDa	0	0	0	7.7582	8.1647	FALSE
Protein ABHD16A OS=Mus musculus GN=Abhd16a PE=1 SV=3	Q9Z1Q2	Abhd16a	63 kDa	0	0	0	1.6333	1.2892	FALSE
Protein arginine methyltransferase NDUFAF7, mitochondrial OS=Mus musculus GN=Ndufaf7 PE=	Q9CWG8	Ndufaf7	48 kDa	0	0	0	0	0.85944	FALSE
Protein arginine N-methyltransferase 5 OS=Mus musculus GN=Prmt5 PE=1 SV=1	A0A0R4J049	Prmt5	73 kDa	0	0	0	4.0833	4.2972	FALSE
Protein arginine N-methyltransferase 7 OS=Mus musculus GN=Prmt7 PE=1 SV=1	Q922X9	Prmt7	78 kDa	0	0	0	0	0.85944	FALSE
Protein BUD31 homolog OS=Mus musculus GN=Bud31 PE=1 SV=1	E0CX20	Bud31	17 kDa	0	0	0	0.81665	1.2892	FALSE
Protein canopy homolog 2 OS=Mus musculus GN=Cnpy2 PE=1 SV=1	Q9QXT0	Cnpy2	21 kDa	0	0	0	1.6333	2.5783	FALSE
Protein canopy homolog 3 OS=Mus musculus GN=Cnpy3 PE=1 SV=1	Q9DAU1	Cnpy3	31 kDa	0	0	0	0	0.85944	FALSE
Protein canopy homolog 4 OS=Mus musculus GN=Cnpy4 PE=1 SV=1	Q8BQ47	Cnpy4	28 kDa	0	0	0	0.81665	0	FALSE
Protein CDV3 OS=Mus musculus GN=Cdv3 PE=1 SV=2	Q4VAA2	Cdv3	30 kDa	0	0	0	2.0416	1.7189	FALSE
Protein DDI1 homolog 2 OS=Mus musculus GN=Ddi2 PE=1 SV=1	A2ADY9	Ddi2	45 kDa	0	0	0	1.225	0	FALSE
Protein DEK OS=Mus musculus GN=Dek PE=1 SV=1	Q7TNV0	Dek	43 kDa	0	0	0	3.2666	2.5783	FALSE
Protein diaphanous homolog 3 OS=Mus musculus GN=Diaph3 PE=1 SV=2	F8WIG5	Diaph3	134 kDa	0	0	0	1.225	0.85944	FALSE
Protein disulfide-isomerase A4 OS=Mus musculus GN=Pdia4 PE=1 SV=1	A0A0R4J0Z1 (+1)	Pdia4	72 kDa	7.3662	6.3914	5.3684	12.25	12.892	FALSE
Protein disulfide-isomerase A5 OS=Mus musculus GN=Pdia5 PE=1 SV=1	Q921X9	Pdia5	59 kDa	0	0	0	1.6333	0	FALSE
Protein disulfide-isomerase TMX3 OS=Mus musculus GN=Tmx3 PE=1 SV=2	Q8BXZ1	Tmx3	52 kDa	0	0	0	1.225	0.85944	FALSE
Protein enabled homolog OS=Mus musculus GN=Enah PE=1 SV=2	Q03173	Enah	86 kDa	0	0	0	2.8583	2.1486	FALSE
Protein FAM114A2 OS=Mus musculus GN=Fam114a2 PE=1 SV=2	Q8VE88	Fam114a2	54 kDa	0	0	0	0.81665	0	FALSE
Protein FAM45A OS=Mus musculus GN=Fam45a PE=1 SV=2	Q9D8N2	Fam45a	40 kDa	0	0	0	0.81665	0	FALSE
Protein FAM49B OS=Mus musculus GN=Fam49b PE=1 SV=1	Q921M7	Fam49b	37 kDa	0	0	0	2.0416	4.2972	FALSE
Protein flightless-1 homolog OS=Mus musculus GN=Flii PE=1 SV=1	Q9JJ28	Flii	145 kDa	0	0	0	3.2666	2.5783	FALSE
Protein FRG1 OS=Mus musculus GN=Frg1 PE=1 SV=2	P97376 (+2)	Frg1	29 kDa	0	0	0	0	2.5783	FALSE
Protein IMPACT OS=Mus musculus GN=Impact PE=1 SV=2	O55091	Impact	36 kDa	0	0	0	1.6333	0.85944	FALSE
Protein incorporated later into tight junctions OS=Mus musculus GN=Tjap1 PE=1 SV=1	I7H459 (+1)	Tjap1	61 kDa	0	0	0	1.225	0	FALSE
Protein kinase C and casein kinase substrate in neurons 2, isoform CRA_a OS=Mus musculus GN=	Q3TDA7 (+1)	Pacsin2	56 kDa	0	0	0	2.45	3.8675	FALSE
Protein kinase C delta type OS=Mus musculus GN=Prkcd PE=1 SV=3	P28867 (+1)	Prkcd	78 kDa	0	0	0	2.45	3.4377	FALSE
Protein kinase C OS=Mus musculus GN=Prkca PE=1 SV=1	Q4VA93	Prkca	77 kDa	0	0	0	2.45	1.7189	FALSE
Protein kinase C OS=Mus musculus GN=Prkci PE=2 SV=1	Q3TJJ5 (+2)	Prkci	67 kDa	0	0	0	0	0.85944	FALSE
Protein kinase, cAMP dependent regulatory, type II alpha OS=Mus musculus GN=Prkar2a PE=1 S	Q8K1M3	Prkar2a	46 kDa	0	0	0	0	2.5783	FALSE
Protein LYRIC OS=Mus musculus GN=Mtdh PE=1 SV=1	Q80WJ7	Mtdh	64 kDa	0	0	0	1.6333	4.7269	FALSE
Protein MEMO1 OS=Mus musculus GN=Memo1 PE=1 SV=1	Q91VH6	Memo1	34 kDa	0	0	0	2.45	3.4377	FALSE
Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1	Q9QYG0	Ndrg2	41 kDa	0	0	0	0.81665	1.2892	FALSE
Protein NEDD1 OS=Mus musculus GN=Nedd1 PE=1 SV=2	P33215	Nedd1	71 kDa	0	0	0	0.81665	1.2892	FALSE
Protein Niban OS=Mus musculus GN=Fam129a PE=1 SV=2	Q3UW53	Fam129a	103 kDa	0	0	0	4.0833	3.008	FALSE
Protein NipSnap homolog 2 OS=Mus musculus GN=Nipsnap2 PE=1 SV=1	O55126 (+2)	Nipsnap2	33 kDa	0	0	0	0	0.85944	FALSE
Protein NipSnap homolog 3B OS=Mus musculus GN=Nipsnap3b PE=1 SV=1	Q9CQE1	Nipsnap3b	28 kDa	0	0	0	0.81665	1.7189	FALSE
Protein Noxp20 OS=Mus musculus GN=Fam114a1 PE=1 SV=1	Q9D281	Fam114a1	61 kDa	0	0	0	4.4916	2.1486	FALSE
Protein O-fucosyltransferase 2 OS=Mus musculus GN=Pofut2 PE=1 SV=1	B2RV73 (+2)	Pofut2	49 kDa	0	0	0	0.81665	0.85944	FALSE
Protein O-GlcNAcase OS=Mus musculus GN=Mgea5 PE=1 SV=2	Q9EQQ9	Mgea5	103 kDa	0	0	0	1.6333	1.2892	FALSE
Protein PBDC1 OS=Mus musculus GN=Pbdc1 PE=1 SV=1	Q9D0B6	Pbdc1	22 kDa	0	0	0	0.81665	0	FALSE
Protein pelota homolog OS=Mus musculus GN=Pelo PE=2 SV=1	Q3THL5 (+1)	Pelo	43 kDa	0	0	0	0.81665	0.85944	FALSE
Protein phosphatase 1 regulatory subunit 12A OS=Mus musculus GN=Ppp1r12a PE=1 SV=2	Q9DBR7	Ppp1r12a	115 kDa	0	0	0	4.4916	4.7269	FALSE
Protein phosphatase 1 regulatory subunit 7 OS=Mus musculus GN=Ppp1r7 PE=1 SV=2	Q3UM45	Ppp1r7	41 kDa	0	0	0	2.0416	0.85944	FALSE
Protein phosphatase 1A OS=Mus musculus GN=Ppm1a PE=1 SV=1	Q9EQE2 (+1)	Ppm1a	36 kDa	0	0	0	2.0416	0	FALSE
Protein phosphatase 1B, magnesium dependent, beta isoform OS=Mus musculus GN=Ppm1b PE=	Q5BKS2 (+1)	Ppm1b	52 kDa	0	0	0	1.6333	2.5783	FALSE
Protein phosphatase 1F OS=Mus musculus GN=Ppm1f PE=1 SV=1	Q8CGA0	Ppm1f	50 kDa	0	0	0	1.225	2.1486	FALSE
Protein phosphatase 1G OS=Mus musculus GN=Ppm1g PE=1 SV=3	Q61074	Ppm1g	59 kDa	0	0	0	2.8583	2.5783	FALSE
Protein phosphatase methylesterase 1 OS=Mus musculus GN=Ppme1 PE=1 SV=5	Q8BVQ5	Ppme1	42 kDa	0	0	0	1.6333	2.1486	FALSE
Protein PRRC1 OS=Mus musculus GN=Prrc1 PE=1 SV=1	Q3UPH1	Prrc1	46 kDa	0	0	0	2.45	0	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Protein PRRC2A OS=Mus musculus GN=Prrc2a PE=1 SV=1	G3UX48 (+1)	Prrc2a	219 kDa	0	0	0	2.0416	2.5783	FALSE
Protein RER1 OS=Mus musculus GN=Rer1 PE=1 SV=1	Q9CQU3	Rer1	23 kDa	0	0	0	0.81665	0.85944	FALSE
Protein S100-A10 OS=Mus musculus GN=S100a10 PE=1 SV=2	P08207 (+2)	S100a10	11 kDa	0	0	0	0	0.85944	FALSE
Protein S100-A4 OS=Mus musculus GN=S100a4 PE=1 SV=1	P07091 (+1)	S100a4	12 kDa	0	0	0	0.81665	0.85944	FALSE
Protein SCAF8 OS=Mus musculus GN=Scaf8 PE=1 SV=1	Q6DID3	Scaf8	140 kDa	0	0	0	1.225	0	FALSE
Protein scribble homolog OS=Mus musculus GN=Scrib PE=1 SV=2	Q80U72	Scrib	174 kDa	0	0	0	0	1.2892	FALSE
Protein SEC13 homolog OS=Mus musculus GN=Sec13 PE=1 SV=3	Q9D1M0	Sec13	36 kDa	0	0	0	2.8583	3.4377	FALSE
Protein sel-1 homolog 1 OS=Mus musculus GN=Sel1l PE=1 SV=1	J3QJX3	Sel1l	82 kDa	0	0	0	0.81665	0	FALSE
Protein SET (Fragment) OS=Mus musculus GN=Set PE=1 SV=1	A2BE93 (+3)	Set	25 kDa	0	0	0	2.8583	2.5783	FALSE
Protein SGT1 homolog OS=Mus musculus GN=Sugt1 PE=1 SV=3	Q9CX34	Sugt1	38 kDa	0	0	0	4.8999	5.1566	FALSE
Protein Simiate OS=Mus musculus GN=Fam206a PE=1 SV=2	Q80ZQ9	Fam206a	22 kDa	0	0	0	0	0.85944	FALSE
Protein Smaug homolog 1 OS=Mus musculus GN=Samd4a PE=1 SV=2	Q8CBY1	Samd4a	78 kDa	0	0	0	1.225	0.85944	FALSE
Protein strawberry notch homolog 1 OS=Mus musculus GN=Sbno1 PE=1 SV=1	B2RRI2 (+2)	Sbno1	154 kDa	0	0	0	0	1.2892	FALSE
Protein transport protein Sec23A OS=Mus musculus GN=Sec23a PE=1 SV=1	E9Q1S3 (+1)	Sec23a	83 kDa	0	0	0	5.7166	4.7269	FALSE
Protein transport protein Sec24A OS=Mus musculus GN=Sec24a PE=1 SV=1	A2AA71 (+1)	Sec24a	119 kDa	0	0	0	1.225	0.85944	FALSE
Protein transport protein Sec31A OS=Mus musculus GN=Sec31a PE=1 SV=2	Q3UPL0	Sec31a	134 kDa	0	0	0	12.25	9.4538	FALSE
Protein tweety homolog 3 OS=Mus musculus GN=Ttyh3 PE=1 SV=1	Q6P5F7	Ttyh3	58 kDa	0	0	0	0	0.85944	FALSE
Protein unc-119 homolog A OS=Mus musculus GN=Unc119 PE=1 SV=1	B1AQD9 (+2)	Unc119	29 kDa	0	0	0	0	0.85944	FALSE
Protein WWC2 OS=Mus musculus GN=Wwc2 PE=1 SV=1	Q6NXJ0	Wwc2	133 kDa	0	0	0	0.81665	0	FALSE
Protein YIPF3 OS=Mus musculus GN=Yipf3 PE=1 SV=1	Q3UDR8	Yipf3	38 kDa	0	0	0	0	0.85944	FALSE
Protein YIPF5 OS=Mus musculus GN=Yipf5 PE=1 SV=1	Q9EQQ2	Yipf5	28 kDa	0	0	0	0.81665	0.85944	FALSE
Protein-glutamine gamma-glutamyltransferase 2 OS=Mus musculus GN=Tgm2 PE=1 SV=4	P21981	Tgm2	77 kDa	0	0	0	1.225	0	FALSE
Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Mus musculus GN=Pcmt1 PE=1 SV=	P23506 (+1)	Pcmt1	25 kDa	0	0	0	1.6333	2.5783	FALSE
Prpsap2 protein OS=Mus musculus GN=Prpsap2 PE=1 SV=1	Q5SWZ0 (+2)	Prpsap2	41 kDa	0	0	0	2.45	2.1486	FALSE
Psap protein OS=Mus musculus GN=Psap PE=2 SV=1	B2RUD7 (+14)	Psap	61 kDa	0	0	0	2.45	3.008	FALSE
Pseudouridylate synthase 7 OS=Mus musculus GN=Pus7 PE=1 SV=1	B7ZNL8 (+1)	Pus7	75 kDa	0	0	0	2.45	3.4377	FALSE
Purine nucleoside phosphorylase OS=Mus musculus GN=Pnp PE=1 SV=2	P23492 (+1)	Pnp	32 kDa	0	3.1957	0	4.8999	5.1566	FALSE
Putative RNA-binding protein Luc7-like 1 OS=Mus musculus GN=Luc7l PE=1 SV=2	Q9CYI4	Luc7l	44 kDa	0	0	0	2.45	2.5783	FALSE
PX domain-containing protein kinase-like protein OS=Mus musculus GN=Pxk PE=1 SV=1	A0A2C9F2B5 (+1)	Pxk	65 kDa	0	0	0	0.81665	0.85944	FALSE
Pyp protein OS=Mus musculus GN=Ppa1 PE=1 SV=1	Q4FK49 (+1)	Ppa1	33 kDa	0	0	0	7.7582	7.7349	FALSE
Pyridoxal kinase OS=Mus musculus GN=Pdxk PE=1 SV=1	Q8K183	Pdxk	35 kDa	0	0	0	0	1.7189	FALSE
Pyridoxal phosphate homeostasis protein OS=Mus musculus GN=Plpbp PE=1 SV=1	Q544R1 (+1)	Plpbp	30 kDa	0	0	0	1.225	1.2892	FALSE
Pyrroline-5-carboxylate reductase 3 OS=Mus musculus GN=Pycr3 PE=1 SV=2	Q9DCC4	Pycr3	29 kDa	0	0	0	0	1.7189	FALSE
Pyrroline-5-carboxylate reductase OS=Mus musculus GN=Pycr1 PE=1 SV=1	Q3UTR5 (+1)	Pycr1	32 kDa	0	0	0	2.0416	0	FALSE
Pyrroline-5-carboxylate reductase OS=Mus musculus GN=Pycr2 PE=2 SV=1	Q3TJ21 (+2)	Pycr2	34 kDa	0	0	0	2.45	2.1486	FALSE
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus mus	P35486 (+1)	Pdha1	43 kDa	0	3.1957	0	3.2666	3.4377	FALSE
Pyruvate kinase PKM OS=Mus musculus GN=Pkm PE=1 SV=4	P52480	Pkm	58 kDa	31.306	23.968	28.632	42.874	48.128	FALSE
Quinone oxidoreductase OS=Mus musculus GN=Cryz PE=1 SV=1	P47199 (+1)	Cryz	35 kDa	0	0	0	1.225	1.2892	FALSE
Rab GDP dissociation inhibitor alpha OS=Mus musculus GN=Gdi1 PE=1 SV=3	P50396	Gdi1	51 kDa	0	0	0	8.5749	8.1647	FALSE
Rab GDP dissociation inhibitor beta OS=Mus musculus GN=Gdi2 PE=1 SV=1	Q61598	Gdi2	51 kDa	5.5246	3.1957	8.9474	11.433	16.329	FALSE
Rab GTPase-activating protein 1 OS=Mus musculus GN=Rabgap1 PE=1 SV=1	A2AWA9 (+1)	Rabgap1	121 kDa	0	0	0	2.0416	0	FALSE
Rab proteins geranylgeranyltransferase component A 1 OS=Mus musculus GN=Chm PE=1 SV=1	Q9QXG2	Chm	74 kDa	0	0	0	0.81665	0	FALSE
Rab-like protein 6 OS=Mus musculus GN=Rabl6 PE=1 SV=2	Q5U3K5	Rabl6	80 kDa	0	0	0	0.81665	0	FALSE
Rab11 family-interacting protein 5 OS=Mus musculus GN=Rab11fip5 PE=1 SV=2	Q8R361	Rab11fip5	70 kDa	0	0	0	1.6333	0.85944	FALSE
RAB14 protein OS=Mus musculus GN=Rab14 PE=1 SV=1	Q50HX4 (+1)	Rab14	24 kDa	3.6831	3.1957	3.5789	4.0833	6.0161	FALSE
RAB1B, member RAS oncogene family, isoform CRA_c OS=Mus musculus GN=Rab1b PE=1 SV=1	Q0PD66 (+1)	Rab1b	22 kDa	0	0	0	2.45	4.2972	FALSE
Rab22B OS=Mus musculus GN=Rab31 PE=1 SV=1	Q3TXV4 (+1)	Rab31	21 kDa	0	0	0	1.6333	0.85944	FALSE
RAB23, member RAS oncogene family, isoform CRA_a OS=Mus musculus GN=Rab23 PE=1 SV=1	Q9D4I9	Rab23	27 kDa	0	0	0	1.225	0	FALSE
Rab3 GTPase-activating protein catalytic subunit OS=Mus musculus GN=Rab3gap1 PE=1 SV=1	A0A1D5RLG3 (+2)	Rab3gap1	111 kDa	0	0	0	0.81665	0.85944	FALSE
Rab3 GTPase-activating protein non-catalytic subunit OS=Mus musculus GN=Rab3gap2 PE=1 SV=	E9QKE4	Rab3gap2	155 kDa	0	0	0	1.6333	0.85944	FALSE
RAB9, member RAS oncogene family (Fragment) OS=Mus musculus GN=Rab9 PE=1 SV=1	A2AFP5 (+2)	Rab9	23 kDa	0	0	0	0.81665	0	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Rac GTPase-activating protein 1 OS=Mus musculus GN=Racgap1 PE=1 SV=1	Q9WVM1	Racgap1	70 kDa	0	0	0	0	1.2892	FALSE
RAC-alpha serine/threonine-protein kinase OS=Mus musculus GN=Akt1 PE=1 SV=2	P31750	Akt1	56 kDa	0	0	0	2.0416	2.5783	FALSE
RAF proto-oncogene serine/threonine-protein kinase OS=Mus musculus GN=Raf1 PE=1 SV=2	Q99N57	Raf1	73 kDa	0	0	0	1.6333	0	FALSE
Ran-binding protein 3 OS=Mus musculus GN=Ranbp3 PE=1 SV=2	Q9CT10	Ranbp3	53 kDa	0	0	0	4.8999	3.4377	FALSE
Ran-binding protein 9 OS=Mus musculus GN=Ranbp9 PE=1 SV=1	E9Q5D6	Ranbp9	76 kDa	0	0	0	0	0.85944	FALSE
RAP1, GTP-GDP dissociation stimulator 1 OS=Mus musculus GN=Rap1gds1 PE=1 SV=1	E9Q912 (+2)	Rap1gds1	66 kDa	0	0	0	2.8583	3.4377	FALSE
Ras and Rab interactor 1 OS=Mus musculus GN=Rin1 PE=1 SV=1	A0A2C9F2A2 (+1)	Rin1	84 kDa	0	0	0	1.225	0.85944	FALSE
Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 OS=Mus musculus GN=Raph1	F2Z4B7 (+1)	Raph1	73 kDa	0	0	0	1.225	0	FALSE
Ras GTPase-activating protein 4 OS=Mus musculus GN=Rasa4 PE=1 SV=1	Q6PFQ7	Rasa4	90 kDa	0	0	0	0.81665	1.7189	FALSE
Ras homolog OS=Mus musculus GN=Rheb PE=2 SV=1	Q9ESR1	Rheb	20 kDa	0	0	0	2.0416	2.1486	FALSE
RAS p21 protein activator 1 OS=Mus musculus GN=Rasa1 PE=2 SV=1	Q91YX7	Rasa1	94 kDa	0	0	0	1.6333	0.85944	FALSE
RAS related protein 1b OS=Mus musculus GN=Rap1b PE=1 SV=1	Q52L50 (+1)	Rap1b	21 kDa	0	0	0	2.45	3.4377	FALSE
Ras suppressor protein 1 OS=Mus musculus GN=Rsu1 PE=1 SV=3	Q01730 (+1)	Rsu1	32 kDa	0	0	0	1.225	0	FALSE
RAS-related C3 botulinum substrate 1 OS=Mus musculus GN=Rac1 PE=1 SV=1	K7Q7T7 (+2)	Rac1	21 kDa	0	3.1957	3.5789	5.3082	5.1566	FALSE
Ras-related GTP-binding protein A OS=Mus musculus GN=Rraga PE=1 SV=1	Q80X95	Rraga	37 kDa	0	0	0	0	0.85944	FALSE
Ras-related GTP-binding protein C OS=Mus musculus GN=Rragc PE=1 SV=1	Q99K70	Rragc	44 kDa	0	0	0	1.6333	1.7189	FALSE
Ras-related protein R-Ras OS=Mus musculus GN=Rras PE=1 SV=1	P10833 (+1)	Rras	24 kDa	0	0	0	1.6333	1.7189	FALSE
Ras-related protein R-Ras2 OS=Mus musculus GN=Rras2 PE=1 SV=1	P62071	Rras2	23 kDa	0	0	0	1.225	1.2892	FALSE
Ras-related protein Rab-10 OS=Mus musculus GN=Rab10 PE=1 SV=1	P61027 (+1)	Rab10	23 kDa	0	0	0	4.8999	4.7269	FALSE
Ras-related protein Rab-12 OS=Mus musculus GN=Rab12 PE=1 SV=1	A2CG35 (+1)	Rab12	32 kDa	0	0	0	1.225	2.1486	FALSE
Ras-related protein Rab-18 OS=Mus musculus GN=Rab18 PE=1 SV=2	P35293 (+1)	Rab18	23 kDa	0	0	0	2.45	2.1486	FALSE
Ras-related protein Rab-1A OS=Mus musculus GN=Rab1A PE=1 SV=3	P62821 (+2)	Rab1A	23 kDa	0	3.1957	3.5789	4.0833	5.5863	FALSE
Ras-related protein Rab-21 OS=Mus musculus GN=Rab21 PE=1 SV=4	P35282 (+2)	Rab21	24 kDa	0	0	0	1.6333	2.5783	FALSE
Ras-related protein Rab-3B OS=Mus musculus GN=Rab3b PE=1 SV=1	A2A7Z6 (+2)	Rab3b	26 kDa	0	0	0	2.0416	2.5783	FALSE
Ras-related protein Rab-6A OS=Mus musculus GN=Rab6a PE=1 SV=4	P35279 (+2)	Rab6a	24 kDa	0	0	0	1.6333	3.008	FALSE
Ras-related protein Rab-7a OS=Mus musculus GN=Rab7a PE=1 SV=2	P51150 (+1)	Rab7a	23 kDa	3.6831	3.1957	0	6.5332	6.8755	FALSE
Ras-related protein Ral-A OS=Mus musculus GN=Rala PE=1 SV=1	P63321 (+1)	Rala	24 kDa	0	0	0	1.6333	0	FALSE
Ras-related protein Rap-2c OS=Mus musculus GN=Rap2c PE=1 SV=1	Q8BU31	Rap2c	21 kDa	0	0	0	2.0416	2.1486	FALSE
RCC1 and BTB domain-containing protein 2 OS=Mus musculus GN=Rcbtb2 PE=1 SV=1	E9Q3B1 (+2)	Rcbtb2	56 kDa	0	0	0	0.81665	0	FALSE
Receptor expression-enhancing protein OS=Mus musculus GN=Reep5 PE=1 SV=1	G3X8R0 (+3)	Reep5	21 kDa	0	0	0	0.81665	0	FALSE
Regulator of nonsense transcripts 1 OS=Mus musculus GN=Upf1 PE=1 SV=2	Q9EPU0	Upf1	124 kDa	7.3662	0	7.1579	11.433	9.4538	FALSE
Renin/prorenin receptor OS=Mus musculus GN=Atp6ap2 PE=1 SV=2	Q1XID4 (+1)	Atp6ap2	39 kDa	0	0	0	0	0.85944	FALSE
Replication factor C (Activator 1) 2 OS=Mus musculus GN=Rfc2 PE=1 SV=1	Q4KL82 (+2)	Rfc2	39 kDa	0	0	0	1.6333	1.2892	FALSE
Replication factor C subunit 1 OS=Mus musculus GN=Rfc1 PE=1 SV=1	A0A0N5E9G7 (+3)	Rfc1	126 kDa	0	0	0	2.8583	2.1486	FALSE
Replication factor C subunit 4 OS=Mus musculus GN=Rfc4 PE=1 SV=1	Q3UI84 (+1)	Rfc4	41 kDa	0	0	0	0.81665	0.85944	FALSE
Reticulon-4 OS=Mus musculus GN=Rtn4 PE=1 SV=2	Q99P72	Rtn4	127 kDa	0	3.1957	7.1579	8.5749	9.8835	FALSE
Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit delta OS=Mus musc	O55057 (+2)	Pde6d	17 kDa	0	0	0	0	0.85944	FALSE
Retinoid-inducible serine carboxypeptidase OS=Mus musculus GN=Scpep1 PE=1 SV=2	Q920A5 (+1)	Scpep1	51 kDa	0	0	0	1.225	0	FALSE
Rho GDP-dissociation inhibitor 1 OS=Mus musculus GN=Arhgdia PE=1 SV=3	Q99PT1	Arhgdia	23 kDa	0	3.1957	3.5789	5.7166	6.4458	FALSE
Rho GDP-dissociation inhibitor 2 OS=Mus musculus GN=Arhgdib PE=1 SV=3	Q61599	Arhgdib	23 kDa	0	0	0	4.4916	3.4377	FALSE
Rho GTPase-activating protein 1 OS=Mus musculus GN=Arhgap1 PE=1 SV=1	A2AH25 (+1)	Arhgap1	54 kDa	0	0	0	5.3082	2.5783	FALSE
Rho guanine nucleotide exchange factor 7 OS=Mus musculus GN=Arhgef7 PE=1 SV=2	Q9ES28	Arhgef7	97 kDa	0	0	0	1.6333	0.85944	FALSE
Rho-associated protein kinase 2 (Fragment) OS=Mus musculus GN=Rock2 PE=1 SV=1	A0A1Y7VMN0 (+1)	Rock2	167 kDa	0	0	0	3.2666	2.5783	FALSE
Rho-related GTP-binding protein RhoB OS=Mus musculus GN=Rhob PE=1 SV=1	P62746 (+1)	Rhob	22 kDa	0	0	0	0	1.2892	FALSE
Rho-related GTP-binding protein RhoC OS=Mus musculus GN=Rhoc PE=1 SV=2	Q62159	Rhoc	22 kDa	0	0	0	4.4916	5.5863	FALSE
Rho-related GTP-binding protein RhoE OS=Mus musculus GN=Rnd3 PE=1 SV=1	P61588	Rnd3	27 kDa	0	0	0	1.225	0	FALSE
Rho-related GTP-binding protein RhoG OS=Mus musculus GN=Rhog PE=1 SV=1	P84096 (+1)	Rhog	21 kDa	0	0	0	2.8583	3.008	FALSE
Ribonuclease H2 subunit A OS=Mus musculus GN=Rnaseh2a PE=1 SV=2	Q9CWY8	Rnaseh2a	34 kDa	0	0	0	0.81665	0	FALSE
Ribonuclease inhibitor OS=Mus musculus GN=Rnh1 PE=1 SV=1	A0A1B0GSG5 (+2)	Rnh1	54 kDa	0	3.1957	3.5789	6.9416	5.5863	FALSE
Ribonucleoside-diphosphate reductase large subunit OS=Mus musculus GN=Rrm1 PE=1 SV=2	P07742	Rrm1	90 kDa	0	0	0	4.4916	4.7269	FALSE
Ribonucleoside-diphosphate reductase subunit M2 OS=Mus musculus GN=Rrm2 PE=1 SV=1	P11157 (+1)	Rrm2	45 kDa	0	0	0	3.2666	3.008	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Ribophorin OS=Mus musculus GN=Rpn2 PE=2 SV=1	Q61833 (+1)	Rpn2	66 kDa	0	0	0	5.3082	6.4458	FALSE
Ribose-phosphate pyrophosphokinase 2 OS=Mus musculus GN=Prps2 PE=1 SV=4	Q9CS42	Prps2	35 kDa	0	0	0	3.2666	4.7269	FALSE
Ribosomal protein L15 OS=Mus musculus GN=Gm10020 PE=3 SV=1	E9QAZ2 (+3)	Gm10020	24 kDa	0	0	0	4.0833	4.2972	FALSE
Ribosomal protein L19 OS=Mus musculus GN=Rpl19 PE=1 SV=1	A2A547 (+2)	Rpl19	23 kDa	0	0	0	2.45	2.5783	FALSE
Ribosomal protein L28 OS=Mus musculus GN=Rpl28 PE=2 SV=1	Q5M9N5	Rpl28	16 kDa	0	0	0	3.2666	3.8675	FALSE
Ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=1	Q564E8 (+1)	Rpl4	47 kDa	0	0	0	14.291	15.47	FALSE
Ribosomal protein L7A OS=Mus musculus GN=Rpl7a PE=2 SV=1	Q5EBG5	Rpl7a	30 kDa	0	0	0	7.3499	7.3052	FALSE
Ribosomal protein S6 kinase alpha-3 OS=Mus musculus GN=Rps6ka3 PE=1 SV=2	P18654	Rps6ka3	84 kDa	0	0	0	3.2666	3.4377	FALSE
Ribosomal protein S6 kinase alpha-4 OS=Mus musculus GN=Rps6ka4 PE=1 SV=2	Q9Z2B9	Rps6ka4	86 kDa	0	0	0	0.81665	0	FALSE
Ribosomal protein S6 kinase beta-1 OS=Mus musculus GN=Rps6kb1 PE=1 SV=2	Q8BSK8	Rps6kb1	59 kDa	0	0	0	0	1.7189	FALSE
Ribosome assembly factor mrt4 OS=Mus musculus GN=Mrto4 PE=1 SV=1	A2AMU9 (+2)	Mrto4	28 kDa	0	0	0	1.225	1.2892	FALSE
Ribosome biogenesis protein WDR12 OS=Mus musculus GN=Wdr12 PE=1 SV=1	Q4V9X1 (+1)	Wdr12	47 kDa	0	0	0	1.6333	0	FALSE
Ribosome maturation protein SBDS OS=Mus musculus GN=Sbds PE=1 SV=4	P70122	Sbds	29 kDa	0	0	0	3.6749	3.8675	FALSE
RIKEN cDNA 2900026A02 gene OS=Mus musculus GN=2900026A02Rik PE=1 SV=1	A0A1D5RLN6 (+1)	2900026A02Rik	43 kDa	0	0	0	0	1.2892	FALSE
RIKEN cDNA 2900064A13, isoform CRA_b OS=Mus musculus GN=Emc7 PE=1 SV=1	Q14C26 (+1)	Emc7	26 kDa	0	0	0	0.81665	1.7189	FALSE
RIKEN cDNA 5730455P16 gene OS=Mus musculus GN=5730455P16Rik PE=1 SV=1	J3KMQ6 (+1)	5730455P16Rik	44 kDa	0	0	0	0.81665	0	FALSE
RIKEN cDNA 9530068E07 gene OS=Mus musculus GN=9530068E07Rik PE=1 SV=1	A0A0A0MQD4 (+3)	9530068E07Rik	27 kDa	0	0	0	0.81665	0	FALSE
RIKEN cDNA C330023M02, isoform CRA_a OS=Mus musculus GN=Naa25 PE=2 SV=1	B2RQV1 (+1)	Naa25	112 kDa	0	0	0	2.0416	0.85944	FALSE
RING-type E3 ubiquitin transferase OS=Mus musculus GN=Arih2 PE=1 SV=1	Q3TK92 (+1)	Arih2	58 kDa	0	0	0	0.81665	0	FALSE
RNA polymerase II subunit A C-terminal domain phosphatase OS=Mus musculus GN=Ctdp1 PE=1	Q7TSG2	Ctdp1	105 kDa	0	0	0	0.81665	0	FALSE
RNA polymerase II-associated protein 3 OS=Mus musculus GN=Rpap3 PE=1 SV=1	Q9D706	Rpap3	74 kDa	0	0	0	2.45	3.4377	FALSE
RNA-binding protein 12 OS=Mus musculus GN=Rbm12 PE=1 SV=3	Q8R4X3	Rbm12	103 kDa	0	0	0	0.81665	0	FALSE
RNA-binding protein 26 OS=Mus musculus GN=Rbm26 PE=1 SV=1	E9PYZ7 (+2)	Rbm26	114 kDa	0	0	0	2.0416	2.1486	FALSE
RNA-binding protein EWS OS=Mus musculus GN=Ewsr1 PE=1 SV=1	Q5SUS9 (+3)	Ewsr1	69 kDa	0	0	0	3.6749	3.008	FALSE
RNA-binding protein OS=Mus musculus GN=Tsn PE=1 SV=1	Q545E6 (+1)	Tsn	26 kDa	0	0	0	0.81665	0	FALSE
Rpl37a protein OS=Mus musculus GN=Rpl37a PE=2 SV=1	Q5M9N6	Rpl37a	9 kDa	0	0	0	3.6749	4.7269	FALSE
RuvB-like 1 OS=Mus musculus GN=Ruvbl1 PE=1 SV=1	P60122 (+2)	Ruvbl1	50 kDa	0	0	3.5789	5.3082	7.7349	FALSE
RuvB-like helicase OS=Mus musculus GN=Ruvbl2 PE=1 SV=1	Q3TXT7 (+2)	Ruvbl2	51 kDa	3.6831	0	0	4.0833	3.8675	FALSE
RWD domain-containing protein 1 OS=Mus musculus GN=Rwdd1 PE=1 SV=1	Q9CQK7	Rwdd1	28 kDa	0	0	0	1.225	1.2892	FALSE
S-adenosyl-L-methionine-dependent tRNA 4-demethylwyosine synthase OS=Mus musculus GN=T	Q8BJM7	Tyw1	82 kDa	0	0	0	0	0.85944	FALSE
S-adenosylmethionine synthase isoform type-2 OS=Mus musculus GN=Mat2a PE=1 SV=2	Q3THS6 (+1)	Mat2a	44 kDa	0	0	0	2.45	1.7189	FALSE
S-formylglutathione hydrolase OS=Mus musculus GN=Esd PE=1 SV=1	H3BKH6 (+1)	Esd	33 kDa	3.6831	0	7.1579	10.616	13.321	FALSE
Sacsin OS=Mus musculus GN=Sacs PE=1 SV=1	E9QNY8 (+1)	Sacs	521 kDa	0	0	0	1.225	0	FALSE
SAPS domain family, member 3, isoform CRA_c OS=Mus musculus GN=Ppp6r3 PE=1 SV=1	G5E8R4 (+1)	Ppp6r3	98 kDa	0	0	0	2.8583	2.5783	FALSE
Schlafen 9 OS=Mus musculus GN=Slfn9 PE=1 SV=1	B1ARD6 (+1)	Slfn9	104 kDa	0	0	0	4.0833	1.7189	FALSE
SCY1-like protein 2 OS=Mus musculus GN=Scyl2 PE=1 SV=1	G5E8J9 (+1)	Scyl2	103 kDa	0	0	0	0	0.85944	FALSE
Sec1 family domain-containing protein 1 OS=Mus musculus GN=Scfd1 PE=1 SV=1	Q8BRF7	Scfd1	72 kDa	0	0	0	0.81665	0.85944	FALSE
SEC14-like protein 1 OS=Mus musculus GN=Sec14l1 PE=1 SV=1	A8Y5H7	Sec14l1	81 kDa	0	0	0	0	0.85944	FALSE
SEC23-interacting protein OS=Mus musculus GN=Sec23ip PE=1 SV=1	G3X928 (+1)	Sec23ip	111 kDa	0	0	0	4.4916	3.4377	FALSE
Sec24 related gene family, member C (S. cerevisiae) OS=Mus musculus GN=Sec24c PE=1 SV=1	A0A286YDI8 (+1)	Sec24c	112 kDa	0	0	0	4.4916	3.8675	FALSE
Sec24-related gene family, member B (S. cerevisiae) OS=Mus musculus GN=Sec24b PE=1 SV=1	Q80ZX0	Sec24b	136 kDa	0	0	0	2.45	2.1486	FALSE
Sec24-related gene family, member D (S. cerevisiae) OS=Mus musculus GN=Sec24d PE=1 SV=1	Q6NXL1	Sec24d	113 kDa	0	0	0	4.0833	3.8675	FALSE
Sec62 protein (Fragment) OS=Mus musculus GN=Sec62 PE=2 SV=1	Q05DA2 (+1)	Sec62	16 kDa	0	0	0	1.6333	1.2892	FALSE
Secernin-2 OS=Mus musculus GN=Scrn2 PE=1 SV=1	Q8VCA8	Scrn2	47 kDa	0	0	0	1.225	0.85944	FALSE
Secretory carrier-associated membrane protein OS=Mus musculus GN=Gm45927 PE=2 SV=1	B2M0S2	Gm45927	89 kDa	0	0	0	2.0416	2.1486	FALSE
Selenocysteine-specific elongation factor OS=Mus musculus GN=Eefsec PE=1 SV=2	Q9JHW4	Eefsec	64 kDa	0	0	0	1.6333	3.8675	FALSE
Selenophosphate synthetase 1 OS=Mus musculus GN=Sephs1 PE=2 SV=1	Q6NZN9 (+1)	Sephs1	43 kDa	0	0	0	2.0416	2.5783	FALSE
Selenoprotein F OS=Mus musculus GN=Selenof PE=1 SV=1	A0A0R4J0K1 (+1)	Selenof	18 kDa	0	0	0	1.225	0.85944	FALSE
Sepiapterin reductase OS=Mus musculus GN=Spr PE=1 SV=1	Q64105 (+1)	Spr	28 kDa	0	0	0	4.8999	3.8675	FALSE
Septin-10 OS=Mus musculus GN=Sept10 PE=1 SV=1	Q8C650	Sept10	52 kDa	0	0	0	0	1.7189	FALSE
Septin-5 OS=Mus musculus GN=Sept5 PE=1 SV=2	Q9Z2Q6	Sept5	43 kDa	0	0	0	1.6333	2.5783	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Septin-7 OS=Mus musculus GN=Sept7 PE=1 SV=2	E9Q1G8	Sept7	51 kDa	0	6.3914	7.1579	8.5749	8.1647	FALSE
Septin-8 OS=Mus musculus GN=Sept8 PE=1 SV=1	B1AQY9 (+3)	Sept8	51 kDa	0	0	0	3.2666	2.5783	FALSE
Septin-9 OS=Mus musculus GN=Sept9 PE=1 SV=1	Q80UG5	Sept9	66 kDa	0	0	0	5.3082	5.1566	FALSE
Sequestosome-1 OS=Mus musculus GN=Sqstm1 PE=1 SV=1	Q64337	Sqstm1	48 kDa	0	0	0	1.6333	2.5783	FALSE
Serine hydrolase-like protein OS=Mus musculus GN=Serhl PE=1 SV=1	Q3U3G8 (+2)	Serhl	36 kDa	0	0	0	0.81665	0.85944	FALSE
Serine hydroxymethyltransferase (Fragment) OS=Mus musculus GN=Shmt1 PE=1 SV=1	G3UYY1 (+2)	Shmt1	49 kDa	0	0	0	3.6749	3.8675	FALSE
Serine protease HTRA2, mitochondrial OS=Mus musculus GN=Htra2 PE=1 SV=1	D3YX27 (+3)	Htra2	46 kDa	0	0	0	1.225	0.85944	FALSE
Serine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Sars PE=1 SV=1	Q8C483	Sars	61 kDa	0	0	5.3684	8.1665	8.5944	FALSE
Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=1	A2A8V8 (+3)	Srrm1	103 kDa	0	0	0	1.225	1.2892	FALSE
Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3	Q8BTI8	Srrm2	295 kDa	0	0	0	1.6333	1.7189	FALSE
Serine/arginine-rich splicing factor 1 OS=Mus musculus GN=Srsf1 PE=1 SV=3	Q6PDM2	Srsf1	28 kDa	0	0	0	1.225	0.85944	FALSE
Serine/arginine-rich splicing factor 2 OS=Mus musculus GN=Srsf2 PE=1 SV=4	Q62093 (+1)	Srsf2	25 kDa	0	0	0	0	2.1486	FALSE
Serine/arginine-rich splicing factor 3 OS=Mus musculus GN=Srsf3 PE=1 SV=1	P84104 (+1)	Srsf3	19 kDa	0	0	0	1.225	1.2892	FALSE
Serine/arginine-rich splicing factor 6 OS=Mus musculus GN=Srsf6 PE=1 SV=1	Q3TWW8	Srsf6	39 kDa	0	0	0	0.81665	1.7189	FALSE
Serine/threonine-protein kinase 3 OS=Mus musculus GN=Stk3 PE=1 SV=1	Q9JI10	Stk3	57 kDa	0	0	0	1.6333	2.1486	FALSE
Serine/threonine-protein kinase A-Raf OS=Mus musculus GN=Araf PE=1 SV=2	P04627	Araf	68 kDa	0	0	0	1.6333	0.85944	FALSE
Serine/threonine-protein kinase DCLK1 OS=Mus musculus GN=Dclk1 PE=1 SV=1	Q9JLM8	Dclk1	84 kDa	0	0	0	2.45	2.5783	FALSE
Serine/threonine-protein kinase N2 OS=Mus musculus GN=Pkn2 PE=1 SV=3	Q8BWW9	Pkn2	112 kDa	0	0	0	2.0416	1.7189	FALSE
Serine/threonine-protein kinase Nek7 OS=Mus musculus GN=Nek7 PE=1 SV=1	Q9ES74	Nek7	35 kDa	0	0	0	1.6333	1.7189	FALSE
Serine/threonine-protein kinase OSR1 OS=Mus musculus GN=Oxsr1 PE=1 SV=1	Q6P9R2	Oxsr1	58 kDa	0	0	0	1.225	3.008	FALSE
Serine/threonine-protein kinase PAK 2 OS=Mus musculus GN=Pak2 PE=1 SV=1	Q8CIN4	Pak2	58 kDa	0	0	0	4.8999	6.4458	FALSE
Serine/threonine-protein kinase WNK1 OS=Mus musculus GN=Wnk1 PE=1 SV=2	P83741	Wnk1	251 kDa	0	0	0	2.0416	2.1486	FALSE
Serine/threonine-protein phosphatase (Fragment) OS=Mus musculus GN=Ppp5c PE=1 SV=1	F7BX26 (+1)	Ppp5c	54 kDa	0	0	0	1.225	1.7189	FALSE
Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B OS=Mus musculus GN=Pp	Q3TT94 (+1)	Ppp2r2a	52 kDa	0	0	0	2.8583	3.4377	FALSE
Serine/threonine-protein phosphatase 2A activator OS=Mus musculus GN=Ptpa PE=2 SV=1	Q8C0E1	Ptpa	37 kDa	0	0	0	1.225	1.7189	FALSE
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Mus musculus GN=	P63330 (+1)	Ppp2ca	36 kDa	3.6831	3.1957	3.5789	4.8999	4.2972	FALSE
Serine/threonine-protein phosphatase 4 catalytic subunit OS=Mus musculus GN=Ppp4c PE=1 SV=	P97470 (+1)	Ppp4c	35 kDa	0	0	0	1.6333	2.1486	FALSE
Serine/threonine-protein phosphatase 4 regulatory subunit 1 OS=Mus musculus GN=Ppp4r1 PE=	E9PX53 (+2)	Ppp4r1	105 kDa	0	0	0	0.81665	0.85944	FALSE
Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=Mus musculus GN=Ppp4r2 PE=	A0A0R4J0U2 (+1)	Ppp4r2	46 kDa	0	0	0	0.81665	1.7189	FALSE
Serine/threonine-protein phosphatase 6 catalytic subunit OS=Mus musculus GN=Ppp6c PE=1 SV=	Q9CQR6	Ppp6c	35 kDa	0	0	0	2.45	1.2892	FALSE
Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A OS=Mus musculus	Q505D1	Ankrd28	113 kDa	0	0	0	0.81665	1.2892	FALSE
Serine/threonine-protein phosphatase CPPED1 OS=Mus musculus GN=Cpped1 PE=1 SV=1	Q8BFS6	Cpped1	35 kDa	0	0	0	0	1.2892	FALSE
Serine/threonine-protein phosphatase OS=Mus musculus GN=Ppp3cb PE=1 SV=1	E0CZ78 (+1)	Ppp3cb	59 kDa	0	0	0	1.225	0	FALSE
Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Mus musculus GN=Pgam5 PE=	Q8BX10	Pgam5	32 kDa	0	0	0	0.81665	0.85944	FALSE
Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Mus musculus GN=Ppp1ca	P62137 (+1)	Ppp1ca	38 kDa	0	0	0	3.6749	3.4377	FALSE
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Mus musculus GN=Ppp1	P63087 (+2)	Ppp1cc	37 kDa	0	0	0	3.6749	3.008	FALSE
Serrate RNA effector molecule homolog OS=Mus musculus GN=Srrt PE=1 SV=1	Q99MR6	Srrt	100 kDa	0	0	0	1.6333	1.2892	FALSE
Serum paraoxonase/arylesterase 2 OS=Mus musculus GN=Pon2 PE=1 SV=2	Q62086	Pon2	40 kDa	0	0	0	1.225	0	FALSE
Serum paraoxonase/lactonase 3 OS=Mus musculus GN=Pon3 PE=1 SV=2	Q62087	Pon3	39 kDa	0	0	0	1.6333	0	FALSE
SET and MYND domain-containing protein 5 OS=Mus musculus GN=Smyd5 PE=1 SV=2	Q3TYX3	Smyd5	47 kDa	0	0	0	0.81665	1.2892	FALSE
Set1/Ash2 histone methyltransferase complex subunit ASH2 OS=Mus musculus GN=Ash2l PE=1 S	Q91X20	Ash2l	68 kDa	0	0	0	0	0.85944	FALSE
Sgpl1 protein OS=Mus musculus GN=Sgpl1 PE=2 SV=1	Q4FK38 (+2)	Sgpl1	64 kDa	0	0	0	4.0833	2.5783	FALSE
SH3 domain-binding glutamic acid-rich-like protein OS=Mus musculus GN=Sh3bgrl PE=2 SV=1	Q3U9A8 (+1)	Sh3bgrl	13 kDa	0	0	0	1.6333	1.2892	FALSE
SH3-domain GRB2-like 1 OS=Mus musculus GN=Sh3gl1 PE=1 SV=1	Q3TRJ7 (+2)	Sh3gl1	42 kDa	0	0	0	1.225	3.4377	FALSE
SHC SH2 domain-binding protein 1 OS=Mus musculus GN=Shcbp1 PE=1 SV=1	Q9Z179	Shcbp1	76 kDa	0	0	0	0	1.2892	FALSE
Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acads PE=1 S	Q07417	Acads	45 kDa	0	0	0	2.45	2.1486	FALSE
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Aca	Q9DBL1	Acadsb	48 kDa	0	0	0	2.0416	1.2892	FALSE
Sialic acid synthase OS=Mus musculus GN=Nans PE=1 SV=1	Q99J77	Nans	40 kDa	0	0	0	4.0833	4.7269	FALSE
Sigma 1 receptor variant SR-1E OS=Mus musculus GN=Sigmar1 PE=2 SV=1	B7ZJH9 (+1)	Sigmar1	18 kDa	0	0	0	0.81665	0	FALSE
Signal peptidase complex catalytic subunit SEC11 OS=Mus musculus GN=Sec11a PE=1 SV=1	D3YTS1 (+4)	Sec11a	28 kDa	0	0	0	1.225	1.7189	FALSE
Signal peptidase complex subunit 1 OS=Mus musculus GN=Spcs1 PE=2 SV=3	Q9D958	Spcs1	18 kDa	0	0	0	0.81665	0	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Signal peptidase complex subunit 3 OS=Mus musculus GN=Spcs3 PE=1 SV=1	Q6ZWQ7	Spcs3	20 kDa	0	0	0	0.81665	0	FALSE
Signal recognition particle 54 kDa protein OS=Mus musculus GN=Srp54 PE=1 SV=2	P14576	Srp54	56 kDa	0	0	0	0	0.85944	FALSE
Signal recognition particle receptor subunit alpha OS=Mus musculus GN=Srpra PE=1 SV=1	Q9DBG7	Srpra	70 kDa	0	0	0	3.2666	2.1486	FALSE
Signal recognition particle subunit SRP68 OS=Mus musculus GN=Srp68 PE=1 SV=2	Q8BMA6	Srp68	71 kDa	0	0	0	2.0416	0.85944	FALSE
Signal recognition particle subunit SRP72 OS=Mus musculus GN=Srp72 PE=1 SV=1	F8VQC1	Srp72	75 kDa	0	0	0	2.8583	2.5783	FALSE
Signal sequence receptor, delta, isoform CRA_b OS=Mus musculus GN=Ssr4 PE=1 SV=1	Q3TVJ8 (+2)	Ssr4	19 kDa	0	0	0	1.6333	2.5783	FALSE
Signal transducer and activator of transcription 3 OS=Mus musculus GN=Stat3 PE=1 SV=2	P42227 (+2)	Stat3	88 kDa	0	0	0	3.2666	3.008	FALSE
Signal transducer and activator of transcription 5B OS=Mus musculus GN=Stat5b PE=1 SV=1	P42232	Stat5b	90 kDa	0	0	0	1.6333	0.85944	FALSE
Signal transducer and activator of transcription OS=Mus musculus GN=Stat2 PE=2 SV=1	Q9QZE4	Stat2	106 kDa	0	0	0	2.0416	0	FALSE
Signal transducer and activator of transcription OS=Mus musculus GN=Stat6 PE=2 SV=1	Q8R4D4	Stat6	94 kDa	0	0	0	1.225	1.2892	FALSE
Signal transducing adapter molecule 1 OS=Mus musculus GN=Stam PE=1 SV=3	P70297 (+2)	Stam	60 kDa	0	0	0	0.81665	1.2892	FALSE
Signal transducing adapter molecule 2 OS=Mus musculus GN=Stam2 PE=1 SV=1	O88811 (+1)	Stam2	57 kDa	0	0	0	1.225	0	FALSE
Single-stranded DNA binding protein 1 OS=Mus musculus GN=Ssbp1 PE=1 SV=1	Q8R2K3	Ssbp1	17 kDa	0	0	0	1.225	1.7189	FALSE
Sister chromatid cohesion protein PDS5 homolog A OS=Mus musculus GN=Pds5a PE=1 SV=3	Q6A026	Pds5a	150 kDa	0	0	0	2.0416	1.2892	FALSE
Sister chromatid cohesion protein PDS5 homolog B OS=Mus musculus GN=Pds5b PE=1 SV=1	F8WHU5 (+1)	Pds5b	165 kDa	0	0	0	2.0416	2.1486	FALSE
Slk protein OS=Mus musculus GN=Slk PE=2 SV=1	A2RRK3 (+1)	Slk	138 kDa	0	0	0	4.0833	3.8675	FALSE
Small acidic protein OS=Mus musculus GN=Smap PE=1 SV=1	Q9R0P4	Smap	20 kDa	0	0	0	1.6333	1.2892	FALSE
Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Mus musculus GN=S	Q8BJU0	Sgta	34 kDa	0	0	0	1.6333	3.008	FALSE
Small nuclear ribonucleoprotein Sm D3 OS=Mus musculus GN=Snrpd3 PE=1 SV=1	P62320 (+1)	Snrpd3	14 kDa	0	0	0	0.81665	0.85944	FALSE
Small ubiquitin-related modifier 2 OS=Mus musculus GN=Sumo2 PE=1 SV=1	D3Z794 (+2)	Sumo2	8 kDa	0	0	0	0.81665	1.2892	FALSE
Snx4 protein OS=Mus musculus PE=2 SV=1	Q80X54 (+1)		47 kDa	0	0	0	2.45	1.2892	FALSE
Sodium-coupled neutral amino acid transporter 2 OS=Mus musculus GN=Slc38a2 PE=1 SV=1	Q8CFE6	Slc38a2	56 kDa	0	0	0	0	0.85944	FALSE
Sorbitol dehydrogenase OS=Mus musculus GN=Sord PE=1 SV=3	Q64442	Sord	38 kDa	0	0	0	0.81665	1.2892	FALSE
Sorcin OS=Mus musculus GN=Sri PE=1 SV=1	Q6P069	Sri	22 kDa	0	0	0	1.6333	3.008	FALSE
Sorting and assembly machinery component 50 homolog OS=Mus musculus GN=Samm50 PE=1 S	Q8BGH2	Samm50	52 kDa	0	0	0	0.81665	1.7189	FALSE
Sorting nexin 3, isoform CRA_b OS=Mus musculus GN=Snx3 PE=1 SV=1	Q78ZM0 (+2)	Snx3	19 kDa	0	0	0	2.0416	3.008	FALSE
Sorting nexin OS=Mus musculus GN=Snx5 PE=2 SV=1	Q3TJN6 (+1)	Snx5	47 kDa	0	0	0	0.81665	1.7189	FALSE
Sorting nexin-18 OS=Mus musculus GN=Snx18 PE=1 SV=1	Q91ZR2	Snx18	68 kDa	0	0	0	1.6333	0.85944	FALSE
Sorting nexin-2 OS=Mus musculus GN=Snx2 PE=1 SV=2	Q9CWK8	Snx2	58 kDa	0	0	0	4.4916	3.8675	FALSE
Sorting nexin-27 OS=Mus musculus GN=Snx27 PE=1 SV=2	Q3UHD6	Snx27	61 kDa	0	0	0	1.225	2.5783	FALSE
Sorting nexin-6 OS=Mus musculus GN=Snx6 PE=1 SV=2	Q6P8X1	Snx6	47 kDa	0	0	0	2.0416	1.2892	FALSE
Sorting nexin-7 OS=Mus musculus GN=Snx7 PE=1 SV=1	F8WI30	Snx7	51 kDa	0	0	0	3.2666	3.008	FALSE
SPARC OS=Mus musculus GN=Sparc PE=1 SV=1	A0A1L1SSH9 (+3)	Sparc	38 kDa	0	0	0	1.6333	2.5783	FALSE
Spastic paraplegia 20, spartin (Troyer syndrome) homolog (human) OS=Mus musculus GN=Spg20	D3Z3F8 (+2)	Spg20	63 kDa	0	0	0	1.6333	2.1486	FALSE
Spectrin alpha chain, non-erythrocytic 1 OS=Mus musculus GN=Sptan1 PE=1 SV=4	P16546	Sptan1	285 kDa	0	3.1957	0	9.7998	4.2972	FALSE
Spectrin beta chain, non-erythrocytic 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2	Q62261	Sptbn1	274 kDa	0	4.7936	0	11.433	6.4458	FALSE
Sperm-associated antigen 7 OS=Mus musculus GN=Spag7 PE=1 SV=1	Q7TNE3	Spag7	26 kDa	0	0	0	1.225	1.2892	FALSE
Sphingosine-1-phosphate phosphatase 1, isoform CRA_a OS=Mus musculus GN=Sgpp1 PE=1 SV=1	Q3UDY2 (+1)	Sgpp1	48 kDa	0	0	0	0.81665	0.85944	FALSE
Spliceosome RNA helicase Ddx39b OS=Mus musculus GN=Ddx39b PE=1 SV=1	Q9Z1N5	Ddx39b	49 kDa	0	0	0	2.0416	3.4377	FALSE
Splicing factor 1 OS=Mus musculus GN=Sf1 PE=1 SV=1	D3YZC9	Sf1	62 kDa	0	0	0	2.0416	2.1486	FALSE
Splicing factor 3a, subunit 3 OS=Mus musculus GN=Sf3a3 PE=1 SV=1	Q58E59 (+1)	Sf3a3	59 kDa	0	0	0	0.81665	0	FALSE
Splicing factor 3b, subunit 3 OS=Mus musculus GN=Sf3b3 PE=2 SV=1	B2RSV4 (+1)	Sf3b3	136 kDa	0	0	0	5.3082	4.7269	FALSE
Squamous cell carcinoma antigen recognized by T-cells 3 OS=Mus musculus GN=Sart3 PE=1 SV=1	Q9JLI8	Sart3	110 kDa	0	0	0	2.0416	3.4377	FALSE
Src substrate cortactin OS=Mus musculus GN=Cttn PE=1 SV=2	Q60598	Cttn	61 kDa	0	0	0	4.4916	3.8675	FALSE
SRSF protein kinase 1 OS=Mus musculus GN=Srpk1 PE=1 SV=2	O70551 (+1)	Srpk1	73 kDa	0	0	0	0	1.2892	FALSE
StAR-related lipid transfer protein 13 OS=Mus musculus GN=Stard13 PE=1 SV=5	Q923Q2	Stard13	125 kDa	0	0	0	0	0.85944	FALSE
Stathmin OS=Mus musculus GN=Stmn1 PE=1 SV=1	D3Z5N2 (+4)	Stmn1	17 kDa	0	0	0	0.81665	0.85944	FALSE
Sterile alpha motif domain-containing protein 9-like OS=Mus musculus GN=Samd9l PE=1 SV=1	E9PX59 (+1)	Samd9l	182 kDa	0	0	0	5.3082	0	FALSE
Stimulator of interferon genes protein OS=Mus musculus GN=Tmem173 PE=1 SV=2	Q3TBT3	Tmem173	43 kDa	0	0	0	0.81665	0	FALSE
Stomatin-like protein 2, mitochondrial OS=Mus musculus GN=Stoml2 PE=1 SV=1	Q99JB2	Stoml2	38 kDa	0	0	0	2.45	1.7189	FALSE
Stonin-1 OS=Mus musculus GN=Ston1 PE=1 SV=2	Q8CDJ8	Ston1	82 kDa	0	0	0	1.225	1.2892	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Striatin OS=Mus musculus GN=Strn PE=1 SV=1	F8WH41 (+1)	Strn	69 kDa	0	0	0	1.225	1.2892	FALSE
Striatin-3 OS=Mus musculus GN=Strn3 PE=1 SV=1	B2RQS1	Strn3	78 kDa	0	0	0	1.6333	0.85944	FALSE
Stromal cell-derived factor 2 OS=Mus musculus GN=Sdf2 PE=1 SV=1	A0A0R4IZW9 (+2)	Sdf2	24 kDa	0	0	0	1.225	0.85944	FALSE
Stromal cell-derived factor 2-like protein 1 OS=Mus musculus GN=Sdf2l1 PE=1 SV=2	Q9ESP1	Sdf2l1	24 kDa	0	0	0	0.81665	0	FALSE
Structural maintenance of chromosomes flexible hinge domain-containing protein 1 OS=Mus mus	Q6P5D8	Smchd1	226 kDa	0	0	0	3.6749	4.2972	FALSE
Structural maintenance of chromosomes protein 1A OS=Mus musculus GN=Smc1a PE=1 SV=4	Q9CU62	Smc1a	143 kDa	0	0	0	0.81665	1.2892	FALSE
Structural maintenance of chromosomes protein 2 OS=Mus musculus GN=Smc2 PE=1 SV=2	Q8CG48	Smc2	134 kDa	3.6831	0	0	5.7166	6.4458	FALSE
Structural maintenance of chromosomes protein OS=Mus musculus GN=Smc3 PE=1 SV=1	Q1HL32 (+2)	Smc3	142 kDa	0	0	0	6.1249	5.1566	FALSE
Structural maintenance of chromosomes protein OS=Mus musculus GN=Smc4 PE=1 SV=1	E9Q2X6 (+1)	Smc4	144 kDa	0	0	0	4.4916	2.1486	FALSE
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Mus musculus GN	Q8K2B3	Sdha	73 kDa	0	3.1957	5.3684	7.3499	8.1647	FALSE
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Mus musculus GN=S	Q9CQA3	Sdhb	32 kDa	0	0	0	3.2666	3.8675	FALSE
Succinate dehydrogenase cytochrome b560 subunit, mitochondrial OS=Mus musculus GN=Sdhc P	Q9CZB0	Sdhc	18 kDa	0	0	0	1.6333	1.2892	FALSE
Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Mus musculus GN=Su	Q9WUM5	Suclg1	36 kDa	0	0	0	2.0416	1.2892	FALSE
Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Mus musculus GN=Suclg2 PE	Q9Z2I8	Suclg2	47 kDa	0	0	0	2.8583	3.008	FALSE
Succinate-CoA ligase subunit beta (Fragment) OS=Mus musculus GN=Sucla2 PE=2 SV=1	Q3UCC6 (+1)	Sucla2	51 kDa	0	0	0	2.45	1.7189	FALSE
Sulfatase-modifying factor 1 OS=Mus musculus GN=Sumf1 PE=1 SV=2	Q8R0F3	Sumf1	41 kDa	0	0	0	1.225	0	FALSE
Sulfurtransferase OS=Mus musculus GN=Mpst PE=1 SV=1	Q3UW66 (+2)	Mpst	33 kDa	0	0	0	1.225	0	FALSE
SUMO-activating enzyme subunit 1 OS=Mus musculus GN=Sae1 PE=1 SV=1	Q9R1T2	Sae1	39 kDa	0	0	0	4.8999	3.008	FALSE
SUMO-activating enzyme subunit 2 OS=Mus musculus GN=Uba2 PE=1 SV=1	Q9Z1F9	Uba2	71 kDa	0	0	0	4.4916	5.1566	FALSE
SUMO-conjugating enzyme UBC9 (Fragment) OS=Mus musculus GN=Ube2i PE=1 SV=1	G3UYP0 (+1)	Ube2i	12 kDa	0	0	0	0.81665	1.7189	FALSE
SUN domain-containing protein 2 OS=Mus musculus GN=Sun2 PE=1 SV=3	Q8BJS4	Sun2	82 kDa	0	0	0	2.0416	1.7189	FALSE
Superoxide dismutase [Cu-Zn] OS=Mus musculus GN=Sod1 PE=1 SV=2	P08228	Sod1	16 kDa	3.6831	3.1957	0	5.7166	6.4458	FALSE
Superoxide dismutase [Mn], mitochondrial OS=Mus musculus GN=Sod2 PE=1 SV=3	P09671 (+1)	Sod2	25 kDa	0	0	0	1.6333	1.2892	FALSE
Suppressor of Ty 16 OS=Mus musculus GN=Supt16 PE=1 SV=1	G3X956	Supt16	120 kDa	0	0	0	6.1249	6.4458	FALSE
Surfeit gene 4, isoform CRA_a OS=Mus musculus GN=Surf4 PE=1 SV=1	Q545Q2 (+1)	Surf4	30 kDa	0	0	0	1.225	0	FALSE
Survival of motor neuron-related-splicing factor 30 OS=Mus musculus GN=Smndc1 PE=1 SV=1	Q8BGT7	Smndc1	27 kDa	0	0	0	0	0.85944	FALSE
SWI/SNF complex subunit SMARCC1 OS=Mus musculus GN=Smarcc1 PE=1 SV=2	P97496 (+1)	Smarcc1	123 kDa	0	0	0	1.225	1.2892	FALSE
Switch-associated protein 70 OS=Mus musculus GN=Swap70 PE=1 SV=2	Q6A028	Swap70	69 kDa	0	0	0	1.6333	0	FALSE
Synaptic functional regulator FMR1 OS=Mus musculus GN=Fmr1 PE=1 SV=1	P35922 (+1)	Fmr1	69 kDa	0	0	0	2.45	2.1486	FALSE
Synaptobrevin homolog YKT6 OS=Mus musculus GN=Ykt6 PE=1 SV=1	Q9CQW1	Ykt6	22 kDa	0	0	0	2.0416	2.5783	FALSE
Synaptojanin-2-binding protein OS=Mus musculus GN=Synj2bp PE=1 SV=1	Q9D6K5	Synj2bp	16 kDa	0	0	0	0.81665	0.85944	FALSE
Syntaxin 5A OS=Mus musculus GN=Stx5a PE=1 SV=1	H3BJ02 (+1)	Stx5a	29 kDa	0	0	0	0	0.85944	FALSE
Syntaxin-4 OS=Mus musculus GN=Stx4 PE=1 SV=1	P70452	Stx4	34 kDa	0	0	0	1.225	0.85944	FALSE
Syntaxin-binding protein 1 OS=Mus musculus GN=Stxbp1 PE=1 SV=2	O08599	Stxbp1	68 kDa	0	0	0	2.0416	1.7189	FALSE
Syntaxin-binding protein 3 OS=Mus musculus GN=Stxbp3 PE=1 SV=1	Q60770	Stxbp3	68 kDa	0	0	0	1.225	0	FALSE
TANK-binding kinase 1 OS=Mus musculus GN=Tbk1 PE=1 SV=1	A1L361 (+1)	Tbk1	83 kDa	0	0	0	0.81665	0.85944	FALSE
TAP1-cas OS=Mus musculus castaneus GN=Tap1 PE=2 SV=1	Q64333 (+1)	Tap1	79 kDa	0	0	0	2.8583	0	FALSE
Tapasin OS=Mus musculus GN=Tapbp PE=1 SV=1	Q3TCU5 (+6)	Tapbp	50 kDa	0	0	0	1.6333	1.2892	FALSE
Taxilin alpha, isoform CRA_a OS=Mus musculus GN=Txlna PE=2 SV=1	Q3UD58 (+1)	Txlna	62 kDa	0	0	0	1.225	1.2892	FALSE
TBC1 domain family member 15 OS=Mus musculus GN=Tbc1d15 PE=2 SV=1	Q4TVN0 (+2)	Tbc1d15	76 kDa	0	0	0	2.45	3.008	FALSE
TBC1 domain family member 4 OS=Mus musculus GN=Tbc1d4 PE=1 SV=1	E0CX53 (+1)	Tbc1d4	147 kDa	0	0	0	0	1.2892	FALSE
TBC1 domain family member 8B OS=Mus musculus GN=Tbc1d8b PE=1 SV=1	A3KGB4 (+1)	Tbc1d8b	128 kDa	0	0	0	1.6333	0	FALSE
Tctex-1 OS=Mus musculus PE=2 SV=1	A1E5T5 (+1)		12 kDa	0	0	0	0.81665	0.85944	FALSE
Tensin-3 OS=Mus musculus GN=Tns3 PE=1 SV=1	Q5SSZ5	Tns3	156 kDa	0	0	0	3.6749	5.1566	FALSE
Terminal uridylyltransferase 7 OS=Mus musculus GN=Zcchc6 PE=1 SV=1	E9PUA2 (+1)	Zcchc6	167 kDa	0	0	0	1.6333	0	FALSE
Testin OS=Mus musculus GN=Tes PE=1 SV=2	Q921W7	Tes	48 kDa	0	0	0	9.3915	9.0241	FALSE
Testis-expressed gene 264 OS=Mus musculus GN=Tex264 PE=1 SV=1	E9Q137 (+1)	Tex264	34 kDa	0	0	0	1.225	0.85944	FALSE
Testis-expressed protein 30 OS=Mus musculus GN=Tex30 PE=1 SV=1	Q3TUU5	Tex30	25 kDa	0	0	0	0	0.85944	FALSE
Tetraspanin OS=Mus musculus GN=Tspan6 PE=2 SV=1	Q3TV84 (+1)	Tspan6	27 kDa	0	0	0	0	0.85944	FALSE
Tetraspanin-31 OS=Mus musculus GN=Tspan31 PE=1 SV=1	Q9CQ88	Tspan31	23 kDa	0	0	0	0	0.85944	FALSE
Tetratricopeptide repeat domain 37 OS=Mus musculus GN=Ttc37 PE=1 SV=1	F8VPK0	Ttc37	174 kDa	0	0	0	2.45	1.7189	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Tetratricopeptide repeat protein 1 OS=Mus musculus GN=Ttc1 PE=1 SV=1	Q91Z38	Ttc1	33 kDa	0	0	0	0	0.85944	FALSE
Tetratricopeptide repeat protein 33 OS=Mus musculus GN=Ttc33 PE=1 SV=1	Q9D6K7	Ttc33	29 kDa	0	0	0	0	0.85944	FALSE
Thioredoxin domain-containing protein 17 OS=Mus musculus GN=Txndc17 PE=1 SV=1	Q9CQM5	Txndc17	14 kDa	0	0	0	2.0416	2.1486	FALSE
Thioredoxin domain-containing protein 9 (Fragment) OS=Mus musculus GN=Txndc9 PE=1 SV=1	A0A0A6YWP9 (+2)	Txndc9	20 kDa	0	0	0	0.81665	0.85944	FALSE
Thioredoxin reductase 1, cytoplasmic OS=Mus musculus GN=Txnrd1 PE=1 SV=3	Q9JMH6	Txnrd1	67 kDa	0	3.1957	0	5.3082	6.4458	FALSE
Thioredoxin-related transmembrane protein 1 OS=Mus musculus GN=Tmx1 PE=1 SV=1	Q8VBT0	Tmx1	31 kDa	0	0	0	0	0.85944	FALSE
Thioredoxin-related transmembrane protein 2 OS=Mus musculus GN=Tmx2 PE=1 SV=1	D3Z2J6 (+1)	Tmx2	30 kDa	0	0	0	0.81665	0	FALSE
THO complex subunit 4 OS=Mus musculus GN=Alyref PE=1 SV=3	O08583	Alyref	27 kDa	0	0	0	1.225	1.2892	FALSE
Threonine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Tars PE=1 SV=2	Q9D0R2	Tars	83 kDa	0	3.1957	5.3684	11.841	13.751	FALSE
THUMP domain-containing protein 1 OS=Mus musculus GN=Thumpd1 PE=1 SV=1	Q99J36	Thumpd1	39 kDa	0	0	0	1.225	0	FALSE
Thy-1 membrane glycoprotein (Fragment) OS=Mus musculus GN=Thy1 PE=1 SV=1	A0A1L1SUX8 (+2)	Thy1	14 kDa	0	0	0	1.225	0	FALSE
Thymidine kinase, cytosolic OS=Mus musculus GN=Tk1 PE=1 SV=3	P04184	Tk1	26 kDa	0	0	0	1.225	2.1486	FALSE
Thymidylate synthase OS=Mus musculus GN=Tyms PE=1 SV=1	P07607 (+2)	Tyms	35 kDa	0	0	0	1.6333	3.008	FALSE
Thymocyte nuclear protein 1 OS=Mus musculus GN=Thyn1 PE=1 SV=1	Q91YJ3	Thyn1	26 kDa	0	0	0	0.81665	0.85944	FALSE
Thyroid hormone receptor interactor 11 OS=Mus musculus GN=Trip11 PE=1 SV=1	E9Q512	Trip11	226 kDa	0	0	0	1.225	0	FALSE
Thyroid hormone receptor interactor 6 OS=Mus musculus GN=Trip6 PE=1 SV=1	B2RS30 (+2)	Trip6	51 kDa	0	0	0	2.45	2.1486	FALSE
Tight junction protein ZO-1 OS=Mus musculus GN=Tjp1 PE=1 SV=2	P39447	Tjp1	195 kDa	0	0	0	0.81665	1.2892	FALSE
TIP41-like protein OS=Mus musculus GN=Tiprl PE=1 SV=1	Q8BH58	Tiprl	31 kDa	0	0	0	1.6333	2.1486	FALSE
Tissue-type plasminogen activator OS=Mus musculus GN=Plat PE=1 SV=3	P11214	Plat	63 kDa	0	0	0	0	1.2892	FALSE
TNFRSF1A-associated via death domain OS=Mus musculus GN=Tradd PE=1 SV=1	B2RRZ7 (+1)	Tradd	35 kDa	0	0	0	0.81665	1.2892	FALSE
Torsin-1A-interacting protein 1 OS=Mus musculus GN=Tor1aip1 PE=1 SV=3	Q921T2	Tor1aip1	67 kDa	0	0	0	1.225	0.85944	FALSE
Torsin-1A-interacting protein 2 OS=Mus musculus GN=Tor1aip2 PE=1 SV=1	Q8BYU6	Tor1aip2	54 kDa	0	0	0	0.81665	0	FALSE
Torsin-3A OS=Mus musculus GN=Tor3a PE=1 SV=2	Q9ER38	Tor3a	44 kDa	0	0	0	1.6333	0	FALSE
Transaldolase OS=Mus musculus GN=Taldo1 PE=1 SV=1	A0A1B0GR11 (+1)	Taldo1	42 kDa	0	0	0	4.0833	3.8675	FALSE
Transcription elongation factor A protein 1 OS=Mus musculus GN=Tcea1 PE=1 SV=2	P10711 (+1)	Tcea1	34 kDa	0	0	0	5.7166	5.1566	FALSE
Transcription elongation factor SPT5 OS=Mus musculus GN=Supt5h PE=1 SV=1	O55201	Supt5h	121 kDa	0	0	0	2.8583	2.5783	FALSE
Transcription factor BTF3 OS=Mus musculus GN=Btf3 PE=1 SV=3	Q64152	Btf3	22 kDa	0	0	0	3.2666	3.008	FALSE
Transcription factor BTF3 OS=Mus musculus GN=Btf3l4 PE=1 SV=1	A2A7Z4 (+1)	Btf3l4	17 kDa	0	0	0	0.81665	0	FALSE
Transcriptional coactivator YAP1 OS=Mus musculus GN=Yap1 PE=1 SV=2	P46938	Yap1	52 kDa	0	0	0	2.8583	2.1486	FALSE
Transcriptional repressor p66 alpha OS=Mus musculus GN=Gatad2a PE=1 SV=1	E9QMN5 (+1)	Gatad2a	67 kDa	0	0	0	0.81665	0.85944	FALSE
Transducin beta-like protein 2 OS=Mus musculus GN=Tbl2 PE=1 SV=2	Q9R099	Tbl2	50 kDa	0	0	0	4.0833	3.8675	FALSE
Transforming growth factor beta-1-induced transcript 1 protein OS=Mus musculus GN=Tgfb1i1 P	Q62219	Tgfb1i1	50 kDa	0	0	0	3.2666	0	FALSE
Transketolase OS=Mus musculus GN=Tkt PE=1 SV=1	P40142	Tkt	68 kDa	9.2077	11.185	14.316	17.558	21.916	FALSE
Translation initiation factor eIF-2B subunit epsilon OS=Mus musculus GN=Eif2b5 PE=1 SV=1	Q8CHW4	Eif2b5	80 kDa	0	0	0	2.45	2.5783	FALSE
Translocation protein SEC63 homolog OS=Mus musculus GN=Sec63 PE=1 SV=4	Q8VHE0	Sec63	88 kDa	0	0	0	2.8583	2.5783	FALSE
Transmembrane 9 superfamily member 3 OS=Mus musculus GN=Tm9sf3 PE=1 SV=1	Q9ET30	Tm9sf3	68 kDa	0	0	0	3.2666	3.4377	FALSE
Transmembrane 9 superfamily member 4 OS=Mus musculus GN=Tm9sf4 PE=1 SV=1	Q8BH24	Tm9sf4	75 kDa	0	0	0	2.45	2.1486	FALSE
Transmembrane 9 superfamily member OS=Mus musculus GN=Tm9sf1 PE=1 SV=1	D3Z6X7 (+2)	Tm9sf1	67 kDa	0	0	0	0	1.2892	FALSE
Transmembrane 9 superfamily member OS=Mus musculus GN=Tm9sf2 PE=2 SV=1	Q8C7F9	Tm9sf2	75 kDa	0	0	0	2.0416	2.5783	FALSE
Transmembrane emp24 domain containing 1 OS=Mus musculus GN=Tmed1 PE=2 SV=1	B2RRM5 (+1)	Tmed1	25 kDa	0	0	0	0.81665	0.85944	FALSE
Transmembrane emp24 domain-containing protein 10 OS=Mus musculus GN=Tmed10 PE=1 SV=1	Q9D1D4	Tmed10	25 kDa	0	0	0	3.2666	2.5783	FALSE
Transmembrane emp24 domain-containing protein 4 OS=Mus musculus GN=Tmed4 PE=1 SV=1	Q8R1V4	Tmed4	26 kDa	0	0	0	1.6333	2.1486	FALSE
Transmembrane emp24 protein transport domain containing 5 OS=Mus musculus GN=Tmed5 PE	A2RS96 (+1)	Tmed5	26 kDa	0	0	0	0	0.85944	FALSE
Transmembrane p24-trafficking protein 7 OS=Mus musculus GN=Tmed7 PE=1 SV=1	D3YZZ5 (+1)	Tmed7	25 kDa	0	0	0	1.6333	2.5783	FALSE
Transmembrane protein 11, mitochondrial OS=Mus musculus GN=Tmem11 PE=1 SV=1	E9Q933 (+1)	Tmem11	20 kDa	0	0	0	0.81665	1.2892	FALSE
Transmembrane protein 120A OS=Mus musculus GN=Tmem120a PE=1 SV=1	Q8C1E7	Tmem120a	41 kDa	0	0	0	0.81665	0	FALSE
Transmembrane protein 165 OS=Mus musculus GN=Tmem165 PE=1 SV=2	P52875	Tmem165	35 kDa	0	0	0	0.81665	0.85944	FALSE
Transmembrane protein 176B OS=Mus musculus GN=Tmem176b PE=1 SV=1	Q9R1Q6	Tmem176b	28 kDa	0	0	0	0.81665	1.2892	FALSE
Transmembrane protein 214 OS=Mus musculus GN=Tmem214 PE=1 SV=1	Q8BM55	Tmem214	76 kDa	0	0	0	1.225	0	FALSE
Transmembrane protein 43 OS=Mus musculus GN=Tmem43 PE=1 SV=1	Q9DBS1	Tmem43	45 kDa	0	0	0	1.225	1.7189	FALSE
Transmembrane protein 87A OS=Mus musculus GN=Tmem87a PE=1 SV=1	A2AQJ5 (+2)	Tmem87a	64 kDa	0	0	0	0	0.85944	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Transport and Golgi organization protein 1 homolog OS=Mus musculus GN=Mia3 PE=1 SV=2	Q8BI84	Mia3	214 kDa	0	0	0	1.225	0	FALSE
Transportin 3 OS=Mus musculus GN=Tnpo3 PE=2 SV=1	Q6DI95 (+1)	Tnpo3	104 kDa	0	0	0	3.2666	3.008	FALSE
Transportin-1 OS=Mus musculus GN=Tnpo1 PE=1 SV=2	Q8BFY9	Tnpo1	102 kDa	0	0	0	3.6749	3.8675	FALSE
Trifunctional purine biosynthetic protein adenosine-3 OS=Mus musculus GN=Gart PE=1 SV=3	Q64737	Gart	108 kDa	0	0	0	9.3915	8.1647	FALSE
Trim47 protein (Fragment) OS=Mus musculus GN=Trim47 PE=2 SV=1	Q497Z1 (+1)	Trim47	70 kDa	0	0	0	1.6333	1.2892	FALSE
Trimethyllysine dioxygenase, mitochondrial OS=Mus musculus GN=Tmlhe PE=1 SV=2	Q91ZE0	Tmlhe	50 kDa	0	0	0	0	0.85944	FALSE
TRIO and F-actin-binding protein OS=Mus musculus GN=Triobp PE=1 SV=3	Q99KW3	Triobp	223 kDa	0	0	0	0.81665	0	FALSE
Tripartite motif protein 3, isoform CRA_a OS=Mus musculus GN=Trim3 PE=1 SV=2	D3YUY7 (+1)	Trim3	81 kDa	0	0	0	0.81665	0	FALSE
Tripartite motif-containing 28 OS=Mus musculus GN=Trim28 PE=2 SV=1	Q5EBP9 (+1)	Trim28	89 kDa	0	0	0	7.3499	7.3052	FALSE
Tripartite motif-containing protein 16 OS=Mus musculus GN=Trim16 PE=1 SV=2	Q99PP9	Trim16	63 kDa	0	0	0	0	0.85944	FALSE
Tripeptidyl-peptidase 1 OS=Mus musculus GN=Tpp1 PE=1 SV=2	O89023 (+2)	Tpp1	61 kDa	0	0	0	1.6333	1.2892	FALSE
tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit WDR4 OS=Mus musculus GN=Wdr4	Q9EP82	Wdr4	46 kDa	0	0	0	0.81665	1.7189	FALSE
tRNA (guanine(26)-N(2))-dimethyltransferase OS=Mus musculus GN=Trmt1 PE=2 SV=1	Q8R2M8	Trmt1	68 kDa	0	0	0	1.6333	1.2892	FALSE
tRNA (uracil-5-)-methyltransferase homolog A OS=Mus musculus GN=Trmt2a PE=1 SV=1	E9PUQ7 (+3)	Trmt2a	68 kDa	0	0	0	0	0.85944	FALSE
tRNA pseudouridine synthase OS=Mus musculus GN=Pus1 PE=2 SV=1	Q3TT85 (+1)	Pus1	44 kDa	0	0	0	2.0416	3.008	FALSE
Tropomodulin-3 OS=Mus musculus GN=Tmod3 PE=1 SV=1	Q9JHJ0	Tmod3	40 kDa	0	0	0	1.225	0	FALSE
TSC22 domain family, member 2 OS=Mus musculus GN=Tsc22d2 PE=1 SV=1	E9Q7M2	Tsc22d2	78 kDa	0	0	0	0	1.2892	FALSE
Tubby-related protein 3 OS=Mus musculus GN=Tulp3 PE=1 SV=1	O88413	Tulp3	51 kDa	0	0	0	0	1.2892	FALSE
Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1	P68369	Tuba1a	50 kDa	0	0	0	40.016	39.104	FALSE
Tubulin beta-3 chain OS=Mus musculus GN=Tubb3 PE=1 SV=1	Q9ERD7	Tubb3	50 kDa	0	0	0	24.908	27.072	FALSE
Tubulin gamma-1 chain OS=Mus musculus GN=Tubg1 PE=1 SV=1	P83887 (+1)	Tubg1	51 kDa	0	0	0	2.0416	2.1486	FALSE
Tubulin--tyrosine ligase-like protein 12 OS=Mus musculus GN=Ttll12 PE=1 SV=1	Q3UDE2	Ttll12	74 kDa	0	0	0	6.1249	7.3052	FALSE
Tubulin-folding cofactor B OS=Mus musculus GN=Tbcb PE=1 SV=2	Q9D1E6	Tbcb	27 kDa	0	0	0	1.225	0.85944	FALSE
Tubulin-specific chaperone D OS=Mus musculus GN=Tbcd PE=1 SV=1	Q8BYA0	Tbcd	133 kDa	0	0	0	3.2666	1.2892	FALSE
Tumor protein D52 (Fragment) OS=Mus musculus GN=Tpd52 PE=1 SV=1	D3Z7X7	Tpd52	23 kDa	0	0	0	0	1.7189	FALSE
Twinfilin-1 OS=Mus musculus GN=Twf1 PE=1 SV=2	Q91YR1	Twf1	40 kDa	0	0	0	2.45	2.5783	FALSE
Twinfilin-2 OS=Mus musculus GN=Twf2 PE=1 SV=1	Q9Z0P5	Twf2	39 kDa	0	0	0	0	1.2892	FALSE
Twisted gastrulation protein homolog 1 OS=Mus musculus GN=Twsg1 PE=1 SV=1	Q9EP52	Twsg1	25 kDa	0	0	0	0	0.85944	FALSE
Type 2 phosphatidylinositol 4,5-bisphosphate 4-phosphatase OS=Mus musculus GN=Pip4p2 PE=1	Q9CZX7	Pip4p2	28 kDa	0	0	0	0	0.85944	FALSE
Tyrosine--tRNA ligase OS=Mus musculus GN=Yars PE=1 SV=1	A2A7S7	Yars	63 kDa	0	0	0	4.8999	7.3052	FALSE
Tyrosine-protein kinase CSK OS=Mus musculus GN=Csk PE=1 SV=2	P41241 (+1)	Csk	51 kDa	0	0	0	0	0.85944	FALSE
Tyrosine-protein kinase Fer OS=Mus musculus GN=Fer PE=1 SV=2	P70451	Fer	95 kDa	0	0	0	0.81665	0.85944	FALSE
Tyrosine-protein kinase OS=Mus musculus GN=Jak1 PE=2 SV=1	Q3URU8	Jak1	133 kDa	0	0	0	1.225	1.2892	FALSE
Tyrosine-protein kinase OS=Mus musculus GN=Src PE=1 SV=1	F8WI90 (+1)	Src	60 kDa	0	0	0	0.81665	1.7189	FALSE
Tyrosine-protein kinase OS=Mus musculus GN=Syk PE=1 SV=1	E9PWE9 (+3)	Syk	66 kDa	0	0	0	0	1.2892	FALSE
Tyrosine-protein phosphatase non-receptor type 1 OS=Mus musculus GN=Ptpn1 PE=1 SV=2	P35821 (+2)	Ptpn1	50 kDa	0	0	0	2.45	2.5783	FALSE
Tyrosine-protein phosphatase non-receptor type 11 OS=Mus musculus GN=Ptpn11 PE=1 SV=2	P35235	Ptpn11	68 kDa	0	0	0	5.3082	4.2972	FALSE
Tyrosine-protein phosphatase non-receptor type 12 OS=Mus musculus GN=Ptpn12 PE=1 SV=3	P35831	Ptpn12	87 kDa	0	0	0	0	0.85944	FALSE
Tyrosine-protein phosphatase non-receptor type 2 OS=Mus musculus GN=Ptpn2 PE=1 SV=2	Q06180	Ptpn2	47 kDa	0	0	0	0.81665	0.85944	FALSE
Tyrosyl-DNA phosphodiesterase 2 OS=Mus musculus GN=Tdp2 PE=1 SV=1	Q9JJX7	Tdp2	41 kDa	0	0	0	0.81665	1.2892	FALSE
U2 small nuclear ribonucleoprotein A' OS=Mus musculus GN=Snrpa1 PE=1 SV=2	P57784	Snrpa1	28 kDa	0	0	0	0	0.85944	FALSE
U2 small nuclear ribonucleoprotein B'' OS=Mus musculus GN=Snrpb2 PE=1 SV=1	Q9CQI7	Snrpb2	25 kDa	0	0	0	0	0.85944	FALSE
U2 snRNP auxiliary factor large subunit OS=Mus musculus GN=U2af2 PE=1 SV=1	Q3KQM4 (+3)	U2af2	34 kDa	0	0	0	0.81665	2.1486	FALSE
U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Mus musculus GN=Snrnp200 PE=1 SV=1	Q6P4T2	Snrnp200	245 kDa	0	0	0	0	0.85944	FALSE
U6 small nuclear RNA (adenine-(43)-N(6))-methyltransferase OS=Mus musculus GN=Mettl16 PE=1	Q5SW15 (+1)	Mettl16	67 kDa	0	0	0	0	0.85944	FALSE
Ubiquilin-2 OS=Mus musculus GN=Ubqln2 PE=1 SV=2	Q9QZM0	Ubqln2	67 kDa	0	0	0	6.9416	8.1647	FALSE
Ubiquitin carboxyl-terminal hydrolase (Fragment) OS=Mus musculus GN=Uchl1 PE=2 SV=1	Q3TCH2 (+1)	Uchl1	25 kDa	0	0	0	0.81665	0	FALSE
Ubiquitin carboxyl-terminal hydrolase 10 OS=Mus musculus GN=Usp10 PE=1 SV=3	P52479	Usp10	87 kDa	0	0	0	0	1.2892	FALSE
Ubiquitin carboxyl-terminal hydrolase 14 OS=Mus musculus GN=Usp14 PE=1 SV=3	Q9JMA1	Usp14	56 kDa	0	0	0	7.7582	6.0161	FALSE
Ubiquitin carboxyl-terminal hydrolase 15 OS=Mus musculus GN=Usp15 PE=1 SV=1	Q8R5H1	Usp15	112 kDa	0	0	0	1.225	1.7189	FALSE
Ubiquitin carboxyl-terminal hydrolase 19 OS=Mus musculus GN=Usp19 PE=1 SV=1	A0A0A6YWX1 (+3)	Usp19	146 kDa	0	0	0	0	1.2892	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Ubiquitin carboxyl-terminal hydrolase 24 OS=Mus musculus GN=Usp24 PE=1 SV=1	B1AY13 (+1)	Usp24	294 kDa	0	0	0	0	1.2892	FALSE
Ubiquitin carboxyl-terminal hydrolase 47 OS=Mus musculus GN=Usp47 PE=1 SV=2	Q8BY87	Usp47	157 kDa	0	0	0	6.5332	8.1647	FALSE
Ubiquitin carboxyl-terminal hydrolase 5 OS=Mus musculus GN=Usp5 PE=1 SV=1	P56399 (+1)	Usp5	96 kDa	3.6831	3.1957	5.3684	6.9416	8.1647	FALSE
Ubiquitin carboxyl-terminal hydrolase 7 OS=Mus musculus GN=Usp7 PE=1 SV=1	F8VPX1 (+1)	Usp7	128 kDa	0	0	0	0.81665	2.1486	FALSE
Ubiquitin carboxyl-terminal hydrolase 8 OS=Mus musculus GN=Usp8 PE=1 SV=2	Q80U87	Usp8	123 kDa	0	0	0	0.81665	0.85944	FALSE
Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Mus musculus GN=Uchl3 PE=1 SV=2	Q9JKB1	Uchl3	26 kDa	0	0	0	1.6333	3.4377	FALSE
Ubiquitin carboxyl-terminal hydrolase isozyme L5 OS=Mus musculus GN=Uchl5 PE=1 SV=2	Q9WUP7	Uchl5	38 kDa	0	0	0	2.8583	2.1486	FALSE
Ubiquitin conjugation factor E4 B OS=Mus musculus GN=Ube4b PE=1 SV=3	Q9ES00	Ube4b	133 kDa	0	0	0	2.45	3.008	FALSE
Ubiquitin recognition factor in ER-associated degradation protein 1 OS=Mus musculus GN=Ufd1 P	P70362 (+1)	Ufd1	34 kDa	0	0	0	1.225	2.5783	FALSE
Ubiquitin thioesterase OTUB1 OS=Mus musculus GN=Otub1 PE=1 SV=1	D3YWF6 (+1)	Otub1	28 kDa	0	0	0	2.45	3.008	FALSE
Ubiquitin-activating enzyme E1, Chr X OS=Mus musculus GN=Uba1 PE=1 SV=1	B9EHN0 (+1)	Uba1	118 kDa	14.732	19.174	19.684	21.641	21.056	FALSE
Ubiquitin-conjugating enzyme E2 E2 OS=Mus musculus GN=Ube2e2 PE=2 SV=1	Q91W82	Ube2e2	22 kDa	0	0	0	1.225	1.2892	FALSE
Ubiquitin-conjugating enzyme E2 H OS=Mus musculus GN=Ube2h PE=1 SV=1	P62257 (+1)	Ube2h	21 kDa	0	0	0	1.225	0	FALSE
Ubiquitin-conjugating enzyme E2 J1 OS=Mus musculus GN=Ube2j1 PE=1 SV=2	Q9JJZ4	Ube2j1	35 kDa	0	0	0	1.225	0	FALSE
Ubiquitin-conjugating enzyme E2 K OS=Mus musculus GN=Ube2k PE=1 SV=3	P61087 (+1)	Ube2k	22 kDa	0	0	0	2.0416	2.1486	FALSE
Ubiquitin-conjugating enzyme E2 L3 OS=Mus musculus GN=Ube2l3 PE=1 SV=1	P68037 (+1)	Ube2l3	18 kDa	0	0	0	1.225	2.1486	FALSE
Ubiquitin-conjugating enzyme E2 Z OS=Mus musculus GN=Ube2z PE=1 SV=2	Q3UE37	Ube2z	38 kDa	0	0	0	2.8583	4.2972	FALSE
Ubiquitin-like domain-containing CTD phosphatase 1 OS=Mus musculus GN=Ublcp1 PE=1 SV=1	Q8BGR9	Ublcp1	37 kDa	0	0	0	1.225	0.85944	FALSE
Ubiquitin-like modifier-activating enzyme 5 OS=Mus musculus GN=Uba5 PE=1 SV=2	Q8VE47	Uba5	45 kDa	0	0	0	0.81665	1.2892	FALSE
Ubiquitin-protein ligase E3A OS=Mus musculus GN=Ube3a PE=1 SV=2	O08759 (+1)	Ube3a	100 kDa	0	0	0	0.81665	0	FALSE
UBX domain containing 2, isoform CRA_a OS=Mus musculus GN=Ubxn4 PE=1 SV=1	A0A0R4J078	Ubxn4	56 kDa	0	0	0	1.225	1.2892	FALSE
UBX domain-containing protein 1 OS=Mus musculus GN=Ubxn1 PE=1 SV=1	Q922Y1	Ubxn1	34 kDa	0	0	0	1.225	0	FALSE
UDP-glucose:glycoprotein glucosyltransferase 1 OS=Mus musculus GN=Uggt1 PE=1 SV=4	Q6P5E4	Uggt1	176 kDa	0	4.7936	5.3684	11.433	8.1647	FALSE
UDP-glucuronosyltransferase 1-7C OS=Mus musculus GN=Ugt1a7c PE=1 SV=1	Q6ZQM8	Ugt1a7c	60 kDa	0	0	0	3.2666	1.7189	FALSE
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Mus mu	Q8CGY8	Ogt	117 kDa	0	0	0	0.81665	0.85944	FALSE
UDP-N-acetylhexosamine pyrophosphorylase OS=Mus musculus GN=Uap1 PE=1 SV=1	A0A0R4J085 (+3)	Uap1	58 kDa	0	0	0	2.0416	1.7189	FALSE
UDP-N-acetylhexosamine pyrophosphorylase-like protein 1 OS=Mus musculus GN=Uap1l1 PE=1 S	Q3TW96 (+1)	Uap1l1	57 kDa	0	0	0	1.6333	2.1486	FALSE
Ufm1-specific protease 2 OS=Mus musculus GN=Ufsp2 PE=1 SV=1	Q99K23	Ufsp2	53 kDa	0	0	0	1.6333	1.2892	FALSE
UMP-CMP kinase 2, mitochondrial OS=Mus musculus GN=Cmpk2 PE=1 SV=2	Q3U5Q7	Cmpk2	50 kDa	0	0	0	0.81665	0	FALSE
UMP-CMP kinase OS=Mus musculus GN=Cmpk1 PE=1 SV=1	A0A0R4J093 (+1)	Cmpk1	26 kDa	0	0	0	1.6333	2.1486	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Alg5 PE=2 SV=3	Q9CTE8 (+1)	Alg5	40 kDa	0	0	0	0	1.2892	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Ap1g1 PE=2 SV=1	Q8CC03	Ap1g1	77 kDa	0	0	0	2.0416	0.85944	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Dnm1l PE=2 SV=1	Q3U4P3	Dnm1l	79 kDa	0	0	0	4.4916	3.8675	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Gmppa PE=2 SV=1	Q3UNC0 (+1)	Gmppa	47 kDa	0	0	0	2.8583	1.2892	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Golga3 PE=2 SV=1	Q3UZV1	Golga3	106 kDa	0	0	0	0.81665	0	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Gsr PE=2 SV=1	Q3U9R7 (+1)	Gsr	49 kDa	0	0	0	2.8583	3.008	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Kpna4 PE=2 SV=1	Q3UGH8	Kpna4	68 kDa	0	0	0	0.81665	0	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Nqo2 PE=2 SV=1	Q9CVF5 (+2)	Nqo2	31 kDa	0	0	0	1.6333	1.2892	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Pak1ip1 PE=2 SV=1	Q3UX26 (+1)	Pak1ip1	41 kDa	0	0	0	0	1.2892	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Pmpca PE=2 SV=1	Q3TY06	Pmpca	58 kDa	0	0	0	1.225	1.2892	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Pmpcb PE=2 SV=1	Q3TET5 (+1)	Pmpcb	54 kDa	0	0	0	1.6333	0	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Ppat PE=2 SV=1	Q3TKC5 (+3)	Ppat	53 kDa	0	0	0	1.225	2.1486	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Prdx5 PE=2 SV=1	Q3UWS9	Prdx5	21 kDa	0	0	0	1.6333	1.2892	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Prepl PE=2 SV=1	Q8BKS6 (+1)	Prepl	76 kDa	0	0	0	0.81665	0	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Prmt3 PE=2 SV=1	Q3U2K1 (+1)	Prmt3	59 kDa	0	0	0	0.81665	1.2892	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Rdx PE=2 SV=1	Q3TH46 (+1)	Rdx	77 kDa	0	0	0	8.1665	7.3052	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Rexo2 PE=2 SV=1	Q3TAV0 (+3)	Rexo2	25 kDa	0	0	0	1.225	0.85944	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Sumf2 PE=2 SV=1	Q3TM08 (+1)	Sumf2	34 kDa	0	0	0	1.6333	1.7189	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus GN=Wdr1 PE=2 SV=1	Q3U136	Wdr1	70 kDa	0	0	0	15.516	12.892	FALSE
Uncharacterized protein (Fragment) OS=Mus musculus PE=2 SV=1	Q3TV85		48 kDa	0	0	0	2.45	3.008	FALSE
Uncharacterized protein C17orf62 homolog OS=Mus musculus PE=1 SV=2	Q3TYS2		21 kDa	0	0	0	1.225	1.2892	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Uncharacterized protein C1orf198 homolog OS=Mus musculus PE=1 SV=1	Q8C3W1		35 kDa	0	0	0	0.81665	0.85944	FALSE
Uncharacterized protein C7orf50 homolog OS=Mus musculus PE=1 SV=3	Q9CXL3		22 kDa	0	0	0	0	0.85944	FALSE
Uncharacterized protein FLJ45252 homolog OS=Mus musculus PE=1 SV=2	Q6PIU9		38 kDa	0	0	0	1.225	1.7189	FALSE
Uncharacterized protein OS=Mus musculus GN=Aars PE=2 SV=1	Q3UD67 (+1)	Aars	107 kDa	0	0	0	11.433	9.8835	FALSE
Uncharacterized protein OS=Mus musculus GN=Abcd3 PE=2 SV=1	Q3U645	Abcd3	75 kDa	0	0	0	1.225	1.2892	FALSE
Uncharacterized protein OS=Mus musculus GN=Acp2 PE=2 SV=1	Q3UZN1	Acp2	47 kDa	0	0	0	0.81665	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Acsl4 PE=2 SV=1	Q8BW44 (+2)	Acsl4	74 kDa	0	0	0	1.225	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Actb PE=2 SV=1	Q3UBP6	Actb	42 kDa	0	0	0	61.657	60.161	FALSE
Uncharacterized protein OS=Mus musculus GN=Aldh9a1 PE=2 SV=1	Q3THE7	Aldh9a1	54 kDa	0	0	0	3.6749	4.2972	FALSE
Uncharacterized protein OS=Mus musculus GN=Anapc4 PE=2 SV=1	Q3TI31 (+2)	Anapc4	92 kDa	0	0	0	1.6333	2.5783	FALSE
Uncharacterized protein OS=Mus musculus GN=Arhgef10 PE=2 SV=1	Q3UGZ6 (+1)	Arhgef10	148 kDa	0	0	0	0	0.85944	FALSE
Uncharacterized protein OS=Mus musculus GN=Arl3 PE=1 SV=1	Q543P7 (+1)	Arl3	20 kDa	0	0	0	1.6333	1.7189	FALSE
Uncharacterized protein OS=Mus musculus GN=Atl2 PE=2 SV=1	Q8BYP9	Atl2	47 kDa	0	0	0	0.81665	1.2892	FALSE
Uncharacterized protein OS=Mus musculus GN=Atp6v1b2 PE=2 SV=1	A0A1S6GWG6 (+1)	Atp6v1b2	59 kDa	0	0	0	2.8583	3.8675	FALSE
Uncharacterized protein OS=Mus musculus GN=Baiap2 PE=2 SV=1	Q3UKP6 (+1)	Baiap2	58 kDa	0	0	0	0	0.85944	FALSE
Uncharacterized protein OS=Mus musculus GN=Bcap31 PE=2 SV=1	Q3U9U5 (+1)	Bcap31	28 kDa	0	0	0	2.0416	1.2892	FALSE
Uncharacterized protein OS=Mus musculus GN=Bcl2l13 PE=2 SV=1	Q3TNR7 (+1)	Bcl2l13	47 kDa	0	0	0	0.81665	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Birc6 PE=2 SV=1	A0A1S6GWH3 (+3)	Birc6	532 kDa	0	0	0	6.1249	6.8755	FALSE
Uncharacterized protein OS=Mus musculus GN=Cars PE=2 SV=1	Q3UXN3 (+1)	Cars	95 kDa	0	0	0	4.8999	3.8675	FALSE
Uncharacterized protein OS=Mus musculus GN=Cdk14 PE=2 SV=1	Q8BN81 (+1)	Cdk14	38 kDa	0	0	0	0.81665	1.2892	FALSE
Uncharacterized protein OS=Mus musculus GN=Cdk4 PE=2 SV=1	Q8BP21	Cdk4	34 kDa	0	0	0	2.8583	3.008	FALSE
Uncharacterized protein OS=Mus musculus GN=Cnot2 PE=2 SV=1	A0A1S6GWJ6 (+3)	Cnot2	61 kDa	0	0	0	1.225	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Cyp7b1 PE=2 SV=1	Q3USU4 (+2)	Cyp7b1	58 kDa	0	0	0	2.0416	1.2892	FALSE
Uncharacterized protein OS=Mus musculus GN=Dctn4 PE=2 SV=1	Q3TQY2	Dctn4	52 kDa	0	0	0	2.8583	2.5783	FALSE
Uncharacterized protein OS=Mus musculus GN=Dhrs4 PE=2 SV=1	Q3UIB5 (+1)	Dhrs4	28 kDa	0	0	0	1.225	1.2892	FALSE
Uncharacterized protein OS=Mus musculus GN=Dkc1 PE=2 SV=1	Q3TM67 (+1)	Dkc1	57 kDa	0	0	0	0	0.85944	FALSE
Uncharacterized protein OS=Mus musculus GN=Dok1 PE=2 SV=1	Q3UWF9	Dok1	53 kDa	0	0	0	1.225	0.85944	FALSE
Uncharacterized protein OS=Mus musculus GN=Edc3 PE=1 SV=1	A0ELI5 (+1)	Edc3	56 kDa	0	0	0	0.81665	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Eef2 PE=2 SV=1	Q3UZ14	Eef2	95 kDa	22.099	30.359	25.053	31.033	35.237	FALSE
Uncharacterized protein OS=Mus musculus GN=Eif4b PE=2 SV=1	Q3TDD8 (+2)	Eif4b	69 kDa	0	3.1957	3.5789	4.4916	7.3052	FALSE
Uncharacterized protein OS=Mus musculus GN=Eif4h PE=2 SV=1	Q3V244 (+2)	Eif4h	27 kDa	0	0	0	3.6749	3.8675	FALSE
Uncharacterized protein OS=Mus musculus GN=Erp44 PE=2 SV=1	Q3URM4 (+1)	Erp44	47 kDa	0	0	0	2.8583	3.008	FALSE
Uncharacterized protein OS=Mus musculus GN=Etf1 PE=2 SV=1	Q3TDF8 (+3)	Etf1	49 kDa	0	0	0	5.7166	3.8675	FALSE
Uncharacterized protein OS=Mus musculus GN=Exosc4 PE=1 SV=1	Q542B0 (+1)	Exosc4	26 kDa	0	0	0	0.81665	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Fbxo2 PE=1 SV=1	Q3USR5 (+1)	Fbxo2	34 kDa	0	0	0	0	0.85944	FALSE
Uncharacterized protein OS=Mus musculus GN=Fubp3 PE=2 SV=1	Q3ULP9	Fubp3	62 kDa	0	0	0	3.2666	3.008	FALSE
Uncharacterized protein OS=Mus musculus GN=Galk2 PE=1 SV=1	Q3U3H5 (+2)	Galk2	51 kDa	0	0	0	0.81665	1.7189	FALSE
Uncharacterized protein OS=Mus musculus GN=Gclc PE=2 SV=1	Q3UNA7	Gclc	73 kDa	0	0	0	0	2.5783	FALSE
Uncharacterized protein OS=Mus musculus GN=Gnl3 PE=2 SV=1	Q3TK27 (+1)	Gnl3	61 kDa	0	0	0	0	1.2892	FALSE
Uncharacterized protein OS=Mus musculus GN=Gpnmb PE=2 SV=1	Q3TAV1 (+4)	Gpnmb	64 kDa	0	0	0	0.81665	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Gtf2b PE=2 SV=1	Q3UNY0	Gtf2b	35 kDa	0	0	0	0	2.1486	FALSE
Uncharacterized protein OS=Mus musculus GN=Heatr3 PE=2 SV=1	Q3USC0 (+1)	Heatr3	74 kDa	0	0	0	1.6333	2.1486	FALSE
Uncharacterized protein OS=Mus musculus GN=Hmgcl PE=2 SV=1	Q3UMP2	Hmgcl	34 kDa	0	0	0	0	0.85944	FALSE
Uncharacterized protein OS=Mus musculus GN=Ilf2 PE=2 SV=1	Q3UXI9 (+1)	Ilf2	43 kDa	0	0	0	1.225	1.7189	FALSE
Uncharacterized protein OS=Mus musculus GN=Lamb1 PE=2 SV=1	Q3UHL7	Lamb1	202 kDa	0	0	7.1579	8.9832	10.313	FALSE
Uncharacterized protein OS=Mus musculus GN=Lamp2 PE=2 SV=1	Q9CZU7	Lamp2	46 kDa	0	0	0	2.8583	2.5783	FALSE
Uncharacterized protein OS=Mus musculus GN=Lman1 PE=2 SV=1	Q3U944 (+1)	Lman1	61 kDa	0	0	0	5.3082	2.5783	FALSE
Uncharacterized protein OS=Mus musculus GN=Luc7l2 PE=2 SV=1	Q3UZ17 (+1)	Luc7l2	45 kDa	0	0	0	2.8583	2.1486	FALSE
Uncharacterized protein OS=Mus musculus GN=Map3k20 PE=2 SV=1	Q3TRG2	Map3k20	51 kDa	0	0	0	2.45	3.8675	FALSE
Uncharacterized protein OS=Mus musculus GN=Mogs PE=2 SV=1	Q3U026 (+2)	Mogs	92 kDa	0	0	0	2.45	2.5783	FALSE
Uncharacterized protein OS=Mus musculus GN=Mrpl19 PE=2 SV=1	Q3URF5 (+1)	Mrpl19	34 kDa	0	0	0	0	0.85944	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Uncharacterized protein OS=Mus musculus GN=Mrpl39 PE=2 SV=1	Q8CCX9 (+1)	Mrpl39	35 kDa	0	0	0	0	0.85944	FALSE
Uncharacterized protein OS=Mus musculus GN=Naga PE=2 SV=1	Q3U6T2 (+1)	Naga	47 kDa	0	0	0	0	1.2892	FALSE
Uncharacterized protein OS=Mus musculus GN=Ndrg3 PE=1 SV=1	Q544I1 (+1)	Ndrg3	42 kDa	0	0	0	1.225	1.2892	FALSE
Uncharacterized protein OS=Mus musculus GN=Nelfa PE=2 SV=1	Q3UK41 (+1)	Nelfa	58 kDa	0	0	0	0.81665	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Nfkb2 PE=1 SV=1	Q3UG25 (+2)	Nfkb2	97 kDa	0	0	0	1.6333	2.1486	FALSE
Uncharacterized protein OS=Mus musculus GN=Npc2 PE=2 SV=1	Q3U3C2 (+1)	Npc2	16 kDa	0	0	0	2.0416	1.7189	FALSE
Uncharacterized protein OS=Mus musculus GN=Npepl1 PE=2 SV=1	Q3TCV9 (+3)	Npepl1	56 kDa	0	0	0	1.6333	0.85944	FALSE
Uncharacterized protein OS=Mus musculus GN=Npm3 PE=2 SV=1	Q3TAH3 (+1)	Npm3	19 kDa	0	0	0	0.81665	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Nrbp1 PE=2 SV=1	Q3TCW5 (+1)	Nrbp1	60 kDa	0	0	0	1.6333	1.2892	FALSE
Uncharacterized protein OS=Mus musculus GN=Nsun2 PE=2 SV=1	A0A1S6GWH4 (+2)	Nsun2	88 kDa	0	0	0	7.3499	10.313	FALSE
Uncharacterized protein OS=Mus musculus GN=Nup133 PE=2 SV=1	Q8CDZ5 (+1)	Nup133	129 kDa	0	0	0	0.81665	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Nup43 PE=2 SV=1	Q3UJY4 (+1)	Nup43	42 kDa	0	0	0	1.225	1.2892	FALSE
Uncharacterized protein OS=Mus musculus GN=Ogfr PE=2 SV=1	Q3UF10 (+1)	Ogfr	63 kDa	0	0	0	2.8583	1.2892	FALSE
Uncharacterized protein OS=Mus musculus GN=Parp12 PE=2 SV=1	Q3U0S1 (+1)	Parp12	80 kDa	0	0	0	1.6333	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Pcid2 PE=2 SV=1	Q8BNM3	Pcid2	45 kDa	0	0	0	0.81665	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Pcyox1 PE=2 SV=1	Q3TVT6 (+2)	Pcyox1	56 kDa	0	0	0	2.0416	2.1486	FALSE
Uncharacterized protein OS=Mus musculus GN=Pdcd6 PE=2 SV=1	Q8C5M4	Pdcd6	22 kDa	0	0	0	0	2.1486	FALSE
Uncharacterized protein OS=Mus musculus GN=Pdlim1 PE=2 SV=1	Q3TZ17	Pdlim1	36 kDa	5.5246	0	5.3684	7.7582	6.8755	FALSE
Uncharacterized protein OS=Mus musculus GN=Pigs PE=2 SV=1	Q3U643 (+2)	Pigs	62 kDa	0	0	0	0.81665	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Pigt PE=2 SV=1	Q3U047 (+1)	Pigt	65 kDa	0	0	0	1.225	0.85944	FALSE
Uncharacterized protein OS=Mus musculus GN=Polr2c PE=2 SV=1	Q3UUX3	Polr2c	38 kDa	0	0	0	0.81665	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Prep PE=2 SV=1	Q3TCS0 (+2)	Prep	81 kDa	0	0	0	11.025	13.321	FALSE
Uncharacterized protein OS=Mus musculus GN=Psmc4 PE=2 SV=1	Q3TUN5	Psmc4	47 kDa	0	0	0	0.81665	1.7189	FALSE
Uncharacterized protein OS=Mus musculus GN=Psmc5 PE=2 SV=1	A0A1S6GWH1 (+1)	Psmc5	47 kDa	0	0	0	4.8999	4.2972	FALSE
Uncharacterized protein OS=Mus musculus GN=Psmd2 PE=2 SV=1	Q3TI61 (+3)	Psmd2	100 kDa	3.6831	6.3914	7.1579	11.841	9.4538	FALSE
Uncharacterized protein OS=Mus musculus GN=Ptcd3 PE=2 SV=1	Q3UK51	Ptcd3	78 kDa	0	0	0	1.225	0.85944	FALSE
Uncharacterized protein OS=Mus musculus GN=Ptges3 PE=2 SV=1	Q3TJG6 (+1)	Ptges3	19 kDa	0	0	0	3.6749	3.4377	FALSE
Uncharacterized protein OS=Mus musculus GN=Pura PE=2 SV=1	Q8C6E9	Pura	35 kDa	0	0	0	0.81665	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Rabggta PE=2 SV=1	Q3UIH7 (+1)	Rabggta	65 kDa	0	0	0	0	0.85944	FALSE
Uncharacterized protein OS=Mus musculus GN=Rela PE=2 SV=1	Q8BTL4	Rela	60 kDa	0	0	0	0	1.2892	FALSE
Uncharacterized protein OS=Mus musculus GN=Rhoa PE=2 SV=1	Q3TN61 (+2)	Rhoa	22 kDa	0	0	0	4.8999	5.5863	FALSE
Uncharacterized protein OS=Mus musculus GN=Rnf126 PE=1 SV=1	Q3U3G2 (+1)	Rnf126	34 kDa	0	0	0	0.81665	1.2892	FALSE
Uncharacterized protein OS=Mus musculus GN=Rps11 PE=2 SV=1	Q9DB79	Rps11	19 kDa	5.5246	6.3914	0	6.5332	6.8755	FALSE
Uncharacterized protein OS=Mus musculus GN=Rsl1d1 PE=2 SV=1	Q3TAJ5	Rsl1d1	44 kDa	0	0	0	0.81665	2.1486	FALSE
Uncharacterized protein OS=Mus musculus GN=Rtca PE=2 SV=1	Q3TIJ4 (+3)	Rtca	39 kDa	0	0	0	1.225	1.7189	FALSE
Uncharacterized protein OS=Mus musculus GN=Sec23b PE=2 SV=1	Q3TAW4 (+4)	Sec23b	86 kDa	0	0	3.5789	5.7166	5.1566	FALSE
Uncharacterized protein OS=Mus musculus GN=Sf3a1 PE=2 SV=1	Q3TVM1 (+1)	Sf3a1	89 kDa	0	0	0	1.225	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Sh3kbp1 PE=2 SV=1	Q3TA88 (+1)	Sh3kbp1	73 kDa	0	3.1957	0	4.8999	3.4377	FALSE
Uncharacterized protein OS=Mus musculus GN=Slc12a4 PE=2 SV=1	Q3TWV2 (+4)	Slc12a4	121 kDa	0	0	0	0.81665	2.5783	FALSE
Uncharacterized protein OS=Mus musculus GN=Slc2a1 PE=2 SV=1	Q3U2J2	Slc2a1	54 kDa	0	0	0	0.81665	1.7189	FALSE
Uncharacterized protein OS=Mus musculus GN=Snd1 PE=2 SV=1	Q3TW51 (+2)	Snd1	102 kDa	0	4.7936	3.5789	14.291	12.462	FALSE
Uncharacterized protein OS=Mus musculus GN=Snx1 PE=2 SV=1	Q3TI63 (+3)	Snx1	59 kDa	0	0	0	3.6749	3.008	FALSE
Uncharacterized protein OS=Mus musculus GN=Ssr1 PE=2 SV=1	Q3TV94 (+1)	Ssr1	32 kDa	0	0	0	1.225	0.85944	FALSE
Uncharacterized protein OS=Mus musculus GN=Stub1 PE=2 SV=1	Q3TYJ0 (+1)	Stub1	35 kDa	0	0	0	0.81665	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Tfg PE=2 SV=1	Q9D828 (+1)	Tfg	42 kDa	0	0	0	2.45	2.1486	FALSE
Uncharacterized protein OS=Mus musculus GN=Tmed9 PE=2 SV=1	Q3TFU8 (+3)	Tmed9	31 kDa	0	0	0	1.225	2.1486	FALSE
Uncharacterized protein OS=Mus musculus GN=Tmpo PE=2 SV=1	Q3UR33 (+1)	Tmpo	50 kDa	0	3.1957	0	4.4916	3.4377	FALSE
Uncharacterized protein OS=Mus musculus GN=Tollip PE=2 SV=1	Q8BQL7 (+1)	Tollip	30 kDa	0	0	0	0.81665	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Tomm70a PE=2 SV=1	Q3TSX8 (+2)	Tomm70a	68 kDa	0	0	0	2.0416	2.1486	FALSE
Uncharacterized protein OS=Mus musculus GN=Trim25 PE=2 SV=1	Q3TU94 (+2)	Trim25	68 kDa	0	0	0	1.225	0	FALSE
Uncharacterized protein OS=Mus musculus GN=Tsc2 PE=2 SV=1	Q3UHB2 (+1)	Tsc2	201 kDa	0	0	0	0.81665	1.2892	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
Uncharacterized protein OS=Mus musculus GN=Txnl1 PE=2 SV=1	Q3U8R9 (+1)	Txnl1	32 kDa	0	0	0	5.7166	5.5863	FALSE
Uncharacterized protein OS=Mus musculus GN=Ube2d3 PE=2 SV=1	Q3U5V6 (+1)	Ube2d3	17 kDa	0	0	0	1.225	1.2892	FALSE
Uncharacterized protein OS=Mus musculus GN=Ubqln1 PE=2 SV=1	Q3T992 (+1)	Ubqln1	59 kDa	0	0	0	6.9416	7.7349	FALSE
Uncharacterized protein OS=Mus musculus GN=Ubr2 PE=2 SV=1	Q3UHE0 (+1)	Ubr2	199 kDa	0	0	0	0.81665	0.85944	FALSE
Uncharacterized protein OS=Mus musculus GN=Vat1 PE=2 SV=1	Q3TXD3 (+3)	Vat1	43 kDa	0	3.1957	0	3.6749	5.5863	FALSE
Uncharacterized protein OS=Mus musculus GN=Vdac1 PE=2 SV=1	Q3THL7 (+1)	Vdac1	31 kDa	0	0	3.5789	5.3082	7.3052	FALSE
Uncharacterized protein OS=Mus musculus GN=Vdac3 PE=2 SV=1	Q3TTN3 (+2)	Vdac3	31 kDa	3.6831	3.1957	3.5789	5.3082	6.0161	FALSE
Uncharacterized protein OS=Mus musculus GN=Wasl PE=1 SV=1	Q3TXX8 (+4)	Wasl	54 kDa	0	0	0	0	0.85944	FALSE
Uncharacterized protein OS=Mus musculus GN=Wbp11 PE=2 SV=1	Q3UKQ3 (+1)	Wbp11	70 kDa	0	0	0	0.81665	0.85944	FALSE
Uncharacterized protein OS=Mus musculus GN=Wbp2 PE=2 SV=1	Q9DBP6	Wbp2	37 kDa	0	0	0	0	0.85944	FALSE
Uncharacterized protein OS=Mus musculus GN=Wdr6 PE=2 SV=1	Q3TEZ2 (+1)	Wdr6	122 kDa	0	0	0	1.225	2.5783	FALSE
Uncharacterized protein OS=Mus musculus GN=Wls PE=2 SV=1	Q8CDZ6	Wls	47 kDa	0	0	0	1.225	0.85944	FALSE
Uncharacterized protein OS=Mus musculus GN=Zfp622 PE=2 SV=1	Q3U343 (+1)	Zfp622	53 kDa	0	0	0	1.6333	1.2892	FALSE
Uncharacterized protein OS=Mus musculus PE=2 SV=1	Q8C9L6 (+1)		87 kDa	0	0	0	2.8583	3.008	FALSE
Uncharacterized protein OS=Mus musculus PE=2 SV=1	Q3U8H8		14 kDa	0	0	0	0.81665	0.85944	FALSE
Unconventional myosin-Ib OS=Mus musculus GN=Myo1b PE=1 SV=1	E9Q580 (+3)	Myo1b	126 kDa	0	0	0	2.0416	2.5783	FALSE
Unconventional myosin-Ic OS=Mus musculus GN=Myo1c PE=1 SV=2	Q9WTI7	Myo1c	122 kDa	0	0	0	8.5749	10.743	FALSE
Unconventional myosin-Ie OS=Mus musculus GN=Myo1e PE=1 SV=1	E9Q634	Myo1e	127 kDa	0	0	0	0	0.85944	FALSE
Unconventional myosin-IXb OS=Mus musculus GN=Myo9b PE=1 SV=1	A0A1D5RLD1 (+2)	Myo9b	223 kDa	0	0	0	0	1.2892	FALSE
Unconventional prefoldin RPB5 interactor OS=Mus musculus GN=Uri1 PE=1 SV=2	Q3TLD5	Uri1	59 kDa	0	0	0	1.225	0	FALSE
UPF0160 protein MYG1, mitochondrial OS=Mus musculus GN=Myg1 PE=1 SV=1	Q9JK81	Myg1	43 kDa	0	0	0	4.0833	3.8675	FALSE
UPF0696 protein C11orf68 homolog OS=Mus musculus GN=Bles03 PE=1 SV=1	Q8VD62	Bles03	28 kDa	0	0	0	0	0.85944	FALSE
Uroporphyrinogen decarboxylase OS=Mus musculus GN=Urod PE=1 SV=2	P70697	Urod	41 kDa	0	0	0	0.81665	0	FALSE
UTP–glucose-1-phosphate uridylyltransferase OS=Mus musculus GN=Ugp2 PE=2 SV=1	Q3U548 (+2)	Ugp2	56 kDa	0	0	0	4.4916	3.4377	FALSE
UV excision repair protein RAD23 homolog B OS=Mus musculus GN=Rad23b PE=1 SV=2	P54728 (+3)	Rad23b	44 kDa	0	0	0	3.2666	1.2892	FALSE
V-type proton ATPase catalytic subunit A OS=Mus musculus GN=Atp6v1a PE=1 SV=2	P50516	Atp6v1a	68 kDa	0	0	0	2.8583	5.1566	FALSE
V-type proton ATPase subunit C OS=Mus musculus GN=Atp6v1c1 PE=2 SV=1	Q3TG21 (+2)	Atp6v1c1	44 kDa	0	0	0	0.81665	0.85944	FALSE
V-type proton ATPase subunit H OS=Mus musculus GN=Atp6v1h PE=1 SV=1	Q8BVE3 (+2)	Atp6v1h	56 kDa	0	0	0	1.6333	0.85944	FALSE
Vacuolar protein sorting 36 (Yeast) OS=Mus musculus GN=Vps36 PE=1 SV=1	Q3TSR1 (+1)	Vps36	44 kDa	0	0	0	1.225	0.85944	FALSE
Vacuolar protein sorting-associated protein 11 homolog OS=Mus musculus GN=Vps11 PE=1 SV=3	Q91W86	Vps11	108 kDa	0	0	0	0	0.85944	FALSE
Vacuolar protein sorting-associated protein 26A OS=Mus musculus GN=Vps26a PE=1 SV=1	P40336	Vps26a	38 kDa	0	0	0	2.45	3.008	FALSE
Vacuolar protein sorting-associated protein 26B OS=Mus musculus GN=Vps26b PE=1 SV=1	Q8C0E2	Vps26b	39 kDa	0	0	0	1.225	0	FALSE
Vacuolar protein sorting-associated protein 29 OS=Mus musculus GN=Vps29 PE=1 SV=1	Q9QZ88	Vps29	20 kDa	0	0	0	2.45	2.5783	FALSE
Vacuolar protein sorting-associated protein 45 OS=Mus musculus GN=Vps45 PE=1 SV=1	P97390 (+1)	Vps45	65 kDa	0	0	0	1.225	0	FALSE
Vacuolar protein sorting-associated protein 4B OS=Mus musculus GN=Vps4b PE=1 SV=2	P46467 (+1)	Vps4b	49 kDa	0	0	0	2.45	1.2892	FALSE
Vasodilator-stimulated phosphoprotein OS=Mus musculus GN=Vasp PE=1 SV=4	P70460	Vasp	40 kDa	0	0	0	2.0416	2.1486	FALSE
Vesicle transport protein GOT1B OS=Mus musculus GN=Golt1b PE=1 SV=1	Q9CR60	Golt1b	15 kDa	0	0	0	1.225	1.2892	FALSE
Vesicle-associated membrane protein 3 OS=Mus musculus GN=Vamp3 PE=1 SV=1	P63024	Vamp3	11 kDa	0	0	0	0.81665	1.7189	FALSE
Vesicle-associated membrane protein 8 OS=Mus musculus GN=Vamp8 PE=1 SV=1	A0A0R4J0R1 (+1)	Vamp8	11 kDa	0	0	0	0.81665	0.85944	FALSE
Vesicle-associated membrane protein, associated protein B and C OS=Mus musculus GN=Vapb PE	Q8BH80 (+1)	Vapb	27 kDa	0	0	0	2.0416	3.4377	FALSE
Vesicle-fusing ATPase OS=Mus musculus GN=Nsf PE=1 SV=2	P46460	Nsf	83 kDa	0	0	0	2.8583	3.4377	FALSE
Vesicle-trafficking protein SEC22b OS=Mus musculus GN=Sec22b PE=1 SV=3	O08547	Sec22b	25 kDa	0	0	0	2.0416	2.1486	FALSE
Vesicular integral-membrane protein VIP36 OS=Mus musculus GN=Lman2 PE=1 SV=2	Q9DBH5	Lman2	40 kDa	0	0	0	5.3082	4.2972	FALSE
von Willebrand factor A domain-containing protein 5A OS=Mus musculus GN=Vwa5a PE=1 SV=2	Q99KC8	Vwa5a	87 kDa	0	0	0	3.2666	1.7189	FALSE
von Willebrand factor A domain-containing protein 8 OS=Mus musculus GN=Vwa8 PE=1 SV=2	Q8CC88	Vwa8	213 kDa	0	0	0	0	1.2892	FALSE
Wars protein OS=Mus musculus GN=Wars PE=2 SV=1	Q4FJZ4	Wars	54 kDa	0	0	0	2.45	3.4377	FALSE
WASH complex subunit 2 OS=Mus musculus GN=Washc2 PE=1 SV=1	Q6PGL7	Washc2	145 kDa	0	0	0	1.6333	0.85944	FALSE
WD repeat and HMG-box DNA-binding protein 1 OS=Mus musculus GN=Wdhd1 PE=1 SV=2	P59328	Wdhd1	124 kDa	0	0	0	3.6749	6.0161	FALSE
WD repeat domain phosphoinositide-interacting protein 1 OS=Mus musculus GN=Wipi1 PE=1 SV	Q8R3E3	Wipi1	49 kDa	0	0	0	0	0.85944	FALSE
WD repeat domain phosphoinositide-interacting protein 2 OS=Mus musculus GN=Wipi2 PE=1 SV	Q80W47	Wipi2	48 kDa	0	0	0	1.225	1.2892	FALSE
WD repeat domain phosphoinositide-interacting protein 3 OS=Mus musculus GN=Wdr45b PE=1 S	Q9CR39	Wdr45b	38 kDa	0	0	0	0.81665	1.2892	FALSE

Identified Proteins (2666)	Accession Number	Alternate ID	MW	VPSko-biotin	ctrl-biotin	VPSoe-biotin	ctrl lysate	VPSoe lysate	enriched?
WD40 repeat-containing protein SMU1 OS=Mus musculus GN=Smu1 PE=2 SV=2	Q3UKJ7	Smu1	58 kDa	0	0	0	0.81665	0	FALSE
Wings apart-like protein homolog OS=Mus musculus GN=Wapl PE=1 SV=2	Q65Z40	Wapl	134 kDa	0	0	0	1.225	2.1486	FALSE
Wiskott-Aldrich syndrome protein family member 2 OS=Mus musculus GN=Wasf2 PE=1 SV=1	Q8BH43	Wasf2	54 kDa	0	0	0	3.2666	2.1486	FALSE
X-prolyl aminopeptidase OS=Mus musculus GN=Xpnpep1 PE=2 SV=1	Q3UKF5 (+1)	Xpnpep1	70 kDa	0	0	0	2.8583	3.8675	FALSE
X-ray repair cross-complementing protein 5 OS=Mus musculus GN=Xrcc5 PE=1 SV=4	P27641	Xrcc5	83 kDa	0	0	0	2.0416	1.7189	FALSE
Xanthine dehydrogenase/oxidase OS=Mus musculus GN=Xdh PE=1 SV=5	Q00519	Xdh	147 kDa	0	0	0	6.9416	8.5944	FALSE
XIAP-associated factor 1 OS=Mus musculus GN=Xaf1 PE=1 SV=3	Q5NBU8	Xaf1	31 kDa	0	0	0	0.81665	0	FALSE
Y+L amino acid transporter 2 OS=Mus musculus GN=Slc7a6 PE=1 SV=1	Q8BGK6	Slc7a6	57 kDa	0	0	0	1.225	0	FALSE
Zinc finger C2HC domain-containing protein 1A OS=Mus musculus GN=Zc2hc1a PE=1 SV=1	Q8BJH1	Zc2hc1a	35 kDa	0	0	0	1.225	0.85944	FALSE
Zinc finger CCCH domain-containing protein 15 OS=Mus musculus GN=Zc3h15 PE=1 SV=2	Q3TIV5	Zc3h15	48 kDa	0	0	0	2.45	3.4377	FALSE
Zinc finger CCCH type-containing 7B OS=Mus musculus GN=Zc3h7b PE=1 SV=1	F8VPP8	Zc3h7b	110 kDa	0	0	0	0	0.85944	FALSE
Zinc finger CCCH-type antiviral protein 1 OS=Mus musculus GN=Zc3hav1 PE=1 SV=1	D3Z5I1	Zc3hav1	113 kDa	0	0	0	4.0833	2.1486	FALSE
Zinc finger protein 330 OS=Mus musculus GN=Znf330 PE=1 SV=1	Q922H9	Znf330	36 kDa	0	0	0	0	1.2892	FALSE
Zinc finger protein ZPR1 (Fragment) OS=Mus musculus GN=Zpr1 PE=1 SV=1	F8WHU9 (+3)	Zpr1	42 kDa	0	0	0	1.6333	1.2892	FALSE
Zinc finger protein-like 1 OS=Mus musculus GN=Zfpl1 PE=1 SV=1	Q9DB43	Zfpl1	34 kDa	0	0	0	1.225	0	FALSE
Zinc finger Ran-binding domain-containing protein 2 OS=Mus musculus GN=Zranb2 PE=1 SV=1	B2RRT9 (+2)	Zranb2	37 kDa	0	0	0	0	1.7189	FALSE
Zinc metallopeptidase, STE24 homolog (S. cerevisiae) OS=Mus musculus GN=Zmpste24 PE=1 SV=	B9EHY2 (+1)	Zmpste24	55 kDa	0	0	0	1.6333	1.2892	FALSE
Zinc phosphodiesterase ELAC protein 2 OS=Mus musculus GN=Elac2 PE=1 SV=1	B1ATP7 (+2)	Elac2	92 kDa	0	0	0	2.8583	3.4377	FALSE
Zinc transporter 7 OS=Mus musculus GN=Slc30a7 PE=1 SV=1	Q9JKN1	Slc30a7	42 kDa	0	0	0	0.81665	1.2892	FALSE