Title	Purification of rod and cone outer segment from carp retina and proteomic analysis of their membrane proteins
Author(s)	深川, 貴志
Citation	大阪大学, 2017, 博士論文
Version Type	VoR
URL	https://doi.org/10.18910/67056
rights	
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Doctor Thesis

Purification of rod and cone outer segment from carp retina and proteomic analysis of their membrane proteins.

(コイ網膜からの桿体と錐体の外節の精製及び
それらに含まれる膜蛋白質のプロテオミクス解析)

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June 2017

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Contents

Abstract

Rods and cones are both photoreceptors in the retina, but they are different in many aspects including the light response characteristics and, for example, cell morphology and metabolism. These differences would be caused by differences in proteins expressed in rods and cones. To understand the molecular bases of these differences between rods and cones, one of the ways is to compare proteins expressed in rods and cones, and to find those expressed specifically or dominantly. In the present study, I am interested in proteins in the outer segment (OS), the site responsible for generation of rod- or cone-characteristic light responses and also the site showing different morphology between rods and cones. For this, I established a method to purify the OS and the inner segment (IS) of rods and also of cones from purified carp rods and cones, respectively, using sucrose density gradient.

In this study, I was interested in proteins tightly bound to the membranes of rod OS or cone OS. To identify these proteins, I analyzed proteins in some selected regions of an SDS-gel of washed membranes of the OS and the IS obtained from both rods and cones, with Liquid Chromatography-tandem Mass Spectrometry (LC-MS/MS) using a protein database constructed from carp retina. By comparing the lists of the proteins found in the OS and the IS of both rods and cones, I found some proteins present in rod OS membranes or cone OS membranes specifically or dominantly, in addition to the proteins already known to be present specifically in rod OS or cone OS.

Introduction

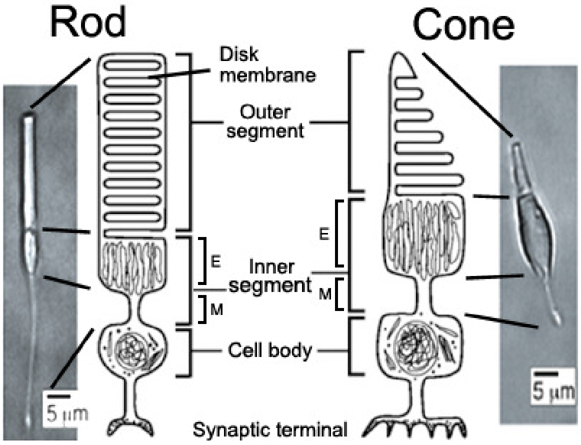

Fig 1. Micrograph and schematic of carp rod and cone.
A mechanically dissociated carp rod (left) and cone (right). Both consist of four parts, outer segment, inner segment, cell body and synaptic terminal. E: ellipsoid. M: myoid. Scale bar, 5 μm throughout. This figure was modified from Figure 1A in Kawamura and Tachibanaki (2008).

In the vertebrate retina, there are two types of photoreceptors, rods and cones. Both photoreceptors have a common structure with four regions: outer segment (OS), inner segment (IS), cell body and synaptic terminal (Fig 1).The OS is the specialized region to convert captured light signals into electrical signals. For this, OS contains molecular machineries to generate a light response. The molecular machinery, called phototransduction cascade, has been well studied in rods, and now is one of the well-known trimeric G-protein coupled signaling pathways (Pugh and Lamb, 1993, Kawamura and Tachibanaki, 2008, Fu and Yau, 2007). For cones, it is known that proteins homologous or identical to those found in rods are expressed, and thus homologous signaling pathways are present in cones.

Rods and cones show different characteristics in light responses (Kawamura and Tachibanaki, 2008, Fu and Yau, 2007). The light responses in cones are much briefer than in rods (Fig 2A and B), and this enables cones to pick up the changes of light signals with higher time resolution than rods. In addition, the light sensitivity is higher in rods than in cones. Fig 2C shows flash intensity-response amplitude relations in carp rods and red-sensitive cones. The light sensitivity of rods is >100 fold higher than that of cones. Because of the difference in sensitivity, rods and cones mediate night vision and daylight vision, respectively. One possibility of these differences is that activities and/or expression levels of phototransduction proteins are different between rods and cones. Carp (*Cyprinus carpio*) is so far the only animal from which we can obtain purified cones in a quantity large enough to do biochemical studies (Tachibanaki *et al.*, 2001). In previous studies, using purified rods and cones from the retina of carp, it was found that the signal amplification is lower, and termination of each reaction is much faster in cones than rods (Tachibanaki *et al.*, 2005, Takemoto *et al.*, 2009, Tachibanaki *et al.*, 2012, Koshitani *et al.*, 2014). These findings so far explain qualitatively the differences in light responses between rods and cones.

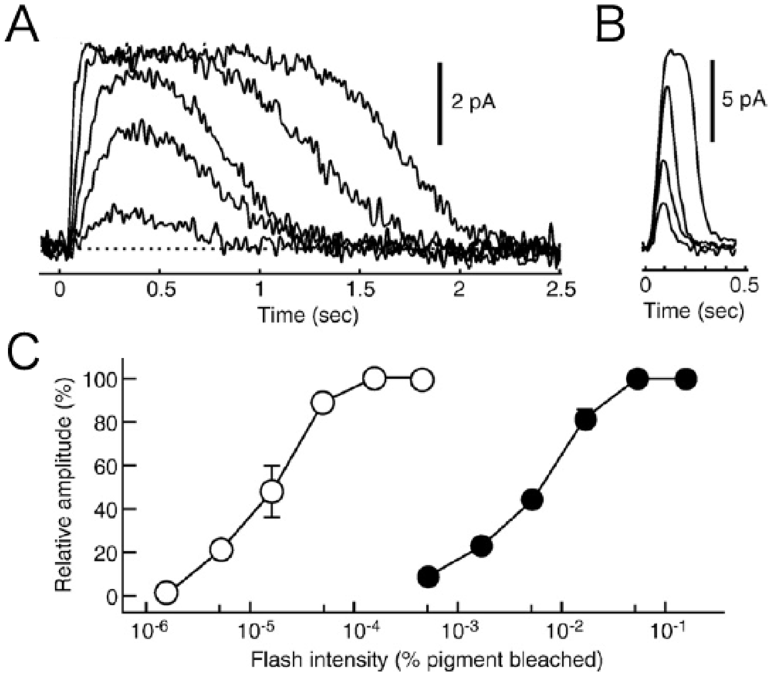

Fig 2. Characterization of carp rod and cone light response.
(A): A flash response family of a rod. Outer segment membrane current was recorded with a suction electrode by giving light flashes of various intensities at time 0 and they are superimposed. (B): A flash response family of a cone. Outer segment membrane current was recorded with a suction electrode by giving light flashes of various intensities at time 0 and they are superimposed. (C): Light intensity-response relations of rods (open circles) and red-sensitive cones (closed circles) shown in (B). This figure was adopted from Figure 1B, C and D in Kawamura and Tachibanaki (2008).

In addition, there is morphological differences in the OS shape and OS structure between rods and cones. As shown in Fig 1, the basic structure of the rod and the cone are similar but the OS shape is a rod-like shape in rods, whereas it is conical shape in cones. Also, the detailed membrane structure is different. In rod OS (ROS), about 1000 disk membranes are stacked and surrounded by a plasma membrane, while in cone OS (COS), the plasma membrane invaginates repeatedly to form a tightly stacked lamellae structure. Such differences seem to be caused by the differences in proteins involved in morphogenesis and preservation of OS, but little is known about such proteins.

As described above, phototransduction mechanisms have been studied already. However, it is still possible that proteins other than known ones are present in ROS or COS and that they contribute to the differences in the light responses between rods and cones. In addition, there could be ROS- or COS-specific protein(s) that contribute to the differences in morphology between rods and cones. To examine these possibilities, it would be most effective to compare proteins expressed in ROS and those in COS. The method to obtain purified ROS has been known for many years, but for COS, its purification method has not been known, mainly because of difficulties in obtaining purified cones in a quantity large enough to manipulate. In the present study, first using sucrose density gradient, I prepared purified COS and ROS from purified carp cones and rods, respectively. In the purified rods and cones in carp, the IS consisting of ellipsoid plus myoid and the OS are both preserved, so that I can also obtain purified IS.

In the present study, I focused on the proteins tightly bound to ROS or COS membranes, so that I prepared ROS and COS membranes washed intensively (washed ROS or washed COS membranes). I also obtained rod inner segment (RIS) membranes and cone inner segment (CIS) membranes similarly. To identify proteins tightly bound to ROS or COS membranes, I analyzed proteins in the regions outside of visual pigment bands in the SDS-PAGE gel of the washed ROS, RIS, COS and CIS membranes with Liquid Chromatography-tandem Mass Spectrometry (LC-MS/MS) using a protein database constructed from carp retina. By comparing the lists of the proteins found in the above four kinds of membranes, I tried to find proteins expressed specifically or dominantly in ROS or COS membranes (ROS- or COS-specific/dominant proteins), and listed such candidate proteins in this study.

Materials and Methods

Chemicals and antibodies

All chemical reagents were purchased from Nacalai Tesque (Kyoto, Japan). Monoclonal anti-chicken Na^+/K^+ ATPase alpha subunit antibody (a5) was obtained from Developmental Studies Hybridoma Bank (Iowa, USA). Anti-human TOM20 antibody (sc-11415) and anti-human neurocalcin delta antibody (NBP2-15037) were obtained from Santa Cruz Biotechnology (Texas, USA) and Novus Biologicals (Colorado, USA), respectively. Polyclonal anti-carp mitochondrial aspartate aminotransferase 2 (mAAT) antiserum was raised against its peptide fragment (Ser28-Lys428; AB793727) in mice by Mr. Komatsu in the lab which I belonged to. Peroxidase-conjugated anti-mouse IgG antibody and anti-rabbit IgG antibody were obtained from Kirkegaard & Perry Laboratories (Maryland, USA). Alexa488-conjugated anti-rabbit IgG antibody and Alexa568-conjugated anti-mouse IgG antibody were obtained from Thermo Fisher Scientific (Massachusetts, USA).

Preparation of purified carp rod and cone photoreceptors

Carp (*Cyprinus carpio*: 25-30 cm in length) were purchased from Hirose Carp (Fukushima, Japan). Animal care was conducted according to the institutional guidelines.

Rod and cone photoreceptors were purified from carp retina as described in Tachibanaki *et al.* (2001) (Fig 3). Briefly, rods and cones were mechanically dissociated from the retina by tapping the retina using a paintbrush in Ringer's solution (119.9 mM NaCl, 2.6 mM KCl, 0.5 mM $CaCl_2$, 0.5 mM $MgCl_2$, 0.5 mM $MgSO_4$, 1 mM $NaHCO_3$, 16 mM glucose, 0.5 mM NaH_2PO_4, 4 mM HEPES, pH 7.5). Detached cells retained the OS and the IS containing of ellipsoid plus myoid, but lacked the cell body and the synaptic terminal (Kawamura and Tachibanaki, 2008). Then, the rods and cones were separated using Percoll stepwise density gradients. Purified rods and cones were washed twice with a potassium gluconate buffer (115 mM potassium gluconate, 2.5 mM KCl, 2 mM $MgCl_2$, 0.1 mM $CaCl_2$, 0.2 mM EGTA, 1 mM dithiothreitol, 10 mM HEPES, pH 7.5) because by this wash, most of contaminated red blood cells were blasted and their soluble proteins were mostly removed in the supernatant while rods and cones remained intact. In previous studies, contamination of cones in the purified rods and that of rods in purified cones were both estimated < 1 % (Tachibanaki *et al.*, 2001). Purified cells were suspended in Ringer's solution.

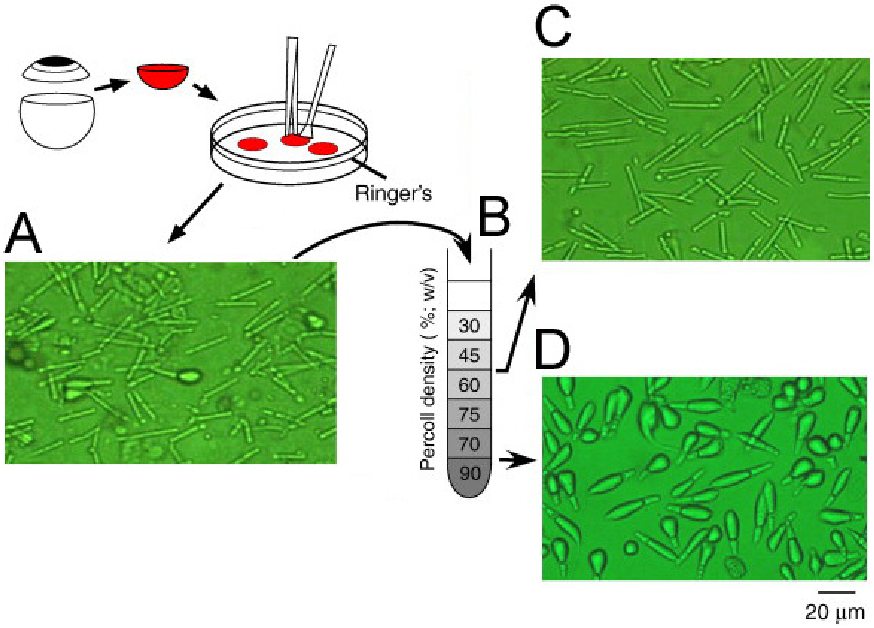

Fig 3. Purification of rods and cones from carp retina
Rods and cones were brushed off the retina. The mixture of rods and cones (A) was layered on the top of a stepwise Percoll gradient. After centrifugation rods were obtained at the 45/60 % interface (B) and cones were obtained at the 75/90 % interface (C). Scale bar, 20 µm throughout. This figure was modified from Figure 3 in Kawamura and Tachibanaki (2008).

Separation of OS membranes from IS membranes in purified cells.

Purified rods were suspended in Ringer's solution and purified cones were suspended in 2 x Ringer's solution (For unknown reasons, separation of OS and IS in cones was more effective when 2 x Ringer's solution was used). Then, each suspension (~800 µL) was passed through a 27-gauge needle 15 times using a 1 mL syringe to mechanically dissociated OS and IS from purified rods or cones. During this procedure, cytoplasmic proteins were probably eluted out from the OS or the IS. The resultant suspension of a mixture of separated OS and IS membranes of rods or cones were then placed on top of a stepwise sucrose density gradient in Ringer's solution in a test tube, and centrifuged for an hour at 190,000 × g at 4 °C. With the above procedure, I obtained a fraction rich of ROS membranes and that of RIS membranes from purified rods, and those rich of COS and CIS membranes from purified cones (see **Results and Discussion**).

Preparation of polyclonal antiserum against calnexin

To raise antiserum against calnexin, partial peptide corresponding to Ile506 - Lys593 of carp calnexin (AB894402.1) was expressed as a GST-fusion protein. The coding region of calnexin was amplified from a carp retinal cDNA library (Shimauchi-Matsukawa *et al.*, 2005) by PCR with a pair of primers, each of which contained a site for a restriction enzyme. The sequences of the primers were: 5'-TCCTCTTCTGCTGCACTG-3' (forward) and 5'-TCATTTCCTGTTTCTGGGAGA -3' (reverse). The *BamHI*- and *XhoI*-digested amplified region was inserted into *BamHI/XhoI* sites of expression vector, pGEX-5X-1 (GE Healthcare, USA). The recombinant plasmid was introduced into E.coli BL21DE3 (Novagen). The expression and purification of the recombinant protein was carried out according to the manufacture's instruction. The fusion protein was used to raise anti-calnexin antiserum in mice. The antisera obtained from mice were confirmed to react specifically to calnexin peptide, Ile506 - Lys593, in its N-terminal maltose-binding protein (MBP) fusion form.

Quantitative evaluation of Contamination of IS or OS membranes

To evaluate the purity of membranes separated with sucrose density gradient centrifugation described above, OS- or IS-specific marker proteins were quantified in each separated membrane fraction. As a marker of OS membranes, visual pigments were quantified spectrophotometrically as described Tachibanaki *et al.* (2001), Okano *et al.* (1989) and Yamaoka *et al.* (2015). As markers of IS membranes, F1 ATPase beta subunit, TOM20, calnexin, and Na^+/K^+ ATPase alpha subunit were quantified. F1 ATPase beta subunit and TOM20 localize to the inner and outer membranes of mitochondria contained in IS, respectively. Calnexin and Na^+/K^+ ATPase alpha subunit localize to the endoplasmic reticulum membranes and plasma membranes in IS. The amount of F1 ATPase beta subunit was quantified with Oriole (Bio-Rad Laboratories, California, USA) staining after SDS-PAGE using bovine serum albumin (BSA) as a molar standard. The amounts of Na^+/K^+ ATPase alpha subunit, calnexin and TOM20 were measured by quantitative immunoblot analysis as described Tachibanaki *et al.* (2005). Briefly, the obtained fractions were transferred onto PVDF membranes (Immobilon-P Transfer Membrane, MERCKMILLIPORE, Darmstadt, Germany) after SDS-PAGE. The membranes were washed in TBS (100 mM Tris, 0.9 % NaCl, pH 7.5) and incubated in TBS containing anti-chicken Na^+/K^+ ATPase alpha subunit antibody (at 1:250 dilution), anti-carp calnexin antiserum (at 1:200 dilution) or anti-human TOM20 antibody (at 1:100 dilution) at 4 °C overnight. After the membranes were washed in TBS, incubation was continued in TBS containing the secondary antibody at room temperature for an hour. After the membranes were washed in TBS, visualization of the immunoreactive protein bands was carried out according to the manufacturer's protocol

(Chemi-Lumi One L, Nacalai Tesque, Kyoto, Japan). The amounts of marker proteins were measured with the amount of visual pigments.

Construction of a database of proteins expressed in carp retina

For the comparative proteomic analysis of rod and cone proteins in the OS and the IS membranes, a database of proteins expressed in carp retina was constructed as described below. Retinal total RNA was extracted from carp retina using TRI reagent (Sigma-Aldrich, California, USA) according to the manufacturer's protocol. Subsequent RNA quality check, RNA sequence library preparation and RNA sequencing were performed at Hokkaido System Science (Hokkaido, Japan. Raw sequence data were submitted to DDBJ Sequence Read Archive (DRA) under accession number DRA004555 (Bioproject ID: PRJDB4664)). Then, the acquired sequences were assembled as contigs by a de novo RNA-seq data assembly method at Hokkaido System Science using Trinity (version r20130225, k-mer 25). The assembled 258,867 contigs were BLASTX searched against NCBI vertebrate_other protein database (release 69, E-value 1e-5) using BLAST+ (version 2.2.29+). A total of 124,947 contigs hit with this search was each annotated with the top hit NCBI gene name and the species name. The contigs that were not identified by the BLAST search were removed from the analysis hereafter. Next, the annotated contigs were translated from DNA sequences to amino acid sequences using TransDecoder (version r20140704). As a result, 125,175 amino acid sequences were obtained. The increase of the number of sequences from the number of contigs was caused by the presence of contigs that have candidate of multiple start codons. The number of amino acid sequences was more than that of all carp genes, 52,610, reported previously (Xu *et al.*, 2014), due to the presence of the splicing variants and the polymorphism in UTR regions and partially in coding regions. The DNA sequences coding same amino acid sequences but having different DNA sequences in UTR regions were not merged at this stage. Then, using acquired data of the sequences, a sequence database of carp retinal proteins was constructed (Fukagawa *et al.*, 2016), and used for the following proteomic analysis.

Liquid chromatography-tandem mass spectrometry (LC-MS/MS) analysis

In this study, I focused on proteins tightly bound to membranes. Therefore, in the LC-MS/MS analysis, I used washed membranes prepared from ROS, RIS, COS and CIS membranes. ROS, RIS, COS and CIS membranes were washed intensively by centrifugation (190,000 x g, 10 min, 4 °C) with a low salt buffer (4 mM HEPES, 1 mM EDTA, pH 7.5) twice and subsequently with a high pH buffer (100 mM Na_2CO_3, pH 11.5) four times to remove soluble and membrane-associated peripheral proteins. The washed membranes were dissolved in SDS-PAGE sample buffer (62.5 mM Tris, 10 % (w/v) glycerol, 100 mM dithiothreitol, 2.3 % SDS, 0.01 % (w/v) bromophenol blue), and kept on ice for more than 1 hour. After solubilization, membranes were subjected to SDS-PAGE, and gels were silver-stained. Then, four regions of each lane (Fig 8E) were subjected to in-gel digestion for subsequent LC-MS/MS analysis. The regions corresponding to rhodopsin monomer (30~40 kDa), dimer (55~65 kDa), and trimer (75~100 kDa) were omitted from the regions for the analysis in ROS-rich fractions to avoid the masking effect caused by massive mount of peptide derived from rhodopsin (about 95 % of total protein amount in ROS-rich fraction). Also in the analyses of other membranes, the same regions were omitted to compare the localized proteins impartially between rod and cone membranes, and also between the OS and IS membranes. Then the proteins in gels were digested by in-gel tryptic cleavage, and resultant peptides were extracted from the gel (Rosenfeld *et al.*, 1992). The peptides were subjected to shotgun proteomic analysis using QTRAP®5500 LC-MS/MS System (AB SCIEX) and Mascot software (version 2.4, Matrix Science, Boston, USA).

Identification of proteins specifically/dominantly expressed in ROS or COS

The amount of a protein analyzed with LC-MS/MS can be quantified with the value of emPAI (Ishihama *et al.*, 2005), which is calculated from the number of the observed peptides divided by the number of the observable peptides per protein in the MS analysis and is an index of the amount of each protein in a sample analyzed with LC-MS/MS. Because OS- and IS-rich fractions were contaminated with IS and OS membranes, respectively, I calculated the portion of a protein detected in the ROS-rich fraction by dividing the emPAI value of a protein in the ROS-rich fraction with the sum of its value in the ROS-rich and the RIS-rich fractions (ROS/(ROS+RIS) in Table 2). Proteins with ROS/(ROS+RIS) < 0.5, which indicates that the protein is detected more in the RIS-rich fraction, are not listed in Table 2. In addition, proteins also found in COS-rich fraction are eliminated under the criteria that their emPAI values in COS-rich fraction, obtained from the same number of cones, i. e., 5×10^4 cones, were more than 1/10 of those in ROS-rich fraction. In Table 2, proteins showing ROS/(ROS+RIS) > 0.8 are shown, based on the fact that many of the known ROS-specific proteins are present with ROS/(ROS+RIS) > 0.8 (see proteins indicated in red bold). In addition, those proteins showing emPAI values lower than 1/100 of that of a protein most abundantly detected, i. e., rhodopsin showing 35.41 emPAI value in the ROS-rich fraction, are eliminated in Table 2. It should be mentioned that the regions corresponding to rhodopsin bands were omitted in the LC-MS/MS analysis (Fig 8E), but that was not completely removed and detected because of its massive expression. In the above process, ROS and COS volume differences (Yamaoka *et al.*, 2015) were taken into account to compare the emPAI values in the equal volume. Proteins in Table 2 are listed in descending order of ROS/(ROS+RIS).

Similarly, I calculated the portion of a protein detected in the COS-rich fraction in Table 3. In this case, guanine nucleotide-binding protein G(t) subunit alpha-2 or cone transducin alpha subunit showing 28.3 emPAI value in the COS-rich fraction, was used as the most abundantly detected protein. It should be mentioned that cone transducin alpha subunit is a ~40 kDa protein. Proteins of this molecular mass may have been quantified only partially in my LC-MS/MS analysis on the proteins in the limited regions (Fig 8E). In other words, the emPAI value of cone transducin alpha subunit could be much higher when all of them were analyzed.

Immunological analysis on the localization of neurocalcin-delta B in cones

To investigate the subcellular localization of Neurocalcin-delta B (NCALD) in cones, immunoblot analysis was applied to separated ROS, RIS, COS and CIS membranes as described in Tachibanaki *et al.* (2005) using anti-human Neurocalcin-delta (NCALD) antibody (at 1:100 dilution), and immunocytochemical analysis was applied to isolated cones as described in Arinobu *et al.* (2010) with some modifications. Briefly, mechanically isolated carp photoreceptors were suspended in a carp Ringer's solution supplemented with 4% (w/v) paraformaldehyde and then incubated for 12 hours at 4 °C in dark. Then they were mounted on a silane-coated slide glass and permeabilized with PBS (137 mM NaCl, 2.7 mM KCl, 8.1 mM Na_2HPO_4, 1.5 mM NaH_2PO_4, pH 7.4) containing 1% (w/v) Triton X-100 for 5 min, air-dried and blocked with PBS containing 0.2% (w/v) Triton X-100 and 1.5 % (v/v) normal goat serum. Mounted cells were then washed with PBS for three times, and incubated for an hour at room temperature with a solution containing anti-human NCALD antibody (at 1:75 dilution) and anti-mitochondrial aspartate aminotransferase 2 (mAAT) antiserum (at 1:300 dilution). Then the cells were washed with PBS three times, and incubated at room temperature for 30 min with mixture of Alexa488-conjugated anti-rabbit IgG (at 1:200 dilution) to detect NCALD and Alexa568-conjugated anti-mouse IgG (at 1:300 dilution) to detect mAAT.

Results and Discussion

Purify of each of OS and IS membranes

In this study, I originally intended to identify soluble and membrane-bound proteins expressed specifically or dominantly in cone OS. It would be ideal to detect proteins expressed in purified cone OS and compare them with proteins expressed in cone IS, rod OS and rod IS. For this purpose, I first tried to isolate intact OS containing soluble and membrane-bound proteins from purified carp rods mechanically with the mechanical method reported previously for frog rod OS showing typical rod-shape (Woodruff *et al.*, 1979). However, the attempt was not successful because I observed only deteriorated rod OS in carp after mechanical separation (see Fig 4E, for example). Thus, in this study, I tried to obtain OS membranes, instead of intact OS, from purified carp rods and cones. The procedure is shown in Fig 4. Purified rods (Fig 4A) and cones (Fig 4B) were mechanically disrupted to separate the OS and the IS (Fig 4C and D). A mixture of deteriorated and separated OS and IS was placed on top of a stepwise sucrose density gradient, 36/50 % (w/v) for rods and 36/70 % (w/v) for cones, in a test tube, and then centrifuged to separate them (Fig 4E and G for rods, and Fig 4F and H for cones). At this stage, OS and IS were disrupted and they were practically in the form of membranes. These membranes in each interface were collected and suspended in Ringer's solution.

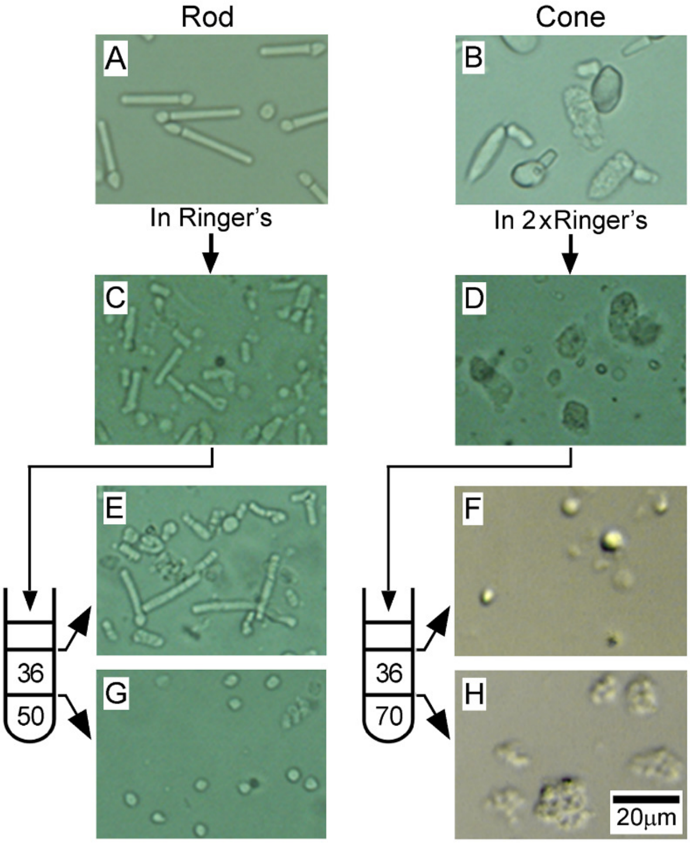

Fig 4. Purification of OS and IS membranes from purified rods and cones.
Differential interference contrast microscopic (DIC) images of the cell fractions in each step of the purification are shown. Purified carp rods (A) and cones (B) were passed through a 27-gauge needle to dissociate the OS from the IS, and the resultant broken rods (C) and cones (D) were layered on a sucrose density gradient made in a test tube (drawings in the left of E/G and F/H) to centrifuge. The number in the drawings shows the density of sucrose (%, w/v). Separated membranes at upper (E, F) and lower (G, H) interfaces were collected. Scale bar, 20 μm throughout.

To evaluate how effectively the separation of OS and IS membranes was achieved with this procedure, membranes obtained at upper interface (Fig 4E for rods and F for cones) and those at the lower interface (Fig 4G for rods and H for cones) were probed quantitatively with five membrane protein markers: visual pigments for the OS, F1 ATPase beta subunit for IS mitochondrial inner membranes (Schwaiger *et al.*, 1987), TOM20 for IS mitochondrial outer membranes (Ramage *et al.*, 1993, Xie *et al.*, 2005), Na^+/K^+ ATPase alpha subunit for IS plasma membranes (Wetzel *et al.*, 1999, Kwok *et al.*, 2008), and calnexin for IS ER membranes (Hammond and Helenius, 1994, Lakkaraju *et al.*, 2012).

Visual pigments in the membranes of starting purified rods and cones, and in the obtained fractions from upper interfaces (Fig 4E for rods and F for cones) and lower interfaces (Fig 4G for rods and H for cones) were quantified spectrophotometrically (Fig 5). Membranes obtained at each interface were suspended in Ringer's solution of the volume same as that of the initial total membranes obtained from purified rods and cones. In the followings, I describe total membranes obtained from starting purified rods or cones as just initial rod or cone membranes, and indicate the content of a protein in each upper or lower fraction as the % of the content in the initial membranes. In the case of rods (Fig 5A), the rod visual pigment, rhodopsin, was mainly distributed at upper interface (Upper fraction in Fig 5A, middle panel) after the separation. Distribution of rhodopsin at the upper interface was 86.2 % (n = 3, Table 1) of the initial rod membranes (Initial in Fig 5A, left panel). In contrast, visual pigments in the lower interfaces were negligible (Lower fraction in Fig 5A, right panel). When the initial rod membranes and membranes both the upper and the lower fractions of rods were subjected to SDS-PAGE (Fig 6A), two or three thick bands of rhodopsin (arrowheads in Fig 6A) were detected in the initial rod membranes (Fig 6A, Initial) and in rod membranes in the upper fraction (Fig 6A, Upper). The lower (~35 kDa) and higher (~70 kDa and ~150 kDa) molecular masses of rhodopsin band are those of monomer, dimer and tetramer, respectively. In contrast, in the lower fraction (Fig 6A, Lower), rhodopsin bands were practically not detected. All of the results shown in Fig 5A and Fig 6A showed that ROS membranes were collected in the upper fraction almost exclusively.

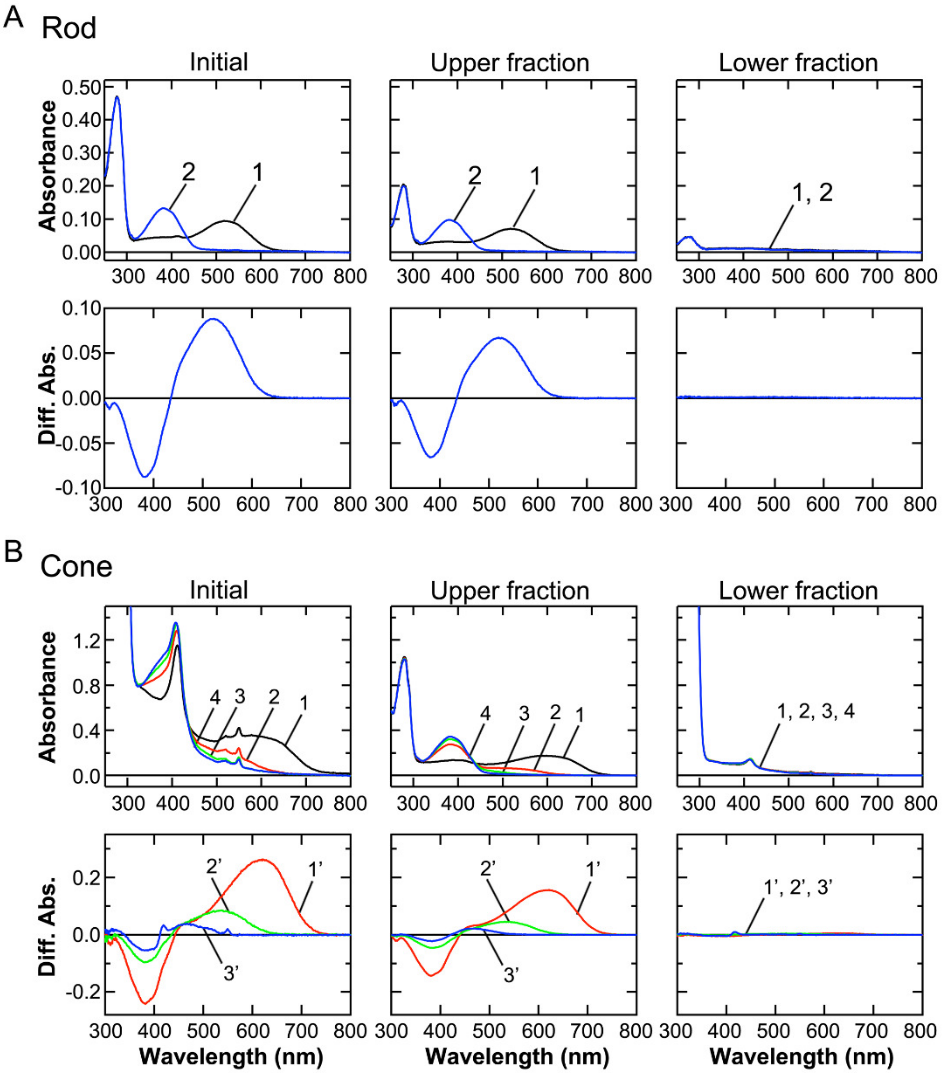

Fig 5. Quantification of visual pigments.

Quantity of visual pigments was measured spectrophotometically in three types of rod (A) and cone (B) preparations: membranes from purified cells as initial materials (Initial), membranes in the upper (Upper fraction) and lower (Lower fraction) fraction. (A) Rhodopsin content was measured in the initial rod membranes (left panels), in the upper and lower fraction (middle and right panels, respectively), all obtained from the same number of cells and suspended in the same volume of Ringer's solution. In each of upper panels, curve 1 (black) shows the absorption spectrum before bleach, and curve 2 (blue) shows the spectrum after complete bleach of rhodopsin with illumination of >440 nm light. Curve 2 was subtracted from curve 1 in each of the upper panel to obtain a difference spectrum, which is shown in the corresponding lower panel. From positive absorption by rhodopsin (λ_{max} = 522 nm), relative rhodopsin content was determined. (B) Contents of red-, green-, and blue-sensitive pigments were measured in the initial purified cone membranes (left panels), in the upper and lower faction ((middle and right panels, respectively). In each of upper panels, curve 1 (black) shows absorption spectrum before bleach. Red-sensitive pigment was first bleached with >675 nm light (curve 2), and then green-sensitive pigment with >600 nm light (curve 3) and finally blue-sensitive pigment with >440 nm light (curve 4). Curve 2 was subtracted from curve 1 to obtain a difference spectrum of red-sensitive pigment, which is shown in the corresponding lower panel (red curve 1', λ_{max} = 622 nm). Similarly, difference spectra were obtained for green-sensitive pigment (green curve 2', i.e., curve 2 – curve 3; λ_{max} = 535 nm) and for blue-sensitive pigment (blue curve 3', i.e., curve 3 – curve 4; λ_{max} = 460 nm) to determine the relative contents of these pigments.

Table 1. Recovery of membranes after separation of OS and IS.

Localization	**Outer segment membrane**	**Inner segment, Mitochondrial membranes**		**Inner segment, Plasma membranes**	**Inner segment, ER membranes**
		Inner membranes	**Outer membranes**		
Protein	**Visual pigment**	**F1 ATPase beta subunit**	**TOM20**	**Na$^+$/K$^+$ ATPase alpha subunit**	**Calnexin**
Rod upper fraction	86.2 ± 13.4 %	N.D.	9.1 ± 0.4 %.	65.7 ± 9.5 %	26.5 ± 4.3 %
Rod lower fraction	0.9 ± 0.2 %	84.8 ± 4.3 %	42.5 ± 7.0 %	40.2 ± 1.2 %	9.9 ± 3.1 %
Cone upper fraction	54.5 ± 3.2 %	3.5 ± 0.9 %	6.86 ± 1.5 %	49.0 ± 8.0 %	35.5 ± 3.1 %
Cone lower fraction	3.5 ± 0.2 %	54.6 ± 4.4 %	58.2 ± 12.3 %	10.9 ± 1.6 %	38.4 ± 5.3 %

Each value is shown as mean ±S.E in 3 independent measurements. N.D., signals not detected.

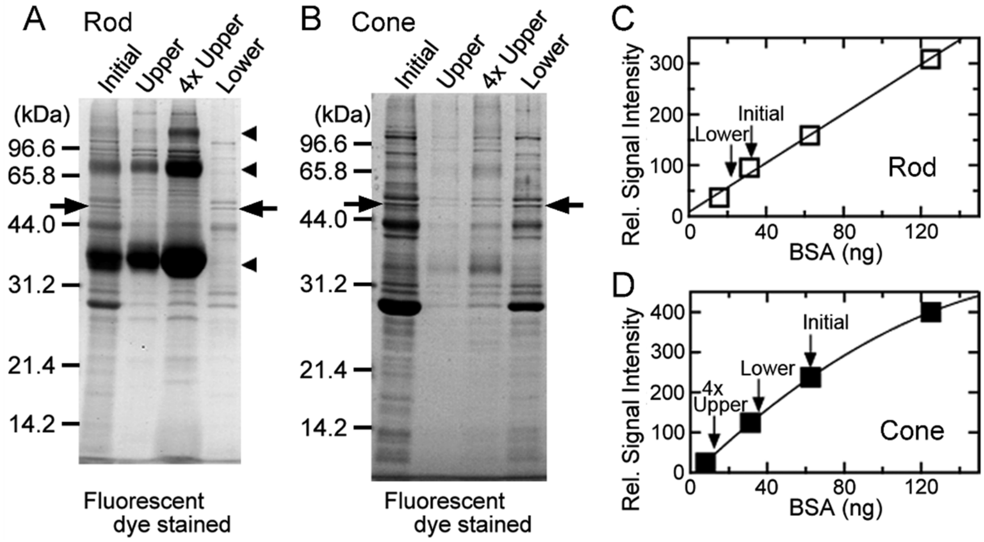

Fig 6. Quantification of F1 ATPase beta subunit.

Quantities of F1 ATPase beta subunit were determined by SDS-PAGE in four rod (A) and four cone (B) membrane preparations. (A) Rod membranes as initial materials (Initial), and rod upper and rod lower fractions (Upper and Lower, respectively) were subjected to SDS-PAGE. The gels were stained with a fluorescent dye, Oriole. In the lane labeled as 4×Upper, 4 times volume of the upper fraction was applied to quantify the amount of F1 ATPase beta subunit precisely. Arrowheads indicate the monomer, dimer and tetramer bands of rhodopsin, and arrows indicate the band of F1 ATPase beta subunit. (B) Similar SDS-PAGE pattern using four cone membrane preparations. (C) An example of quantification of F1 ATPase beta subunit with Oriole staining in four rod membrane preparations. A calibration curve was obtained with Oriole staining using known amounts of BSA (open rectangles and filled line), which was performed in parallel with SDS-PAGE of the rod membrane preparations. From the signal intensity of F1 ATPase beta subunit in (A), the amount of F1 ATPase beta subunit was quantified in four rod membrane preparations using the calibration curve (downward arrows). Note that F1 ATPase beta subunit was not detected in upper fractions in (A). (D) Similar quantification in four cone membrane preparations.

In the case of cones, red-, green-, and blue-sensitive cone visual pigments were also dominantly detected in the membranes at the upper interface (Fig 5B, left and middle panels) as in the case of rods, but distribution of the cone pigments in the upper fraction was lower than that of rods: it was 54.5 % in cones (n = 3, Table 1) while it was 86.2 % in rods as mentioned above. The amount of the cone visual pigments in the lower fraction was almost negligible similarly as in rods (Fig 5B, right panel). These results clearly show that both the rod and cone OS membranes were collected effectively at the upper interface (Ringer's solution/36 % sucrose interface) and therefore in the upper fraction, and there were little contaminations of OS membranes in the lower fractions.

Next, separation of IS membrane was examined. First, separation of inner mitochondrial membranes was examined by quantifying its marker protein, F1 ATPase beta subunit, in the upper and the lower fractions of both rods and cones. When the initial rod membranes and membranes in the upper and lower fractions of rods (Fig 6A), or those of cones (Fig 6B) were subjected to SDS-PAGE, a band was detected at 55 kDa (arrows) in the lane of initial rod membranes (Fig 6A, Initial) and that of initial cone membranes (Fig 6B, Initial). This band was identified as carp F1 ATPase beta subunit (AB023582.1) by mass spectrometry, and was also clearly detected in the lower fractions of both rods and cones (Upper in Fig 6A and B, respectively). The amount of F1 ATPase beta subunit in each of fractions (Initial, Upper, 4×Upper and Lower) was quantified by measuring the Oriole fluorescent signals of the band in each lane using BSA as a molar standard (Fig 6C and D) and the results showed that the mitochondrial inner membrane marker was detected minimally in the upper fraction (not detected in rods and 3.5 % in cones) and mainly in the lower fraction (84.8 % in rods and 54.6 % in cones) (Table1, F1 ATPase beta subunit).

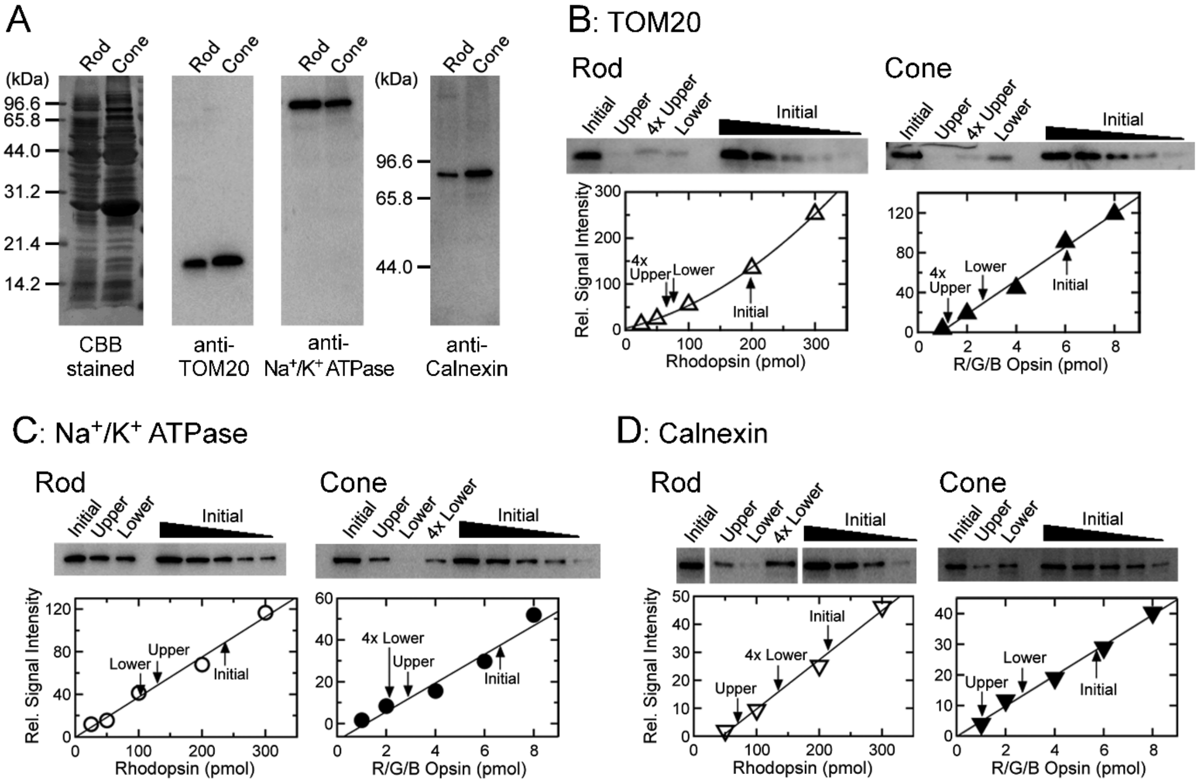

Fig 7. Estimation of separation of OS and IS membranes using TOM20, Na$^+$/K$^+$ ATPase alpha subunit and calnexin as marker proteins.

(A) Specificity of antibodies used to detect TOM20, Na$^+$/K$^+$ ATPase alpha subunit and that of anti-calnexin antiserum. Purified rod membranes containing 200 pmol of rhodopsin and cone membranes containing 6 pmol of cone total pigments were subjected to SDS-PAGE and were stained with Coomassie Brilliant Blue (left panel) or probed with antibodies or antiserum against each protein (right three panels). (B-D) Quantitative immunoblot analyses of TOM20 (B), Na$^+$/K$^+$ ATPase alpha subunit (C) and calnexin (D). In the upper panels in each of (B) - (D), purified rod membranes containing 200 pmol of rhodopsin or purified cone membranes containing 6 pmol of total cone pigments (Initial), upper and lower membrane fractions obtained from the same number of the purified cells (Upper and Lower, respectively), and a diluted series of initial rod and cone membranes were subjected to SDS-PAGE. These membranes were probed with antibodies or antiserum against each marker protein. To detect the amounts of target proteins precisely, 4 times volume of samples were applied when necessary (4×). The amount of a target protein in each of the membranes was determined with a calibration line obtained from immunoblot signals obtained in a diluted series of initial rod or cone membranes. In the lower panels in each of (B) - (D), examples of quantification are shown. The quantity of a target protein in each fraction is indicated by an arrow in lower panels. With this estimation, one can determine how much % of the target protein is present in each of the membranes as compared with the amount in the initial rod or cone membranes of the same cell number.

Then, separation of other membranes in the cellular organelles in the IS, IS plasma membranes, mitochondrial outer membranes and ER membranes, were examined. Those membranes in these fractions were probed with quantitative immunoblot analyses using marker proteins: TOM20 for mitochondrial outer membranes, Na^+/K^+ ATPase alpha subunit for IS plasma membranes and calnexin for ER membranes (Fig 7). As shown in Fig 7A, each of antibodies or antiserum used in the analysis detected a single band in purified rod and cone membranes, and the molecular mass of each of the detected band corresponded to the known value of the target protein. These results indicated that used antibodies and antiserum reacted to target proteins selectively. Next, the three marker proteins were quantified in initial rod and cone membranes and in the upper and the lower fractions (Fig 7B-D and Table 1). Fig 7B shows an example of the quantification of TOM20, a marker of mitochondrial outer membrane. This marker was detected in the upper fraction to some extent (9.1 % in rods and 6.9 % in cones), but much more in the lower fraction (42.5 % in rods and 58.2 % in cones) similarly as mitochondrial inner membrane marker, F1 ATPase beta subunit.

The IS plasma membrane marker, Na^+/K^+ ATPase alpha subunit, was detected in both the upper and the lower fractions, but the marker was present slightly more in the upper fraction: the percentage of the marker present in the upper fractions was 65.7 % in rods and 49.0 % in cones, and in the lower fractions, it was 40.2 % in rods and 10.9 % in cones (Fig 7C and Table 1). Calnexin, an ER membrane marker, was also present in both the upper and the lower fraction as IS plasma membranes. This marker was slightly enriched in the upper fraction in rods (26.5 % in the upper fraction and 9.9 % in the lower fraction) but detected almost equally in both fractions in cones (35.5 % in the upper fraction and 38.4 % in the lower fraction) (Fig 7D and Table 1).

From these results, it is concluded that upper fraction exclusively contains OS membranes together with some of IS membranes (mitochondrial inner and outer membranes, IS plasma membranes plus ER membranes) and lower fraction contains mainly mitochondrial membranes and some of the IS plasma membranes and ER membranes. For convenience, upper fraction is called as OS-rich fraction and lower fraction is called as IS-rich fraction. To distinguish each fraction between rods and cones, rod OS-rich fraction is called as ROS-rich fraction. Similarly the terms of RIS-rich fraction (rod IS-rich fraction), COS-rich fraction (cone OS-rich fraction) and CIS-rich fraction (cone IS-rich fraction) are used in the followings.

Although the OS-rich fraction contains OS membranes exclusively, it also contains some of the IS membranes: IS plasma membranes, ER membranes and less abundantly mitochondrial inner and outer membranes. The membranes used are all from purified rods and cones. These purified cells contain OS and also IS consisting of the ellipsoid and the myoid but lacking the nucleus and the terminal (Kawamura and Tachibanaki, 2008). From consideration of the structural basis of purified rods and cones, IS plasma membranes and ER membranes are probably present mush less than mitochondrial membranes and also much less than membranes of highly membranous OS. For this reason, contamination of IS plasma membranes and that of ER membranes would be limited in OS-rich fraction of both rods and cones.

In the present study, I focused on the proteins expressed specifically/dominantly in ROS or COS. Estimation of the amount of a marker protein shown above was based on the percentage of the proteins found in each of the membrane fractions comparing with that in the initial rod or cone membranes. In the COS-rich fraction, 3.5-6.9 % contamination of CIS proteins was observed (Table 1). Note that this contamination is the percentage of the total CIS proteins, and therefore, the actual contamination of CIS proteins is dependent on the total CIS proteins and total COS proteins. Previous estimation of the volumes of COS and CIS in carp showed that the CIS volume is ~6 times higher than the COS volume (Yamaoka *et al.*, 2015). Based on this volume ratio, I estimated the actual contamination of CIS proteins in COS-rich fraction. I assume an extreme case that the membrane density and protein density in the membranes are the same in COS and CIS. In this case, based on the distribution of visual pigment (~55 % of pigments in the initial COS membranes) and those of CIS proteins (TOM20 and F1 ATPase beta subunit; 3.5-6.9 % in the initial CIS membranes) in COS-rich fraction shown in Table 1, the calculation showed that the amount of the contaminated CIS proteins, mainly those in the mitochondrial inner and outer membranes, could be equivalent to the amount of the COS proteins in the COS-rich fraction (COS proteins: CIS proteins = ~55 % × 1: 3.5-6.9 % × 6). On the contrary, COS protein contamination in the CIS-rich fraction could be negligible (COS proteins: CIS proteins = 3.5 % × 1: 54.6-58.2 % × 6). Because contamination of CIS proteins in the COS-rich fraction cannot be ignored, I tried to identify proteins specifically/dominantly present in COS by excluding the proteins found in CIS-rich fraction which was contaminated with COS membranes minimally. Similar volume consideration was made for the amount of RIS proteins contaminated in ROS-rich fraction. In the ROS-rich fraction, 86.2 % of visual pigment, a ROS specific marker protein, was recovered, while the most abundant proteins in the RIS, mitochondrial inner and outer membrane proteins (F1 ATPase beta subunit and TOM20, respectively) were present in ROS-rich fraction at the amount of 9.1 % at the maximum (see Table 1). When the volume difference (ROS volume: RIS volume = 4:1, (Yamaoka *et al.*, 2015)) is taken into consideration, contamination of mitochondrial proteins in ROS-rich fraction is negligible (ROS proteins: mitochondrial proteins = 86.2 % × 4: 9.1 % × 1). The amount of other IS proteins such as IS plasma membrane proteins and inner segment ER membrane proteins are also little for the amount of ROS proteins in ROS-rich fraction. However, the amount of IS plasma membrane proteins and ER membrane proteins in ROS-rich fraction are equal to or larger than the amount of those in RIS-rich fraction (see Table 1). Therefore, because ROS proteins contamination in RIS-rich fraction are little (ROS proteins: RIS proteins = 0.9 % × 4: 42.5-84.8 % × 1), it is possible to efficiently identify proteins specifically/ dominantly present in ROS by excluding the proteins which found and are rich in RIS-rich fraction.

Identification of proteins specifically/dominantly expressed in ROS or COS

To identify ROS- or COS-specific/dominant proteins, I made a list of proteins detected in each of the ROS-rich, RIS-rich, COS-rich, and CIS-rich fractions using shotgun proteomic analysis by LC-MS/MS. ROS-rich fraction contains contaminated RIS membranes to some extent. It is also contaminated with COS and CIS membranes, which are potentially present in purified rods in a small amount (Tachibanaki *et al.*, 2001). Similarly, COS-rich fraction contains contaminated CIS membranes significantly, and also contaminated with ROS and RIS membranes and red blood cell membranes, which are potentially present in purified cones in a small amount. Then, to find proteins present specifically/dominantly in ROS, the proteins found in RIS-rich and COS-rich fractions were excluded from the list of the proteins detected in the ROS-rich fraction. With this comparison, not only the common proteins found in both ROS-rich and COS-rich fractions but also the RIS proteins contaminated or commonly present in ROS-rich fraction can be excluded. To find proteins present specifically/dominantly in COS, the same treatment was also carried out for COS-rich fraction.

In this study, I focused on the proteins tightly bound to membranes as the first step to identify proteins specifically/dominantly expressed in ROS or COS because only membranes were obtained (see above). For this purpose, membranes in each of the ROS-rich, RIS-rich, COS-rich, and CIS-rich fractions were washed to remove soluble and membrane-associated peripheral proteins as much as possible. SDS-PAGE patterns of the membranes in each of the fractions before wash (Fig 8A-D, Initial) and the final washed membranes (Fig 8A-D, Washed) are shown in Fig 8A-D. SDS-PAGE pattern of supernatants after washes with low salt buffer twice and with high pH buffer four times (Fig 8A-D, Low salt wash sup and High pH wash sup, respectively) showed that most of the removable proteins were washed away from the membranes.

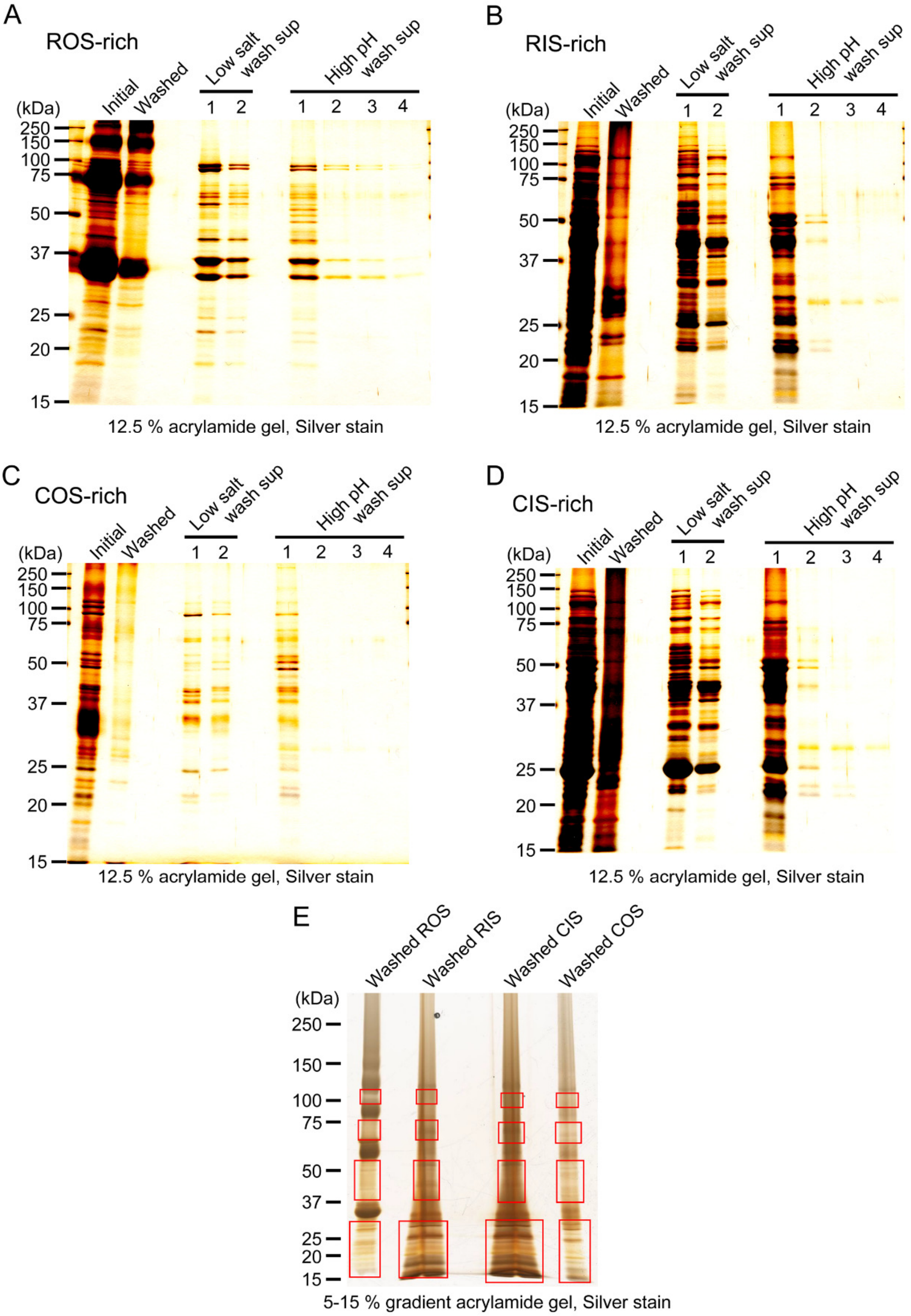

Fig 8. Preparation of washed membranes for LC-MS/MS.

Membranes in ROS-rich (A), RIS-rich (B), COS-rich (C) and CIS-rich (D) fractions were intensively washed with a low salt buffer and a high pH buffer to eliminate soluble and peripheral membrane proteins as much as possible. In (A) - (D), SDS-PAGE patterns of the membranes prepared from initial membranes (Initial), the membranes finally obtained after intensive washes

(Washed), and supernatants obtained during washes (Low salt wash sup 1-2 and High pH wash sup 1-4) are shown for membranes prepared from each fraction. In (E), an example of a gel subjected to LC-MS/MS analysis is shown. Washed membranes obtained from ROS-, RIS-, COS-, and CIS-rich fractions were subjected to SDS-PAGE, and boxed areas of each lane were cut out of the gel and subjected to in gel digestion for LC-MS/MS analysis. Membranes used for SDS-PAGE in each of the lane in (E) were obtained from 10^6 rods (Washed ROS), 4.7×10^5 rods (Washed RIS), 1.2×10^5 cones (Washed CIS) and 2.5×10^4 cones (Washed COS).

These washed membranes in each of fractions shown in Fig 8A-D were then subjected to SDS-PAGE to separate proteins for the analysis with LC-MS/MS. In the ROS-rich fraction, visual pigment, rhodopsin, is the most abundant protein (approx. 95 %). Proteins separated in the gel were digested for LC-MS/MS analysis, but massive amount of rhodopsin probably impedes the LC-MS/MS analysis by masking other proteolytic products when it is included. For this reason, rhodopsin band, monomer at 30~40 kDa, dimer at 55~65 kDa and trimer at 80~90 kDa, were excluded in LC-MS/MS analysis. In the analysis of proteins in other fractions, the same regions were omitted in order to compare the proteins equally. The regions indicated by four rectangles in each lane in Fig 8E were subjected to proteolysis and analyzed with LC-MS/MS. As a result, 648, 971, 1,064 and 629 proteins were identified from washed ROS-rich, RIS-rich, CIS-rich and COS-rich fraction, respectively (Supplemental Table S1-4).

Then, I identified proteins specifically/dominantly present in the ROS-rich or COS-rich fraction (Table 2 and 3, respectively). For these purposes, I used the emPAI (exponentially modified protein abundance index) value, which has been reported to be proportional to the amount of a protein present in a sample used for LC-MS/MS analysis (Ishihama *et al.*, 2005). Briefly, I used emPAI values obtained from the same number of the cells as an index of the amount of a protein present in the washed membranes. First, I calculated the portion of a protein in the ROS-rich fraction in a total amount of that protein in ROS-rich and RIS-rich fractions (shown as ROS/(ROS+RIS) in Table 2). With this procedure, I excluded proteins present more in RIS-rich fraction (i. e., those proteins showing ROS/(ROS+RIS)<0.5). The same treatment was applied to the proteins in COS-rich and CIS-rich fractions to exclude CIS proteins. In addition, proteins found in both ROS-rich and COS-rich fractions to similar extent were excluded: for example, when a protein in COS-rich fraction shows the emPAI value of >1/10 of that in ROS-rich fraction, this protein was regarded as the protein expressed in both ROS and COS. Furthermore, in Tables 2 and 3, I excluded the proteins showing the emPAI value <1/100 of the maximum value of the most abundant protein in ROS or COS (see Materials and Methods). After this manipulation, 132 proteins and 48 proteins remained in the list of proteins specifically/dominantly found in ROS-rich and COS-rich fraction, respectively. Note that ideally, but not actually, proteins present in the rhodopsin bands or visual pigments bands were not analyzed, and those present at the region close to these bands were not analyzed correctly.

Table 2. List of probable proteins present almost exclusively in ROS-rich fraction.

Protein*	Molecular Mass	emPAI		ROS
		ROS-rich	RIS-rich	(ROS+RIS)
[#]peripherin-2 (Travis *et al.*, 1991)	21 kDa	37.89	0	1
rod outer segment membrane protein 1 (Moritz and Molday, 1996)	25 kDa	11.87	0	1
retinal guanylyl cyclase 2 (Dizhoor *et al.*, 1994, Lowe *et al.*, 1995, Yang *et al.*, 1995)	**124 kDa**	**11.27**	**0**	**1**
PREDICTED: olfactory guanylyl cyclase GC-D isoform X3 (Dizhoor *et al.*, 1994, Lowe *et al.*, 1995, Yang *et al.*, 1995)	**88 kDa**	**9**	**0**	**1**
retinal guanylyl cyclase 2 (Dizhoor *et al.*, 1994, Lowe *et al.*, 1995, Yang *et al.*, 1995)	**125 kDa**	**7.78**	**0**	**1**
uncharacterized protein LOC100005305 (Azadi *et al.*, 2010)	11 kDa	5.06	0	1
ADP-ribosylation factor-like protein 8B-A	21 kDa	4.15	0	1
[#]PREDICTED: pleckstrin homology domain-containing family B member 1 isoform X1 (Xu *et al.*, 1999)	21 kDa	4.15	0	1
PREDICTED: uncharacterized protein LOC571872 isoform X1 (Kwok *et al.*, 2008)	23 kDa	3.63	0	1
olfactory guanylyl cyclase GC-D (Dizhoor *et al.*, 1994, Lowe *et al.*, 1995, Yang *et al.*, 1995)	**34 kDa**	**3.26**	**0**	**1**
ras-related protein Rab-18 (Kwok *et al.*, 2008)	23 kDa	3.05	0	1
ADP-ribosylation factor-like protein 8A	25 kDa	3.04	0	1
PREDICTED: olfactory guanylyl cyclase GC-D isoform X2 (Dizhoor *et al.*, 1994, Lowe *et al.*, 1995, Yang *et al.*, 1995)	**26 kDa**	**2.9**	**0**	**1**
PREDICTED: ADP-ribosylation factor-like protein 13B-like isoform X5	27 kDa	2.67	0	1
ras-related protein Rab-11A (Kwok *et al.*, 2008, Ying *et al.*, 2016)	22 kDa	2.57	0	1
dnaJ homolog subfamily C member 5G	22 kDa	2.53	0	1
PREDICTED: protein RD3-like (Azadi *et al.*, 2010)	24 kDa	2.24	0	1
small GTPase RhoA	22 kDa	1.64	0	1
synaptobrevin homolog YKT6 (Kwok *et al.*, 2008)	22 kDa	1.57	0	1
uncharacterized protein LOC449549 (Gordiyenko *et al.*, 2010)	23 kDa	1.49	0	1
ras-related protein Ral-A	23 kDa	1.48	0	1
PREDICTED: tubulin beta-4B chain-like, partial	16 kDa	1.42	0	1
PREDICTED: ras-related protein Rab-28 isoform X2 (Roosing *et al.*, 2013)	25 kDa	1.35	0	1
[#]peripherin 2b (retinal degeneration, slow) (Travis *et al.*, 1991)	39 kDa	1.29	0	1
guanylyl cyclase 3 (Fu and Yau, 2007, Kawamura and Tachibanaki, 2008)	**123 kDa**	**1.22**	**0**	**1**
[ER]PREDICTED: GTP-binding protein SAR1b-like (Bar-Peled and Raikhel, 1997)	13 kDa	1.19	0	1
[%]PREDICTED: regulator of G-protein signaling 9-binding protein B (Tachibanaki *et al.*, 2012, Hu *et al.*, 2003)	28 kDa	1.16	0	1
guanylyl cyclase 3 (Fu and Yau, 2007, Kawamura and Tachibanaki, 2008)	**128 kDa**	**1.15**	**0**	**1**
PREDICTED: alpha/beta hydrolase domain-containing protein 17A	28 kDa	1.12	0	1

PREDICTED: protein RD3-like (Azadi *et al.*, 2010)	24 kDa	1.09	0	1
$^{\#}$retinol dehydrogenase 8a (Miyazono *et al.*, 2008)	35 kDa	1.02	0	1
PREDICTED: josephin-2 isoform X1	21 kDa	0.96	0	1
PREDICTED: ADP-ribosylation factor 2	16 kDa	0.93	0	1
PREDICTED: uncharacterized protein si:dkey-182g1.3	16 kDa	0.93	0	1
$^{\#}$PREDICTED: peripherin-2 (Travis *et al.*, 1991)	39 kDa	0.9	0	1
PREDICTED: vesicle transport through interaction with t-SNAREs homolog 1A isoform X1	26 kDa	0.72	0	1
PREDICTED: phospholipid-transporting ATPase IB isoform X6	134 kDa	0.67	0	1
$^{\%}$PREDICTED: regulator of G-protein signaling 9 isoform X1 (Tachibanaki *et al.*, 2012)	57 kDa	0.66	0	1
histone 2, H2a	14 kDa	0.65	0	1
PREDICTED: cGMP-gated cation channel alpha-1 (Weitz *et al.*, 2002, Zheng *et al.*, 2002)	**36 kDa**	**0.65**	**0**	**1**
guanine nucleotide-binding protein subunit beta-5 (Hu *et al.*, 2003)	43 kDa	0.64	0	1
rho-related gtp-binding protein rhoc	22 kDa	0.62	0	1
ras homolog gene family, member A	22 kDa	0.61	0	1
PREDICTED: ras-related protein Rab-30	15 kDa	0.61	0	1
ras-related protein Rab-8A (Deretic *et al.*, 1995, Kwok *et al.*, 2008, Ying *et al.*, 2016)	23 kDa	0.59	0	1
PREDICTED: CSC1-like protein 2 isoform X2	87 kDa	0.58	0	1
PREDICTED: sodium/potassium/calcium exchanger 1 isoform X1 (Kim *et al.*, 1998)	**80 kDa**	**0.57**	**0**	**1**
^{Mt}PREDICTED: choline transporter-like protein 1 (Michel and Bakovic, 2009)	72 kDa	0.49	0	1
PREDICTED: protein-L-isoaspartate(D-aspartate) O-methyltransferase isoform X1	26 kDa	0.49	0	1
ragulator complex protein LAMTOR1	18 kDa	0.49	0	1
PREDICTED: CSC1-like protein 2	47 kDa	0.47	0	1
PREDICTED: uncharacterized protein si:rp71-36a1.2	28 kDa	0.46	0	1
uncharacterized protein LOC100001558 (Weitz *et al.*, 2002, Zheng *et al.*, 2002)	**19 kDa**	**0.46**	**0**	**1**
PREDICTED: tetratricopeptide repeat protein 8-like isoform X1	58 kDa	0.45	0	1
PREDICTED: protein tyrosine phosphatase type IVA 2-like isoform X3	19 kDa	0.44	0	1
PREDICTED: E3 ubiquitin-protein ligase RNF170-like	29 kDa	0.44	0	1
PREDICTED: solute carrier family 41 member 1	40 kDa	0.42	0	1
^{IS}ADP-ribosylation factor-like protein 1 (Van *et al.*,2001)	20 kDa	0.41	0	1
palmitoyltransferase ZDHHC2	42 kDa	0.41	0	1
ADP-ribosylation factor-like protein 3	20 kDa	0.41	0	1
signal recognition particle receptor subunit beta	31 kDa	0.41	0	1
PREDICTED: ras-related protein Rap-2c	21 kDa	0.4	0	1
PREDICTED: casein kinase I isoform gamma-1-like isoform X2	53 kDa	0.4	0	1

alpha/beta hydrolase domain-containing protein 17C	32 kDa	0.4	0	1
cell division control protein 42 homolog	21 kDa	0.39	0	1
PREDICTED: F-box/LRR-repeat protein 20	45 kDa	0.38	0	1
syntaxin 5	34 kDa	0.36	0	1
ras-related protein Rab-24	23 kDa	0.36	0	1
^{IS}receptor expression-enhancing protein 6 (Arno *et al.*, 2016)	23 kDa	0.35	0	1
uncharacterized protein LOC101884052	11 kDa	0.35	0	1
$^{\#}$peripherin-2 (Travis *et al.*, 1991)	18 kDa	13.19	0.06	0.996
PREDICTED: pyruvate kinase PKM isoform X1	60 kDa	9.33	0.07	0.992
neurotrimin isoform 1 precursor	38 kDa	3.08	0.03	0.992
rod outer segment membrane protein 1 (Moritz and Molday, 1996)	40 kDa	9.09	0.08	0.991
PREDICTED: cadherin-related family member 1-like isoform X2 (Rattner *et al.*, 2001)	99 kDa	0.61	0.01	0.984
uncharacterized protein LOC492355	23 kDa	2.41	0.04	0.982
$^{\#}$peripherin-2 (Travis *et al.*, 1991)	20 kDa	6.1	0.11	0.982
PREDICTED: cGMP-gated cation channel alpha-1 (Weitz *et al.*, 2002, Zheng *et al.*, 2002)	**63 kDa**	**2.31**	**0.05**	**0.979**
lysophosphatidylcholine acyltransferase 2	60 kDa	0.62	0.02	0.974
rhodopsin	**40 kDa**	**35.41**	**0.96**	**0.974**
$^{\#}$peripherin-2 (Travis *et al.*, 1991)	20 kDa	1.9	0.05	0.973
PREDICTED: ADP-ribosylation factor-like protein 13B-like isoform X5	42 kDa	1.77	0.05	0.973
PREDICTED: red-sensitive opsin-1 isoform X1	**41 kDa**	**0.85**	**0.02**	**0.972**
ras-related protein Rab-18-B (Kwok *et al.*, 2008)	23 kDa	1.5	0.04	0.971
ras-related protein Rap-1b-like (Kwok *et al.*, 2008)	21 kDa	3.51	0.11	0.971
PREDICTED: cGMP-gated cation channel alpha-1 (Weitz *et al.*, 2002, Zheng *et al.*, 2002)	**63 kDa**	**2.13**	**0.07**	**0.969**
putative Ras-related protein Rab-42	18 kDa	1.7	0.06	0.967
PREDICTED: ras-related protein Rab-7a isoform X1 (Gordiyenko *et al.*, 2010)	24 kDa	1.11	0.04	0.963
PREDICTED: ras-related protein Rab-10	23 kDa	3.73	0.16	0.959
ras-related protein Rab-2A	24 kDa	16.19	0.76	0.955
PREDICTED: ras-related protein Rab-11B (Kwok *et al.*, 2008)	25 kDa	5.48	0.28	0.951
PREDICTED: phospholipid scramblase 2	26 kDa	1.55	0.08	0.95
^{ER}transmembrane protein 33 (Urade *et al.*, 2014)	29 kDa	0.64	0.04	0.948
epidermal retinol dehydrogenase 2	34 kDa	1.09	0.06	0.946
ADP-ribosylation factor-like protein 6	21 kDa	1.73	0.11	0.942
ras-related protein Rap-1b precursor (Kwok *et al.*, 2008)	21 kDa	2.86	0.18	0.942
^{IS}ubiquitin-60S ribosomal protein L40 (Perrelet, 1972)	12 kDa	1.37	0.09	0.939
PREDICTED: cadherin-related family member 5-like isoform X2	17 kDa	0.83	0.06	0.933
^{ER}PREDICTED: GTP-binding protein SAR1b (Bar-Peled and Raikhel, 1997)	22 kDa	0.6	0.05	0.93
ADP-ribosylation factor-like 15a	23 kDa	0.59	0.04	0.93

ras-related protein Rab-35	20 kDa	2.35	0.18	0.928
dolichol-phosphate mannosyltransferase subunit 1	28 kDa	0.46	0.04	0.928
PREDICTED: uncharacterized protein LOC571872 isoform X1 (Kwok *et al.*, 2008)	32 kDa	7.97	0.62	0.927
^{IS}40S ribosomal protein S3a (Perrelet, 1972)	33 kDa	0.39	0.03	0.926
^{ER}ER membrane protein complex subunit 3 (Christianson *et al.*, 2010)	30 kDa	1.3	0.11	0.919
uncharacterized protein LOC393228	21 kDa	0.93	0.1	0.9
ras-related protein Rab-5B (Shelby *et al.*, 2015)	24 kDa	0.82	0.09	0.898
peroxisomal membrane protein 11B	25 kDa	0.76	0.09	0.897
^{IS}PREDICTED: 40S ribosomal protein S3-like isoform X1 (Perrelet, 1972)	28 kDa	0.65	0.08	0.895
ras-related protein Rab-14	24 kDa	1.81	0.21	0.894
PREDICTED: ras-related protein Rab-1A-like isoform X1	22 kDa	5.63	0.67	0.893
ras-related protein Rab-1B (Kwok *et al.*, 2008)	22 kDa	5.57	0.67	0.893
^{IS}40S ribosomal protein S10 (Perrelet, 1972)	20 kDa	0.41	0.05	0.891
PREDICTED: cadherin-related family member 5-like isoform X2	44 kDa	1.08	0.13	0.89
ras-related protein Rab-5C (Shelby *et al.*, 2015)	37 kDa	1.86	0.25	0.88
ras-related protein Rab-1B (Kwok *et al.*, 2008)	19 kDa	2.06	0.29	0.875
RAB11a, member RAS oncogene family, like (Kwok *et al.*, 2008, Ying *et al.*, 2016)	20 kDa	1.86	0.27	0.873
^{ER}alpha-1,3/1,6-mannosyltransferase ALG2 (Thiel *et al.*, 2003)	46 kDa	0.48	0.07	0.872
PREDICTED: sphingomyelin phosphodiesterase 2 isoform X1	48 kDa	0.45	0.07	0.871
rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha (Catty *et al.*, 1992)	**99 kDa**	**0.44**	**0.06**	**0.871**
^{IS}60S ribosomal protein L9 (Perrelet, 1972)	22 kDa	0.62	0.1	0.86
N-acetyltransferase 14	32 kDa	0.4	0.07	0.856
RAB5A, member RAS oncogene family, a (Shelby *et al.*, 2015)	24 kDa	2.31	0.39	0.856
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	24 kDa	0.8	0.15	0.844
^{IS}40S ribosomal protein S5 (Perrelet, 1972)	25 kDa	0.77	0.14	0.844
^{IS}nicastrin precursor (Baulac *et al.*, 2003)	42 kDa	0.41	0.08	0.84
immunity-related GTPase family, q2	42 kDa	1.35	0.26	0.838
^{ER}vesicle-trafficking protein SEC22b-A (Nakajima *et al.*, 2004)	24 kDa	1.07	0.21	0.836
^{ER}uncharacterized protein LOC100127828 (Moon and Horton, 2003)	34 kDa	0.86	0.18	0.826
RAB1A, member RAS oncogene family	28 kDa	1.44	0.31	0.825
guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 (Lerea *et al.*, 1986)	**37 kDa**	**16.62**	**3.61**	**0.821**
^{IS}protein NDRG1 isoform 1 (Takita *et al.*, 2016)	42 kDa	3.23	0.77	0.808

*Proteins already known to be specifically expressed in ROS are indicated in red bold, and those known to be expressed in other portions of a rod or in other cells are indicated with color background. Yellow background: proteins expressed in both ROS and COS, including those expressed in ROS, but their expression in COS not confirmed.

Yellow background: proteins abundantly expressed in ROS and less abundantly in COS ($^{\#}$), or those abundantly expressed in COS and less abundantly in ROS ($^{\%}$).

Green background: proteins detected in purified ROS disk membranes.

Gray background: COS-specific proteins (blue bold), ER specific proteins (^{ER}), mitochondrial protein (^{Mt}) and IS proteins (^{IS}).

The values of emPAI shown are those obtained in the washed membranes of 30×10^4 rods.

Table 3. List of probable proteins present almost exclusively in COS-rich fraction.

Protein*	Molecular Mass	emPAI		$\frac{COS}{(COS+CIS)}$
		COS-rich	CIS-rich	
^{IS}creatine kinase b-type (Sistermans *et al.*, 1995)	16 kDa	1.92	0	1
ADP-ribosylation factor 1	21 kDa	1.34	0	1
protein RD3 (Azadi *et al.*, 2010)	15 kDa	1.04	0	1
^{IS}retinoschisin precursor (Molday *et al.*, 2007)	22 kDa	0.62	0	1
PREDICTED: guanine nucleotide-binding protein G(i) subunit alpha-1	40 kDa	0.56	0	1
PREDICTED: guanine nucleotide-binding protein subunit alpha-13-like	34 kDa	0.52	0	1
PREDICTED: gamma-glutamyltransferase 5 isoform X1	62 kDa	0.5	0	1
PREDICTED: cyclic nucleotide-gated cation channel beta-3-like isoform X2 (Biel *et al.*, 1999)	**28 kDa**	**0.47**	**0**	**1**
carbonic anhydrase (Hageman *et al.*, 1991)	29 kDa	0.45	0	1
PREDICTED: cadherin-related family member 5-like isoform X2	20 kDa	0.41	0	1
neurocalcin-delta B	22 kDa	0.38	0	1
PREDICTED: cyclic nucleotide-gated channel cone photoreceptor subunit alpha isoform X2 (Biel *et al.*, 1999)	**81 kDa**	**0.36**	**0**	**1**
PREDICTED: flotillin 1a isoform X1	47 kDa	0.35	0	1
ras-related protein Rab-43	23 kDa	0.35	0	1
^{ER}vitamin K epoxide reductase complex subunit 1-like protein 1 (Westhofen *et al.*, 2011)	12 kDa	0.34	0	1
PREDICTED: ras-related protein Rab-35-like	24 kDa	0.34	0	1
PREDICTED: Fc receptor-like protein 5 isoform X2	12 kDa	0.33	0	1
PREDICTED: SH3-containing GRB2-like protein 3-interacting protein 1 isoform X2	12 kDa	0.32	0	1
synaptic vesicle glycoprotein 2B	12 kDa	0.32	0	1
PREDICTED: uncharacterized protein LOC100334801 isoform X2	26 kDa	0.31	0	1
guanine nucleotide-binding protein G(i) subunit alpha-2	41 kDa	0.3	0	1
ubiquitin-like 3b	13 kDa	0.3	0	1
ras-related GTP-binding protein C	13 kDa	0.29	0	1
band 3 anion transport protein (211V-519E) (Schlüter and Drenckhahn, 1986)	35 kDa	3.68	0.08	0.98
cyclic nucleotide-gated channel cone photoreceptor subunit alpha-like (Biel *et al.*, 1999)	**82 kDa**	**0.56**	**0.02**	**0.974**
PREDICTED: ammonium transporter Rh type A isoform X1 (Iwamoto *et al.*, 1998)	12 kDa	3.2	0.11	0.967
flotillin-1	41 kDa	2.14	0.1	0.955
band 3 anion transport protein (92M-191C) (Schlüter and Drenckhahn, 1986)	11 kDa	5.06	0.27	0.949
flotillin-2a	47 kDa	2.12	0.12	0.947
guanine nucleotide-binding protein G(t) subunit alpha-2 (Lerea *et al.*, 1986)	**40 kDa**	**28.3**	**2.02**	**0.933**

opsin-1, short-wave-sensitive 1	**39 kDa**	**0.44**	**0.03**	**0.933**
band 3 anion transport protein (562G-810W) (Schlüter and Drenckhahn, 1986)	27 kDa	1.17	0.1	0.923
$^{\%}$PREDICTED: regulator of G-protein signaling 9-binding protein-like (Tachibanaki *et al.*, 2012, Hu *et al.*, 2003)	27 kDa	6.33	0.63	0.909
^{ER}signal peptidase complex subunit 3 (Kalies and Hartmann, 1996)	20 kDa	1.39	0.14	0.909
^{IS}PREDICTED: metal transporter CNNM4 (Parry *et al.*, 2009, Polok *et al.*, 2009)	35 kDa	0.66	0.08	0.898
^{IS}brain creatine kinase b (Sistermans *et al.*, 1995)	43 kDa	0.52	0.06	0.895
adipocyte plasma membrane-associated protein	47 kDa	1	0.12	0.893
green-sensitive opsin-4	**39 kDa**	**2.04**	**0.25**	**0.892**
$^{\%}$PREDICTED: regulator of G-protein signaling 9 isoform X2 (Tachibanaki *et al.*, 2012)	62 kDa	0.9	0.11	0.889
guanine nucleotide-binding protein G(o) subunit alpha	40 kDa	1.44	0.19	0.885
protein kinase, cAMP-dependent, regulatory, type II, alpha A	45 kDa	0.62	0.09	0.872
synaptotagmin II	47 kDa	0.36	0.06	0.867
G-protein-coupled receptor kinase 7A (Rinner *et al.*, 2005)	**62 kDa**	**3.49**	**0.56**	**0.863**
^{ER}dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit precursor (Yamagata *et al.*, 1997)	51 kDa	0.63	0.11	0.854
solute carrier family 2, facilitated glucose transporter member 1	53 kDa	0.61	0.1	0.854
peroxiredoxin-2	22 kDa	0.62	0.13	0.831
PREDICTED: sodium/potassium/calcium exchanger 2-like isoform X2 (Li *et al.*, 2006)	**68 kDa**	**0.45**	**0.1**	**0.816**
cone cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha' (Stearns *et al.*, 2007)	**98 kDa**	**0.39**	**0.1**	**0.8**

*Proteins already known to be specifically expressed in COS are indicated in blue bold, and those known to be expressed in other portions of a cone or in other cells are indicated with color background.

Gray background: IS proteins (^{IS}) and ER specific proteins (^{ER}).

Yellow background: proteins expressed in both ROS and COS, or those abundantly expressed in COS and less abundantly in ROS ($^{\%}$).

Blue background: cone specific protein present both in OS and IS.

Pink background: red blood cell specific proteins.

The values of emPAI shown are those obtained in the washed membranes of 5 × 10^4 cones.

Among the 132 proteins found in ROS-rich fraction, 13 proteins are already known to be present only in ROS (shown in red bold in Table 2) and 23 proteins are known to be expressed abundantly in ROS although they are also known to be expressed in COS (proteins with yellow background in Table 2). Additionally, the other 13 proteins are known to be detected in highly purified ROS disk membranes (proteins with green background in Table 2) (Kwok *et al.*, 2008). These facts ensure that the proteins with higher expression in ROS than COS remained in the list and the strategy to identify ROS-specific/dominant proteins is valid. On the one hand, 21 proteins that are known not to be localized at ROS also remained in the list (proteins with gray background in Table 2). With lowering the (ROS/ROS+RIS) value, number of proteins expressed not in the OS seems to be increased. The remaining 62 proteins without special indication in Table 2 could be specifically/dominantly separated into the ROS-rich fraction during the membrane separation. In general, with increasing the value of (ROS/ROS+RIS), the possibility that the protein is expressed specifically/dominantly in ROS would be higher.

Similarly, 48 proteins are listed in Table 3. Among them, 9 proteins are already known to be present only in COS (shown in blue bold in Table 3). The other three proteins are known to be present in both ROS and COS (with yellow background), and two of them ($^{\%}$) showing more than 20 times higher expression levels in COS than in ROS (Tachibanaki *et al.*, 2012) are also listed in Table 3. These facts ensure that the strategy to identify COS-specific/dominant proteins is valid. However, 11 proteins that are known not to be localized in COS also remained in the list (proteins with gray and pink background in Table 3). Unlike ROS-rich fraction, there was little relation between these proteins and (COS/COS+CIS) values. The remaining 24 proteins without special indication in Table 3 could be specifically/dominantly separated into the COS-rich fraction during the membrane separation.

These results that proteins known to be localized outside of ROS or COS were found in Tables 2 and 3 may suggest that there is a local density difference in membranes to induce membrane contamination in my membrane separation using density gradient. In any event, the results indicate that these lists (Tables 2 and 3) contain ROS- or COS-specific/dominant proteins but that their exact localization should be confirmed with alternative ways such as immunocytochemistry.

Localization of NCALD in cone

Validation of my separation of membranes was tested by using one of the candidate proteins, neurocalcin delta B (NCALD), which was detected specifically in the COS-rich fraction in my study. NCALD has been reported to be expressed in amacrine cells and ganglion cells (Nakano *et al.*, 1992), and its localization is also recognized in CIS (Krishnan *et al.*, 2004) but not in COS. As shown in Tables 3, S3 and S4, NCALD was detected in COS but not in CIS, and not in ROS or RIS (Tables S1 and S2).

Localization of NCALD was examined in isolated cones. As has been reported previously (Krishnan *et al.*, 2004), NCALD was present in IS (anti-NCALD in Fig 9A) similarly as mitochondrial aspartate aminotransferase 2 (anti-mAAT in Fig 9A), a marker protein of mitochondrial inner membranes in IS (Masuda *et al.*, 2016). In addition, some punctate NCALD signals were detected also in COS (Fig 9A, anti-NCALD) in the apical region of a COS as well as at the base of a COS, possibly the calycal process. The apparent discrepancy between this immunocytochemistry (mainly present in CIS and slightly in COS) and the result of LC-MS/MS analysis shown in Table 3 (only present in COS membranes) could be due to the difference in the membranes probed in these studies: in immunocytochemistry, native membranes in living cells were probed while in the LC-MS/MS analysis, membranes intensively washed were used. This possibility was examined with immunoblot.

In immunoblot analysis in non-washed membranes of ROS-rich and RIS-rich fractions (ROS-rich and RIS-rich in Fig 9C), NCALD signals was not observed (arrowhead), while positive signals in non-washed COS-rich and CIS-rich fractions were detected (COS-rich and CIS-rich in Fig 9C). The intensity of the signal was higher in the CIS-rich fraction (the number of purified cones used in Fig 9C was smaller for CIS-rich fraction, see legend to Fig 9C), which is in agreement with the immunocytochemical study shown in Fig 9A. However, in membranes intensively washed (washed membranes), which were used for LC-MS/MS analysis, NCALD signal was not detected (Fig 9D, arrowhead) even when the membranes applied for SDS-PAGE increased by 12.5 times for washed COS membrane and 50 times for washed CIS membranes (Washed COS and Washed CIS, respectively in Fig 9D) than those used in Fig 9C.

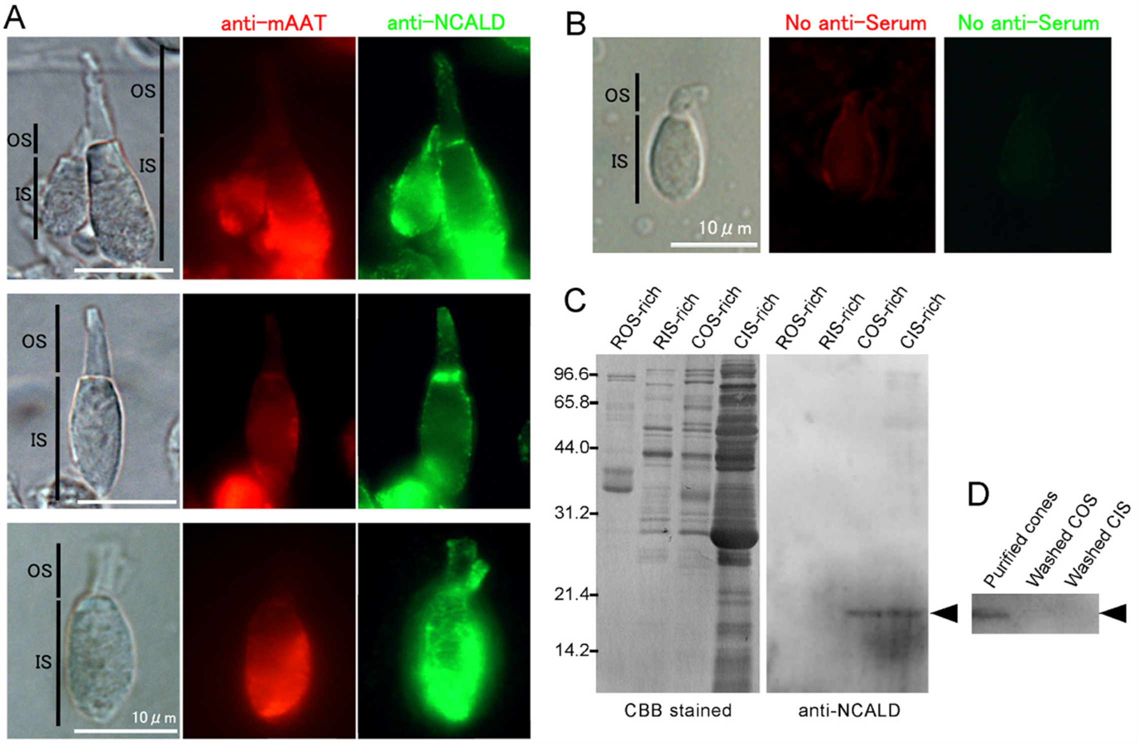

Fig 9. Subcellular localization of neurocalcin δ B (NCALD) in rods and cones.
(A) DIC images (left panels) of double (top), single (middle) and twin (bottom) cones, and immunofluorescent images of antiserum against anti-mAAT (middle panels) and those of NCALD (right panels). Scale bars, 10 μm. OS, outer segment. IS, inner segment. (B) Negative control of (A) with use of control mouse serum (middle for mAAT) and rabbit serum (right for NCALD). A cone was only faintly labeled with these control sera. (C) Immunoblot analysis of non-washed membranes in ROS-, RIS-, COS- and CIS-rich fractions (ROS-rich, RIS-rich, COS-rich and CIS-rich, respectively). Membranes in these fractions were subjected to SDS-PAGE and were stained with CBB or probed with antibody against NCALD. NCALD signals were observed in membranes of COS-rich and CIS-rich fractions (arrowhead). The membranes of ROS- and RIS-rich fraction were obtained from 2.0 × 10^5 rods. The membranes of COS- and CIS-rich fraction were obtained from 2.0 × 10^5 and 5.0 × 10^4 cones, respectively, to observe similar intensity of immunoblot signals of NCALD. (D) Immunoblot signals of NCALD (arrowhead) on membranes obtained from 2.0 × 10^5 purified cone membranes (Purified cones), washed COS membranes obtained from 2.5 × 10^6 purified cones (Washed COS) and washed CIS membrane obtained from 2.5 × 10^6 purified cones (Washed CIS).

Neurocalcin is a member of the neuronal calcium sensor family (Burgoyne, 2007, Ames and Lim, 2012), and is thought to be soluble under low Ca^{2+} conditions. Therefore, it is possible that most of NCALD were removed from membranes during the wash of membranes used for LC-MS/MS analysis, because Ca^{2+} concentration in washing buffers were low. This would be the reason why NCALD was not detected in washed CIS-rich membranes. Previous studies showed that NCALD is able to interact directly with retinal guanylyl cyclase 1 (ROS-GC1) (Krishnan *et al.*, 2004), which is known to be localized to ROS membranes. In carp cones, cone guanylate cyclase (GC-C (Takemoto *et al.*, 2009) or guanylyl cyclase 3) is expressed as the homolog of bovine ROS-GC1. GC-C was detected in COS-rich fraction in my LC-MS/MS analysis (Table S3). It is possible that a few amount of NCALD, which is bound to GC-C in washed COS-rich membranes and is enough to be detected in the LC-MS/MS analysis (Tables 3 and S4) but not in immunoblot analysis (Fig 9D). GC-C was actually detected in the LC-MS/MS analysis in the washed COS-rich fraction but not in the washed CIS-rich fraction (Tables S3 and S4, respectively). However, GC-C was also detected in ROS-rich fraction (Tables 2 and S1) probably because of contamination of cones in purified rod preparation (Tachibanaki *et al.*, 2001). It is the reason why GC-C is not listed in Table 3.

Proteomic analysis on proteins expressed in OS and IS in rods and cones

It has been known that rods and cones are different in many aspects. For example, phototransduction in OS is different (Pugh and Lamb, 1993, Kawamura and Tachibanaki, 2008, Fu and Yau, 2007), OS morphology is different (Pugh and Lamb, 1993, Kawamura and Tachibanaki, 2008, Fu and Yau, 2007), energy metabolism is different (Okawa *et al.*, 2008), and so on. In previous studies, by transcriptomic analysis of purified rods and cones, proteins or genes that are specifically or dominantly expressed in ether rods or cones were found (Akimoto *et al.*, 2006, Tsuji *et al.*, 2007, Shimauchi-Matukawa *et al.*, 2008). These proteins or genes are potentially the candidates participating in the differences between rods and cones. However, it is not easy to identify their functional roles generally. On this point, it is very probable that those proteins are expressed at the site where the difference is observed. In this study, a method to obtain OS and IS membranes effectively from purified rods and cones was established and the quantity was large enough to perform biochemical studies. Then, I actually succeeded in identifying a protein that localized to COS membranes but not in CIS, ROS and RIS membranes (Fig 9), although these membranes were intensively washed. Therefore, these results could contribute to the study aiming at finding proteins specifically expressed at appropriate site, OS or IS in rods or cones, to exert their specific functions.

Future perspectives

In this study, I established a method to obtain OS and IS membranes effectively from purified rods and cones, and found some candidates of ROS- or COS-specific/ dominant proteins. I believe that functional analysis of these proteins will elucidate the mechanisms of the differences in function and structure between rods and cones.

By the way, in my study, LC-MS/MS analysis was performed except for rhodopsin bands in ROS-rich fraction and the same regions in RIS-, COS- and CIS-rich fractions because I thought that massive amount of rhodopsin probably impedes the LC-MS/MS analysis by masking other proteolytic products when it is included. However, LC-MS/MS analysis of all proteins in purified ROS membrane were performed (Skiba *et al.*, 2013) and their result suggested that massive amount of rhodopsin had little impedance in LC-MS/MS analysis. From this, LC-MS/MS analysis in all regions of all fractions I prepared is potentially possible, and it is expected that more new ROS- or COS-specific/dominant proteins can be found.

I focused on the proteins tightly bound to membranes as the first step and found some candidates of ROS- or COS-specific/dominant proteins. Unfortunately, soluble proteins and peripheral membrane proteins were not included in my study, but ROS- or COS-specific/dominant proteins should be found in such a group of proteins. In particular, analysis of soluble proteins is difficult because soluble proteins were lost during purification of OS and IS membranes. On the one hand, analysis of peripheral membrane proteins is possible when one uses ROS, RIS, COS and CIS membranes before washing or the supernatants obtained during washes. It is possible to extend my study by using these preparations in elucidating the molecular mechanism of the differences between rods and cones. I hope that that my current study will contribute to those studies.

So far, I focused on ROS- or COS-specific/dominant proteins because phototransduction cascade exists in OS, but it is possible to focus on RIS- or CIS-specific/dominant proteins. The IS has a function mainly to produce energy, and IS size are greatly different between rods and cones (Fig 1). Also, it is known that cones have more energy requirements than rods (Okawa *et al.*, 2008). From this, it is possible that qualitative and/or quantitative functional differences, and structural differences are present between RIS and CIS. On this point, it will be interesting to focus on IS with finding RIS- or CIS-specific/dominant proteins, which I believe practically possible.

To elucidate the molecular mechanisms of the differences between rods and cones, I believe that knockout study is very effective. Unfortunately, knockout study in carp is very difficult because of its slow growth rate and large size of breeding facility.

However, in zebrafish (*Danio rerio*) which is a kind of model animal and the most closely related to carp, knockout analysis can be rather easily performed by genome editing. First of all, using knockout zebrafish of NCALD newly found as a protein not localized in ROS but localized in COS in this study, I would like to investigate whether light response is changed. As already mentioned, NCALD is able to interact directly with ROS-GC1 (see **Results and Discussion**) and active ROS-GC1 (Krishnan *et al.*, 2004). High activation of guanylate cyclase (GC) in light response is known to be related to briefer response (Takemoto *et al.*, 2009). If light response is changed in NCALD knockout zebrafish, it is possible that NCALD contributes to the characteristic light response of cones including briefer response by interacting directly with and activating GC-C. I believe that to investigate the function of NCALD in COS will elucidate one of the differences of molecular bases between rods and cones.

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Acknowledgment

I thank Professor Seiji Takashima and Dr. Kazumasa Takafuji at Osaka University for discussion and performing MS analysis, and Mr. Yuki Komatsu in our lab for preparing anti-mAAT antiserum against carp mAAT.

I express gratitude to Professor Satoru Kawamura and Associate Professor Shuji Tachibanaki for invaluable discussions and suggestions throughout this study. I thank Professor Nobuhiko Yamamoto, Professor Seiji Takashima and Professor Yasushi Hiraoka for critical readings of this thesis. I thank all members of Kawamura laboratory for various discussions and supports.

Table S1. Identified proteins in washed ROS-rich fraction.

Proteins in washed ROS-rich fraction were identified with LC-MS/MS analysis and are listed in descending order of emPAI values for 5×10^5 rods.

	Identified proteins in washed ROS-rich fraction	Molecular mass	emPAI
1	uncharacterized protein LOC100145214	33 kDa	7.7948
2	peripherin-2	21 kDa	6.1222
3	rhodopsin	40 kDa	5.7215
4	guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	37 kDa	2.6851
5	ras-related protein Rab-2A	24 kDa	2.6161
6	peripherin-2	18 kDa	2.1304
7	rod outer segment membrane protein 1	25 kDa	1.9179
8	retinal guanylyl cyclase 2 (guanylate cyclase retinal rod2 [Cyprinus carpio])	124 kDa	1.8202
9	guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	37 kDa	1.7943
10	PREDICTED: pyruvate kinase PKM isoform X1	60 kDa	1.5077
11	rod outer segment membrane protein 1	40 kDa	1.4684
12	PREDICTED: olfactory guanylyl cyclase GC-D isoform X3 (guanylate cyclase retinal rod1 [Cyprinus carpio])	88 kDa	1.4548
13	ATP synthase F(0) complex subunit B1, mitochondrial	31 kDa	1.3896
14	PREDICTED: uncharacterized protein LOC571872 isoform X1	32 kDa	1.2876
15	retinal guanylyl cyclase 2 (guanylate cyclase retinal rod2 [Cyprinus carpio])	125 kDa	1.2573
16	voltage-dependent anion-selective channel protein 2	30 kDa	1.0218
17	peripherin-2	20 kDa	0.9849
18	PREDICTED: ras-related protein Rab-1A-like isoform X1	22 kDa	0.9094
19	ras-related protein Rab-1B	22 kDa	0.8998
20	PREDICTED: ras-related protein Rab-11B	25 kDa	0.8862
21	uncharacterized protein LOC100005305	11 kDa	0.8181
22	PREDICTED: solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3a isoform X2	40 kDa	0.7296
23	PREDICTED: sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3Fa isoform X2	40 kDa	0.7255
24	PREDICTED: pleckstrin homology domain-containing family B member 1 isoform X1	21 kDa	0.6706
25	ADP-ribosylation factor-like protein 8B-A	21 kDa	0.6706
26	voltage-dependent anion-selective channel protein 1	31 kDa	0.6616
27	PREDICTED: ATP synthase subunit gamma, mitochondrial isoform X1	33 kDa	0.6449
28	PREDICTED: tubulin beta-4B chain-like	31 kDa	0.643
29	PREDICTED: ras-related protein Rab-10	23 kDa	0.6025
30	PREDICTED: uncharacterized protein LOC571872 isoform X1	23 kDa	0.5861
31	mitochondrial 2-oxoglutarate/malate carrier protein	38 kDa	0.5717
32	ras-related protein Rap-1b-like	21 kDa	0.5664
33	ATP synthase subunit alpha, mitochondrial	33 kDa	0.5559
34	PREDICTED: prohibitin isoform X2	22 kDa	0.5396
35	PREDICTED: prohibitin	22 kDa	0.5346
36	ADP/ATP translocase 3	27 kDa	0.5263
37	olfactory guanylyl cyclase GC-D (guanylate cyclase retinal rod1 [Cyprinus carpio])	34 kDa	0.5262
38	protein NDRG1 isoform 1	42 kDa	0.5211
39	putative tubulin beta chain variant 1	20 kDa	0.5103
40	prohibitin 2a	35 kDa	0.4993
41	neurotrimin isoform 1 precursor	38 kDa	0.4975
42	ras-related protein Rab-18	23 kDa	0.4926
43	ADP-ribosylation factor-like protein 8A	25 kDa	0.4906
44	PREDICTED: olfactory guanylyl cyclase GC-D isoform X2 (guanylate cyclase retinal rod1 [Cyprinus carpio])	26 kDa	0.4683
45	ras-related protein Rap-1b precursor	21 kDa	0.4628
46	PREDICTED: ADP-ribosylation factor-like protein 13B-like isoform X5	27 kDa	0.432
47	ras-related protein Rab-11A	22 kDa	0.4156
48	dnaJ homolog subfamily C member 5G	22 kDa	0.4086
49	uncharacterized protein LOC492355	23 kDa	0.3888
50	PREDICTED: voltage-dependent anion-selective channel protein 2	11 kDa	0.3817
51	ras-related protein Rab-35	20 kDa	0.379

52	PREDICTED: cGMP-gated cation channel alpha-1	63 kDa	0.374
53	RAB5A, member RAS oncogene family, a	24 kDa	0.3736
54	voltage-dependent anion-selective channel protein 2-like	30 kDa	0.3663
55	PREDICTED: protein RD3-like	24 kDa	0.3623
56	PREDICTED: ATP synthase subunit alpha, mitochondrial	27 kDa	0.3572
57	PREDICTED: cGMP-gated cation channel alpha-1	63 kDa	0.3443
58	PREDICTED: uncharacterized protein LOC571872 isoform X1	12 kDa	0.3431
59	protein disulfide-isomerase TMX3 precursor	47 kDa	0.3406
60	long-chain fatty acid transport protein 4	25 kDa	0.3365
61	ras-related protein Rab-1B	19 kDa	0.3323
62	ATP synthase subunit O, mitochondrial	26 kDa	0.3271
63	synaptosomal-associated protein 25-B	23 kDa	0.3179
64	peripherin-2	20 kDa	0.3062
65	PREDICTED: prohibitin-2	27 kDa	0.3038
66	ras-related protein Rab-5C	37 kDa	0.3011
67	RAB11a, member RAS oncogene family, like	20 kDa	0.3009
68	PREDICTED: tubulin alpha chain	45 kDa	0.2956
69	ras-related protein Rab-14	24 kDa	0.2927
70	PREDICTED: ADP-ribosylation factor-like protein 13B-like isoform X5	42 kDa	0.2853
71	ADP-ribosylation factor-like protein 6	21 kDa	0.2792
72	creatine kinase S-type, mitochondrial	47 kDa	0.2761
73	PREDICTED: creatine kinase S-type, mitochondrial isoform X2	47 kDa	0.2751
74	putative Ras-related protein Rab-42	18 kDa	0.2746
75	cytochrome c-1	36 kDa	0.2686
76	small GTPase RhoA	22 kDa	0.2642
77	synaptobrevin homolog YKT6	22 kDa	0.2544
78	ATPase, Na+/K+ transporting, beta 2b polypeptide	34 kDa	0.2521
79	PREDICTED: phospholipid scramblase 2	26 kDa	0.2508
80	PREDICTED: phosphate carrier protein, mitochondrial-like isoform X1	34 kDa	0.2484
81	PREDICTED: tubulin beta-2B chain-like isoform 1	55 kDa	0.2433
82	PREDICTED: voltage-dependent anion-selective channel protein 2	11 kDa	0.243
83	ras-related protein Rab-18-B	23 kDa	0.2418
84	uncharacterized protein LOC449549	23 kDa	0.2401
85	ATP synthase subunit g, mitochondrial	11 kDa	0.2396
86	ras-related protein Ral-A	23 kDa	0.2384
87	PREDICTED: ATPase, Na+/K+ transporting, beta 2b polypeptide isoform X1	24 kDa	0.2351
88	RAB1A, member RAS oncogene family	28 kDa	0.2331
89	PREDICTED: tubulin beta-4B chain-like, partial	16 kDa	0.2301
90	PREDICTED: LOW QUALITY PROTEIN: actin, gamma 1	40 kDa	0.2296
91	voltage-dependent anion-selective channel protein 2	20 kDa	0.2266
92	ubiquitin-60S ribosomal protein L40	12 kDa	0.2209
93	NAD(P) transhydrogenase, mitochondrial	114 kDa	0.2185
94	PREDICTED: ras-related protein Rab-28 isoform X2	25 kDa	0.2185
95	immunity-related GTPase family, q2	42 kDa	0.2181
96	PREDICTED: vesicle-associated membrane protein 2-like	12 kDa	0.2153
97	catechol-O-methyltransferase a	30 kDa	0.2119
98	ER membrane protein complex subunit 3	30 kDa	0.2107
99	peripherin 2b (retinal degeneration, slow)	39 kDa	0.2078
100	60S ribosomal protein L18	22 kDa	0.2022
101	PREDICTED: tubulin alpha-1C chain	45 kDa	0.1988
102	guanylyl cyclase 3 (guanylate cyclase retinal cone [Cyprinus carpio])	123 kDa	0.1967
103	PREDICTED: GTP-binding protein SAR1b-like	13 kDa	0.193
104	PREDICTED: regulator of G-protein signaling 9-binding protein B	28 kDa	0.1869
105	guanylyl cyclase 3 (guanylate cyclase retinal cone [Cyprinus carpio])	128 kDa	0.1853
106	PREDICTED: alpha/beta hydrolase domain-containing protein 17A	28 kDa	0.1808
107	PREDICTED: ras-related protein Rab-7a isoform X1	24 kDa	0.18
108	PREDICTED: protein RD3-like	24 kDa	0.1765
109	epidermal retinol dehydrogenase 2	34 kDa	0.1765
110	PREDICTED: cadherin-related family member 5-like isoform X2	44 kDa	0.1752

111	vesicle-trafficking protein SEC22b-A	24 kDa	0.1722
112	PREDICTED: L-lactate dehydrogenase B-B chain isoform X3	19 kDa	0.1705
113	PREDICTED: NADH dehydrogenase	20 kDa	0.1692
114	PREDICTED: tubulin alpha chain-like	50 kDa	0.1692
115	retinol dehydrogenase 8a	35 kDa	0.1652
116	mitochondrial inner membrane protein	83 kDa	0.1614
117	PREDICTED: josephin-2 isoform X1	21 kDa	0.1549
118	PREDICTED: ADP-ribosylation factor 2	16 kDa	0.1509
119	uncharacterized protein LOC393228	21 kDa	0.1507
120	S-arrestin	44 kDa	0.1503
121	PREDICTED: uncharacterized protein si:dkey-182g1.3	16 kDa	0.1496
122	rhodopsin kinase	27 kDa	0.1481
123	PREDICTED: transmembrane emp24 domain-containing protein 7 isoform X2	27 kDa	0.1465
124	reticulon-4	22 kDa	0.1447
125	PREDICTED: peripherin-2	39 kDa	0.1447
126	NADH-cytochrome b5 reductase 1	28 kDa	0.1442
127	reticulon-4	22 kDa	0.1438
128	ras-related protein Rab-3A	28 kDa	0.1405
129	erlin-2 precursor	40 kDa	0.14
130	uncharacterized protein LOC100127828	34 kDa	0.1396
131	guanine nucleotide-binding protein G(t) subunit alpha-2	40 kDa	0.1395
132	PREDICTED: mitochondrial glutamate carrier 1	34 kDa	0.139
133	PREDICTED: red-sensitive opsin-1 isoform X1	41 kDa	0.138
134	PREDICTED: cadherin-related family member 5-like isoform X2	17 kDa	0.1338
135	vesicle-associated membrane protein-associated protein A	30 kDa	0.133
136	PREDICTED: ras-related protein Rab-6A isoform X2	24 kDa	0.1325
137	ras-related protein Rab-5B	24 kDa	0.1317
138	60S ribosomal protein L24	18 kDa	0.1295
139	CDP-diacylglycerol--inositol 3-phosphatidyltransferase	24 kDa	0.1294
140	40S ribosomal protein S5	25 kDa	0.1242
141	PREDICTED: saccharopine dehydrogenase-like oxidoreductase-like	12 kDa	0.124
142	peroxisomal membrane protein 11B	25 kDa	0.1228
143	PREDICTED: LOW QUALITY PROTEIN: 40S ribosomal protein S13-like	19 kDa	0.1227
144	PREDICTED: ADP-dependent glucokinase isoform X2	58 kDa	0.1199
145	PREDICTED: ER membrane protein complex subunit 1 isoform X1	111 kDa	0.1193
146	sorting and assembly machinery component 50 homolog A	52 kDa	0.1182
147	sodium/potassium-transporting ATPase subunit alpha-3	113 kDa	0.1173
148	ADP-ribosylation factor-like protein 9	26 kDa	0.1162
149	PREDICTED: vesicle transport through interaction with t-SNAREs homolog 1A isoform X1	26 kDa	0.1162
150	cytochrome c oxidase subunit 4 isoform 1, mitochondrial	20 kDa	0.1149
151	PREDICTED: phospholipid-transporting ATPase IB isoform X6	134 kDa	0.1089
152	PREDICTED: regulator of G-protein signaling 9 isoform X1	57 kDa	0.1066
153	PREDICTED: ER membrane protein complex subunit 1 isoform X1	114 kDa	0.1065
154	rhodopsin kinase	64 kDa	0.1061
155	histone 2, H2a	14 kDa	0.1048
156	PREDICTED: 40S ribosomal protein S3-like isoform X1	28 kDa	0.1045
157	PREDICTED: cGMP-gated cation channel alpha-1	36 kDa	0.1044
158	transmembrane protein 33	29 kDa	0.104
159	guanine nucleotide-binding protein subunit beta-5	43 kDa	0.1034
160	very-long-chain enoyl-CoA reductase	36 kDa	0.1028
161	retinol dehydrogenase-like	36 kDa	0.1024
162	lysophosphatidylcholine acyltransferase 2	60 kDa	0.1002
163	creatine kinase U-type, mitochondrial	22 kDa	0.1001
164	60S ribosomal protein L9	22 kDa	0.1001
165	rho-related gtp-binding protein rhoc	22 kDa	0.0995
166	retinol dehydrogenase 13	37 kDa	0.0994
167	PREDICTED: mitochondrial pyruvate carrier 2	14 kDa	0.0991
168	PREDICTED: cadherin-related family member 1-like isoform X2	99 kDa	0.0988
169	ras homolog gene family, member A	22 kDa	0.0983

170	PREDICTED: ras-related protein Rab-30	15 kDa	0.0982
171	PREDICTED: 60S ribosomal protein L6	30 kDa	0.0979
172	PREDICTED: GTP-binding protein SAR1b	22 kDa	0.0977
173	PREDICTED: 40S ribosomal protein S9-like	22 kDa	0.0971
174	hexokinase-1	54 kDa	0.0961
175	ADP-ribosylation factor-like 15a	23 kDa	0.0954
176	ras-related protein Rab-8A	23 kDa	0.0954
177	NADH dehydrogenase 1 beta subcomplex subunit 6	15 kDa	0.0947
178	40S ribosomal protein S25	15 kDa	0.0931
179	PREDICTED: CSC1-like protein 2 isoform X2	87 kDa	0.093
180	hexokinase-1	71 kDa	0.0929
181	surfeit gene 4, like	23 kDa	0.0927
182	Beta-centractin	15 kDa	0.0923
183	PREDICTED: sodium/potassium/calcium exchanger 1 isoform X1	80 kDa	0.0922
184	solute carrier family 3 (amino acid transporter heavy chain), member 2b	57 kDa	0.0897
185	NADH dehydrogenase	58 kDa	0.0887
186	PREDICTED: NADH dehydrogenase (ubiquinone) complex I, assembly factor 6	33 kDa	0.0875
187	isocitrate dehydrogenase	50 kDa	0.0861
188	PREDICTED: threonine dehydratase, mitochondrial-like isoform X2	60 kDa	0.0843
189	LETM1 and EF-hand domain-containing protein 1, mitochondrial	86 kDa	0.0843
190	dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	69 kDa	0.0835
191	sideroflexin-4	35 kDa	0.0825
192	acyl-CoA synthetase long-chain family member 3b	79 kDa	0.0822
193	DDRGK domain-containing protein 1 precursor	35 kDa	0.0822
194	malate dehydrogenase, mitochondrial	35 kDa	0.0801
195	PREDICTED: choline transporter-like protein 1	72 kDa	0.08
196	PREDICTED: oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) isoform X3	26 kDa	0.0798
197	PREDICTED: protein-L-isoaspartate(D-aspartate) O-methyltransferase isoform X1	26 kDa	0.0794
198	PREDICTED: 40S ribosomal protein S24	17 kDa	0.0794
199	PREDICTED: regulator of G-protein signaling 9-binding protein-like	27 kDa	0.079
200	ragulator complex protein LAMTOR1	18 kDa	0.0788
201	60S ribosomal protein L14	18 kDa	0.0782
202	epimerase family protein SDR39U1	36 kDa	0.078
203	alpha-1,3/1,6-mannosyltransferase ALG2	46 kDa	0.0779
204	PREDICTED: actin, aortic smooth muscle	18 kDa	0.0777
205	PREDICTED: arylacetamide deacetylase isoform X1	47 kDa	0.0755
206	PREDICTED: CSC1-like protein 2	47 kDa	0.0753
207	dolichol-phosphate mannosyltransferase subunit 1	28 kDa	0.0747
208	PREDICTED: uncharacterized protein si:rp71-36a1.2	28 kDa	0.0743
209	uncharacterized protein LOC100001558	19 kDa	0.0739
210	PREDICTED: sphingomyelin phosphodiesterase 2 isoform X1	48 kDa	0.073
211	PREDICTED: tetratricopeptide repeat protein 8-like isoform X1	58 kDa	0.0728
212	green-sensitive opsin-4	39 kDa	0.0725
213	PREDICTED: protein tyrosine phosphatase type IVA 2-like isoform X3	19 kDa	0.071
214	rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha	99 kDa	0.0708
215	PREDICTED: E3 ubiquitin-protein ligase RNF170-like	29 kDa	0.0704
216	plasminogen receptor (KT)	20 kDa	0.0692
217	PREDICTED: syntaxin-12 isoform X1	30 kDa	0.0686
218	PREDICTED: solute carrier family 41 member 1	40 kDa	0.0686
219	PREDICTED: potassium voltage-gated channel subfamily B member 2	93 kDa	0.0676
220	signal peptidase complex subunit 3	20 kDa	0.0674
221	mitochondrial carrier homolog 2	31 kDa	0.0669
222	ADP-ribosylation factor-like protein 1	20 kDa	0.0666
223	nicastrin precursor	42 kDa	0.0664
224	methyltransferase like 7A precursor	31 kDa	0.0663
225	palmitoyltransferase ZDHHC2	42 kDa	0.0662
226	PREDICTED: cadherin-related family member 5-like isoform X2	20 kDa	0.0662
227	40S ribosomal protein S10	20 kDa	0.0662

228	ADP-ribosylation factor-like protein 3	20 kDa	0.0662
229	signal recognition particle receptor subunit beta	31 kDa	0.0661
230	ADP-ribosylation factor 1	21 kDa	0.0654
231	PREDICTED: ras-related protein Rap-2c	21 kDa	0.0654
232	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	21 kDa	0.0646
233	PREDICTED: casein kinase I isoform gamma-1-like isoform X2	53 kDa	0.0646
234	alpha/beta hydrolase domain-containing protein 17C	32 kDa	0.0642
235	N-acetyltransferase 14	32 kDa	0.064
236	PREDICTED: FAS-associated factor 2-like isoform X1	54 kDa	0.0636
237	PREDICTED: NADH dehydrogenase	21 kDa	0.0634
238	cell division control protein 42 homolog	21 kDa	0.0634
239	calmegin precursor	66 kDa	0.0628
240	synaptophysin b isoform 1	33 kDa	0.0625
241	40S ribosomal protein S3a	33 kDa	0.0625
242	PREDICTED: mitochondrial ubiquitin ligase activator of nfkb 1-A	33 kDa	0.061
243	PREDICTED: F-box/LRR-repeat protein 20	45 kDa	0.0606
244	PREDICTED: V-type proton ATPase subunit S1	34 kDa	0.0588
245	PREDICTED: transmembrane emp24 domain-containing protein 2	23 kDa	0.0586
246	ras-related protein Rab-24	23 kDa	0.0582
247	phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	11 kDa	0.0578
248	receptor expression-enhancing protein 6	23 kDa	0.0573
249	PREDICTED: uncharacterized protein LOC101884052	11 kDa	0.0572
250	PREDICTED: ADP-ribosylation factor-like protein 3	23 kDa	0.057
251	ras-related C3 botulinum toxin substrate 2	23 kDa	0.057
252	mitochondrial chaperone BCS1	48 kDa	0.0567
253	sideroflexin-3	36 kDa	0.0567
254	HIG1 domain family member 1A	11 kDa	0.0566
255	thioredoxin-related transmembrane protein 2-B precursor	36 kDa	0.0563
256	PREDICTED: gamma-glutamyltransferase 5	60 kDa	0.056
257	PREDICTED: aspartyl/asparaginyl beta-hydroxylase isoform X6	11 kDa	0.056
258	PREDICTED: voltage-dependent anion-selective channel protein 3 isoform X3	36 kDa	0.0557
259	PREDICTED: voltage-dependent anion-selective channel protein 3 isoform X3	36 kDa	0.0557
260	PREDICTED: 40S ribosomal protein S8	24 kDa	0.055
261	ELMO domain-containing protein 2 precursor	24 kDa	0.0544
262	PREDICTED: NADH dehydrogenase	12 kDa	0.0543
263	PREDICTED: reticulon-3-B-like isoform X2	25 kDa	0.0536
264	selenoprotein T1a precursor	12 kDa	0.0527
265	PREDICTED: cyclic nucleotide-gated cation channel beta-1 isoform X2	116 kDa	0.0524
266	histone 1, H4, like	12 kDa	0.0522
267	PREDICTED: uncharacterized protein LOC100707031 isoform X1	12 kDa	0.0517
268	PREDICTED: 40S ribosomal protein S2	12 kDa	0.0512
269	Bardet-Biedl syndrome 5 protein homolog	39 kDa	0.0511
270	PREDICTED: ADP-dependent glucokinase isoform X2	26 kDa	0.0503
271	mitochondrial ATP synthase subunit f	13 kDa	0.0502
272	mitochondrial pyruvate carrier 1	13 kDa	0.0502
273	PREDICTED: 26S proteasome non-ATPase regulatory subunit 1-like	148 kDa	0.0501
274	PREDICTED: vesicle-associated membrane protein-associated protein A-like	26 kDa	0.0501
275	PREDICTED: vesicle-associated membrane protein-associated protein A-like	26 kDa	0.0501
276	guanine nucleotide-binding protein G(o) subunit alpha	40 kDa	0.0497
277	PREDICTED: calnexin isoform X1	67 kDa	0.0494
278	PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like	27 kDa	0.0494
279	uncharacterized protein LOC100124614	13 kDa	0.0493
280	PREDICTED: prominin-1 isoform X1	95 kDa	0.0491
281	PREDICTED: l-isoaspartyl protein carboxyl methyltransferase, like isoform X2	27 kDa	0.0489
282	phosducin	27 kDa	0.0485
283	PREDICTED: ceroid-lipofuscinosis, neuronal 6a isoform X1	19 kDa	0.0484
284	PREDICTED: transmembrane emp24 domain-containing protein 9 isoform X1	27 kDa	0.0482
285	mannose-P-dolichol utilization defect 1 protein	27 kDa	0.0478
286	very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 2	28 kDa	0.047

287	PREDICTED: protein XRP2 isoform X1	42 kDa	0.0469
288	PREDICTED: UDP-N-acetylglucosamine transporter isoform X1	14 kDa	0.0467
289	ATP synthase F(0) complex subunit C3, mitochondrial	14 kDa	0.0463
290	fatty aldehyde dehydrogenase	28 kDa	0.0462
291	3-hydroxyacyl-CoA dehydrogenase type-2	28 kDa	0.046
292	PREDICTED: hexokinase-1-like	14 kDa	0.0459
293	PREDICTED: solute carrier family 1 (glial high affinity glutamate transporter), member 2a isoform X2	58 kDa	0.0456
294	PREDICTED: coiled-coil-helix-coiled-coil-helix domain-containing protein 6, mitochondrial isoform X2	29 kDa	0.0456
295	aquaporin-9	29 kDa	0.0456
296	PREDICTED: alkaline phosphatase, tissue-nonspecific isozyme isoform X2	58 kDa	0.0455
297	PREDICTED: retinal-specific ATP-binding cassette transporter isoform X1	265 kDa	0.0453
298	histone 2, H2a	14 kDa	0.0451
299	PREDICTED: uncharacterized protein LOC565091 isoform X1	14 kDa	0.0451
300	40S ribosomal protein S4, X isoform	29 kDa	0.0446
301	basigin precursor	45 kDa	0.044
302	alpha/beta hydrolase domain-containing protein 14A	30 kDa	0.0435
303	calcium-binding mitochondrial carrier protein Aralar1	76 kDa	0.0434
304	protein RD3	15 kDa	0.0433
305	PREDICTED: surfeit locus protein 4	30 kDa	0.0432
306	excitatory amino acid transporter 2	61 kDa	0.0429
307	F-box/LRR-repeat protein 2	46 kDa	0.0427
308	NADH dehydrogenase 1 beta subcomplex subunit 4	15 kDa	0.0426
309	membrane magnesium transporter 1 precursor	15 kDa	0.0426
310	prominin-1 precursor	94 kDa	0.0422
311	ES1 protein, mitochondrial precursor	31 kDa	0.042
312	PREDICTED: SEC14-like protein 3 isoform X1	31 kDa	0.0417
313	PREDICTED: GTPase HRas-like	15 kDa	0.0416
314	PREDICTED: dehydrogenase/reductase SDR family member 7B isoform X1	31 kDa	0.0415
315	PREDICTED: progestin and adipoQ receptor family member 4-like	31 kDa	0.0415
316	flotillin-2a	47 kDa	0.0413
317	uncharacterized protein LOC562845	31 kDa	0.041
318	mitochondrial dicarboxylate carrier	32 kDa	0.0409
319	PREDICTED: lipid phosphate phosphohydrolase 1 isoform X1	32 kDa	0.0407
320	serum/glucocorticoid regulated kinase 1-like	48 kDa	0.0403
321	NADH dehydrogenase 1 alpha subcomplex subunit 6	16 kDa	0.04
322	PREDICTED: rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit beta	99 kDa	0.0397
323	PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2	116 kDa	0.0394
324	ATPase, Na+/K+ transporting, beta 2a polypeptide	16 kDa	0.0392
325	PREDICTED: aspartate beta-hydroxylase isoform X2	33 kDa	0.0391
326	protein NipSnap homolog 2	33 kDa	0.0388
327	trifunctional enzyme subunit beta, mitochondrial	50 kDa	0.0387
328	creatine kinase b-type	16 kDa	0.0386
329	PREDICTED: lipid phosphate phosphohydrolase 1-like	33 kDa	0.0385
330	mitochondrial import receptor subunit TOM20 homolog B	16 kDa	0.0383
331	PREDICTED: casein kinase I isoform gamma-2 isoform X1	51 kDa	0.0381
332	ubiquitin-conjugating enzyme E2Nb	16 kDa	0.038
333	uncharacterized protein LOC492776	16 kDa	0.038
334	PREDICTED: hydroxyacylglutathione hydrolase, mitochondrial isoform X1	34 kDa	0.0378
335	protein-S-isoprenylcysteine O-methyltransferase	34 kDa	0.0378
336	PREDICTED: uncharacterized protein LOC100694464	17 kDa	0.0375
337	60S ribosomal protein L22	17 kDa	0.0375
338	mitochondrial import inner membrane translocase subunit TIM44	52 kDa	0.0373
339	protein disulfide-isomerase TMX3 precursor	52 kDa	0.0372
340	PREDICTED: retinol dehydrogenase 12-like	34 kDa	0.0371
341	PREDICTED: NADH dehydrogenase	17 kDa	0.037
342	inactive hydroxysteroid dehydrogenase-like protein 1	35 kDa	0.0368
343	dehydrogenase/reductase (SDR family) member 13a, duplicate 3	35 kDa	0.0368
344	uncharacterized protein LOC100135257	35 kDa	0.0365

345	elongation of very long chain fatty acids-like 4	35 kDa	0.0365
346	PREDICTED: uncharacterized protein LOC100126019 isoform X1	107 kDa	0.0362
347	protein YIF1A	35 kDa	0.036
348	PREDICTED: 40S ribosomal protein S23-like	17 kDa	0.036
349	PREDICTED: creatine kinase S-type, mitochondrial isoform X2	17 kDa	0.0357
350	PREDICTED: 60S ribosomal protein L23	17 kDa	0.0357
351	peptidyl-prolyl cis-trans isomerase A	18 kDa	0.0355
352	PREDICTED: 60S ribosomal protein L12	18 kDa	0.0353
353	alpha-internexin	55 kDa	0.0352
354	optic atrophy 3 protein homolog	18 kDa	0.035
355	60S ribosomal protein L26	18 kDa	0.035
356	protein lunapark-A	36 kDa	0.035
357	PREDICTED: PI-PLC X domain-containing protein 2-like	37 kDa	0.0348
358	60S ribosomal protein L27a	18 kDa	0.0348
359	PREDICTED: mitochondrial fission process protein 1-like	18 kDa	0.0344
360	coiled-coil domain-containing protein 47 precursor	56 kDa	0.0343
361	ATP synthase subunit d, mitochondrial	18 kDa	0.0341
362	uncharacterized protein LOC100127838	18 kDa	0.0341
363	PREDICTED: 60S ribosomal protein L23a	18 kDa	0.0341
364	PREDICTED: 60S ribosomal protein L27-like	18 kDa	0.0341
365	40S ribosomal protein S18	18 kDa	0.0339
366	PREDICTED: histidine triad nucleotide-binding protein 3 isoform X1	18 kDa	0.0339
367	40S ribosomal protein S16	18 kDa	0.0337
368	coiled-coil domain-containing protein 126	18 kDa	0.0337
369	uncharacterized protein LOC100005305	19 kDa	0.0335
370	neutral amino acid transporter B(0)	57 kDa	0.0334
371	coiled-coil domain-containing protein 126	19 kDa	0.0333
372	golgin A7 family, member Ba	19 kDa	0.0333
373	PREDICTED: atlastin-3 isoform X1	58 kDa	0.033
374	glutathione S-transferase theta-like	19 kDa	0.0329
375	stomatin-like protein 2, mitochondrial	39 kDa	0.0322
376	pyruvate dehydrogenase E1 component subunit beta, mitochondrial	39 kDa	0.0322
377	PREDICTED: protein ATP1B4	39 kDa	0.0322
378	fatty-acid amide hydrolase 2-A	59 kDa	0.0322
379	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	40 kDa	0.0317
380	uncharacterized protein LOC570464 precursor	20 kDa	0.0317
381	PREDICTED: potassium voltage-gated channel subfamily V member 2	60 kDa	0.0316
382	keratin, type II cytoskeletal 8	61 kDa	0.0315
383	golgin A7 family, member Ba	20 kDa	0.0315
384	eukaryotic translation initiation factor 2 subunit 2	20 kDa	0.0315
385	apoptosis-inducing factor 2	41 kDa	0.0312
386	PREDICTED: peroxiredoxin-5, mitochondrial-like	20 kDa	0.0308
387	PREDICTED: 40S ribosomal protein S2	20 kDa	0.0308
388	PREDICTED: ADP-ribosylation factor 6-like	20 kDa	0.0308
389	PREDICTED: protein tyrosine phosphatase type IVA 3-like isoform X3	20 kDa	0.0308
390	PREDICTED: 11-cis retinol dehydrogenase isoform X1	41 kDa	0.0304
391	transmembrane protein 30Aa	42 kDa	0.0303
392	PREDICTED: photoreceptor outer segment membrane glycoprotein 2-like isoform X1	42 kDa	0.0303
393	LIM domain and actin-binding protein 1	20 kDa	0.0301
394	PREDICTED: signal peptidase complex catalytic subunit SEC11A-like	21 kDa	0.0301
395	ADP-ribosylation factor-like protein 5A	21 kDa	0.0301
396	PREDICTED: guanine nucleotide-binding protein subunit alpha-11-like isoform X1	42 kDa	0.0299
397	PREDICTED: exportin-1-like, partial	21 kDa	0.0299
398	guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-3	21 kDa	0.0294
399	brain creatine kinase b	43 kDa	0.0294
400	PREDICTED: translocon-associated protein subunit gamma	21 kDa	0.0293
401	PREDICTED: cell division control protein 42 homolog isoform X1	21 kDa	0.0289
402	aspartate aminotransferase 2	43 kDa	0.0289
403	PREDICTED: glutaminase a isoform X1	66 kDa	0.0289

404	PREDICTED: transmembrane and coiled-coil domains protein 1-like	21 kDa	0.0288
405	peripherin 2, like	21 kDa	0.0288
406	outer dense fiber of sperm tails 2b	22 kDa	0.0286
407	ADP-ribosylation-like factor 6 interacting protein 5	22 kDa	0.0286
408	PREDICTED: ras-related C3 botulinum toxin substrate 1	22 kDa	0.0286
409	AFG3-like protein 2	89 kDa	0.0286
410	PREDICTED: guanine nucleotide-binding protein G(s) subunit alpha isoform X2	44 kDa	0.0283
411	phosphatidylinositide phosphatase SAC1-B	67 kDa	0.0281
412	protein kinase, cAMP-dependent, regulatory, type II, alpha A	45 kDa	0.028
413	ras-related protein R-Ras	22 kDa	0.0279
414	PREDICTED: glucose-induced degradation protein 8 homolog	22 kDa	0.0277
415	PREDICTED: charged multivesicular body protein 6-like isoform X1	22 kDa	0.0276
416	PREDICTED: transmembrane protein 126A isoform X1	22 kDa	0.0274
417	protein phosphatase 2, regulatory subunit B', epsilon isoform a	22 kDa	0.0274
418	synaptotagmin II	47 kDa	0.0269
419	PREDICTED: cadherin-related family member 5-like isoform X2	23 kDa	0.0269
420	adipocyte plasma membrane-associated protein	47 kDa	0.0268
421	membrane-associated progesterone receptor component 2	24 kDa	0.0261
422	PREDICTED: metal transporter CNNM4	24 kDa	0.0261
423	PREDICTED: NADPH--cytochrome P450 reductase isoform X1	48 kDa	0.026
424	glutamine synthetase 1	24 kDa	0.0257
425	60S ribosomal protein L15	24 kDa	0.0256
426	protein THEM6 precursor	24 kDa	0.0256
427	HD domain-containing protein 2	24 kDa	0.0256
428	PREDICTED: neural cell adhesion molecule 1 isoform X1	74 kDa	0.0255
429	protein THEM6 precursor	24 kDa	0.0255
430	NADH dehydrogenase	24 kDa	0.0253
431	PREDICTED: dephospho-CoA kinase domain-containing protein-like isoform X2	24 kDa	0.0253
432	transmembrane emp24 domain-containing protein 10 precursor	24 kDa	0.0252
433	rho GTPase-activating protein 1	50 kDa	0.0251
434	PREDICTED: serine/threonine-protein kinase NIM1-like	50 kDa	0.025
435	60S ribosomal protein L10	25 kDa	0.025
436	motile sperm domain-containing protein 1	25 kDa	0.025
437	PREDICTED: testis-expressed sequence 264 protein-like	25 kDa	0.025
438	cytochrome b-c1 complex subunit 2, mitochondrial	50 kDa	0.0249
439	rab GDP dissociation inhibitor beta	51 kDa	0.0247
440	60S ribosomal protein L10a	25 kDa	0.0246
441	tubulin gamma-1 chain	51 kDa	0.0244
442	phosphatidylinositide phosphatase SAC1-A	51 kDa	0.0243
443	dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit precursor	51 kDa	0.0242
444	UBX domain-containing protein 4	52 kDa	0.0241
445	transmembrane protein 147	25 kDa	0.0241
446	60S ribosomal protein L17	25 kDa	0.0241
447	PREDICTED: ras-related protein Rab-9B	25 kDa	0.0241
448	PREDICTED: phosphatidate cytidylyltransferase 1	52 kDa	0.0239
449	Probable saccharopine dehydrogenase	26 kDa	0.0237
450	solute carrier family 2, facilitated glucose transporter member 1	53 kDa	0.0236
451	squalene synthase	53 kDa	0.0236
452	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	26 kDa	0.0234
453	PREDICTED: coiled-coil domain-containing protein 136-like isoform X1	53 kDa	0.0233
454	CAAX prenyl protease 1 homolog	53 kDa	0.0233
455	BRI3-binding protein precursor	26 kDa	0.0231
456	peroxisomal biogenesis factor 3	26 kDa	0.0231
457	uncharacterized protein LOC619200	27 kDa	0.0229
458	ATP synthase subunit s, mitochondrial	27 kDa	0.0228
459	PREDICTED: probable ATP-dependent RNA helicase ddx6	54 kDa	0.0228
460	PREDICTED: fatty aldehyde dehydrogenase-like	55 kDa	0.0226
461	PREDICTED: sterol 26-hydroxylase, mitochondrial	27 kDa	0.0225
462	PREDICTED: ribosomal protein S6 kinase alpha-3 isoform X1	83 kDa	0.0224

463	sorting and assembly machinery component 50 homolog B	27 kDa	0.0224
464	PREDICTED: ATP synthase subunit beta, mitochondrial-like	56 kDa	0.0221
465	PREDICTED: sodium-coupled neutral amino acid transporter 3-like isoform X1	56 kDa	0.0219
466	ER membrane protein complex subunit 10 isoform 1 precursor	28 kDa	0.0217
467	PREDICTED: ankyrin repeat domain-containing protein 33B	57 kDa	0.0216
468	thioredoxin-dependent peroxide reductase, mitochondrial	28 kDa	0.0215
469	V-type proton ATPase subunit D	28 kDa	0.0215
470	60S ribosomal protein L7	29 kDa	0.0214
471	T-complex protein 1 subunit beta	58 kDa	0.0213
472	PREDICTED: importin-5 isoform X1	119 kDa	0.0209
473	prenylcysteine oxidase 1 precursor	59 kDa	0.0208
474	neuronal membrane glycoprotein M6-b	30 kDa	0.0206
475	catechol O-methyltransferase	30 kDa	0.0205
476	PREDICTED: protein phosphatase 1 regulatory subunit 16A	61 kDa	0.0204
477	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2b isoform X1	92 kDa	0.0203
478	60S ribosomal protein L7a	30 kDa	0.0203
479	PREDICTED: calcium signal-modulating cyclophilin ligand isoform X1	30 kDa	0.0203
480	microtubule-associated protein RP/EB family member 3	30 kDa	0.0201
481	aquaporin 1	30 kDa	0.02
482	PREDICTED: tetraspanin-5-like isoform X1	31 kDa	0.0199
483	E3 ubiquitin-protein ligase MARCH5	31 kDa	0.0193
484	acyl-CoA-binding domain-containing protein 5-B	32 kDa	0.0192
485	surfeit locus protein 1	32 kDa	0.0191
486	B-cell receptor-associated protein 31	32 kDa	0.0191
487	thioredoxin-related transmembrane protein 1 precursor	32 kDa	0.019
488	uncharacterized protein C18orf19 homolog B	32 kDa	0.0189
489	PREDICTED: rap1 GTPase-GDP dissociation stimulator 1-like isoform X1	32 kDa	0.0188
490	PREDICTED: protein FAM57A-like	32 kDa	0.0187
491	PREDICTED: cyclic nucleotide-gated cation channel beta-3 isoform X4	66 kDa	0.0186
492	trimeric intracellular cation channel type B	33 kDa	0.0185
493	PREDICTED: serine protease 33-like	33 kDa	0.0185
494	phosphatidylinositol N-acetylglucosaminyltransferase subunit Q	67 kDa	0.0184
495	PREDICTED: E3 ubiquitin-protein ligase CHIP isoform X2	33 kDa	0.0184
496	N-ethylmaleimide-sensitive factor attachment protein, beta	33 kDa	0.0183
497	PREDICTED: uncharacterized protein LOC323326 isoform X1	33 kDa	0.0183
498	PREDICTED: synembryn-A-like isoform X2	67 kDa	0.0183
499	RPE-retinal G protein-coupled receptor	33 kDa	0.0182
500	pyrroline-5-carboxylate reductase 1a	34 kDa	0.018
501	PREDICTED: protein CLN8 isoform X1	34 kDa	0.018
502	mitochondrial carnitine/acylcarnitine carrier protein CACL	34 kDa	0.018
503	PREDICTED: protein SCO1 homolog, mitochondrial	34 kDa	0.0179
504	60S acidic ribosomal protein P0	34 kDa	0.0177
505	solute carrier family 7, member 3	70 kDa	0.0176
506	mitochondrial Rho GTPase 2	70 kDa	0.0176
507	retinal G protein coupled receptor b	35 kDa	0.0176
508	cyclin-dependent kinase 5 activator 2	35 kDa	0.0174
509	peroxisomal membrane protein PMP34	35 kDa	0.0174
510	PREDICTED: CAAX prenyl protease 2	35 kDa	0.0172
511	PREDICTED: heme oxygenase 2	36 kDa	0.017
512	glycerophosphodiester phosphodiesterase domain-containing protein 1	36 kDa	0.0167
513	protein SCO2 homolog, mitochondrial	36 kDa	0.0167
514	PREDICTED: meckelin isoform X2	111 kDa	0.0166
515	PREDICTED: transmembrane protein 43-like	37 kDa	0.0165
516	PREDICTED: xyloside xylosyltransferase 1 isoform X1	37 kDa	0.0165
517	limbic system-associated membrane protein precursor	37 kDa	0.0164
518	solute carrier family 35 member B1	37 kDa	0.0164
519	casein kinase 1, alpha 1	38 kDa	0.0161
520	inositol monophosphatase 3	37 kDa	0.0161
521	PREDICTED: epoxide hydrolase 1, partial	38 kDa	0.0161

522	PREDICTED: uncharacterized protein si:ch211-132g1.3 isoform X6	38 kDa	0.016
523	PREDICTED: tumor suppressor candidate 3	38 kDa	0.0159
524	metal transporter CNNM2	38 kDa	0.0159
525	abhydrolase domain-containing protein 16A	38 kDa	0.0158
526	PREDICTED: monoacylglycerol lipase abhd6-A	38 kDa	0.0158
527	dynamin-1-like protein	77 kDa	0.0158
528	PREDICTED: cadherin-related family member 2	39 kDa	0.0157
529	PREDICTED: ATP-dependent 6-phosphofructokinase, liver type-like	39 kDa	0.0155
530	erlin-1 precursor	39 kDa	0.0155
531	eukaryotic translation initiation factor 4A, isoform 1A	39 kDa	0.0155
532	PREDICTED: ATP-dependent RNA helicase DDX3X isoform X6	79 kDa	0.0154
533	PREDICTED: ATP-dependent zinc metalloprotease YME1L1 isoform X1	79 kDa	0.0154
534	opsin-1, short-wave-sensitive 2	39 kDa	0.0154
535	opsin-1, short-wave-sensitive 1	39 kDa	0.0154
536	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	80 kDa	0.0153
537	PREDICTED: cyclic nucleotide-gated channel rod photoreceptor subunit alpha-like	82 kDa	0.015
538	PREDICTED: electrogenic sodium bicarbonate cotransporter 1 isoform X2	123 kDa	0.0149
539	cAMP-dependent protein kinase catalytic subunit beta	41 kDa	0.0149
540	PREDICTED: presenilins-associated rhomboid-like protein, mitochondrial	41 kDa	0.0149
541	flotillin-1	41 kDa	0.0149
542	PREDICTED: ribosomal protein S6 kinase alpha-1 isoform X1	83 kDa	0.0148
543	mitochondrial trifunctional protein, alpha subunit	83 kDa	0.0147
544	reticulon-1 isoform 1	83 kDa	0.0147
545	PREDICTED: choline transporter-like protein 1 isoform X2	83 kDa	0.0146
546	probable hydrolase PNKD	41 kDa	0.0146
547	thromboxane-A synthase	42 kDa	0.0145
548	PREDICTED: reticulon-1 isoform X1	85 kDa	0.0144
549	PREDICTED: peroxisomal membrane protein PEX14	43 kDa	0.0141
550	solute carrier family 43 member 3	43 kDa	0.0139
551	acyl-CoA:lysophosphatidylglycerol acyltransferase 1	43 kDa	0.0139
552	reticulon-1 isoform 1	88 kDa	0.0139
553	monoacylglycerol lipase ABHD12	44 kDa	0.0138
554	PREDICTED: protein EFR3 homolog B isoform X2	91 kDa	0.0133
555	26S protease regulatory subunit 8	46 kDa	0.0131
556	PREDICTED: dyslexia-associated protein KIAA0319-like protein homolog isoform X1	93 kDa	0.0131
557	PREDICTED: protein NDRG3 isoform X1	46 kDa	0.013
558	PREDICTED: butyrophilin subfamily 3 member A1-like	46 kDa	0.013
559	PREDICTED: regulator of microtubule dynamics protein 2 isoform X1	47 kDa	0.0129
560	saccharopine dehydrogenase b	47 kDa	0.0128
561	ectonucleotide pyrophosphatase/phosphodiesterase family member 6 precursor	47 kDa	0.0127
562	26S proteasome non-ATPase regulatory subunit 3	48 kDa	0.0126
563	PREDICTED: required for meiotic nuclear division protein 1 homolog isoform X1	48 kDa	0.0125
564	PREDICTED: basic leucine zipper and W2 domain-containing protein 1-A	48 kDa	0.0125
565	palmitoyltransferase ZDHHC17	48 kDa	0.0124
566	PREDICTED: ubiquinol-cytochrome c reductase core protein II isoform X1	49 kDa	0.0124
567	PREDICTED: protein GPR108	49 kDa	0.0123
568	PREDICTED: calcium-binding mitochondrial carrier protein SCaMC-2-B isoform X2	49 kDa	0.0123
569	TLD domain-containing protein 1	50 kDa	0.0121
570	PREDICTED: LOW QUALITY PROTEIN: long-chain-fatty-acid--CoA ligase 6	50 kDa	0.0121
571	PREDICTED: oxysterol-binding protein-related protein 1-like	50 kDa	0.012
572	AP-2 complex subunit mu-A isoform 1	50 kDa	0.012
573	PREDICTED: uncharacterized protein si:ch211-11k18.4	51 kDa	0.0119
574	peroxisomal multifunctional enzyme type 2	51 kDa	0.0118
575	dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	51 kDa	0.0117
576	cytochrome P450, family 20, subfamily A, polypeptide 1	52 kDa	0.0116
577	PREDICTED: V-type proton ATPase subunit S1	52 kDa	0.0116
578	citrate synthase, mitochondrial precursor	52 kDa	0.0116
579	epoxide hydrolase 1	52 kDa	0.0115
580	cytochrome b-c1 complex subunit 1, mitochondrial	52 kDa	0.0115

581	mitochondrial dynamics protein MID49	52 kDa	0.0115
582	ectonucleotide pyrophosphatase/phosphodiesterase family member 5 precursor	53 kDa	0.0114
583	PREDICTED: sodium-coupled neutral amino acid transporter 3	53 kDa	0.0113
584	NADH dehydrogenase	53 kDa	0.0113
585	PREDICTED: S-arrestin	53 kDa	0.0112
586	PREDICTED: abhydrolase domain-containing protein 8	53 kDa	0.0112
587	PREDICTED: protein LYRIC isoform X1	53 kDa	0.0112
588	PREDICTED: microtubule-associated protein futsch-like	217 kDa	0.0112
589	zinc transporter 1	54 kDa	0.0112
590	dihydrolipoyl dehydrogenase, mitochondrial	54 kDa	0.0112
591	PREDICTED: probable ATP-dependent RNA helicase ddx6-like isoform X2	54 kDa	0.011
592	V-type proton ATPase subunit H isoform 1	55 kDa	0.0109
593	T-complex protein 11-like protein 1	56 kDa	0.0107
594	6-phosphogluconate dehydrogenase, decarboxylating isoform 1	56 kDa	0.0107
595	dol-P-Man:Man(7)GlcNAc(2)-PP-Dol alpha-1,6-mannosyltransferase precursor	56 kDa	0.0106
596	GDP-Man:Man(3)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase isoform 1	57 kDa	0.0106
597	PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP8 isoform X1	57 kDa	0.0105
598	PREDICTED: protein phosphatase 3, catalytic subunit, gamma isoform-like isoform X1	57 kDa	0.0104
599	T-complex protein 1 subunit zeta	58 kDa	0.0104
600	PREDICTED: protein phosphatase 3, catalytic subunit, gamma isoform isoform X1	58 kDa	0.0104
601	PREDICTED: cell adhesion molecule 3 isoform X1	58 kDa	0.0102
602	PREDICTED: glycerol kinase isoform X4	59 kDa	0.0102
603	PREDICTED: serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform	59 kDa	0.0102
604	amine oxidase	59 kDa	0.0102
605	PREDICTED: lysophosphatidylcholine acyltransferase 1-like	59 kDa	0.0102
606	PREDICTED: peroxisomal N(1)-acetyl-spermine/spermidine oxidase	59 kDa	0.0101
607	T-complex protein 1 subunit epsilon	59 kDa	0.0101
608	PREDICTED: voltage-dependent calcium channel subunit alpha-2/delta-1-like	120 kDa	0.01
609	uncharacterized protein LOC619266 precursor	60 kDa	0.01
610	PREDICTED: calcium-activated potassium channel subunit alpha-1 isoform X15	60 kDa	0.01
611	PREDICTED: cyclin-dependent kinase 17 isoform X1	60 kDa	0.01
612	EH-domain containing 1a	60 kDa	0.01
613	non-specific lipid-transfer protein	60 kDa	0.0099
614	methylmalonate-semialdehyde dehydrogenase	61 kDa	0.0099
615	PREDICTED: brain-specific angiogenesis inhibitor 1-associated protein 2 isoform X1	61 kDa	0.0098
616	delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial precursor	62 kDa	0.0097
617	zinc transporter 9	64 kDa	0.0094
618	PREDICTED: acetolactate synthase-like protein isoform X1	67 kDa	0.0089
619	PREDICTED: sodium/potassium/calcium exchanger 2-like isoform X2	68 kDa	0.0088
620	chaperone activity of bc1 complex-like, mitochondrial	70 kDa	0.0086
621	cleft lip and palate transmembrane protein 1 homolog	72 kDa	0.0083
622	78 kDa glucose-regulated protein precursor	72 kDa	0.0083
623	PREDICTED: LOW QUALITY PROTEIN: long-chain-fatty-acid--CoA ligase 6	75 kDa	0.008
624	transmembrane 9 superfamily member 4 precursor	75 kDa	0.0079
625	PREDICTED: protein PTHB1 isoform X1	76 kDa	0.0079
626	sphingomyelin phosphodiesterase 3	76 kDa	0.0078
627	ATP-binding cassette sub-family B member 8, mitochondrial	77 kDa	0.0078
628	PREDICTED: potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 3-like	79 kDa	0.0075
629	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	81 kDa	0.0074
630	disintegrin and metalloproteinase domain-containing protein 10 precursor	85 kDa	0.007
631	aconitate hydratase, mitochondrial	86 kDa	0.007
632	PREDICTED: ATP-dependent 6-phosphofructokinase, platelet type isoform X2	86 kDa	0.0069
633	PREDICTED: retinal-specific ATP-binding cassette transporter isoform X2	261 kDa	0.0069
634	heat shock protein HSP 90-beta	89 kDa	0.0067
635	PREDICTED: paraplegin	92 kDa	0.0065
636	PREDICTED: 2-oxoglutarate dehydrogenase, mitochondrial	93 kDa	0.0064
637	PREDICTED: prominin-1-A isoform X10	94 kDa	0.0064
638	PREDICTED: oxysterol-binding protein-related protein 8-like	98 kDa	0.0061

639	cone cGMP−specific 3',5'−cyclic phosphodiesterase subunit alpha'	98 kDa	0.0061
640	PREDICTED: cleavage and polyadenylation specificity factor subunit 1 isoform X1	99 kDa	0.006
641	PREDICTED: bifunctional heparan sulfate N−deacetylase/N−sulfotransferase 1	102 kDa	0.0058
642	PREDICTED: transmembrane and TPR repeat−containing protein 3	105 kDa	0.0057
643	PREDICTED: AP−1 complex subunit beta−1 isoform X2	107 kDa	0.0055
644	sorting nexin−25	111 kDa	0.0054
645	PREDICTED: sorting nexin−14 isoform X2	113 kDa	0.0053
646	PREDICTED: uncharacterized protein KIAA1614 homolog isoform X1	115 kDa	0.0052
647	PREDICTED: solute carrier family 12 member 7 isoform X5	121 kDa	0.0049
648	PREDICTED: oxygen−regulated protein 1	232 kDa	0.0026

Table S2. Identified proteins in washed RIS-rich fraction.

Poteins in washed RIS-rich fraction were identified with LC-MS/MS analysis and are listed in descending order of emPAI values for 5×10^5 rods.

	Identified proteins in washed RIS-rich fraction	Molecular mass	emPAI
1	uncharacterized protein LOC100145214	33 kDa	733.05
2	ATP synthase F(0) complex subunit B1, mitochondrial	31 kDa	21.616
3	voltage-dependent anion-selective channel protein 1	31 kDa	11.403
4	PREDICTED: ATP synthase subunit alpha, mitochondrial	27 kDa	8.7106
5	creatine kinase S-type, mitochondrial	47 kDa	8.4939
6	PREDICTED: creatine kinase S-type, mitochondrial isoform X2	27 kDa	8.4926
7	PREDICTED: uncharacterized protein LOC100707031 isoform X1	12 kDa	8.3582
8	PREDICTED: creatine kinase S-type, mitochondrial isoform X2	47 kDa	7.7687
9	voltage-dependent anion-selective channel protein 2	30 kDa	6.5886
10	PREDICTED: sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3Fa isoform X2	40 kDa	6.4744
11	PREDICTED: prohibitin isoform X2	22 kDa	5.7014
12	ATP synthase subunit g, mitochondrial	11 kDa	5.4627
13	creatine kinase S-type, mitochondrial	11 kDa	3.4905
14	serine/threonine-protein kinase MAK	11 kDa	3.2093
15	prohibitin 2a	35 kDa	2.9052
16	PREDICTED: prohibitin	22 kDa	2.8865
17	HIG1 domain family member 1A	11 kDa	2.8453
18	cytochrome b-c1 complex subunit 1, mitochondrial	52 kDa	2.818
19	PREDICTED: solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3a isoform X2	40 kDa	2.6469
20	voltage-dependent anion-selective channel protein 2-like	30 kDa	2.3697
21	PREDICTED: retinol dehydrogenase 8-like isoform X1	35 kDa	2.3033
22	mitochondrial 2-oxoglutarate/malate carrier protein	38 kDa	2.2404
23	malate dehydrogenase, mitochondrial	35 kDa	1.9284
24	PREDICTED: creatine kinase S-type, mitochondrial isoform X2	17 kDa	1.8764
25	PREDICTED: NADH dehydrogenase	15 kDa	1.8277
26	NADH dehydrogenase 1 beta subcomplex subunit 4	15 kDa	1.7781
27	ATP synthase subunit d, mitochondrial	18 kDa	1.6005
28	calcium-binding mitochondrial carrier protein Aralar1	76 kDa	1.4904
29	prohibitin 2-like	27 kDa	1.4654
30	ATP synthase subunit alpha, mitochondrial	33 kDa	1.404
31	ATP synthase subunit O, mitochondrial	26 kDa	1.3261
32	ADP/ATP translocase 3	27 kDa	1.2792
33	PREDICTED: NADH dehydrogenase	20 kDa	1.2519
34	PREDICTED: NADH dehydrogenase	19 kDa	1.2519
35	calcium-binding mitochondrial carrier protein Aralar1	60 kDa	1.1102
36	PREDICTED: hexokinase-1-like	14 kDa	1.0688
37	cytochrome c oxidase subunit 4 isoform 1, mitochondrial	20 kDa	1.0395
38	PREDICTED: NADH dehydrogenase	12 kDa	1.0008
39	PREDICTED: ATP synthase subunit gamma, mitochondrial isoform X1	33 kDa	0.9213
40	mitochondrial import receptor subunit TOM40 homolog	36 kDa	0.8869
41	isocitrate dehydrogenase	50 kDa	0.8761
42	PREDICTED: voltage-dependent anion-selective channel protein 2	11 kDa	0.8756
43	PREDICTED: prohibitin-2	27 kDa	0.8586
44	PREDICTED: voltage-dependent anion-selective channel protein 2	11 kDa	0.85
45	dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	69 kDa	0.7958
46	CDGSH iron sulfur domain 1	12 kDa	0.7186
47	PREDICTED: tubulin beta-4B chain-like	31 kDa	0.7144
48	PREDICTED: voltage-dependent anion-selective channel protein 3 isoform X3	36 kDa	0.7131
49	uncharacterized protein LOC541492	13 kDa	0.7088
50	PREDICTED: coiled-coil-helix-coiled-coil-helix domain-containing protein 6, mitochondrial isoform X2	29 kDa	0.707
51	mitochondrial import receptor subunit TOM40 homolog	36 kDa	0.7066

52	PREDICTED: NADH dehydrogenase	25 kDa	0.6935
53	PREDICTED: LOW QUALITY PROTEIN: actin, gamma 1	40 kDa	0.6866
54	ATPase, Na+/K+ transporting, beta 2b polypeptide	34 kDa	0.68
55	PREDICTED: pyruvate dehydrogenase E1 alpha 1 isoform X1	45 kDa	0.6756
56	S-arrestin	44 kDa	0.6623
57	PREDICTED: voltage-dependent anion-selective channel protein 3 isoform X3	36 kDa	0.642
58	PREDICTED: ATP synthase subunit beta, mitochondrial-like	56 kDa	0.6347
59	hexokinase-1	11 kDa	0.6334
60	sorting and assembly machinery component 50 homolog B	23 kDa	0.6189
61	PREDICTED: calcium-binding mitochondrial carrier protein Aralar2 isoform X1	15 kDa	0.6177
62	PREDICTED: L-lactate dehydrogenase B-B chain isoform X3	19 kDa	0.5989
63	PREDICTED: NADH dehydrogenase	14 kDa	0.591
64	uncharacterized protein LOC100135302	20 kDa	0.5895
65	PREDICTED: NADH dehydrogenase	17 kDa	0.5848
66	guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	37 kDa	0.5839
67	NADH dehydrogenase 1 alpha subcomplex subunit 11	16 kDa	0.5819
68	mitochondrial import receptor subunit TOM70	65 kDa	0.5705
69	PREDICTED: mitochondrial pyruvate carrier 2	14 kDa	0.5548
70	guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	37 kDa	0.531
71	sorting and assembly machinery component 50 homolog A	52 kDa	0.5031
72	NADH dehydrogenase 1 beta subcomplex subunit 6	15 kDa	0.5021
73	PREDICTED: threonine dehydratase, mitochondrial-like isoform X2	60 kDa	0.4921
74	NADH dehydrogenase 1 alpha subcomplex subunit 6	16 kDa	0.4489
75	NADH dehydrogenase (ubiquinone) 1 subunit c2	13 kDa	0.4395
76	aspartate aminotransferase 2a	48 kDa	0.4383
77	cytochrome c-1	36 kDa	0.4087
78	putative tubulin beta chain variant 1	20 kDa	0.3935
79	voltage-dependent anion-selective channel protein 2	20 kDa	0.3776
80	uncharacterized protein LOC100135302	23 kDa	0.3768
81	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	80 kDa	0.3711
82	mitochondrial NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 5	22 kDa	0.3702
83	mitochondrial chaperone BCS1	48 kDa	0.3687
84	PREDICTED: ATPase, Na+/K+ transporting, beta 2b polypeptide isoform X1	24 kDa	0.3639
85	cytochrome b-c1 complex subunit 2, mitochondrial	50 kDa	0.3558
86	aspartate aminotransferase 2	43 kDa	0.3536
87	NADH dehydrogenase	41 kDa	0.3475
88	NADH dehydrogenase	31 kDa	0.3435
89	sodium/potassium-transporting ATPase subunit alpha-3	113 kDa	0.3395
90	PREDICTED: phosphate carrier protein, mitochondrial-like isoform X1	34 kDa	0.3353
91	PREDICTED: threo-3-hydroxyaspartate ammonia-lyase-like	41 kDa	0.332
92	NADH dehydrogenase	53 kDa	0.329
93	cytochrome c oxidase subunit 4 isoform 1, mitochondrial	20 kDa	0.3265
94	plasminogen receptor (KT)	20 kDa	0.3223
95	sideroflexin-3	36 kDa	0.311
96	PREDICTED: peroxiredoxin-5, mitochondrial-like	20 kDa	0.306
97	PREDICTED: calcium-binding mitochondrial carrier protein Aralar2 isoform X1	48 kDa	0.3028
98	NADH dehydrogenase	58 kDa	0.2958
99	solute carrier family 25, member 23	31 kDa	0.2892
100	NAD(P) transhydrogenase, mitochondrial	114 kDa	0.2842
101	PREDICTED: vesicle-associated membrane protein-associated protein A-like	26 kDa	0.283
102	PREDICTED: vesicle-associated membrane protein-associated protein A-like	26 kDa	0.283
103	stomatin-like protein 2, mitochondrial	39 kDa	0.2785
104	PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like	27 kDa	0.2751
105	stomatin-like protein 2, mitochondrial	39 kDa	0.275
106	PREDICTED: pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial isoform X1	25 kDa	0.2739
107	PREDICTED: ubiquinol-cytochrome c reductase core protein II isoform X1	49 kDa	0.2723
108	LETM1 and EF-hand domain-containing protein 1, mitochondrial	86 kDa	0.2666
109	protein disulfide-isomerase TMX3 precursor	47 kDa	0.2645
110	mitochondrial inner membrane protein	83 kDa	0.2592

111	reticulon-4-interacting protein 1 homolog, mitochondrial	42 kDa	0.2566
112	mitochondrial import inner membrane translocase subunit Tim17-B	18 kDa	0.2565
113	protein NipSnap homolog 2	33 kDa	0.2554
114	voltage-dependent anion-selective channel protein 2	20 kDa	0.2532
115	mitochondrial pyruvate carrier 1	13 kDa	0.2434
116	solute carrier family 25, member 23	23 kDa	0.2278
117	citrate synthase, mitochondrial precursor	52 kDa	0.2185
118	apolipoprotein O	24 kDa	0.2167
119	cytochrome c oxidase subunit VIIa polypeptide 3	16 kDa	0.2071
120	PREDICTED: mitochondrial glutamate carrier 1	34 kDa	0.2071
121	cytochrome c oxidase subunit Vaa	16 kDa	0.2042
122	PREDICTED: tubulin alpha chain-like	12 kDa	0.2021
123	dihydrolipoyl dehydrogenase, mitochondrial	54 kDa	0.2018
124	hexokinase-1	54 kDa	0.2009
125	ES1 protein, mitochondrial precursor	31 kDa	0.2005
126	transmembrane protein 256 precursor	12 kDa	0.1984
127	PREDICTED: ubiquinol-cytochrome c reductase core protein II isoform X1	40 kDa	0.1957
128	PREDICTED: uncharacterized protein LOC571872 isoform X1	12 kDa	0.1948
129	NADH dehydrogenase	12 kDa	0.1913
130	alpha-enolase	47 kDa	0.186
131	PREDICTED: NADH dehydrogenase	21 kDa	0.1825
132	PREDICTED: apoptosis-inducing factor 1, mitochondrial isoform X3	68 kDa	0.181
133	succinyl-CoA ligase	51 kDa	0.1776
134	PREDICTED: glutaryl-CoA dehydrogenase, mitochondrial-like	49 kDa	0.1759
135	PREDICTED: apoptosis-inducing factor 1, mitochondrial isoform X1	48 kDa	0.1759
136	NADH dehydrogenase	13 kDa	0.1755
137	mitochondrial carrier homolog 2	31 kDa	0.1739
138	heat shock cognate 71 kDa protein	42 kDa	0.1735
139	isocitrate dehydrogenase	40 kDa	0.1722
140	erlin-2 precursor	40 kDa	0.1713
141	cytochrome c oxidase subunit 6A1, mitochondrial	13 kDa	0.1698
142	enoyl-CoA hydratase, mitochondrial	31 kDa	0.1691
143	solute carrier family 25, member 23	31 kDa	0.1691
144	PREDICTED: LOW QUALITY PROTEIN: long-chain-fatty-acid--CoA ligase 6	50 kDa	0.1667
145	isocitrate dehydrogenase	43 kDa	0.1665
146	PREDICTED: NADH dehydrogenase	43 kDa	0.1648
147	L-lactate dehydrogenase B-A chain	36 kDa	0.1643
148	PREDICTED: isocitrate dehydrogenase	44 kDa	0.1624
149	PREDICTED: cytochrome b-c1 complex subunit 7-like	13 kDa	0.1619
150	pyruvate dehydrogenase E1 component subunit beta, mitochondrial	39 kDa	0.1589
151	translocase of outer mitochondrial membrane 40 homolog, like	35 kDa	0.1584
152	methylmalonate-semialdehyde dehydrogenase	61 kDa	0.1579
153	PREDICTED: uncharacterized protein LOC556653	23 kDa	0.1577
154	NADH-cytochrome b5 reductase 1	28 kDa	0.1561
155	rhodopsin	40 kDa	0.1555
156	PREDICTED: tubulin alpha-1C chain	45 kDa	0.1547
157	hexokinase-1	71 kDa	0.1528
158	uncharacterized protein LOC556781	23 kDa	0.1521
159	isocitrate dehydrogenase	43 kDa	0.152
160	3-hydroxyacyl-CoA dehydrogenase type-2	28 kDa	0.1504
161	mitochondrial import inner membrane translocase subunit tim16	14 kDa	0.1501
162	PREDICTED: gap junction delta-2 protein-like	21 kDa	0.1495
163	retinol dehydrogenase-like	36 kDa	0.1449
164	PREDICTED: tubulin alpha-4A chain-like, partial	22 kDa	0.1426
165	NADH dehydrogenase	24 kDa	0.1419
166	protein QIL1	12 kDa	0.1404
167	creatine kinase U-type, mitochondrial	22 kDa	0.1399
168	PREDICTED: tubulin beta-2B chain-like isoform 1	55 kDa	0.1394
169	PREDICTED: tubulin alpha chain	45 kDa	0.1388

170	OCIA domain-containing protein 1	30 kDa	0.1381
171	trifunctional enzyme subunit beta, mitochondrial	50 kDa	0.1374
172	reticulon-4	22 kDa	0.1374
173	PREDICTED: mitochondrial import inner membrane translocase subunit Tim23	22 kDa	0.1349
174	PREDICTED: protein FAM162B isoform X1	17 kDa	0.1314
175	PREDICTED: complex I assembly factor TIMMDC1, mitochondrial isoform X1	33 kDa	0.1305
176	translocase of outer mitochondrial membrane 40 homolog, like	36 kDa	0.1302
177	ATPase family AAA domain-containing protein 3	69 kDa	0.1242
178	protein NDRG1 isoform 1	42 kDa	0.1242
179	succinate dehydrogenase	61 kDa	0.1235
180	ras-related protein Rab-2A	24 kDa	0.1227
181	uncharacterized protein LOC556781	13 kDa	0.1218
182	succinate dehydrogenase	73 kDa	0.1212
183	PREDICTED: FAS-associated factor 2-like isoform X1	54 kDa	0.1196
184	PREDICTED: presenilins-associated rhomboid-like protein, mitochondrial	41 kDa	0.1181
185	PREDICTED: LOW QUALITY PROTEIN: long-chain-fatty-acid--CoA ligase 6	75 kDa	0.1152
186	mitochondrial import inner membrane translocase subunit Tim23	22 kDa	0.1127
187	PREDICTED: arylacetamide deacetylase isoform X2	16 kDa	0.1101
188	PREDICTED: ras-related protein Rab-1A-like isoform X1	22 kDa	0.1089
189	ATPase family AAA domain-containing protein 3	69 kDa	0.1088
190	coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	37 kDa	0.1085
191	ras-related protein Rab-1B	22 kDa	0.108
192	Tubulin beta-2C chain	11 kDa	0.1069
193	retinol dehydrogenase 13	37 kDa	0.1068
194	PREDICTED: calcium-binding mitochondrial carrier protein SCaMC-2-B isoform X2	49 kDa	0.1065
195	NADH dehydrogenase	17 kDa	0.1065
196	synaptosomal-associated protein 25-B	23 kDa	0.1063
197	aconitate hydratase, mitochondrial	86 kDa	0.1031
198	PREDICTED: tubulin alpha chain-like	50 kDa	0.1025
199	PREDICTED: uncharacterized protein LOC571872 isoform X1	32 kDa	0.1009
200	mitochondrial import inner membrane translocase subunit Tim17-A	17 kDa	0.1009
201	uncharacterized protein LOC541537	27 kDa	0.0992
202	PREDICTED: uncharacterized protein LOC101885612	11 kDa	0.0971
203	PREDICTED: actin, aortic smooth muscle	18 kDa	0.0968
204	mitochondria-eating protein	55 kDa	0.096
205	28S ribosomal protein S36, mitochondrial	12 kDa	0.0957
206	brain creatine kinase b	43 kDa	0.0955
207	sorting and assembly machinery component 50 homolog B	27 kDa	0.0953
208	PREDICTED: NADH dehydrogenase	21 kDa	0.0942
209	elongation factor Tu, mitochondrial	49 kDa	0.0942
210	PREDICTED: mitochondrial fission process protein 1-like	18 kDa	0.0939
211	transmembrane protein 256 precursor	12 kDa	0.0928
212	glutaryl-CoA dehydrogenase a	18 kDa	0.0912
213	sideroflexin-4	35 kDa	0.0909
214	PREDICTED: vesicle-associated membrane protein 2-like	12 kDa	0.0902
215	acylglycerol kinase, mitochondrial precursor	48 kDa	0.0901
216	ras-related protein Rab-3A	28 kDa	0.0898
217	long-chain fatty acid transport protein 4	25 kDa	0.0897
218	histone 1, H4, like	12 kDa	0.0889
219	mitochondrial ubiquitin ligase activator of nfkb 1-A	12 kDa	0.0889
220	PREDICTED: succinate dehydrogenase cytochrome b560 subunit, mitochondrial isoform X1	19 kDa	0.0886
221	PREDICTED: ornithine aminotransferase, mitochondrial	49 kDa	0.0871
222	erlin-1 precursor	39 kDa	0.0859
223	PREDICTED: L-lactate dehydrogenase B-B chain isoform X4	19 kDa	0.0846
224	PREDICTED: S-arrestin	53 kDa	0.0833
225	PREDICTED: arylacetamide deacetylase isoform X1	47 kDa	0.0829
226	cysteine desulfurase, mitochondrial	50 kDa	0.0828
227	PREDICTED: mitochondrial ubiquitin ligase activator of nfkb 1-A	33 kDa	0.0823
228	PREDICTED: ATP-binding cassette sub-family B member 7, mitochondrial	82 kDa	0.0811

229	PREDICTED: stress–70 protein, mitochondrial–like, partial	17 kDa	0.0784
230	ATP–binding cassette sub–family B member 8, mitochondrial	77 kDa	0.0781
231	PREDICTED: cadherin–related family member 5–like isoform X2	20 kDa	0.0776
232	inactive hydroxysteroid dehydrogenase–like protein 1	35 kDa	0.077
233	PREDICTED: growth hormone–inducible transmembrane protein	35 kDa	0.0762
234	erlin–1 precursor	39 kDa	0.0753
235	solute carrier family 25 (mitochondrial carrier: glutamate), member 22	36 kDa	0.0737
236	PREDICTED: malate dehydrogenase 1Aa, NAD (soluble) isoform X1	36 kDa	0.072
237	dihydrolipoyllysine–residue succinyltransferase component of 2–oxoglutarate dehydrogenase complex, mitochondrial	51 kDa	0.0714
238	PREDICTED: calcium–binding mitochondrial carrier protein SCaMC–3–like isoform X1	10 kDa	0.0708
239	PREDICTED: magnesium transporter MRS2 homolog, mitochondrial isoform X1	48 kDa	0.0702
240	vesicle–associated membrane protein–associated protein A	30 kDa	0.0696
241	catechol–O–methyltransferase a	30 kDa	0.0692
242	NADH dehydrogenase (ubiquinone) Fe–S protein 8b	22 kDa	0.0689
243	probable D–lactate dehydrogenase, mitochondrial	53 kDa	0.0687
244	mitochondrial carnitine/acylcarnitine carrier protein CACL	34 kDa	0.0682
245	ADP–ribosylation factor–like protein 9	26 kDa	0.0682
246	PREDICTED: sodium/potassium–transporting ATPase subunit beta–2–like	19 kDa	0.0674
247	PREDICTED: transmembrane protein 126A isoform X1	22 kDa	0.0673
248	PREDICTED: mitochondrial import inner membrane translocase subunit Tim21	27 kDa	0.0656
249	Na+/K+ –ATPase alpha 1 subunit	90 kDa	0.0651
250	PREDICTED: uncharacterized protein LOC556653	35 kDa	0.0647
251	PREDICTED: transmembrane emp24 domain–containing protein 9 isoform X1	27 kDa	0.0644
252	acetyl–CoA acetyltransferase, mitochondrial precursor	48 kDa	0.0628
253	RAB5A, member RAS oncogene family, a	24 kDa	0.0627
254	stress–70 protein, mitochondrial	73 kDa	0.0615
255	very–long–chain enoyl–CoA reductase	36 kDa	0.0615
256	cytochrome c	11 kDa	0.0613
257	metaxin 1	36 kDa	0.0612
258	cytochrome c oxidase subunit IV isoform 2	20 kDa	0.0604
259	PREDICTED: coiled–coil domain–containing protein 136–like isoform X1	53 kDa	0.0602
260	heat shock cognate 71 kDa protein	29 kDa	0.0597
261	protein QIL1	12 kDa	0.0597
262	ATPase, Na+/K+ transporting, beta 2a polypeptide	16 kDa	0.0595
263	PREDICTED: ADP–dependent glucokinase isoform X2	58 kDa	0.0591
264	synaptojanin–2–binding protein	16 kDa	0.0578
265	pyrroline–5–carboxylate reductase 1a	34 kDa	0.0574
266	zinc transporter 9	64 kDa	0.0573
267	PREDICTED: protein SCO1 homolog, mitochondrial	34 kDa	0.0568
268	PREDICTED: dnaJ homolog subfamily C member 11	65 kDa	0.0557
269	PREDICTED: mitochondrial fission factor homolog B isoform X1	34 kDa	0.0555
270	PREDICTED: glutaminase a isoform X1	66 kDa	0.0549
271	calmegin precursor	66 kDa	0.0548
272	COX16 cytochrome c oxidase assembly homolog	13 kDa	0.0546
273	PREDICTED: peptidyl–prolyl cis–trans isomerase FKBP8 isoform X1	57 kDa	0.0545
274	mitochondrial import inner membrane translocase subunit TIM50 precursor	44 kDa	0.054
275	mitochondrial ATP synthase subunit f	13 kDa	0.054
276	60S ribosomal protein L18	22 kDa	0.0539
277	traB domain–containing protein	40 kDa	0.0534
278	probable glutamate––tRNA ligase, mitochondrial precursor	40 kDa	0.0534
279	metaxin–2	31 kDa	0.0531
280	transmembrane protein 11, mitochondrial	27 kDa	0.0528
281	reticulon–4	22 kDa	0.0528
282	78 kDa glucose–regulated protein precursor	72 kDa	0.0527
283	glyceraldehyde–3–phosphate dehydrogenase 2	36 kDa	0.0521
284	60S ribosomal protein L14	18 kDa	0.0518
285	60S ribosomal protein L24	18 kDa	0.0514
286	RAB1A, member RAS oncogene family	28 kDa	0.0496
287	ATP synthase F(0) complex subunit C3, mitochondrial	14 kDa	0.0487

288	serine hydroxymethyltransferase, mitochondrial	57 kDa	0.0483
289	thioredoxin-dependent peroxide reductase, mitochondrial	28 kDa	0.0482
290	60 kDa heat shock protein, mitochondrial	28 kDa	0.048
291	ras-related protein Rab-1B	19 kDa	0.0477
292	acyl-CoA synthetase long-chain family member 3b	79 kDa	0.0464
293	PREDICTED: nuclease EXOG, mitochondrial	39 kDa	0.0464
294	mitochondrial Rho GTPase 2	70 kDa	0.0457
295	uncharacterized protein LOC619266 precursor	60 kDa	0.0455
296	DDRGK domain-containing protein 1 precursor	35 kDa	0.0454
297	PREDICTED: ras-related protein Rab-11B	25 kDa	0.0453
298	PREDICTED: ER membrane protein complex subunit 1 isoform X1	111 kDa	0.045
299	guanine nucleotide-binding protein G(o) subunit alpha	40 kDa	0.045
300	PREDICTED: syntaxin-12 isoform X1	30 kDa	0.0444
301	RAB11a, member RAS oncogene family, like	20 kDa	0.0438
302	PREDICTED: NADH dehydrogenase	20 kDa	0.0438
303	mitochondrial trifunctional protein, alpha subunit	83 kDa	0.0434
304	phosphatidate cytidylyltransferase, mitochondrial precursor	15 kDa	0.0434
305	solute carrier family 3 (amino acid transporter heavy chain), member 2b	57 kDa	0.0432
306	AFG3-like protein 2	89 kDa	0.043
307	glycerophosphodiester phosphodiesterase domain-containing protein 1	36 kDa	0.0428
308	immunity-related GTPase family, q2	42 kDa	0.0423
309	40S ribosomal protein S25	15 kDa	0.0422
310	Beta-centractin	15 kDa	0.0418
311	PREDICTED: ADP-dependent glucokinase isoform X2	26 kDa	0.0417
312	PREDICTED: OCIA domain-containing protein 1 isoform X1	26 kDa	0.0417
313	PREDICTED: mitochondrial fission factor-like isoform X3	26 kDa	0.0417
314	mitochondrial dicarboxylate carrier	32 kDa	0.0416
315	PREDICTED: kynurenine/alpha-aminoadipate aminotransferase, mitochondrial isoform X1	48 kDa	0.0415
316	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	21 kDa	0.0413
317	ras-related protein Rab-5C	37 kDa	0.0411
318	surfeit locus protein 1	32 kDa	0.0411
319	PREDICTED: succinate dehydrogenase	32 kDa	0.0411
320	PREDICTED: oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) isoform X3	26 kDa	0.041
321	PREDICTED: mitochondrial import inner membrane translocase subunit Tim22	21 kDa	0.0407
322	PREDICTED: 2-oxoglutarate dehydrogenase, mitochondrial	93 kDa	0.0406
323	PREDICTED: potassium voltage-gated channel subfamily B member 2	93 kDa	0.0403
324	c3orf33 homolog	16 kDa	0.0395
325	rhodopsin kinase	27 kDa	0.0395
326	PREDICTED: oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) isoform X2	44 kDa	0.0394
327	PREDICTED: NADH dehydrogenase (ubiquinone) complex I, assembly factor 6	33 kDa	0.0394
328	PREDICTED: transmembrane emp24 domain-containing protein 7 isoform X2	27 kDa	0.0391
329	PREDICTED: FUN14 domain-containing protein 2 isoform X1	16 kDa	0.0388
330	eukaryotic translation elongation factor 1 alpha 1-like	50 kDa	0.0387
331	ATPase family AAA domain-containing protein 1-B	22 kDa	0.0386
332	immunoglobulin superfamily member 8 precursor	68 kDa	0.0386
333	mitochondrial import receptor subunit TOM20 homolog B	16 kDa	0.0385
334	uncharacterized protein C2orf47 homolog, mitochondrial	28 kDa	0.0379
335	dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit precursor	51 kDa	0.0377
336	guanine nucleotide-binding protein G(t) subunit alpha-2	40 kDa	0.0372
337	ATP synthase subunit delta, mitochondrial	17 kDa	0.0372
338	PREDICTED: mitochondrial pyruvate carrier 2-like	17 kDa	0.0372
339	protein disulfide-isomerase TMX3 precursor	52 kDa	0.0371
340	uncharacterized protein LOC100127828	34 kDa	0.0371
341	PREDICTED: transmembrane emp24 domain-containing protein 2	23 kDa	0.0369
342	uncharacterized protein LOC100145220	29 kDa	0.0367
343	ubiquinone biosynthesis monooxygenase COQ6	52 kDa	0.0366

344	phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	11 kDa	0.0364
345	PREDICTED: probable UDP-sugar transporter protein SLC35A4 isoform X1	11 kDa	0.0364
346	60 kDa heat shock protein, mitochondrial	29 kDa	0.0362
347	mitochondrial folate transporter/carrier	35 kDa	0.0362
348	phosphatidate cytidylyltransferase, mitochondrial precursor	11 kDa	0.0359
349	PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like, partial	35 kDa	0.0359
350	surfeit gene 4, like	23 kDa	0.0358
351	PREDICTED: ER membrane protein complex subunit 1 isoform X1	114 kDa	0.0355
352	PREDICTED: heme oxygenase 2	36 kDa	0.0354
353	PREDICTED: ras-related protein Rab-6A isoform X2	24 kDa	0.0353
354	cytochrome b-c1 complex subunit Rieske, mitochondrial	30 kDa	0.035
355	PREDICTED: ATP-dependent zinc metalloprotease YME1L1 isoform X1	79 kDa	0.0348
356	40S ribosomal protein S19	18 kDa	0.0348
357	PREDICTED: 60S ribosomal protein L6	30 kDa	0.0348
358	metaxin 1a	36 kDa	0.0347
359	ras-related protein Rab-14	24 kDa	0.0347
360	L-2-hydroxyglutarate dehydrogenase, mitochondrial	12 kDa	0.0346
361	optic atrophy 3 protein homolog	18 kDa	0.0345
362	60S ribosomal protein L15	24 kDa	0.0345
363	PREDICTED: sarcolemmal membrane-associated protein isoform X4	92 kDa	0.0344
364	acyl-CoA dehydrogenase-like	49 kDa	0.0343
365	PREDICTED: 40S ribosomal protein S8	24 kDa	0.0343
366	60S ribosomal protein L27a	18 kDa	0.0343
367	vesicle-trafficking protein SEC22b-A	24 kDa	0.0339
368	PREDICTED: saccharopine dehydrogenase-like oxidoreductase-like	12 kDa	0.0331
369	rab GDP dissociation inhibitor beta	51 kDa	0.033
370	mitochondrial trifunctional protein, alpha subunit	38 kDa	0.0328
371	E3 ubiquitin-protein ligase MARCH5	31 kDa	0.0328
372	PREDICTED: LOW QUALITY PROTEIN: 40S ribosomal protein S13-like	19 kDa	0.0327
373	PREDICTED: ER membrane protein complex subunit 6	12 kDa	0.0327
374	succinate dehydrogenase	32 kDa	0.0326
375	COX15 homolog	51 kDa	0.0326
376	rhodopsin kinase	64 kDa	0.0324
377	COX16 cytochrome c oxidase assembly homolog	12 kDa	0.0323
378	mimitin, mitochondrial	19 kDa	0.032
379	dynamin-like 120 kDa protein, mitochondrial precursor	112 kDa	0.0317
380	delta-1-pyrroline-5-carboxylate synthase	85 kDa	0.0316
381	gamma-enolase	52 kDa	0.0316
382	PREDICTED: NCK-interacting protein with SH3 domain-like	19 kDa	0.0313
383	synaptotagmin II	47 kDa	0.0308
384	PREDICTED: regulator of microtubule dynamics protein 2 isoform X1	47 kDa	0.0308
385	PREDICTED: apoptosis-inducing factor 1, mitochondrial isoform X1	13 kDa	0.0306
386	flotillin 2	47 kDa	0.0305
387	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 precursor	67 kDa	0.0304
388	NADH dehydrogenase	27 kDa	0.0303
389	PREDICTED: pyruvate dehydrogenase protein X component, mitochondrial	54 kDa	0.0303
390	ATP synthase subunit s, mitochondrial	27 kDa	0.03
391	cytochrome c-type heme lyase	34 kDa	0.0299
392	alpha/beta hydrolase domain-containing protein 11	34 kDa	0.0296
393	nucleoside diphosphate kinase A	20 kDa	0.0294
394	uncharacterized protein LOC100127828	34 kDa	0.0293
395	chaperone activity of bc1 complex-like, mitochondrial	70 kDa	0.0292
396	ras-related protein Rab-35	20 kDa	0.0292
397	very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 2	28 kDa	0.0287
398	PREDICTED: protein XRP2 isoform X1	42 kDa	0.0287
399	dnaJ homolog subfamily C member 11	64 kDa	0.0285
400	ras-related protein Rap-1b precursor	21 kDa	0.0284
401	fatty aldehyde dehydrogenase	28 kDa	0.0281
402	mitochondrial-processing peptidase subunit alpha	58 kDa	0.028

403	60S ribosomal protein L7	29 kDa	0.0277
404	uncharacterized protein C18orf19 homolog A	29 kDa	0.0276
405	peptidyl-prolyl cis-trans isomerase FKBP8	44 kDa	0.0275
406	histone 2, H2a	14 kDa	0.0274
407	epimerase family protein SDR39U1	36 kDa	0.0274
408	oxidase (cytochrome c) assembly 1-like	51 kDa	0.0274
409	isochorismatase domain-containing protein 2, mitochondrial	21 kDa	0.0274
410	ADP-ribosylation-like factor 6 interacting protein 5	22 kDa	0.0272
411	peptidyl-prolyl cis-trans isomerase FKBP8	44 kDa	0.0271
412	S-adenosylmethionine mitochondrial carrier protein	29 kDa	0.0271
413	protoporphyrinogen oxidase	52 kDa	0.027
414	heat shock protein 75 kDa, mitochondrial	82 kDa	0.027
415	solute carrier family 2, facilitated glucose transporter member 1	53 kDa	0.0263
416	PREDICTED: transmembrane protein 70, mitochondrial	30 kDa	0.0262
417	PREDICTED: 40S ribosomal protein S9-like	22 kDa	0.0259
418	abhydrolase domain-containing protein 16A	38 kDa	0.0257
419	PREDICTED: ras-related protein Rab-10	23 kDa	0.0256
420	adipocyte plasma membrane-associated protein	47 kDa	0.0252
421	PREDICTED: dnaJ homolog subfamily C member 30	47 kDa	0.0252
422	methyltransferase like 7A precursor	31 kDa	0.0251
423	PREDICTED: progestin and adipoQ receptor family member 4-like	31 kDa	0.025
424	NADH dehydrogenase	48 kDa	0.0242
425	PREDICTED: succinyl-CoA ligase	16 kDa	0.0242
426	CDP-diacylglycerol--inositol 3-phosphatidyltransferase	24 kDa	0.0239
427	protein THEM6 precursor	24 kDa	0.0239
428	protein THEM6 precursor	24 kDa	0.0238
429	synaptophysin b isoform 1	33 kDa	0.0235
430	PREDICTED: aspartate beta-hydroxylase isoform X2	33 kDa	0.0233
431	PREDICTED: protein MGARP isoform X2	41 kDa	0.0233
432	ubiquinol-cytochrome c reductase complex assembly factor 1	33 kDa	0.0233
433	fatty-acid amide hydrolase 1	16 kDa	0.0232
434	PREDICTED: reticulon-3-B-like isoform X2	25 kDa	0.0231
435	PREDICTED: glycerol kinase isoform X4	59 kDa	0.0231
436	translocase of outer mitochondrial membrane 20 homolog a	16 kDa	0.023
437	40S ribosomal protein S5	25 kDa	0.023
438	PREDICTED: calnexin isoform X1	67 kDa	0.0229
439	1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon	42 kDa	0.0229
440	PREDICTED: probable palmitoyltransferase ZDHHC14 isoform X1	16 kDa	0.0227
441	PREDICTED: protein CCSMST1	16 kDa	0.0227
442	glutathione peroxidase 1	16 kDa	0.0227
443	PREDICTED: solute carrier family 25 member 51-like	34 kDa	0.0226
444	PREDICTED: kynurenine--oxoglutarate transaminase 1 isoform X1	51 kDa	0.0225
445	PREDICTED: hydroxyacylglutathione hydrolase, mitochondrial isoform X1	34 kDa	0.0225
446	PREDICTED: uncharacterized protein LOC100694464	17 kDa	0.0223
447	mitochondrial import inner membrane translocase subunit TIM44	52 kDa	0.0222
448	bcl-2-modifying factor	17 kDa	0.0221
449	reticulon-1 isoform 1	17 kDa	0.0221
450	PREDICTED: retinol dehydrogenase 12-like	34 kDa	0.0221
451	PREDICTED: cadherin-related family member 5-like isoform X2	44 kDa	0.0217
452	40S ribosomal protein S7	17 kDa	0.0216
453	PREDICTED: coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial	17 kDa	0.0213
454	PREDICTED: 60S ribosomal protein L9 isoform X2	17 kDa	0.0213
455	PREDICTED: 40S ribosomal protein S24	17 kDa	0.0212
456	lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	54 kDa	0.021
457	PREDICTED: AFG3-like protein 1	27 kDa	0.021
458	PREDICTED: 60S ribosomal protein L12	18 kDa	0.0209
459	protein SCO2 homolog, mitochondrial	36 kDa	0.0207
460	isovaleryl-CoA dehydrogenase, mitochondrial	46 kDa	0.0206

461	PREDICTED: transmembrane protein 43-like	37 kDa	0.0205
462	PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP8 isoform X1	37 kDa	0.0201
463	uncharacterized protein LOC100127838	18 kDa	0.0201
464	PREDICTED: 60S ribosomal protein L23a	18 kDa	0.0201
465	PREDICTED: neutral alpha-glucosidase AB	18 kDa	0.0201
466	coiled-coil domain-containing protein 51	47 kDa	0.02
467	PREDICTED: sodium/potassium-transporting ATPase subunit beta-2-like	18 kDa	0.02
468	PREDICTED: [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	47 kDa	0.02
469	flotillin-2a	47 kDa	0.0199
470	PREDICTED: epoxide hydrolase 1, partial	38 kDa	0.0199
471	40S ribosomal protein S16	18 kDa	0.0198
472	dnaJ homolog subfamily C member 2	48 kDa	0.0197
473	solute carrier family 25 member 40	39 kDa	0.0193
474	PREDICTED: alpha-aminoadipic semialdehyde dehydrogenase	59 kDa	0.019
475	40S ribosomal protein S4, X isoform	29 kDa	0.019
476	mitofusin-2	80 kDa	0.0189
477	PREDICTED: fatty aldehyde dehydrogenase isoform X2	40 kDa	0.0188
478	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 precursor	70 kDa	0.0187
479	carnitine O-palmitoyltransferase 2, mitochondrial	20 kDa	0.0186
480	ER membrane protein complex subunit 3	30 kDa	0.0185
481	methylmalonic aciduria type A protein, mitochondrial	30 kDa	0.0185
482	peripherin-2	20 kDa	0.0184
483	PREDICTED: surfeit locus protein 4	30 kDa	0.0184
484	60S ribosomal protein L7a	30 kDa	0.0184
485	PREDICTED: uncharacterized protein si:ch211-11k18.4	51 kDa	0.0184
486	PREDICTED: very long-chain specific acyl-CoA dehydrogenase, mitochondrial isoform X1	71 kDa	0.0183
487	hydroxysteroid dehydrogenase-like protein 2	51 kDa	0.0182
488	PREDICTED: paraplegin	92 kDa	0.0182
489	PREDICTED: calcium-binding mitochondrial carrier protein SCaMC-3-like isoform X2	41 kDa	0.0182
490	regulator of microtubule dynamics protein 3	51 kDa	0.018
491	PREDICTED: 40S ribosomal protein S2	20 kDa	0.018
492	NADH dehydrogenase 1 beta subcomplex subunit 10	20 kDa	0.018
493	long-chain fatty acid transport protein 4	73 kDa	0.0179
494	mitochondrial dynamics protein MID49	52 kDa	0.0177
495	PREDICTED: epoxide hydrolase 1-like, partial	20 kDa	0.0176
496	PREDICTED: dehydrogenase/reductase SDR family member 7B isoform X1	31 kDa	0.0176
497	PREDICTED: 3 beta-hydroxysteroid dehydrogenase type 7 isoform X1	42 kDa	0.0176
498	60S ribosomal protein L4	43 kDa	0.0172
499	ras-related protein Rap-1b-like	21 kDa	0.0171
500	ADP-ribosylation factor-like protein 6	21 kDa	0.0171
501	translocon-associated protein subunit delta precursor	21 kDa	0.017
502	tryptophan 5-hydroxylase 1	54 kDa	0.017
503	PREDICTED: bcl10-interacting CARD protein isoform X2	21 kDa	0.0169
504	PREDICTED: cytochrome c oxidase subunit 4 isoform 1, mitochondrial	21 kDa	0.0169
505	uncharacterized protein LOC393228	21 kDa	0.0168
506	PREDICTED: protein FAM57A-like	32 kDa	0.0168
507	PREDICTED: fatty aldehyde dehydrogenase-like	55 kDa	0.0167
508	outer dense fiber of sperm tails 2b	22 kDa	0.0166
509	PRA1 family protein 3	22 kDa	0.0166
510	fumarate hydratase, mitochondrial precursor	55 kDa	0.0166
511	60S ribosomal protein L9	22 kDa	0.0163
512	abhydrolase domain-containing protein 4	22 kDa	0.0163
513	PREDICTED: synembryn-A-like isoform X2	67 kDa	0.0163
514	protein kinase, cAMP-dependent, regulatory, type II, alpha A	45 kDa	0.0163
515	ubiquinone biosynthesis protein COQ7 homolog	22 kDa	0.0162
516	carnitine O-palmitoyltransferase 2, mitochondrial	22 kDa	0.0162
517	eukaryotic translation elongation factor 1 alpha 1-like	22 kDa	0.0161
518	solute carrier family 25 member 46	45 kDa	0.016

519	isobutyryl-CoA dehydrogenase, mitochondrial	45 kDa	0.016
520	protein-S-isoprenylcysteine O-methyltransferase	34 kDa	0.016
521	PREDICTED: probable arginine--tRNA ligase, mitochondrial isoform X1	22 kDa	0.016
522	PREDICTED: 10 kDa heat shock protein, mitochondrial isoform X2	11 kDa	0.0159
523	PREDICTED: aarF domain-containing protein kinase 4	11 kDa	0.0159
524	PREDICTED: saccharopine dehydrogenase-like oxidoreductase	11 kDa	0.0159
525	succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	57 kDa	0.0159
526	acyl-CoA dehydrogenase family member 9, mitochondrial	69 kDa	0.0159
527	succinyl-CoA ligase	34 kDa	0.0159
528	dihydroorotate dehydrogenase (quinone), mitochondrial	46 kDa	0.0158
529	aspartate aminotransferase, cytoplasmic	46 kDa	0.0158
530	PREDICTED: 60S ribosomal protein L18a-like	23 kDa	0.0158
531	60S acidic ribosomal protein P0	34 kDa	0.0157
532	mitochondrial ubiquitin ligase activator of nfkb 1-A	23 kDa	0.0156
533	methylglutaconyl-CoA hydratase, mitochondrial	35 kDa	0.0156
534	PREDICTED: transmembrane protein C9orf123 homolog	11 kDa	0.0154
535	saccharopine dehydrogenase b	47 kDa	0.0154
536	PREDICTED: flotillin 1a isoform X1	47 kDa	0.0153
537	PREDICTED: serine protease HTRA2, mitochondrial	47 kDa	0.0153
538	electron transfer flavoprotein subunit alpha, mitochondrial	35 kDa	0.0153
539	ADP-ribosylation factor-like protein 6-interacting protein 1	23 kDa	0.0153
540	PREDICTED: heme oxygenase 2	35 kDa	0.0152
541	transmembrane protein 65	24 kDa	0.015
542	ras-related protein Rab-5B	24 kDa	0.015
543	uncharacterized protein LOC100005854	24 kDa	0.015
544	PREDICTED: required for meiotic nuclear division protein 1 homolog isoform X1	48 kDa	0.0149
545	DnaJ (Hsp40) homolog, subfamily A, member 3B	36 kDa	0.0148
546	protein lunapark-A	36 kDa	0.0147
547	putative hexokinase HKDC1	61 kDa	0.0147
548	delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial precursor	62 kDa	0.0146
549	cytosol aminopeptidase	37 kDa	0.0145
550	transmembrane emp24 domain-containing protein 10 precursor	24 kDa	0.0145
551	probable 28S ribosomal protein S10, mitochondrial	12 kDa	0.0145
552	fructose-bisphosphate aldolase C	37 kDa	0.0145
553	ubiquitin-60S ribosomal protein L40	12 kDa	0.0143
554	phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	12 kDa	0.0143
555	heat shock protein HSP 90-beta	89 kDa	0.0143
556	superoxide dismutase	25 kDa	0.0141
557	peroxisomal membrane protein 11B	25 kDa	0.0141
558	selenoprotein T1a precursor	12 kDa	0.0141
559	PREDICTED: glutaminase kidney isoform, mitochondrial isoform X2	38 kDa	0.014
560	dynamin-1-like protein	77 kDa	0.0139
561	phosphatidate cytidylyltransferase, mitochondrial precursor	12 kDa	0.0139
562	PRELI domain containing 1b	25 kDa	0.0139
563	UBX domain-containing protein 4	52 kDa	0.0138
564	cytochrome P450, family 20, subfamily A, polypeptide 1	52 kDa	0.0138
565	transmembrane protein 147	25 kDa	0.0138
566	NAD-dependent malic enzyme, mitochondrial	65 kDa	0.0138
567	PREDICTED: 40S ribosomal protein S2	12 kDa	0.0136
568	PREDICTED: neural cell adhesion molecule 1b isoform X11	92 kDa	0.0136
569	Probable saccharopine dehydrogenase	26 kDa	0.0135
570	PREDICTED: UPF0562 protein C7orf55 homolog	13 kDa	0.0135
571	probable asparagine--tRNA ligase, mitochondrial	26 kDa	0.0135
572	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	26 kDa	0.0134
573	pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	13 kDa	0.0134
574	diablo, IAP-binding mitochondrial protein a	13 kDa	0.0133
575	PREDICTED: phospholipid scramblase 2	26 kDa	0.0132
576	BRI3-binding protein precursor	26 kDa	0.0132
577	rod outer segment membrane protein 1	40 kDa	0.0132

578	uncharacterized protein LOC100124614	13 kDa	0.0131
579	39S ribosomal protein L17, mitochondrial	13 kDa	0.013
580	flotillin-1	41 kDa	0.013
581	mannose-P-dolichol utilization defect 1 protein	27 kDa	0.0128
582	nicastrin precursor	42 kDa	0.0127
583	PREDICTED: transmembrane protein 186 isoform X1	13 kDa	0.0127
584	carnitine O-acetyltransferase b	70 kDa	0.0126
585	PREDICTED: acyl-CoA-binding domain-containing protein 5A isoform X2	56 kDa	0.0126
586	PREDICTED: proteoglycan 4-like isoform X1	13 kDa	0.0126
587	syntaxin binding protein 1b	57 kDa	0.0124
588	60S ribosomal protein L8	28 kDa	0.0124
589	PREDICTED: 40S ribosomal protein S3-like isoform X1	28 kDa	0.0122
590	solute carrier family 25 member 36-A	28 kDa	0.0122
591	aquaporin-9	29 kDa	0.0122
592	LYR motif containing protein 1	14 kDa	0.0121
593	60S ribosomal protein L30	14 kDa	0.012
594	acyl-coenzyme A thioesterase THEM4	29 kDa	0.012
595	PREDICTED: 40S ribosomal protein S15	14 kDa	0.0119
596	prenylcysteine oxidase 1 precursor	59 kDa	0.0118
597	ES1 protein homolog, mitochondrial	29 kDa	0.0118
598	dehydrogenase/reductase SDR family member 4	29 kDa	0.0117
599	PREDICTED: lymphocyte antigen 6D-like isoform X1	14 kDa	0.0117
600	PREDICTED: AFG3-like protein 1	60 kDa	0.0117
601	PREDICTED: pyruvate kinase PKM isoform X1	60 kDa	0.0117
602	PREDICTED: uncharacterized aarF domain-containing protein kinase 2	14 kDa	0.0116
603	PREDICTED: protein HEG homolog 1 isoform X3	45 kDa	0.0116
604	PREDICTED: potassium voltage-gated channel subfamily V member 2	60 kDa	0.0116
605	ubiquitin-conjugating enzyme E2 J1	30 kDa	0.0115
606	alpha-1,3/1,6-mannosyltransferase ALG2	46 kDa	0.0115
607	PREDICTED: ADP-ribosylation factor-like protein 13A isoform X1	46 kDa	0.0115
608	complement component 1 Q subcomponent-binding protein, mitochondrial	30 kDa	0.0115
609	PREDICTED: ATP synthase-coupling factor 6, mitochondrial isoform X1	15 kDa	0.0115
610	uncharacterized protein LOC447917 precursor	30 kDa	0.0114
611	F-box/LRR-repeat protein 2	46 kDa	0.0114
612	membrane magnesium transporter 1 precursor	15 kDa	0.0114
613	PREDICTED: pre-B-cell leukemia transcription factor-interacting protein 1 isoform X3	15 kDa	0.0114
614	PREDICTED: 40S ribosomal protein S15a isoform X1	15 kDa	0.0113
615	40S ribosomal protein S6	31 kDa	0.0112
616	isoleucine--tRNA ligase, mitochondrial	110 kDa	0.0111
617	propionyl-CoA carboxylase alpha chain, mitochondrial	79 kDa	0.0111
618	PREDICTED: cGMP-gated cation channel alpha-1	63 kDa	0.011
619	Meckel syndrome type 1 protein	15 kDa	0.011
620	ancient ubiquitous protein 1	48 kDa	0.0109
621	transcription factor A, mitochondrial	31 kDa	0.0109
622	holocytochrome c synthetase a	32 kDa	0.0109
623	HIG1 domain family member 2A, mitochondrial	15 kDa	0.0108
624	iron-sulfur cluster assembly 1 homolog, mitochondrial precursor	15 kDa	0.0108
625	PREDICTED: phosphorylase, glycogen, muscle b isoform X1	97 kDa	0.0108
626	PREDICTED: sphingomyelin phosphodiesterase 2 isoform X1	48 kDa	0.0108
627	PREDICTED: LOW QUALITY PROTEIN: metalloendopeptidase OMA1, mitochondrial	16 kDa	0.0108
628	60S ribosomal protein L31	16 kDa	0.0108
629	[3-methyl-2-oxobutanoate dehydrogenase	48 kDa	0.0107
630	N-acetyltransferase 14	32 kDa	0.0107
631	PREDICTED: ethylmalonyl-CoA decarboxylase isoform X1	32 kDa	0.0107
632	protein FAM136A	16 kDa	0.0107
633	solute carrier family 25 member 35	32 kDa	0.0106
634	PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform X1	65 kDa	0.0106
635	PREDICTED: translocon-associated protein subunit alpha-like isoform X3	32 kDa	0.0105

636	PREDICTED: RNA-binding protein Musashi homolog 1-like isoform X1	33 kDa	0.0105
637	NADH dehydrogenase	16 kDa	0.0105
638	PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2	116 kDa	0.0105
639	rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha	99 kDa	0.0105
640	PREDICTED: glycerol-3-phosphate dehydrogenase, mitochondrial isoform X2	66 kDa	0.0105
641	uncharacterized protein LOC560648	16 kDa	0.0104
642	PREDICTED: protein CCSMST1	16 kDa	0.0104
643	RPE-retinal G protein-coupled receptor	33 kDa	0.0103
644	PREDICTED: enoyl-CoA delta isomerase 1, mitochondrial	33 kDa	0.0102
645	epidermal retinol dehydrogenase 2	34 kDa	0.0101
646	PREDICTED: vesicle-fusing ATPase isoform X1	86 kDa	0.01
647	PREDICTED: pre-B-cell leukemia transcription factor-interacting protein 1 isoform X3	17 kDa	0.01
648	solute carrier family 25 member 33	34 kDa	0.0099
649	solute carrier family 25 member 33	34 kDa	0.0099
650	mitochondrial dynamics protein MID51	52 kDa	0.0099
651	PREDICTED: protein transport protein Sec61 subunit alpha-like 1	52 kDa	0.0099
652	FUN14 domain-containing protein 1	17 kDa	0.0098
653	uncharacterized protein LOC100135257	35 kDa	0.0097
654	elongation of very long chain fatty acids-like 4	35 kDa	0.0097
655	uncharacterized protein C15orf61 homolog	17 kDa	0.0097
656	CAAX prenyl protease 1 homolog	53 kDa	0.0096
657	PREDICTED: cadherin-related family member 5-like isoform X2	17 kDa	0.0096
658	PREDICTED: 40S ribosomal protein S23-like	17 kDa	0.0096
659	PREDICTED: LETM1 domain-containing protein LETM2, mitochondrial	54 kDa	0.0096
660	PREDICTED: mitochondrial 10-formyltetrahydrofolate dehydrogenase	90 kDa	0.0096
661	PREDICTED: 60S ribosomal protein L23	17 kDa	0.0095
662	28S ribosomal protein S14, mitochondrial	17 kDa	0.0095
663	peptidyl-prolyl cis-trans isomerase A	17 kDa	0.0095
664	thioredoxin-related transmembrane protein 2-B precursor	36 kDa	0.0095
665	putative Ras-related protein Rab-42	18 kDa	0.0095
666	carnitine O-palmitoyltransferase 2, mitochondrial	18 kDa	0.0094
667	endoplasmin precursor	92 kDa	0.0094
668	glycerophosphodiester phosphodiesterase 1	36 kDa	0.0094
669	PREDICTED: poliovirus receptor-related protein 1-like isoform X2	55 kDa	0.0094
670	PREDICTED: acyl carrier protein, mitochondrial	18 kDa	0.0093
671	uncharacterized protein LOC100135288	18 kDa	0.0093
672	PREDICTED: mitochondrial coenzyme A transporter SLC25A42 isoform X1	36 kDa	0.0093
673	39S ribosomal protein L20, mitochondrial	18 kDa	0.0093
674	PREDICTED: glycerol-3-phosphate acyltransferase 1, mitochondrial	93 kDa	0.0092
675	presequence protease, mitochondrial precursor	18 kDa	0.0092
676	limbic system-associated membrane protein precursor	37 kDa	0.0092
677	calcium/calmodulin-dependent protein kinase type II delta 1 chain isoform 1	56 kDa	0.0092
678	arginase-1	37 kDa	0.0092
679	coiled-coil domain-containing protein 47 precursor	56 kDa	0.0092
680	dehydrogenase/reductase SDR family member 7	37 kDa	0.0091
681	PREDICTED: 60S ribosomal protein L27-like	18 kDa	0.0091
682	succinate dehydrogenase	18 kDa	0.0091
683	PREDICTED: protein GPR107 isoform X1	56 kDa	0.0091
684	40S ribosomal protein S18	18 kDa	0.009
685	inositol monophosphatase 3	37 kDa	0.009
686	PREDICTED: 2-oxoglutarate dehydrogenase-like, mitochondrial	115 kDa	0.009
687	peripherin-2	18 kDa	0.009
688	PREDICTED: T-cell activation inhibitor, mitochondrial	57 kDa	0.009
689	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex 1-like	19 kDa	0.0089
690	PREDICTED: 60S ribosomal protein L21	19 kDa	0.0089
691	PREDICTED: protein ERGIC-53	57 kDa	0.0089
692	PREDICTED: lysine (K)-specific demethylase 6A, like isoform X1	19 kDa	0.0089
693	PREDICTED: translocation protein SEC62	19 kDa	0.0089
694	amine oxidase	59 kDa	0.0087

695	PREDICTED: lysophosphatidylcholine acyltransferase 1-like	59 kDa	0.0087
696	PREDICTED: rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit beta	99 kDa	0.0087
697	cytosolic 5'-nucleotidase 3	39 kDa	0.0086
698	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	40 kDa	0.0085
699	PREDICTED: choline dehydrogenase, mitochondrial	20 kDa	0.0085
700	polyribonucleotide nucleotidyltransferase 1, mitochondrial	60 kDa	0.0084
701	ATPase family AAA domain-containing protein 1-B	20 kDa	0.0084
702	peripherin-2	20 kDa	0.0084
703	mitochondrial ubiquitin ligase activator of NFKB 1	40 kDa	0.0083
704	PREDICTED: probable hydrolase PNKD	20 kDa	0.0083
705	renalase	41 kDa	0.0082
706	PREDICTED: clathrin coat assembly protein AP180 isoform X5	41 kDa	0.0082
707	PREDICTED: protein tyrosine phosphatase type IVA 3-like isoform X3	20 kDa	0.0082
708	PREDICTED: cytochrome c oxidase assembly factor 1 homolog isoform X3	20 kDa	0.0082
709	PREDICTED: coenzyme Q-binding protein COQ10 homolog A, mitochondrial	20 kDa	0.0082
710	alpha-aminoadipic semialdehyde synthase, mitochondrial	105 kDa	0.0081
711	L-threonine 3-dehydrogenase, mitochondrial	42 kDa	0.0081
712	40S ribosomal protein S10	20 kDa	0.0081
713	PREDICTED: cGMP-gated cation channel alpha-1	63 kDa	0.008
714	LIM domain and actin-binding protein 1	20 kDa	0.008
715	PREDICTED: signal peptidase complex catalytic subunit SEC11A-like	21 kDa	0.008
716	PREDICTED: heparan sulfate 2-O-sulfotransferase 1	42 kDa	0.008
717	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	42 kDa	0.008
718	coatomer subunit gamma-2	42 kDa	0.008
719	PREDICTED: protein TsetseEP-like	21 kDa	0.008
720	PREDICTED: ADP-ribosylation factor-like protein 13B-like isoform X5	42 kDa	0.008
721	enoyl-CoA delta isomerase 2, mitochondrial	42 kDa	0.0079
722	PREDICTED: renin receptor isoform X1	42 kDa	0.0079
723	probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial	107 kDa	0.0079
724	cytosol aminopeptidase	21 kDa	0.0078
725	PREDICTED: translocon-associated protein subunit gamma	21 kDa	0.0078
726	39S ribosomal protein L12, mitochondrial	21 kDa	0.0078
727	PREDICTED: cell division control protein 42 homolog isoform X1	21 kDa	0.0077
728	PREDICTED: transmembrane and coiled-coil domains protein 1-like	21 kDa	0.0077
729	PREDICTED: meckelin isoform X2	111 kDa	0.0077
730	Bcl-2/adenovirus E1B 19kD interaction protein XR	22 kDa	0.0076
731	basigin precursor	45 kDa	0.0075
732	phosphoglycerate kinase 1	45 kDa	0.0075
733	neuroplastin precursor	45 kDa	0.0075
734	protein FAM134A	45 kDa	0.0075
735	PREDICTED: protein RER1 isoform X2	22 kDa	0.0075
736	PREDICTED: lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial-like	45 kDa	0.0075
737	1-acyl-sn-glycerol-3-phosphate acyltransferase gamma	45 kDa	0.0074
738	PREDICTED: glucose-induced degradation protein 8 homolog	22 kDa	0.0074
739	tyrosine-protein phosphatase non-receptor type 1	22 kDa	0.0074
740	PREDICTED: GTP-binding protein SAR1b	22 kDa	0.0074
741	28S ribosomal protein S27, mitochondrial	46 kDa	0.0073
742	presequence protease, mitochondrial precursor	115 kDa	0.0073
743	PREDICTED: cytochrome b-c1 complex subunit 6, mitochondrial-like	23 kDa	0.0073
744	2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	46 kDa	0.0072
745	ADP-ribosylation factor-like 15a	23 kDa	0.0072
746	transmembrane protein 160	23 kDa	0.0072
747	PREDICTED: probable peptidyl-tRNA hydrolase isoform X1	23 kDa	0.0072
748	mpv17-like protein 2	23 kDa	0.0072
749	electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	23 kDa	0.0072
750	PREDICTED: short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	47 kDa	0.0071
751	uncharacterized protein LOC492355	23 kDa	0.0071
752	eukaryotic initiation factor 4A-II	47 kDa	0.0071
753	isocitrate dehydrogenase	47 kDa	0.0071

754	ras-related protein Rab-18-B	23 kDa	0.0071
755	PREDICTED: peptidyl-prolyl cis-trans isomerase A-like	23 kDa	0.0071
756	PREDICTED: ras-related protein Rab-7a isoform X1	24 kDa	0.007
757	recoverin	23 kDa	0.007
758	serum/glucocorticoid regulated kinase 1-like	48 kDa	0.0069
759	mitochondrial import inner membrane translocase subunit Tim10 B	24 kDa	0.0069
760	keratin, type I cytoskeletal 18	49 kDa	0.0068
761	PREDICTED: neural cell adhesion molecule 1 isoform X1	74 kDa	0.0068
762	nucleoside diphosphate kinase 7	24 kDa	0.0068
763	ELMO domain-containing protein 2 precursor	24 kDa	0.0067
764	PREDICTED: sialic acid-binding Ig-like lectin 6	24 kDa	0.0067
765	protein FAM173A	24 kDa	0.0067
766	PREDICTED: 60S ribosomal protein L13	24 kDa	0.0067
767	PREDICTED: glucose-6-phosphate translocase	50 kDa	0.0067
768	PREDICTED: amyloid-like protein 2 isoform X2	24 kDa	0.0067
769	60S ribosomal protein L10	25 kDa	0.0067
770	maleylacetoacetate isomerase isoform 2	25 kDa	0.0067
771	PREDICTED: GRAM domain-containing protein 2-like isoform X3	25 kDa	0.0066
772	prolactin regulatory element-binding protein	25 kDa	0.0066
773	hypoxanthine-guanine phosphoribosyltransferase	25 kDa	0.0066
774	60S ribosomal protein L10a	25 kDa	0.0066
775	UMP-CMP kinase	25 kDa	0.0066
776	GTP:AMP phosphotransferase AK3, mitochondrial	25 kDa	0.0065
777	phosphatidylinositide phosphatase SAC1-A	51 kDa	0.0065
778	solute carrier family 25 member 47-A	25 kDa	0.0065
779	28S ribosomal protein S34, mitochondrial	25 kDa	0.0065
780	PREDICTED: V-type proton ATPase subunit S1	52 kDa	0.0064
781	PREDICTED: phosphatidate cytidylyltransferase 1	52 kDa	0.0064
782	PREDICTED: glutaminase kidney isoform, mitochondrial isoform X3	26 kDa	0.0064
783	bcl-2-like protein 13	52 kDa	0.0063
784	N-acylneuraminate cytidylyltransferase	53 kDa	0.0063
785	polyribonucleotide nucleotidyltransferase 1, mitochondrial	26 kDa	0.0063
786	probable leucine--tRNA ligase, mitochondrial	26 kDa	0.0063
787	PREDICTED: dnaJ homolog subfamily C member 30-like isoform X1	26 kDa	0.0062
788	peroxisomal biogenesis factor 3	26 kDa	0.0062
789	PREDICTED: lon protease homolog, mitochondrial	108 kDa	0.0062
790	insulin receptor a precursor	27 kDa	0.0061
791	mitochondrial peptide methionine sulfoxide reductase	27 kDa	0.0061
792	fascin-2	55 kDa	0.0061
793	phosducin	27 kDa	0.006
794	diablo homolog, mitochondrial	27 kDa	0.006
795	PREDICTED: putative Dol-P-Glc:Glc(2)Man(9)GlcNAc(2)-PP-Dol alpha-1,2-glucosyltransferase	55 kDa	0.006
796	triosephosphate isomerase A	27 kDa	0.006
797	PREDICTED: glutathione reductase, mitochondrial isoform X2	27 kDa	0.006
798	methylmalonyl-CoA mutase, mitochondrial	84 kDa	0.006
799	diablo homolog, mitochondrial	27 kDa	0.0059
800	HCLS1-associated protein X-1	28 kDa	0.0059
801	dol-P-Man:Man(7)GlcNAc(2)-PP-Dol alpha-1,6-mannosyltransferase precursor	56 kDa	0.0059
802	aldehyde dehydrogenase 2 family (mitochondrial), tandem duplicate 2	57 kDa	0.0058
803	dolichol-phosphate mannosyltransferase subunit 1	28 kDa	0.0058
804	ER membrane protein complex subunit 10 isoform 1 precursor	28 kDa	0.0058
805	neural cell adhesion molecule 1 precursor	28 kDa	0.0058
806	PREDICTED: Golgi SNAP receptor complex member 1 isoform X1	28 kDa	0.0057
807	PREDICTED: solute carrier family 1 (glial high affinity glutamate transporter), member 2a isoform X2	58 kDa	0.0057
808	transmembrane protein 33	29 kDa	0.0057
809	PREDICTED: cell adhesion molecule 3 isoform X1	58 kDa	0.0056
810	ATP-dependent Clp protease proteolytic subunit, mitochondrial	29 kDa	0.0056
811	PREDICTED: transmembrane protein 101	29 kDa	0.0056

812	28S ribosomal protein S2, mitochondrial	29 kDa	0.0055
813	glutamate dehydrogenase 1b	60 kDa	0.0055
814	dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase	30 kDa	0.0055
815	alpha/beta hydrolase domain-containing protein 14A	30 kDa	0.0055
816	PREDICTED: protein phosphatase 1 regulatory subunit 16A	61 kDa	0.0054
817	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2b isoform X1	92 kDa	0.0054
818	actin-like protein 6A	31 kDa	0.0053
819	PREDICTED: SEC14-like protein 3 isoform X1	31 kDa	0.0052
820	L-2-hydroxyglutarate dehydrogenase, mitochondrial	31 kDa	0.0052
821	T-complex protein 1 subunit gamma	63 kDa	0.0052
822	PREDICTED: G-protein coupled receptor 98 isoform X2	31 kDa	0.0052
823	leucine-rich repeat, immunoglobulin-like and transmembrane domains 1 precursor	64 kDa	0.0051
824	leucine-rich PPR motif-containing protein, mitochondrial	162 kDa	0.0051
825	B-cell receptor-associated protein 31	32 kDa	0.0051
826	thioredoxin-related transmembrane protein 1 precursor	32 kDa	0.0051
827	uncharacterized protein C18orf19 homolog B	32 kDa	0.005
828	PREDICTED: ATP-dependent (S)-NAD(P)H-hydrate dehydratase isoform X10	32 kDa	0.005
829	uncharacterized protein LOC100127834	33 kDa	0.005
830	3-hydroxyisobutyrate dehydrogenase, mitochondrial	33 kDa	0.005
831	40S ribosomal protein S3a	33 kDa	0.005
832	PREDICTED: LOW QUALITY PROTEIN: metalloendopeptidase OMA1, mitochondrial	33 kDa	0.0049
833	3-mercaptopyruvate sulfurtransferase	33 kDa	0.0049
834	PREDICTED: protein FAM134C	33 kDa	0.0049
835	carnitine O-acetyltransferase	68 kDa	0.0048
836	PREDICTED: protein CLN8 isoform X1	34 kDa	0.0048
837	PREDICTED: carnitine palmitoyltransferase 1A isoform X2	69 kDa	0.0048
838	PREDICTED: uncharacterized protein KIAA1467 homolog isoform X1	69 kDa	0.0048
839	40S ribosomal protein SA	34 kDa	0.0048
840	malonyl-CoA decarboxylase, mitochondrial	34 kDa	0.0048
841	solute carrier family 7, member 3	70 kDa	0.0047
842	PREDICTED: transmembrane and TPR repeat-containing protein 3	105 kDa	0.0047
843	enoyl-CoA hydratase domain-containing protein 2, mitochondrial	35 kDa	0.0047
844	dehydrogenase/reductase (SDR family) member 13a, duplicate 3	35 kDa	0.0047
845	PREDICTED: mitochondrial thiamine pyrophosphate carrier isoform X1	35 kDa	0.0047
846	heme oxygenase 2	35 kDa	0.0047
847	glyoxylate reductase/hydroxypyruvate reductase	35 kDa	0.0046
848	PREDICTED: mitochondrial Rho GTPase 1 isoform X4	71 kDa	0.0046
849	PREDICTED: uncharacterized protein LOC100126019 isoform X1	107 kDa	0.0046
850	PREDICTED: CAAX prenyl protease 2	35 kDa	0.0046
851	long-chain fatty acid transport protein 1	72 kDa	0.0046
852	PREDICTED: zinc finger protein-like 1 isoform X1	36 kDa	0.0045
853	methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	72 kDa	0.0045
854	PREDICTED: syntaxin-18 isoform X1	36 kDa	0.0045
855	PREDICTED: coiled-coil domain containing 127a isoform X1	36 kDa	0.0045
856	PREDICTED: trans-Golgi network integral membrane protein 2	36 kDa	0.0045
857	PREDICTED: xyloside xylosyltransferase 1 isoform X1	37 kDa	0.0044
858	uncharacterized protein LOC100170509	75 kDa	0.0043
859	protein phosphatase 1, catalytic subunit, alpha	37 kDa	0.0043
860	PREDICTED: syntaxin-16 isoform X1	38 kDa	0.0043
861	amine oxidase	38 kDa	0.0043
862	neurotrimin isoform 1 precursor	38 kDa	0.0042
863	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial precursor	38 kDa	0.0042
864	PREDICTED: serine/threonine-protein phosphatase PP1-beta catalytic subunit	38 kDa	0.0042
865	PREDICTED: hydroxyindole O-methyltransferase isoform X1	38 kDa	0.0042
866	enkurin domain-containing protein 1	39 kDa	0.0042
867	PREDICTED: tectonic-2	39 kDa	0.0042
868	cell adhesion molecule 1b precursor	39 kDa	0.0042
869	PREDICTED: ATP-dependent 6-phosphofructokinase, liver type-like	39 kDa	0.0041
870	Bardet-Biedl syndrome 5 protein homolog	39 kDa	0.0041

871	eukaryotic translation initiation factor 4A, isoform 1A	39 kDa	0.0041
872	protein phosphatase 1 regulatory subunit 7 isoform 1	40 kDa	0.0041
873	PREDICTED: ATP-dependent zinc metalloprotease YME1L1-like isoform X1	81 kDa	0.004
874	28S ribosomal protein S22, mitochondrial	40 kDa	0.004
875	PREDICTED: tectonic-2	40 kDa	0.004
876	PREDICTED: red-sensitive opsin-1 isoform X1	41 kDa	0.004
877	cAMP-dependent protein kinase catalytic subunit beta	41 kDa	0.004
878	G-protein coupled receptor 98 precursor	82 kDa	0.0039
879	PREDICTED: protein phosphatase 1K, mitochondrial isoform X1	41 kDa	0.0039
880	PREDICTED: transmembrane protein 237A	42 kDa	0.0039
881	PREDICTED: coiled-coil domain-containing protein 136 isoform X2	42 kDa	0.0038
882	PREDICTED: glycine--tRNA ligase	86 kDa	0.0038
883	PREDICTED: peroxisomal membrane protein PEX14	43 kDa	0.0038
884	polymerase delta-interacting protein 2	43 kDa	0.0037
885	3-ketoacyl-CoA thiolase, mitochondrial	43 kDa	0.0037
886	acyl-CoA:lysophosphatidylglycerol acyltransferase 1	43 kDa	0.0037
887	reticulon-1 isoform 1	88 kDa	0.0037
888	monoacylglycerol lipase ABHD12	44 kDa	0.0037
889	PREDICTED: sorting nexin-13 isoform X3	44 kDa	0.0037
890	ATPase family AAA domain-containing protein 1-A isoform 1	44 kDa	0.0037
891	GPI-anchor transamidase precursor	45 kDa	0.0036
892	28S ribosomal protein S5, mitochondrial precursor	45 kDa	0.0036
893	PREDICTED: POC1 centriolar protein homolog A-like	45 kDa	0.0036
894	PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	91 kDa	0.0036
895	PREDICTED: centrosomal protein POC5 isoform X1	45 kDa	0.0035
896	28S ribosomal protein S9, mitochondrial	46 kDa	0.0035
897	28S ribosomal protein S29, mitochondrial	46 kDa	0.0035
898	casein kinase 2, alpha 1 polypeptide	46 kDa	0.0035
899	PREDICTED: peptide chain release factor 1, mitochondrial-like	46 kDa	0.0035
900	PREDICTED: dyslexia-associated protein KIAA0319-like protein homolog isoform X1	93 kDa	0.0035
901	medium-chain specific acyl-CoA dehydrogenase, mitochondrial	46 kDa	0.0035
902	PREDICTED: V-type proton ATPase 116 kDa subunit a isoform 2 isoform X2	47 kDa	0.0034
903	PREDICTED: outer dense fiber protein 2	96 kDa	0.0034
904	PREDICTED: neutral alpha-glucosidase AB	96 kDa	0.0034
905	uncharacterized protein C6orf136 homolog	48 kDa	0.0033
906	glycogen synthase kinase-3 alpha	48 kDa	0.0033
907	PREDICTED: mannosyl-oligosaccharide 1,2-alpha-mannosidase IA isoform X1	48 kDa	0.0033
908	PREDICTED: mannosyl-oligosaccharide glucosidase isoform X1	49 kDa	0.0033
909	adenylyl cyclase-associated protein 1	50 kDa	0.0032
910	PREDICTED: NAD kinase 2, mitochondrial isoform X2	50 kDa	0.0032
911	PREDICTED: oxysterol-binding protein-related protein 1-like	50 kDa	0.0032
912	endoplasmic reticulum resident protein 44	50 kDa	0.0032
913	puromycin-sensitive aminopeptidase	102 kDa	0.0032
914	elongation factor 1-gamma	51 kDa	0.0031
915	evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	52 kDa	0.0031
916	epoxide hydrolase 1	52 kDa	0.0031
917	PREDICTED: monocarboxylate transporter 2	52 kDa	0.0031
918	squalene synthase	53 kDa	0.003
919	PREDICTED: sodium-coupled neutral amino acid transporter 3	53 kDa	0.003
920	PREDICTED: protein LYRIC isoform X1	53 kDa	0.003
921	PREDICTED: AP-2 complex subunit alpha-1 isoform X1	109 kDa	0.003
922	progressive ankylosis-like protein	55 kDa	0.0029
923	V-type proton ATPase subunit H isoform 1	55 kDa	0.0029
924	PREDICTED: succinate-semialdehyde dehydrogenase, mitochondrial isoform X1	55 kDa	0.0029
925	PREDICTED: tudor and KH domain-containing protein isoform X1	56 kDa	0.0029
926	4-aminobutyrate aminotransferase, mitochondrial	56 kDa	0.0029
927	V-type proton ATPase subunit B, brain isoform	56 kDa	0.0028
928	GDP-Man:Man(3)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase isoform 1	57 kDa	0.0028
929	PREDICTED: atlastin-3 isoform X1	58 kDa	0.0028

930	E3 ubiquitin-protein ligase synoviolin precursor	59 kDa	0.0027
931	fatty-acid amide hydrolase 2-A	59 kDa	0.0027
932	PREDICTED: UPF0606 protein KIAA1549 isoform X2	120 kDa	0.0027
933	lysophosphatidylcholine acyltransferase 2	60 kDa	0.0027
934	keratin, type II cytoskeletal 8	61 kDa	0.0026
935	PREDICTED: propionyl-CoA carboxylase beta chain, mitochondrial isoform X1	61 kDa	0.0026
936	PREDICTED: GPI transamidase component PIG-S isoform X2	63 kDa	0.0025
937	PREDICTED: asparagine--tRNA ligase, cytoplasmic	64 kDa	0.0025
938	phenylalanine--tRNA ligase beta subunit	66 kDa	0.0024
939	phosphatidylinositide phosphatase SAC1-B	67 kDa	0.0024
940	PREDICTED: mitochondrial intermediate peptidase	68 kDa	0.0023
941	PREDICTED: V-type proton ATPase catalytic subunit A	68 kDa	0.0023
942	electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	69 kDa	0.0023
943	PREDICTED: aarF domain-containing protein kinase 4	70 kDa	0.0023
944	PREDICTED: long-chain fatty acid transport protein 6-like	70 kDa	0.0023
945	PREDICTED: epidermal growth factor receptor kinase substrate 8 isoform X1	71 kDa	0.0023
946	polyadenylate-binding protein 1	71 kDa	0.0022
947	PREDICTED: signal recognition particle receptor subunit alpha	71 kDa	0.0022
948	cleft lip and palate transmembrane protein 1 homolog	72 kDa	0.0022
949	selenoprotein O	77 kDa	0.0021
950	PREDICTED: striatin-3 isoform X1	79 kDa	0.002
951	PREDICTED: synembryn-A-like	79 kDa	0.002
952	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	81 kDa	0.002
953	PREDICTED: ribosomal protein S6 kinase alpha-3 isoform X1	83 kDa	0.0019
954	probable C-mannosyltransferase DPY19L1	83 kDa	0.0019
955	ATP-dependent RNA helicase SUPV3L1, mitochondrial precursor	86 kDa	0.0019
956	PREDICTED: heat shock 70 kDa protein 4L	93 kDa	0.0017
957	PREDICTED: V-type proton ATPase 116 kDa subunit a isoform 1 isoform X1	96 kDa	0.0017
958	PREDICTED: oxysterol-binding protein-related protein 8-like	98 kDa	0.0016
959	cone cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha'	98 kDa	0.0016
960	PREDICTED: cadherin-related family member 1-like isoform X2	99 kDa	0.0016
961	PREDICTED: pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial-like	99 kDa	0.0016
962	PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1	102 kDa	0.0016
963	PREDICTED: potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 1	102 kDa	0.0016
964	PREDICTED: kinesin-like protein KIFC3 isoform X5	110 kDa	0.0014
965	PREDICTED: spermatogenesis-associated protein 20	115 kDa	0.0014
966	von Willebrand factor A domain-containing protein 8	126 kDa	0.0013
967	PREDICTED: nodal modulator 1	130 kDa	0.0012
968	PREDICTED: PDZ domain-containing protein 8	131 kDa	0.0012
969	PREDICTED: 26S proteasome non-ATPase regulatory subunit 1-like	148 kDa	0.0011
970	PREDICTED: protein fantom isoform X1	215 kDa	0.0007
971	PREDICTED: rootletin isoform X1	226 kDa	0.0007

Table S3. Identified proteins in washed COS-rich fraction.

Proteins in washed COS-rich fraction were identified with LC-MS/MS analysis and are listed in descending order of emPAI values for 5×10^5 cones.

	Identified proteins in washed COS-rich fraction	Molecular mass	emPAI
1	uncharacterized protein LOC100145214	33 kDa	277.27
2	ba1 globin, like	16 kDa	36.229
3	guanine nucleotide-binding protein G(t) subunit alpha-2	40 kDa	28.315
4	voltage-dependent anion-selective channel protein 1	31 kDa	22.103
5	mitochondrial 2-oxoglutarate/malate carrier protein	38 kDa	19.592
6	ATP synthase F(0) complex subunit B1, mitochondrial	31 kDa	14.092
7	voltage-dependent anion-selective channel protein 2	30 kDa	13.789
8	PREDICTED: ATP synthase subunit alpha, mitochondrial	27 kDa	10.735
9	voltage-dependent anion-selective channel protein 2-like	30 kDa	9.6742
10	arrestin-C	40 kDa	8.5749
11	PREDICTED: voltage-dependent anion-selective channel protein 2	11 kDa	7.348
12	PREDICTED: prohibitin isoform X2	22 kDa	7.3326
13	PREDICTED: prohibitin	22 kDa	7.2457
14	ADP/ATP translocase 3	27 kDa	7.2237
15	PREDICTED: solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3a isoform X2	40 kDa	6.9013
16	alpha globin-like	15 kDa	6.5356
17	PREDICTED: regulator of G-protein signaling 9-binding protein-like	27 kDa	6.3251
18	NADH dehydrogenase 1 beta subcomplex subunit 6	15 kDa	5.3325
19	ATP synthase subunit g, mitochondrial	11 kDa	5.1649
20	band 3 anion transport protein	11 kDa	5.0632
21	ATP synthase subunit alpha, mitochondrial	33 kDa	4.4947
22	PREDICTED: uncharacterized protein LOC100707031 isoform X1	12 kDa	4.2863
23	ADP-ribosylation factor-like protein 9	26 kDa	4.0831
24	prohibitin 2a	35 kDa	4.0018
25	band 3 anion transport protein	35 kDa	3.6752
26	PREDICTED: ATP synthase subunit gamma, mitochondrial isoform X1	33 kDa	3.4842
27	PREDICTED: coiled-coil-helix-coiled-coil-helix domain-containing protein 6, mitochondrial isoform X2	29 kDa	3.4397
28	calcium-binding mitochondrial carrier protein Aralar1	76 kDa	3.3774
29	dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	69 kDa	3.2991
30	PREDICTED: ammonium transporter Rh type A isoform X1	12 kDa	3.2045
31	ras-related protein Rab-1B	22 kDa	3.103
32	voltage-dependent anion-selective channel protein 2	20 kDa	3.0643
33	ATP synthase subunit O, mitochondrial	26 kDa	2.9888
34	PREDICTED: phosphate carrier protein, mitochondrial-like isoform X1	34 kDa	2.8384
35	calcium-binding mitochondrial carrier protein Aralar1	60 kDa	2.7242
36	cytochrome c-1	36 kDa	2.571
37	PREDICTED: tubulin beta-4B chain-like	31 kDa	2.5302
38	PREDICTED: ATPase, Na+/K+ transporting, beta 2b polypeptide isoform X1	24 kDa	2.3123
39	ras-related protein Rab-2A	24 kDa	2.3123
40	NADH dehydrogenase 1 beta subcomplex subunit 4	15 kDa	2.222
41	PREDICTED: NADH dehydrogenase	12 kDa	2.187
42	ES1 protein, mitochondrial precursor	31 kDa	2.1733
43	retinol dehydrogenase 13	37 kDa	2.1611
44	ATPase, Na+/K+ transporting, beta 2b polypeptide	34 kDa	2.155
45	flotillin-1	41 kDa	2.1371
46	flotillin-2a	47 kDa	2.1241
47	PREDICTED: calcium-binding mitochondrial carrier protein Aralar2 isoform X1	15 kDa	2.1192
48	histone 1, H4, like	12 kDa	2.0635
49	green-sensitive opsin-4	39 kDa	2.0402
50	PREDICTED: ras-related protein Rab-1A-like isoform X1	22 kDa	2.014
51	PREDICTED: NADH dehydrogenase	20 kDa	1.9289
52	creatine kinase b-type	16 kDa	1.9177

53	PREDICTED: creatine kinase S-type, mitochondrial isoform X2	47 kDa	1.9172
54	peripherin-2	20 kDa	1.8952
55	protein disulfide-isomerase TMX3 precursor	47 kDa	1.8814
56	uncharacterized protein LOC541492	13 kDa	1.8285
57	G-protein-coupled receptor kinase 7A	62 kDa	1.8236
58	PREDICTED: threonine dehydratase, mitochondrial-like isoform X2	60 kDa	1.7725
59	retinol dehydrogenase 8a	35 kDa	1.735
60	mitochondrial import inner membrane translocase subunit tim16	14 kDa	1.7187
61	erlin-2 precursor	40 kDa	1.6659
62	G-protein-coupled receptor kinase 7A	62 kDa	1.6653
63	reticulon-4	22 kDa	1.6103
64	ras-related protein Rab-1B	19 kDa	1.5373
65	sodium/potassium-transporting ATPase subunit alpha-3	113 kDa	1.4576
66	guanine nucleotide-binding protein G(o) subunit alpha	40 kDa	1.4444
67	NADH dehydrogenase 1 alpha subcomplex subunit 6	16 kDa	1.4242
68	PREDICTED: LOW QUALITY PROTEIN: actin, gamma 1	40 kDa	1.421
69	LETM1 and EF-hand domain-containing protein 1, mitochondrial	86 kDa	1.414
70	PREDICTED: ADP-ribosylation factor 2	16 kDa	1.4099
71	signal peptidase complex subunit 3	20 kDa	1.3911
72	PREDICTED: ras-related protein Rab-11B	25 kDa	1.3698
73	CDGSH iron sulfur domain 1	12 kDa	1.3672
74	ubiquitin-60S ribosomal protein L40	12 kDa	1.3672
75	ADP-ribosylation factor 1	21 kDa	1.3378
76	PREDICTED: vesicle-associated membrane protein 2-like	12 kDa	1.3324
77	long-chain fatty acid transport protein 4	25 kDa	1.3264
78	PREDICTED: calcium-binding mitochondrial carrier protein Aralar2 isoform X1	48 kDa	1.2667
79	reticulon-4	22 kDa	1.216
80	PREDICTED: prohibitin-2	27 kDa	1.2107
81	PREDICTED: mitochondrial import inner membrane translocase subunit Tim23	22 kDa	1.1991
82	PREDICTED: ras-related protein Rab-10	23 kDa	1.1746
83	band 3 anion transport protein	27 kDa	1.1697
84	PREDICTED: ATP synthase subunit beta, mitochondrial-like	56 kDa	1.1576
85	NADH-cytochrome b5 reductase 1	28 kDa	1.1502
86	RAB1A, member RAS oncogene family	28 kDa	1.1502
87	reticulon-4-interacting protein 1 homolog, mitochondrial	42 kDa	1.1361
88	PREDICTED: LOW QUALITY PROTEIN: 40S ribosomal protein S13-like	19 kDa	1.1243
89	RAB5A, member RAS oncogene family, a	24 kDa	1.1139
90	PREDICTED: ras-related protein Rab-6A isoform X2	24 kDa	1.1139
91	PREDICTED: succinate dehydrogenase cytochrome b560 subunit, mitochondrial isoform X1	19 kDa	1.1062
92	guanine nucleotide-binding protein subunit beta-5	43 kDa	1.0998
93	OCIA domain-containing protein 1	30 kDa	1.0506
94	PREDICTED: mitochondrial pyruvate carrier 2	14 kDa	1.049
95	putative tubulin beta chain variant 1	20 kDa	1.0392
96	protein RD3	15 kDa	1.0384
97	PREDICTED: voltage-dependent anion-selective channel protein 3 isoform X3	36 kDa	0.9969
98	PREDICTED: voltage-dependent anion-selective channel protein 3 isoform X3	36 kDa	0.9969
99	adipocyte plasma membrane-associated protein	47 kDa	0.9967
100	cytochrome b-c1 complex subunit 1, mitochondrial	52 kDa	0.9894
101	NADH dehydrogenase	58 kDa	0.9887
102	sorting and assembly machinery component 50 homolog A	52 kDa	0.9865
103	PREDICTED: dehydrogenase/reductase SDR family member 7B isoform X1	31 kDa	0.985
104	ras-related protein Rap-1b-like	21 kDa	0.9522
105	ADP-ribosylation factor-like protein 6	21 kDa	0.9522
106	NADH dehydrogenase 1 alpha subcomplex subunit 11	16 kDa	0.9516
107	PREDICTED: ubiquinol-cytochrome c reductase core protein II isoform X1	49 kDa	0.9416
108	creatine kinase U-type, mitochondrial	22 kDa	0.9018
109	PREDICTED: regulator of G-protein signaling 9 isoform X2	62 kDa	0.9007
110	PREDICTED: peripherin-2	39 kDa	0.8957
111	dolichol-phosphate mannosyltransferase subunit 1	28 kDa	0.8834

112	PREDICTED: transmembrane emp24 domain-containing protein 2	23 kDa	0.8563
113	ras-related protein Rab-8A	23 kDa	0.8563
114	serine/threonine-protein kinase MAK	11 kDa	0.8547
115	DDRGK domain-containing protein 1 precursor	35 kDa	0.8532
116	mitochondrial import receptor subunit TOM70	65 kDa	0.838
117	sorting and assembly machinery component 50 homolog B	23 kDa	0.8351
118	PREDICTED: 60S ribosomal protein L9 isoform X2	17 kDa	0.8278
119	HIG1 domain family member 1A	11 kDa	0.8235
120	ER membrane protein complex subunit 3	30 kDa	0.8153
121	ras-related protein Rab-5B	24 kDa	0.815
122	protein NDRG1 isoform 1	42 kDa	0.8101
123	very-long-chain enoyl-CoA reductase	36 kDa	0.8058
124	ras-related protein Rab-14	24 kDa	0.8053
125	PREDICTED: syntaxin-12 isoform X1	30 kDa	0.8037
126	protein THEM6 precursor	24 kDa	0.8005
127	PREDICTED: 40S ribosomal protein S8	24 kDa	0.7958
128	PREDICTED: tubulin alpha chain-like	12 kDa	0.7852
129	PREDICTED: mitochondrial fission process protein 1-like	18 kDa	0.7831
130	transmembrane protein 256 precursor	12 kDa	0.7762
131	transmembrane protein 256 precursor	12 kDa	0.7762
132	cytochrome b-c1 complex subunit 2, mitochondrial	50 kDa	0.7759
133	PREDICTED: reticulon-3-B-like isoform X2	25 kDa	0.7731
134	PREDICTED: saccharopine dehydrogenase-like oxidoreductase-like	12 kDa	0.7674
135	solute carrier family 3 (amino acid transporter heavy chain), member 2b	57 kDa	0.7645
136	PREDICTED: tubulin alpha chain	45 kDa	0.7509
137	dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	51 kDa	0.748
138	calmegin precursor	66 kDa	0.7279
139	mitochondrial ATP synthase subunit f	13 kDa	0.7183
140	PREDICTED: ubiquinol-cytochrome c reductase core protein II isoform X1	40 kDa	0.7172
141	protein NipSnap homolog 2	33 kDa	0.712
142	NADH dehydrogenase (ubiquinone) 1 subunit c2	13 kDa	0.7107
143	transmembrane protein 11, mitochondrial	27 kDa	0.7043
144	PREDICTED: red-sensitive opsin-1 isoform X1	41 kDa	0.6974
145	cytochrome c oxidase subunit IV isoform 2	20 kDa	0.6919
146	PREDICTED: tubulin beta-2B chain-like isoform 1	55 kDa	0.6904
147	ras-related protein Rab-35	20 kDa	0.6779
148	PREDICTED: mitochondrial glutamate carrier 1	34 kDa	0.6776
149	PREDICTED: metal transporter CNNM4	35 kDa	0.6615
150	sideroflexin-3	36 kDa	0.6512
151	trifunctional enzyme subunit beta, mitochondrial	50 kDa	0.6511
152	PREDICTED: hexokinase-1-like	14 kDa	0.6489
153	succinyl-CoA ligase	51 kDa	0.6439
154	PREDICTED: NADH dehydrogenase	21 kDa	0.6433
155	mitochondrial import receptor subunit TOM40 homolog	36 kDa	0.6413
156	mitochondrial import receptor subunit TOM40 homolog	36 kDa	0.6364
157	dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit precursor	51 kDa	0.6301
158	peroxiredoxin-2	22 kDa	0.6233
159	PREDICTED: pyruvate dehydrogenase E1 alpha 1 isoform X1	45 kDa	0.62
160	60S ribosomal protein L9	22 kDa	0.6195
161	vesicle-associated membrane protein-associated protein A	30 kDa	0.6169
162	protein kinase, cAMP-dependent, regulatory, type II, alpha A	45 kDa	0.6162
163	retinoschisin precursor	22 kDa	0.6157
164	solute carrier family 2, facilitated glucose transporter member 1	53 kDa	0.6104
165	PREDICTED: 40S ribosomal protein S9-like	22 kDa	0.6009
166	membrane magnesium transporter 1 precursor	15 kDa	0.5968
167	uncharacterized protein LOC492355	23 kDa	0.5834
168	peripherin 2b (retinal degeneration, slow)	39 kDa	0.5832
169	mitochondrial chaperone BCS1	48 kDa	0.5706

170	elongation factor 1-alpha	48 kDa	0.5674
171	PREDICTED: ras-related protein Rab-7a isoform X1	24 kDa	0.5669
172	AFG3-like protein 2	89 kDa	0.565
173	uncharacterized protein C18orf19 homolog B	32 kDa	0.5577
174	PREDICTED: cyclic nucleotide-gated channel rod photoreceptor subunit alpha-like	82 kDa	0.5572
175	PREDICTED: guanine nucleotide-binding protein G(i) subunit alpha-1	40 kDa	0.556
176	PREDICTED: uncharacterized protein si:dkey-182g1.3	16 kDa	0.5479
177	mitochondrial inner membrane protein	83 kDa	0.5418
178	PREDICTED: LOW QUALITY PROTEIN: long-chain-fatty-acid--CoA ligase 6	50 kDa	0.5399
179	nicastrin precursor	42 kDa	0.538
180	arrestin-C	33 kDa	0.531
181	epidermal retinol dehydrogenase 2	34 kDa	0.5248
182	PREDICTED: guanine nucleotide-binding protein subunit alpha-13-like	34 kDa	0.5248
183	dynamin-1-like protein	77 kDa	0.5221
184	isocitrate dehydrogenase	43 kDa	0.5212
185	brain creatine kinase b	43 kDa	0.518
186	inactive hydroxysteroid dehydrogenase-like protein 1	35 kDa	0.5068
187	dehydrogenase/reductase (SDR family) member 13a, duplicate 3	35 kDa	0.5068
188	uncharacterized protein LOC100135257	35 kDa	0.503
189	40S ribosomal protein S7	17 kDa	0.5024
190	PREDICTED: vesicle-associated membrane protein-associated protein A-like	26 kDa	0.499
191	PREDICTED: vesicle-associated membrane protein-associated protein A-like	26 kDa	0.499
192	PREDICTED: nucleoside diphosphate kinase B isoform X1	17 kDa	0.4987
193	NADH dehydrogenase	53 kDa	0.4981
194	hexokinase-1	71 kDa	0.4976
195	PREDICTED: gamma-glutamyltransferase 5 isoform X1	62 kDa	0.4973
196	PREDICTED: tubulin alpha-1C chain	45 kDa	0.4934
197	NAD-dependent protein deacetylase sirtuin-3, mitochondrial	18 kDa	0.4877
198	PREDICTED: 60S ribosomal protein L12	18 kDa	0.4841
199	optic atrophy 3 protein homolog	18 kDa	0.4806
200	PREDICTED: transmembrane emp24 domain-containing protein 9 isoform X1	27 kDa	0.4798
201	calcium/calmodulin-dependent protein kinase type II delta 1 chain isoform 1	56 kDa	0.4722
202	uncharacterized protein LOC100127838	18 kDa	0.4671
203	very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 2	28 kDa	0.4664
204	PREDICTED: cyclic nucleotide-gated cation channel beta-3-like isoform X2	28 kDa	0.4664
205	40S ribosomal protein S18	18 kDa	0.4639
206	transmembrane protein 33	29 kDa	0.4516
207	carbonic anhydrase	29 kDa	0.4495
208	PREDICTED: ADP-dependent glucokinase isoform X2	58 kDa	0.4478
209	PREDICTED: sodium/potassium/calcium exchanger 2-like isoform X2	68 kDa	0.4467
210	ATPase family AAA domain-containing protein 3	69 kDa	0.4441
211	opsin-1, short-wave-sensitive 2	39 kDa	0.4398
212	opsin-1, short-wave-sensitive 1	39 kDa	0.4398
213	PREDICTED: L-lactate dehydrogenase B-B chain isoform X4	19 kDa	0.4364
214	PREDICTED: L-lactate dehydrogenase B-B chain isoform X3	19 kDa	0.4336
215	cytochrome c oxidase subunit 4 isoform 1, mitochondrial	20 kDa	0.4308
216	PREDICTED: tubulin alpha chain-like	50 kDa	0.4307
217	plasminogen receptor (KT)	20 kDa	0.428
218	ras-related protein Rab-8B	20 kDa	0.428
219	eukaryotic translation elongation factor 1 alpha 1-like	50 kDa	0.4274
220	PREDICTED: potassium voltage-gated channel subfamily B member 2	93 kDa	0.4184
221	NADH dehydrogenase 1 beta subcomplex subunit 10	20 kDa	0.4172
222	PREDICTED: ADP-ribosylation factor 6-like	20 kDa	0.4172
223	mitochondrial carrier homolog 2	31 kDa	0.414
224	ADP-ribosylation factor-like protein 1	20 kDa	0.412
225	PREDICTED: cadherin-related family member 5-like isoform X2	20 kDa	0.4095
226	PREDICTED: epoxide hydrolase 1-like, partial	20 kDa	0.4095
227	immunity-related GTPase family, q2	42 kDa	0.4074
228	LIM domain and actin-binding protein 1	20 kDa	0.407

229	heat shock cognate 71 kDa protein	42 kDa	0.4049
230	zinc transporter 9	64 kDa	0.4025
231	mitochondrial dicarboxylate carrier	32 kDa	0.4023
232	ras-related protein Rap-1b precursor	21 kDa	0.4021
233	hexokinase-1	54 kDa	0.3958
234	cone cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha'	98 kDa	0.3931
235	uncharacterized protein LOC393228	21 kDa	0.3902
236	uncharacterized protein LOC100302470 precursor	21 kDa	0.3902
237	synaptophysin b isoform 1	33 kDa	0.3866
238	PREDICTED: complex I assembly factor TIMMDC1, mitochondrial isoform X1	33 kDa	0.3793
239	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 precursor	67 kDa	0.3773
240	neurocalcin-delta B	22 kDa	0.3769
241	ras homolog gene family, member A	22 kDa	0.3727
242	uncharacterized protein LOC100127828	34 kDa	0.3653
243	PREDICTED: cyclic nucleotide-gated channel cone photoreceptor subunit alpha isoform X2	81 kDa	0.364
244	heat shock protein 75 kDa, mitochondrial	82 kDa	0.3629
245	synaptotagmin II	47 kDa	0.3608
246	PREDICTED: retinol dehydrogenase 8-like isoform X1	35 kDa	0.36
247	phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	11 kDa	0.3579
248	PREDICTED: growth hormone-inducible transmembrane protein	35 kDa	0.3574
249	ras-related protein Rab-18-B	23 kDa	0.3566
250	PREDICTED: [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	47 kDa	0.3559
251	PREDICTED: flotillin 1a isoform X1	47 kDa	0.355
252	uncharacterized protein LOC100135302	23 kDa	0.3547
253	ras-related protein Rab-43	23 kDa	0.3547
254	PREDICTED: uncharacterized protein LOC101884052	11 kDa	0.3541
255	surfeit gene 4, like	23 kDa	0.3528
256	methylmalonate-semialdehyde dehydrogenase	61 kDa	0.3447
257	vitamin K epoxide reductase complex subunit 1-like protein 1	12 kDa	0.3431
258	retinol dehydrogenase-like	36 kDa	0.3426
259	CDP-diacylglycerol--inositol 3-phosphatidyltransferase	24 kDa	0.3418
260	protein THEM6 precursor	24 kDa	0.3401
261	28S ribosomal protein S36, mitochondrial	12 kDa	0.3396
262	guanine nucleotide binding protein (G protein), beta polypeptide 3b	37 kDa	0.3391
263	NADH dehydrogenase	24 kDa	0.3384
264	PREDICTED: dephospho-CoA kinase domain-containing protein-like isoform X2	24 kDa	0.3384
265	PREDICTED: ras-related protein Rab-35-like	24 kDa	0.3384
266	PREDICTED: LOW QUALITY PROTEIN: long-chain-fatty-acid--CoA ligase 6	75 kDa	0.3353
267	phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	12 kDa	0.3327
268	NAD(P) transhydrogenase, mitochondrial	114 kDa	0.3299
269	40S ribosomal protein S5	25 kDa	0.3299
270	PREDICTED: uncharacterized protein LOC571872 isoform X1	12 kDa	0.3294
271	PREDICTED: Fc receptor-like protein 5 isoform X2	12 kDa	0.3294
272	PREDICTED: NADH dehydrogenase	25 kDa	0.3283
273	guanylyl cyclase 3 (guanylate cyclase retinal cone [Cyprinus carpio])	128 kDa	0.327
274	citrate synthase, mitochondrial precursor	52 kDa	0.3198
275	PREDICTED: SH3-containing GRB2-like protein 3-interacting protein 1 isoform X2	12 kDa	0.3168
276	synaptic vesicle glycoprotein 2B	12 kDa	0.3168
277	erlin-1 precursor	39 kDa	0.3154
278	stomatin-like protein 2, mitochondrial	39 kDa	0.3134
279	PREDICTED: ADP-dependent glucokinase isoform X2	26 kDa	0.3113
280	mitochondrial pyruvate carrier 1	13 kDa	0.3108
281	pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	13 kDa	0.3108
282	PREDICTED: phospholipid scramblase 2	26 kDa	0.3069
283	PREDICTED: uncharacterized protein LOC100334801 isoform X2	26 kDa	0.3069
284	cytochrome c oxidase subunit 6A1, mitochondrial	13 kDa	0.3051
285	guanine nucleotide-binding protein G(i) subunit alpha-2	41 kDa	0.3028
286	PREDICTED: mitochondrial import inner membrane translocase subunit Tim21	27 kDa	0.3027

287	phosducin	27 kDa	0.3
288	ubiquitin-like 3b	13 kDa	0.2996
289	mitochondrial trifunctional protein, alpha subunit	83 kDa	0.2989
290	PREDICTED: protein MGARP isoform X2	41 kDa	0.2965
291	mannose-P-dolichol utilization defect 1 protein	27 kDa	0.2959
292	PREDICTED: transmembrane emp24 domain-containing protein 7 isoform X2	27 kDa	0.2946
293	PREDICTED: 40S ribosomal protein S20	13 kDa	0.2942
294	PREDICTED: proteoglycan 4-like isoform X1	13 kDa	0.2916
295	PREDICTED: prostate stem cell antigen-like	13 kDa	0.2916
296	ras-related GTP-binding protein C	13 kDa	0.2916
297	60S ribosomal protein L8	28 kDa	0.2869
298	ATP synthase F(0) complex subunit C3, mitochondrial	14 kDa	0.2866
299	ras-related protein Rab-3A	28 kDa	0.2844
300	PREDICTED: NADH dehydrogenase	43 kDa	0.2821
301	60S ribosomal protein L7	29 kDa	0.282
302	monoacylglycerol lipase ABHD12	44 kDa	0.2797
303	PREDICTED: neuroplastin-like	44 kDa	0.2797
304	histone 2, H2a	14 kDa	0.2793
305	60S ribosomal protein L30	14 kDa	0.2793
306	40S ribosomal protein S4, X isoform	29 kDa	0.2761
307	PREDICTED: lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial-like	45 kDa	0.2706
308	60S ribosomal protein L7a	30 kDa	0.2672
309	PREDICTED: NADH dehydrogenase	15 kDa	0.2658
310	PREDICTED: multiple PDZ domain protein isoform X1	93 kDa	0.2638
311	PREDICTED: ammonium transporter Rh type A-like	15 kDa	0.2637
312	26S protease regulatory subunit 8	46 kDa	0.2634
313	aquaporin 1	30 kDa	0.2629
314	PREDICTED: 40S ribosomal protein S15a isoform X1	15 kDa	0.2616
315	PREDICTED: ankyrin 1, erythrocytic a isoform X12	31 kDa	0.2578
316	PREDICTED: GTPase HRas-like	15 kDa	0.2575
317	PREDICTED: equilibrative nucleoside transporter 1-like	15 kDa	0.2575
318	enoyl-CoA hydratase, mitochondrial	31 kDa	0.2558
319	PREDICTED: ER membrane protein complex subunit 1 isoform X1	111 kDa	0.2557
320	40S ribosomal protein S25	15 kDa	0.2555
321	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	80 kDa	0.254
322	aspartate aminotransferase 2a	48 kDa	0.2539
323	Beta-centractin	15 kDa	0.2535
324	PREDICTED: probable signal peptidase complex subunit 2-like isoform X1	15 kDa	0.2535
325	tubulin, alpha 8 like	48 kDa	0.252
326	PREDICTED: carnitine O-palmitoyltransferase 1, liver isoform isoform X2	48 kDa	0.2482
327	PREDICTED: gamma-aminobutyric acid receptor subunit alpha-6 isoform X1	49 kDa	0.2463
328	PREDICTED: uncharacterized protein LOC571872 isoform X1	32 kDa	0.2453
329	cytochrome c oxidase subunit Vaa	16 kDa	0.2441
330	60S ribosomal protein L28	16 kDa	0.2441
331	microsomal glutathione S-transferase-like	16 kDa	0.2441
332	elongation factor Tu, mitochondrial	49 kDa	0.2427
333	brain creatine kinase	16 kDa	0.2423
334	PREDICTED: FUN14 domain-containing protein 2 isoform X1	16 kDa	0.2388
335	PREDICTED: mitochondrial ubiquitin ligase activator of nfkb 1-A	33 kDa	0.2382
336	RPE-retinal G protein-coupled receptor	33 kDa	0.2382
337	isocitrate dehydrogenase	50 kDa	0.238
338	mitochondrial import receptor subunit TOM20 homolog B	16 kDa	0.2371
339	elongation factor Ts, mitochondrial	34 kDa	0.2365
340	ubiquitin-conjugating enzyme E2Nb	16 kDa	0.2354
341	alpha/beta hydrolase domain-containing protein 11	34 kDa	0.2323
342	ras-related protein Rab-27A	17 kDa	0.2321
343	mitochondrial import inner membrane translocase subunit TIM44	52 kDa	0.2308
344	PREDICTED: equilibrative nucleoside transporter 1-like	34 kDa	0.2307
345	NADH dehydrogenase	17 kDa	0.2305

346	chaperone activity of bc1 complex-like, mitochondrial	70 kDa	0.23
347	PREDICTED: retinol dehydrogenase 12-like	34 kDa	0.2299
348	retinal G protein coupled receptor b	35 kDa	0.2291
349	PREDICTED: NADH dehydrogenase	17 kDa	0.2289
350	PREDICTED: protein transport protein Sec61 subunit alpha-like 1	52 kDa	0.2287
351	ubiquinone biosynthesis monooxygenase COQ6	52 kDa	0.2276
352	G protein-coupled receptor kinase 1 b	17 kDa	0.2242
353	PREDICTED: coiled-coil domain-containing protein 136-like isoform X1	53 kDa	0.2235
354	CAAX prenyl protease 1 homolog	53 kDa	0.2235
355	PREDICTED: 40S ribosomal protein S23-like	17 kDa	0.2227
356	dihydrolipoyl dehydrogenase, mitochondrial	54 kDa	0.222
357	PREDICTED: protein FAM162B isoform X1	17 kDa	0.2212
358	PREDICTED: 40S ribosomal protein S24	17 kDa	0.2212
359	PREDICTED: 60S ribosomal protein L23	17 kDa	0.2212
360	microsomal glutathione S-transferase 1.2	17 kDa	0.2212
361	translocase of outer mitochondrial membrane 40 homolog, like	36 kDa	0.2199
362	putative Ras-related protein Rab-42	18 kDa	0.2197
363	ragulator complex protein LAMTOR1	18 kDa	0.2197
364	microsomal glutathione S-transferase 1.1	18 kDa	0.2197
365	long-chain fatty acid transport protein 4	73 kDa	0.2197
366	lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	54 kDa	0.2195
367	60S ribosomal protein L14	18 kDa	0.2183
368	PREDICTED: fatty aldehyde dehydrogenase-like	55 kDa	0.2171
369	L-lactate dehydrogenase B-A chain	36 kDa	0.217
370	60S ribosomal protein L24	18 kDa	0.2168
371	60S ribosomal protein L26	18 kDa	0.2168
372	60S ribosomal protein L27a	18 kDa	0.2154
373	PREDICTED: ankyrin-1-like	18 kDa	0.2154
374	PREDICTED: multiple PDZ domain protein isoform X1	37 kDa	0.2142
375	mitochondrial import inner membrane translocase subunit Tim17-B	18 kDa	0.214
376	ATP synthase subunit d, mitochondrial	18 kDa	0.2113
377	ras-related protein Rab-5C	37 kDa	0.2108
378	uncharacterized protein LOC559844	37 kDa	0.2101
379	PREDICTED: epoxide hydrolase 1, partial	38 kDa	0.2088
380	40S ribosomal protein S16	18 kDa	0.2086
381	PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP8 isoform X1	57 kDa	0.2075
382	neurotrimin isoform 1 precursor	38 kDa	0.2062
383	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial precursor	38 kDa	0.2049
384	PREDICTED: serine/threonine-protein kinase DCLK1 isoform X1	38 kDa	0.2042
385	acyl-CoA synthetase long-chain family member 3b	79 kDa	0.2006
386	PREDICTED: NCK-interacting protein with SH3 domain-like	19 kDa	0.1997
387	EF-hand calcium-binding domain-containing protein 4A	19 kDa	0.1997
388	PREDICTED: ceroid-lipofuscinosis, neuronal 6a isoform X1	19 kDa	0.1973
389	NADH dehydrogenase	41 kDa	0.1929
390	cytochrome P450, family 27, subfamily C, polypeptide 1	62 kDa	0.1914
391	PREDICTED: cadherin-related family member 1 isoform X2	83 kDa	0.1902
392	uncharacterized protein LOC100158473	20 kDa	0.1894
393	PREDICTED: sterol 26-hydroxylase, mitochondrial	20 kDa	0.1872
394	ER membrane protein complex subunit 4	20 kDa	0.1872
395	phosphatidylinositol N-acetylglucosaminyltransferase subunit H	20 kDa	0.1872
396	PREDICTED: signal peptidase complex catalytic subunit SEC11A-like	21 kDa	0.1862
397	PREDICTED: protein XRP2 isoform X1	42 kDa	0.1853
398	PREDICTED: protein TsetseEP-like	21 kDa	0.1851
399	uncharacterized protein LOC570464 precursor	21 kDa	0.1851
400	enoyl-CoA delta isomerase 2, mitochondrial	42 kDa	0.1837
401	calpain-5	21 kDa	0.1831
402	PREDICTED: vesicle-fusing ATPase isoform X1	86 kDa	0.1825
403	PREDICTED: translocon-associated protein subunit gamma	21 kDa	0.181
404	PREDICTED: cell division control protein 42 homolog isoform X1	21 kDa	0.1791

405	aspartate aminotransferase 2	43 kDa	0.1787
406	PREDICTED: glutaminase a isoform X1	66 kDa	0.1786
407	PREDICTED: transmembrane and coiled-coil domains protein 1-like	21 kDa	0.1781
408	ADP-ribosylation factor-like protein 8B-A	21 kDa	0.1781
409	phosphatidylserine synthase 1	21 kDa	0.1781
410	PREDICTED: cadherin-related family member 5-like isoform X2	44 kDa	0.1773
411	ADP-ribosylation-like factor 6 interacting protein 5	22 kDa	0.1771
412	outer dense fiber of sperm tails 2b	22 kDa	0.1771
413	peptidyl-prolyl cis-trans isomerase FKBP8	44 kDa	0.1768
414	mitochondrial NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 5	22 kDa	0.1753
415	Bcl-2/adenovirus E1B 19kD interaction protein XR	22 kDa	0.1753
416	ADP-ribosylation factor-like 3, like 1	22 kDa	0.1753
417	PREDICTED: guanine nucleotide-binding protein G(s) subunit alpha isoform X2	44 kDa	0.1749
418	recoverin-like	22 kDa	0.1743
419	lactation elevated protein 1 homolog B	22 kDa	0.1743
420	ubiquinone biosynthesis protein COQ7 homolog	22 kDa	0.1734
421	PREDICTED: protein RER1 isoform X2	22 kDa	0.1734
422	rho-related gtp-binding protein rhoc	22 kDa	0.1734
423	synaptobrevin homolog YKT6	22 kDa	0.1707
424	PREDICTED: transmembrane protein 126A isoform X1	22 kDa	0.1698
425	PREDICTED: paraplegin	92 kDa	0.1696
426	F-box/LRR-repeat protein 2	46 kDa	0.1691
427	PREDICTED: flavin reductase (NADPH)-like	23 kDa	0.169
428	ras-related protein Rab-18	23 kDa	0.1681
429	PREDICTED: protein NDRG3 isoform X1	46 kDa	0.1678
430	bcl2-associated X protein, b	23 kDa	0.1672
431	PREDICTED: pyruvate dehydrogenase kinase, isozyme 3 isoform X2	46 kDa	0.1669
432	PREDICTED: regulator of microtubule dynamics protein 2 isoform X1	47 kDa	0.1665
433	PREDICTED: cadherin-related family member 5-like isoform X2	23 kDa	0.1664
434	coiled-coil domain-containing protein 51	47 kDa	0.1649
435	saccharopine dehydrogenase b	47 kDa	0.1649
436	PREDICTED: prominin-1 isoform X1	95 kDa	0.1637
437	PREDICTED: ADP-ribosylation factor-like protein 3	23 kDa	0.1631
438	apolipoprotein O	24 kDa	0.1615
439	PREDICTED: sphingomyelin phosphodiesterase 2 isoform X1	48 kDa	0.1608
440	PREDICTED: NADPH--cytochrome P450 reductase isoform X1	48 kDa	0.1608
441	NADH dehydrogenase	48 kDa	0.1604
442	[3-methyl-2-oxobutanoate dehydrogenase	48 kDa	0.16
443	60S ribosomal protein L15	24 kDa	0.1584
444	PREDICTED: metal transporter CNNM4	74 kDa	0.1578
445	ceramide-1-phosphate transfer protein	24 kDa	0.1576
446	60S ribosomal protein L10	25 kDa	0.1547
447	PREDICTED: ras-related protein Rab-28 isoform X2	25 kDa	0.1532
448	60S ribosomal protein L10a	25 kDa	0.1525
449	PREDICTED: von Willebrand factor A domain-containing protein 1	25 kDa	0.1525
450	peroxisomal membrane protein 11B	25 kDa	0.1518
451	hydroxysteroid dehydrogenase-like protein 2	51 kDa	0.1516
452	PREDICTED: V-type proton ATPase subunit S1	52 kDa	0.1492
453	protein disulfide-isomerase TMX3 precursor	52 kDa	0.1481
454	epoxide hydrolase 1	52 kDa	0.1478
455	Probable saccharopine dehydrogenase	26 kDa	0.1464
456	PREDICTED: OCIA domain-containing protein 1 isoform X1	26 kDa	0.1451
457	PREDICTED: mitochondrial fission factor-like isoform X3	26 kDa	0.1451
458	PREDICTED: sodium-coupled neutral amino acid transporter 3	53 kDa	0.1449
459	PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2	53 kDa	0.1446
460	PREDICTED: abhydrolase domain-containing protein 8	53 kDa	0.1439
461	bcl-2-like protein 1	26 kDa	0.1432
462	NADH dehydrogenase	27 kDa	0.1426
463	PREDICTED: ATP synthase subunit s-like protein isoform X1	27 kDa	0.142

464	ATP synthase subunit s, mitochondrial	27 kDa	0.1414
465	ER membrane protein complex subunit 7 precursor	27 kDa	0.1414
466	G protein-coupled receptor kinase 1 b	54 kDa	0.1411
467	sorting and assembly machinery component 50 homolog B	27 kDa	0.1384
468	transmembrane emp24 domain-containing protein 4 precursor	27 kDa	0.1384
469	PREDICTED: sodium-coupled neutral amino acid transporter 3-like isoform X1	56 kDa	0.1356
470	large neutral amino acids transporter small subunit 1	57 kDa	0.1348
471	uncharacterized protein C2orf47 homolog, mitochondrial	28 kDa	0.1344
472	ER membrane protein complex subunit 10 isoform 1 precursor	28 kDa	0.1344
473	serine hydroxymethyltransferase, mitochondrial	57 kDa	0.1334
474	3-hydroxyacyl-CoA dehydrogenase type-2	28 kDa	0.1333
475	thioredoxin-dependent peroxide reductase, mitochondrial	28 kDa	0.1333
476	PREDICTED: 40S ribosomal protein S3-like isoform X1	28 kDa	0.1328
477	PREDICTED: solute carrier family 1 (glial high affinity glutamate transporter), member 2a isoform X2	58 kDa	0.1323
478	aquaporin-9	29 kDa	0.1323
479	PREDICTED: olfactory guanylyl cyclase GC-D isoform X3 (guanylate cyclase retinal rod1 [Cyprinus carpio])	88 kDa	0.1313
480	UDP glucuronosyltransferase 1 family, polypeptide B1 precursor	29 kDa	0.1312
481	heat shock protein HSP 90-beta	89 kDa	0.1303
482	PREDICTED: lysophosphatidylcholine acyltransferase 1-like	59 kDa	0.13
483	S-adenosylmethionine mitochondrial carrier protein	29 kDa	0.1297
484	neuronal membrane glycoprotein M6-b	30 kDa	0.1276
485	calpain-5	30 kDa	0.1262
486	erythrocyte membrane protein band 4.1b (elliptocytosis 1, RH-linked)	30 kDa	0.1257
487	uncharacterized protein LOC447917 precursor	30 kDa	0.1247
488	prominin-1 precursor	94 kDa	0.123
489	40S ribosomal protein S6	31 kDa	0.1224
490	methyltransferase like 7A precursor	31 kDa	0.1215
491	signal recognition particle receptor subunit beta	31 kDa	0.1211
492	eukaryotic translation initiation factor 3 subunit F	31 kDa	0.1206
493	E3 ubiquitin-protein ligase MARCH5	31 kDa	0.1197
494	erythrocyte band 7 integral membrane protein	32 kDa	0.1193
495	surfeit locus protein 1	32 kDa	0.118
496	integral membrane protein 2B	32 kDa	0.118
497	thioredoxin-related transmembrane protein 1 precursor	32 kDa	0.1176
498	PREDICTED: cadherin-related family member 1-like isoform X2	99 kDa	0.1164
499	PREDICTED: rap1 GTPase-GDP dissociation stimulator 1-like isoform X1	32 kDa	0.1163
500	PREDICTED: translocon-associated protein subunit alpha-like isoform X3	32 kDa	0.1155
501	PREDICTED: aspartate beta-hydroxylase isoform X2	33 kDa	0.1143
502	ubiquinol-cytochrome c reductase complex assembly factor 1	33 kDa	0.1139
503	PREDICTED: mitogen-activated protein kinase 14A-like isoform X2	33 kDa	0.1128
504	PREDICTED: calnexin isoform X1	67 kDa	0.1126
505	PREDICTED: enoyl-CoA delta isomerase 1, mitochondrial	33 kDa	0.1124
506	trifunctional enzyme subunit alpha, mitochondrial	33 kDa	0.1124
507	PREDICTED: protein CLN8 isoform X1	34 kDa	0.1116
508	protein-S-isoprenylcysteine O-methyltransferase	34 kDa	0.1109
509	PREDICTED: mitochondrial fission factor homolog B isoform X1	34 kDa	0.109
510	mitochondrial Rho GTPase 2	70 kDa	0.1089
511	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 precursor	70 kDa	0.1083
512	peroxisomal membrane protein PMP34	35 kDa	0.1076
513	elongation of very long chain fatty acids-like 4	35 kDa	0.1072
514	PREDICTED: very long-chain specific acyl-CoA dehydrogenase, mitochondrial isoform X1	71 kDa	0.1062
515	malate dehydrogenase, mitochondrial	35 kDa	0.1059
516	iron-sulfur protein NUBPL	36 kDa	0.1052
517	thioredoxin-related transmembrane protein 2-B precursor	36 kDa	0.1048
518	disintegrin and metalloproteinase domain-containing protein 10 precursor	36 kDa	0.1048
519	stress-70 protein, mitochondrial	73 kDa	0.1036
520	protein SCO2 homolog, mitochondrial	36 kDa	0.1032

521	DnaJ (Hsp40) homolog, subfamily A, member 3B	36 kDa	0.1032
522	PREDICTED: transmembrane protein 43-like	37 kDa	0.1022
523	phosducin-like protein	37 kDa	0.1019
524	transferrin receptor protein 1	77 kDa	0.0987
525	ATP-binding cassette sub-family B member 8, mitochondrial	77 kDa	0.0986
526	abhydrolase domain-containing protein 16A	38 kDa	0.098
527	ATPase asna1	38 kDa	0.0977
528	cyclin-Y-like protein 1	39 kDa	0.0971
529	heterogeneous nuclear ribonucleoprotein K	39 kDa	0.0962
530	PREDICTED: hydroxymethylbilane synthase a isoform X1	39 kDa	0.0962
531	Bardet-Biedl syndrome 5 protein homolog	39 kDa	0.096
532	eukaryotic translation initiation factor 4A, isoform 1A	39 kDa	0.0957
533	pyruvate dehydrogenase E1 component subunit beta, mitochondrial	39 kDa	0.0951
534	mitofusin-2	80 kDa	0.095
535	lectin, mannose-binding 2-like b precursor	40 kDa	0.0943
536	isocitrate dehydrogenase	40 kDa	0.0935
537	major histocompatibility complex class I UEA precursor	41 kDa	0.0904
538	PREDICTED: synaptotagmin-14 isoform X1	41 kDa	0.0904
539	PREDICTED: annexin A4-like isoform X1	42 kDa	0.0894
540	1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon	42 kDa	0.0889
541	PREDICTED: guanine nucleotide-binding protein subunit alpha-11-like isoform X1	42 kDa	0.0887
542	PREDICTED: ADP-ribosylation factor-like protein 13B-like isoform X5	42 kDa	0.0885
543	HLA-B associated transcript 1	42 kDa	0.088
544	solute carrier family 43 member 3	43 kDa	0.0861
545	reticulon-1 isoform 1	88 kDa	0.0857
546	transducin beta-like protein 2 precursor	44 kDa	0.085
547	ATPase family AAA domain-containing protein 1-A isoform 1	44 kDa	0.0848
548	PREDICTED: mitogen-activated protein kinase 3	44 kDa	0.0844
549	dnaJ homolog subfamily A member 3, mitochondrial	44 kDa	0.0842
550	serine/threonine-protein kinase DCLK2 isoform 1	90 kDa	0.0838
551	basigin precursor	45 kDa	0.0835
552	GPI-anchor transamidase precursor	45 kDa	0.0835
553	neuroplastin precursor	45 kDa	0.0833
554	1-acyl-sn-glycerol-3-phosphate acyltransferase gamma	45 kDa	0.0825
555	endoplasmin precursor	92 kDa	0.0821
556	28S ribosomal protein S27, mitochondrial	46 kDa	0.0818
557	glycosaminoglycan xylosylkinase	46 kDa	0.0812
558	26S proteasome non-ATPase regulatory subunit 3	48 kDa	0.0781
559	PREDICTED: protein tweety homolog 3 isoform X1	48 kDa	0.078
560	PREDICTED: kynurenine/alpha-aminoadipate aminotransferase, mitochondrial isoform X1	48 kDa	0.0778
561	uncharacterized protein C6orf136 homolog	48 kDa	0.0774
562	PREDICTED: required for meiotic nuclear division protein 1 homolog isoform X1	48 kDa	0.0772
563	PREDICTED: apoptosis-inducing factor 1, mitochondrial isoform X1	48 kDa	0.0767
564	keratin, type I cytoskeletal 18	49 kDa	0.0763
565	PREDICTED: calcium-binding mitochondrial carrier protein SCaMC-2-B isoform X2	49 kDa	0.076
566	acyl-CoA dehydrogenase-like	49 kDa	0.076
567	adenylyl cyclase-associated protein 1	50 kDa	0.0751
568	calcium/calmodulin-dependent protein kinase IGa	50 kDa	0.0748
569	erythrocyte membrane protein band 4.1b (elliptocytosis 1, RH-linked)	50 kDa	0.0744
570	elongation factor 1-gamma	51 kDa	0.0731
571	UBX domain-containing protein 4	52 kDa	0.072
572	cytochrome P450, family 20, subfamily A, polypeptide 1	52 kDa	0.072
573	PREDICTED: metal transporter CNNM4	52 kDa	0.072
574	PREDICTED: phosphatidate cytidylyltransferase 1	52 kDa	0.0715
575	vimentin	53 kDa	0.0707
576	26S protease regulatory subunit 7	52 kDa	0.0707
577	squalene synthase	53 kDa	0.0704
578	zinc transporter 1	54 kDa	0.0693
579	PREDICTED: pyruvate dehydrogenase protein X component, mitochondrial	54 kDa	0.0688

580	PREDICTED: FAS-associated factor 2-like isoform X1	54 kDa	0.0687
581	PREDICTED: monocarboxylate transporter 4 isoform X1	55 kDa	0.0681
582	WD repeat-containing protein 37	55 kDa	0.0678
583	V-type proton ATPase subunit H isoform 1	55 kDa	0.0673
584	dynamin-like 120 kDa protein, mitochondrial precursor	112 kDa	0.0671
585	6-phosphogluconate dehydrogenase, decarboxylating isoform 1	56 kDa	0.0659
586	dol-P-Man:Man(7)GlcNAc(2)-PP-Dol alpha-1,6-mannosyltransferase precursor	56 kDa	0.0658
587	annexin 11a isoform 2	56 kDa	0.0658
588	PREDICTED: protein ERGIC-53	57 kDa	0.0646
589	neutral amino acid transporter B(0)	57 kDa	0.0646
590	PREDICTED: protein phosphatase 3, catalytic subunit, gamma isoform-like isoform X1	57 kDa	0.0646
591	T-complex protein 1 subunit beta	58 kDa	0.064
592	prenylcysteine oxidase 1 precursor	59 kDa	0.0624
593	fatty-acid amide hydrolase 2-A	59 kDa	0.0624
594	PREDICTED: pyruvate kinase PKM isoform X1	60 kDa	0.0617
595	PREDICTED: extended synaptotagmin-1 isoform X1	60 kDa	0.0615
596	lysine--tRNA ligase	60 kDa	0.0614
597	keratin, type II cytoskeletal 8	61 kDa	0.0612
598	PREDICTED: ankyrin-1-like isoform X2	184 kDa	0.0611
599	PREDICTED: cGMP-gated cation channel alpha-1	63 kDa	0.0587
600	dnaJ homolog subfamily C member 11	64 kDa	0.058
601	leucine-rich repeat, immunoglobulin-like and transmembrane domains 1 precursor	64 kDa	0.0579
602	phosphatidylinositide phosphatase SAC1-B	67 kDa	0.0549
603	PREDICTED: V-type proton ATPase catalytic subunit A	68 kDa	0.0541
604	PREDICTED: carnitine palmitoyltransferase 1A isoform X2	69 kDa	0.0539
605	acyl-CoA dehydrogenase family member 9, mitochondrial	69 kDa	0.0537
606	PREDICTED: aarF domain-containing protein kinase 4	70 kDa	0.0532
607	solute carrier family 7, member 3	70 kDa	0.0531
608	polyadenylate-binding protein 1	71 kDa	0.0522
609	PREDICTED: signal recognition particle receptor subunit alpha	71 kDa	0.0522
610	cleft lip and palate transmembrane protein 1 homolog	72 kDa	0.0516
611	long-chain fatty acid transport protein 1	72 kDa	0.0515
612	78 kDa glucose-regulated protein precursor	72 kDa	0.0512
613	succinate dehydrogenase	73 kDa	0.0508
614	PREDICTED: caseinolytic peptidase B protein homolog	74 kDa	0.0497
615	PREDICTED: ATP-dependent RNA helicase DDX3X isoform X6	79 kDa	0.0467
616	MAGUK p55 subfamily member 5-A	80 kDa	0.0462
617	PREDICTED: ATP-binding cassette sub-family B member 7, mitochondrial	82 kDa	0.0451
618	PREDICTED: ribosomal protein S6 kinase alpha-3 isoform X1	83 kDa	0.0443
619	methylmalonyl-CoA mutase, mitochondrial	84 kDa	0.0441
620	transferrin receptor 1b	86 kDa	0.043
621	PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	91 kDa	0.0404
622	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2b isoform X1	92 kDa	0.0403
623	PREDICTED: neural cell adhesion molecule 1b isoform X11	92 kDa	0.0401
624	PREDICTED: prominin-1-A isoform X10	94 kDa	0.0393
625	PREDICTED: patched domain-containing protein 3	97 kDa	0.038
626	PREDICTED: dynamin 1a isoform X5	99 kDa	0.0371
627	PREDICTED: solute carrier family 12 member 7 isoform X5	121 kDa	0.0304
628	PREDICTED: electrogenic sodium bicarbonate cotransporter 1 isoform X2	123 kDa	0.0299
629	PREDICTED: uncharacterized protein LOC102079324	130 kDa	0.0282

Table S4. Identified proteins in washed CIS-rich fraction.
Proteins in washed CIS-rich fraction were identified with LC-MS/MS analysis and are listed in descending order of emPAI values for 5×10^5 cones.

	Identified proteins in washed CIS-rich fraction	Molecular mass	emPAI
1	uncharacterized protein LOC100145214	33 kDa	7847
2	ATP synthase F(0) complex subunit B1, mitochondrial	31 kDa	2258
3	PREDICTED: prohibitin isoform X2	22 kDa	314.23
4	voltage-dependent anion-selective channel protein 1	31 kDa	177.58
5	PREDICTED: prohibitin	22 kDa	158.55
6	PREDICTED: creatine kinase S-type, mitochondrial isoform X2	27 kDa	85.687
7	ATP synthase subunit g, mitochondrial	11 kDa	77.77
8	PREDICTED: ATP synthase subunit alpha, mitochondrial	27 kDa	76.757
9	voltage-dependent anion-selective channel protein 2	30 kDa	72.567
10	mitochondrial 2-oxoglutarate/malate carrier protein	38 kDa	66.02
11	PREDICTED: voltage-dependent anion-selective channel protein 2	11 kDa	57.343
12	PREDICTED: creatine kinase S-type, mitochondrial isoform X2	47 kDa	47.71
13	cytochrome b-c1 complex subunit 1, mitochondrial	52 kDa	43.7
14	ATP synthase subunit d, mitochondrial	18 kDa	39.82
15	PREDICTED: uncharacterized protein LOC100707031 isoform X1	12 kDa	36.977
16	prohibitin 2a	35 kDa	33.777
17	PREDICTED: prohibitin-2	27 kDa	33.76
18	creatine kinase S-type, mitochondrial	47 kDa	32.798
19	PREDICTED: retinol dehydrogenase 8-like isoform X1	35 kDa	29.97
20	PREDICTED: NADH dehydrogenase	15 kDa	29.018
21	PREDICTED: NADH dehydrogenase	14 kDa	26.823
22	voltage-dependent anion-selective channel protein 2-like	30 kDa	26.292
23	prohibitin 2-like	27 kDa	25.383
24	PREDICTED: L-lactate dehydrogenase B-B chain isoform X3	19 kDa	24.783
25	PREDICTED: solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3a isoform X2	40 kDa	24.575
26	PREDICTED: ATP synthase subunit gamma, mitochondrial isoform X1	33 kDa	19.243
27	ATP synthase subunit alpha, mitochondrial	33 kDa	18.732
28	ES1 protein, mitochondrial precursor	31 kDa	18.641
29	serine/threonine-protein kinase MAK	11 kDa	18.142
30	NADH dehydrogenase 1 beta subcomplex subunit 4	15 kDa	17.471
31	ADP/ATP translocase 3	27 kDa	16.99
32	PREDICTED: NADH dehydrogenase	19 kDa	16.812
33	uncharacterized protein LOC541492	13 kDa	16.12
34	ATP synthase subunit O, mitochondrial	26 kDa	15.708
35	NADH dehydrogenase 1 alpha subcomplex subunit 11	16 kDa	14.404
36	PREDICTED: NADH dehydrogenase	20 kDa	14.001
37	PREDICTED: NADH dehydrogenase	25 kDa	13.02
38	PREDICTED: threonine dehydratase, mitochondrial-like isoform X2	60 kDa	12.608
39	ADP-ribosylation factor-like protein 9	26 kDa	12.599
40	PREDICTED: voltage-dependent anion-selective channel protein 3 isoform X3	36 kDa	12.562
41	mitochondrial import receptor subunit TOM70	65 kDa	12.518
42	sorting and assembly machinery component 50 homolog B	23 kDa	12.399
43	malate dehydrogenase, mitochondrial	35 kDa	12.138
44	ba1 globin, like	16 kDa	12.076
45	cytochrome c oxidase subunit 4 isoform 1, mitochondrial	20 kDa	11.65
46	cytochrome b-c1 complex subunit 1, mitochondrial	13 kDa	11.245
47	mitochondrial pyruvate carrier 1	13 kDa	10.912
48	mitochondrial import inner membrane translocase subunit tim16	14 kDa	10.712
49	calcium-binding mitochondrial carrier protein Aralar1	76 kDa	10.452
50	PREDICTED: voltage-dependent anion-selective channel protein 3 isoform X3	36 kDa	10.25
51	PREDICTED: cytochrome b-c1 complex subunit 7-like	13 kDa	9.4493
52	PREDICTED: threo-3-hydroxyaspartate ammonia-lyase-like	41 kDa	9.414
53	mitochondrial import receptor subunit TOM40 homolog	36 kDa	9.3517

54	stomatin–like protein 2, mitochondrial	39 kDa	9.2827
55	calcium–binding mitochondrial carrier protein Aralar1	60 kDa	9.1383
56	HIG1 domain family member 1A	11 kDa	8.7413
57	PREDICTED: ATP synthase subunit beta, mitochondrial–like	56 kDa	8.4217
58	arrestin–C	40 kDa	8.2907
59	mitochondrial NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 5	22 kDa	8.091
60	PREDICTED: coiled–coil–helix–coiled–coil–helix domain–containing protein 6, mitochondrial isoform X2	29 kDa	8.0897
61	PREDICTED: phosphate carrier protein, mitochondrial–like isoform X1	34 kDa	7.9053
62	PREDICTED: NADH dehydrogenase	12 kDa	7.742
63	cytochrome c oxidase subunit IV isoform 2	20 kDa	7.485
64	PREDICTED: pyruvate dehydrogenase E1 alpha 1 isoform X1	45 kDa	7.336
65	dihydrolipoyllysine–residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	69 kDa	7.2543
66	sideroflexin–3	36 kDa	7.1363
67	stomatin–like protein 2, mitochondrial	39 kDa	7.1153
68	PREDICTED: NADH dehydrogenase	17 kDa	7.0023
69	NADH dehydrogenase	41 kDa	6.9657
70	cytochrome c oxidase subunit VIIa polypeptide 3	16 kDa	6.909
71	PREDICTED: voltage–dependent anion–selective channel protein 2	11 kDa	6.7737
72	plasminogen receptor (KT)	20 kDa	6.554
73	NADH dehydrogenase 1 beta subcomplex subunit 6	15 kDa	6.357
74	NADH dehydrogenase (ubiquinone) 1 subunit c2	13 kDa	6.0537
75	sorting and assembly machinery component 50 homolog A	52 kDa	6.0447
76	aspartate aminotransferase 2a	48 kDa	5.9803
77	cytochrome c–1	36 kDa	5.9553
78	mitochondrial chaperone BCS1	48 kDa	5.938
79	cytochrome c oxidase subunit 6A1, mitochondrial	13 kDa	5.9023
80	NADH dehydrogenase	24 kDa	5.8123
81	NADH dehydrogenase	31 kDa	5.646
82	CDGSH iron sulfur domain 1	12 kDa	5.5593
83	PREDICTED: mitochondrial pyruvate carrier 2	14 kDa	5.542
84	cytochrome c oxidase subunit 4 isoform 1, mitochondrial	20 kDa	5.5203
85	mitochondrial import receptor subunit TOM40 homolog	36 kDa	5.4667
86	histone 1, H4, like	12 kDa	5.142
87	PREDICTED: calcium–binding mitochondrial carrier protein Aralar2 isoform X1	48 kDa	4.8943
88	PREDICTED: calcium–binding mitochondrial carrier protein Aralar2 isoform X1	15 kDa	4.7787
89	cytochrome b–c1 complex subunit 2, mitochondrial	50 kDa	4.7677
90	trifunctional enzyme subunit beta, mitochondrial	50 kDa	4.7373
91	PREDICTED: pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial isoform X1	25 kDa	4.669
92	alpha globin–like	15 kDa	4.5913
93	isocitrate dehydrogenase	50 kDa	4.306
94	NADH dehydrogenase	53 kDa	4.2797
95	reticulon–4–interacting protein 1 homolog, mitochondrial	42 kDa	4.219
96	retinol dehydrogenase 13	37 kDa	4.108
97	NADH–cytochrome b5 reductase 1	28 kDa	3.9437
98	apolipoprotein O	24 kDa	3.9143
99	PREDICTED: ubiquinol–cytochrome c reductase core protein II isoform X1	49 kDa	3.7547
100	protein NipSnap homolog 2	33 kDa	3.6203
101	inactive hydroxysteroid dehydrogenase–like protein 1	35 kDa	3.568
102	NADH dehydrogenase 1 alpha subcomplex subunit 6	16 kDa	3.4727
103	LETM1 and EF–hand domain–containing protein 1, mitochondrial	86 kDa	3.3119
104	aspartate aminotransferase 2	43 kDa	3.2839
105	voltage–dependent anion–selective channel protein 2	20 kDa	2.9212
106	PREDICTED: mitochondrial glutamate carrier 1	34 kDa	2.9134
107	translocase of outer mitochondrial membrane 40 homolog, like	35 kDa	2.8674
108	mitochondrial dicarboxylate carrier	32 kDa	2.842
109	PREDICTED: ubiquinol–cytochrome c reductase core protein II isoform X1	40 kDa	2.8386
110	ADP–ribosylation factor–like protein 9	25 kDa	2.8341

111	NADH dehydrogenase	58 kDa	2.8289
112	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	80 kDa	2.7294
113	succinyl-CoA ligase	51 kDa	2.6793
114	translocase of outer mitochondrial membrane 40 homolog, like	36 kDa	2.6352
115	NADH dehydrogenase	13 kDa	2.5723
116	NADH dehydrogenase (ubiquinone) 1 subunit c2	13 kDa	2.5723
117	isocitrate dehydrogenase	43 kDa	2.5709
118	PREDICTED: NADH dehydrogenase	43 kDa	2.5394
119	PREDICTED: coiled-coil domain-containing protein 136-like isoform X1	53 kDa	2.5324
120	PREDICTED: isocitrate dehydrogenase	44 kDa	2.4932
121	PREDICTED: mitochondrial fission process protein 1-like	18 kDa	2.4453
122	cytochrome c oxidase subunit Vaa	18 kDa	2.3777
123	28S ribosomal protein S36, mitochondrial	12 kDa	2.2468
124	heat shock cognate 71 kDa protein	42 kDa	2.2293
125	ATPase family AAA domain-containing protein 3	69 kDa	2.2163
126	3-hydroxyacyl-CoA dehydrogenase type-2	28 kDa	2.1361
127	PREDICTED: uncharacterized protein LOC556653	23 kDa	2.1319
128	PREDICTED: hexokinase-1-like	14 kDa	2.1305
129	uncharacterized protein C18orf19 homolog B	32 kDa	2.1159
130	PREDICTED: NADH dehydrogenase	21 kDa	2.0971
131	NADH dehydrogenase	12 kDa	2.0714
132	cytochrome c oxidase subunit Vaa	16 kDa	2.0471
133	guanine nucleotide-binding protein G(t) subunit alpha-2	40 kDa	2.0231
134	enoyl-CoA hydratase, mitochondrial	31 kDa	1.9767
135	OCIA domain-containing protein 1	30 kDa	1.9289
136	reticulon-4	22 kDa	1.9169
137	pyruvate dehydrogenase E1 component subunit beta, mitochondrial	39 kDa	1.9136
138	methylmalonate-semialdehyde dehydrogenase	61 kDa	1.8848
139	NADH dehydrogenase	17 kDa	1.822
140	retinol dehydrogenase-like	36 kDa	1.8206
141	L-lactate dehydrogenase B-A chain	36 kDa	1.8206
142	sideroflexin-4	35 kDa	1.8005
143	PREDICTED: presenilins-associated rhomboid-like protein, mitochondrial	41 kDa	1.7799
144	coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	37 kDa	1.7621
145	ATPase family AAA domain-containing protein 3	69 kDa	1.7604
146	PREDICTED: complex I assembly factor TIMMDC1, mitochondrial isoform X1	33 kDa	1.7283
147	PREDICTED: NADH dehydrogenase	21 kDa	1.7263
148	PREDICTED: L-lactate dehydrogenase B-B chain isoform X4	19 kDa	1.7052
149	uncharacterized protein LOC100135302	20 kDa	1.6653
150	putative tubulin beta chain variant 1	20 kDa	1.6459
151	mitochondrial inner membrane protein	83 kDa	1.6335
152	PREDICTED: LOW QUALITY PROTEIN: actin, gamma 1	40 kDa	1.6204
153	creatine kinase U-type, mitochondrial	22 kDa	1.619
154	isocitrate dehydrogenase	43 kDa	1.6078
155	PREDICTED: calcium-binding mitochondrial carrier protein SCaMC-2-B isoform X2	49 kDa	1.5994
156	PREDICTED: vesicle-associated membrane protein-associated protein A-like	26 kDa	1.5929
157	PREDICTED: vesicle-associated membrane protein-associated protein A-like	26 kDa	1.5929
158	thioredoxin-dependent peroxide reductase, mitochondrial	28 kDa	1.5892
159	mitochondrial import inner membrane translocase subunit Tim17-B	18 kDa	1.5758
160	protein QIL1	12 kDa	1.5631
161	PREDICTED: nuclease EXOG, mitochondrial	39 kDa	1.5583
162	transmembrane protein 256 precursor	12 kDa	1.5345
163	PREDICTED: very long-chain specific acyl-CoA dehydrogenase, mitochondrial isoform X1	71 kDa	1.5216
164	PREDICTED: dehydrogenase/reductase SDR family member 7B isoform X1	31 kDa	1.5171
165	glutaryl-CoA dehydrogenase a	18 kDa	1.5004
166	isocitrate dehydrogenase	40 kDa	1.4881
167	ATP-binding cassette sub-family B member 8, mitochondrial	77 kDa	1.4777
168	sorting and assembly machinery component 50 homolog B	27 kDa	1.464
169	NAD(P) transhydrogenase, mitochondrial	114 kDa	1.4534

170	PREDICTED: calcium/calmodulin-dependent protein kinase type II delta 1 chain isoform X3	28 kDa	1.4404
171	dihydrolipoyl dehydrogenase, mitochondrial	54 kDa	1.4384
172	metaxin 1	36 kDa	1.4365
173	PREDICTED: LOW QUALITY PROTEIN: long-chain-fatty-acid--CoA ligase 6	50 kDa	1.4107
174	PREDICTED: mitochondrial fission factor-like isoform X4	24 kDa	1.3838
175	COX16 cytochrome c oxidase assembly homolog	13 kDa	1.3807
176	mitochondrial carrier homolog 2	31 kDa	1.3454
177	PREDICTED: tubulin beta-4B chain-like	31 kDa	1.3266
178	reticulon-4	22 kDa	1.3162
179	PREDICTED: choline dehydrogenase, mitochondrial	25 kDa	1.2768
180	ATPase, Na+/K+ transporting, beta 2b polypeptide	34 kDa	1.2638
181	[3-methyl-2-oxobutanoate dehydrogenase	48 kDa	1.2509
182	PREDICTED: retinol dehydrogenase 12-like	34 kDa	1.2403
183	AFG3-like protein 2	89 kDa	1.2328
184	cytochrome b-c1 complex subunit Rieske, mitochondrial	30 kDa	1.2288
185	PREDICTED: probable UDP-sugar transporter protein SLC35A4 isoform X1	11 kDa	1.2058
186	PREDICTED: presenilins-associated rhomboid-like protein, mitochondrial-like isoform X2	11 kDa	1.2058
187	elongation factor Tu, mitochondrial	49 kDa	1.1921
188	erlin-2 precursor	40 kDa	1.1837
189	ADP-ribosylation factor-like protein 6	21 kDa	1.1684
190	acetyl-CoA acetyltransferase, mitochondrial precursor	48 kDa	1.1577
191	PREDICTED: mitochondrial import inner membrane translocase subunit Tim22	21 kDa	1.1569
192	ras-related protein Rab-2A	24 kDa	1.1561
193	solute carrier family 25 (mitochondrial carrier: glutamate), member 22	36 kDa	1.1538
194	PREDICTED: mitochondrial fission factor-like isoform X3	26 kDa	1.1463
195	mitochondrial import receptor subunit TOM20 homolog B	16 kDa	1.1448
196	PREDICTED: glutaryl-CoA dehydrogenase, mitochondrial-like	49 kDa	1.1278
197	zinc transporter 9	64 kDa	1.1104
198	citrate synthase, mitochondrial precursor	52 kDa	1.0972
199	PREDICTED: stress-70 protein, mitochondrial-like, partial	17 kDa	1.0902
200	PREDICTED: tubulin alpha chain-like	12 kDa	1.0861
201	mitochondrial trifunctional protein, alpha subunit	83 kDa	1.071
202	transmembrane protein 256 precursor	12 kDa	1.0682
203	PREDICTED: coiled-coil domain-containing protein 136-like isoform X1	30 kDa	1.0538
204	PREDICTED: kynurenine/alpha-aminoadipate aminotransferase, mitochondrial isoform X1	48 kDa	1.0501
205	PREDICTED: ras-related protein Rab-1A-like isoform X1	22 kDa	1.0436
206	PREDICTED: nucleoside diphosphate kinase B isoform X1	17 kDa	1.0402
207	ras-related protein Rab-1B	22 kDa	1.0343
208	succinate dehydrogenase	61 kDa	1.0337
209	mitochondrial import inner membrane translocase subunit Tim17-A	17 kDa	1.0283
210	regulator of microtubule dynamics protein 3	51 kDa	1.0172
211	PREDICTED: protein FAM162B isoform X1	17 kDa	1.0167
212	PREDICTED: peroxiredoxin-5, mitochondrial-like	20 kDa	1.0114
213	succinate dehydrogenase	73 kDa	1.0022
214	pyrroline-5-carboxylate reductase 1a	34 kDa	0.9856
215	uncharacterized protein LOC100135302	23 kDa	0.9732
216	histone H2AX	15 kDa	0.972
217	dnaJ homolog subfamily C member 11	64 kDa	0.9565
218	methylglutaconyl-CoA hydratase, mitochondrial	35 kDa	0.9354
219	PREDICTED: FAS-associated factor 2-like isoform X1	54 kDa	0.9249
220	dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	51 kDa	0.9224
221	PREDICTED: dephospho-CoA kinase domain-containing protein-like isoform X2	24 kDa	0.9039
222	PREDICTED: LOW QUALITY PROTEIN: long-chain-fatty-acid--CoA ligase 6	75 kDa	0.891
223	ubiquinone biosynthesis monooxygenase COQ6	52 kDa	0.8882
224	metaxin 1a	36 kDa	0.8661
225	PREDICTED: tubulin alpha chain	45 kDa	0.8658

226	NADH dehydrogenase (ubiquinone) Fe-S protein 8b	22 kDa	0.8573
227	hexokinase-1	54 kDa	0.8501
228	ATP synthase F(0) complex subunit C3, mitochondrial	14 kDa	0.8416
229	PREDICTED: transmembrane protein 126A isoform X1	22 kDa	0.8358
230	histone 2, H2a	14 kDa	0.8304
231	uncharacterized protein C18orf19 homolog A	29 kDa	0.8156
232	histone 2, H2a	14 kDa	0.8087
233	hexokinase-1	11 kDa	0.8001
234	PREDICTED: apoptosis-inducing factor 1, mitochondrial isoform X3	68 kDa	0.7994
235	regulator of microtubule dynamics protein 3	35 kDa	0.7984
236	cysteine desulfurase, mitochondrial	50 kDa	0.7902
237	hexokinase-1	71 kDa	0.7863
238	protein disulfide-isomerase TMX3 precursor	47 kDa	0.7839
239	PREDICTED: coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial	17 kDa	0.7803
240	PREDICTED: tubulin alpha-1C chain	45 kDa	0.7769
241	PREDICTED: mitochondrial import inner membrane translocase subunit Tim21	27 kDa	0.7623
242	protein NDRG1 isoform 1	42 kDa	0.7588
243	ubiquinone biosynthesis monooxygenase COQ6	52 kDa	0.7533
244	PREDICTED: uncharacterized protein LOC101885612	11 kDa	0.7513
245	cytochrome c	11 kDa	0.7513
246	optic atrophy 3 protein homolog	18 kDa	0.7487
247	vesicle-associated membrane protein-associated protein A	30 kDa	0.7465
248	PREDICTED: gap junction delta-2 protein-like	21 kDa	0.7351
249	PREDICTED: dnaJ homolog subfamily C member 11	65 kDa	0.7321
250	PREDICTED: protein SCO1 homolog, mitochondrial	34 kDa	0.7261
251	PREDICTED: hydroxyacylglutathione hydrolase, mitochondrial isoform X1	34 kDa	0.7261
252	uncharacterized protein LOC100127838	18 kDa	0.7193
253	PREDICTED: ATP-binding cassette sub-family B member 7, mitochondrial	82 kDa	0.716
254	L-2-hydroxyglutarate dehydrogenase, mitochondrial	31 kDa	0.7117
255	PREDICTED: uncharacterized protein LOC571872 isoform X1	12 kDa	0.7078
256	PREDICTED: mitochondrial fission factor homolog B isoform X1	34 kDa	0.707
257	stress-70 protein, mitochondrial	73 kDa	0.7019
258	mitochondrial trifunctional protein, alpha subunit	38 kDa	0.6997
259	PREDICTED: protein MGARP isoform X2	41 kDa	0.6936
260	mitochondrial import inner membrane translocase subunit Tim23	22 kDa	0.6933
261	PREDICTED: uncharacterized protein LOC556653	35 kDa	0.6888
262	mitochondrial ubiquitin ligase activator of nfkb 1-A	12 kDa	0.6878
263	COX16 cytochrome c oxidase assembly homolog	12 kDa	0.6878
264	phosphatidate cytidylyltransferase, mitochondrial precursor	12 kDa	0.6878
265	uncharacterized protein LOC100145220	29 kDa	0.6777
266	PREDICTED: apoptosis-inducing factor 1, mitochondrial isoform X1	48 kDa	0.6765
267	PREDICTED: mitochondrial import inner membrane translocase subunit Tim23	22 kDa	0.6713
268	PREDICTED: pyrroline-5-carboxylate reductase 2-like	16 kDa	0.6675
269	calcium/calmodulin-dependent protein kinase type II delta 1 chain isoform 1	56 kDa	0.6639
270	aconitate hydratase, mitochondrial	86 kDa	0.6634
271	mitochondrial ATP synthase subunit f	13 kDa	0.6508
272	PREDICTED: choline dehydrogenase, mitochondrial	20 kDa	0.643
273	translocase of outer mitochondrial membrane 20 homolog a	16 kDa	0.6392
274	PREDICTED: cytochrome b-c1 complex subunit Rieske, mitochondrial-like	26 kDa	0.6391
275	PREDICTED: [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	47 kDa	0.6342
276	arrestin-C	33 kDa	0.6335
277	PREDICTED: regulator of G-protein signaling 9-binding protein-like	27 kDa	0.6307
278	uncharacterized protein LOC541537	27 kDa	0.6307
279	PREDICTED: ATP-binding cassette sub-family B member 10, mitochondrial	30 kDa	0.6231
280	acylglycerol kinase, mitochondrial precursor	48 kDa	0.6225
281	delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial precursor	62 kDa	0.6219
282	PREDICTED: ATPase, Na+/K+ transporting, beta 2b polypeptide isoform X1	24 kDa	0.6172
283	PREDICTED: glutaminase a isoform X1	66 kDa	0.6105

284	PREDICTED: mitochondrial pyruvate carrier 2-like	17 kDa	0.6069
285	PREDICTED: uncharacterized aarF domain-containing protein kinase 5 isoform X1	42 kDa	0.6033
286	PREDICTED: sterol 26-hydroxylase, mitochondrial	20 kDa	0.6001
287	60S ribosomal protein L15	24 kDa	0.5996
288	abhydrolase domain-containing protein 16A	38 kDa	0.5985
289	PREDICTED: growth hormone-inducible transmembrane protein	35 kDa	0.5898
290	uncharacterized protein C2orf47 homolog, mitochondrial	28 kDa	0.5809
291	PREDICTED: tubulin alpha chain-like	50 kDa	0.5754
292	PREDICTED: ATP-dependent zinc metalloprotease YME1L1 isoform X1	79 kDa	0.5752
293	60 kDa heat shock protein, mitochondrial	28 kDa	0.5705
294	3-ketoacyl-CoA thiolase, mitochondrial	43 kDa	0.5674
295	carnitine O-palmitoyltransferase 2, mitochondrial	18 kDa	0.5611
296	very-long-chain enoyl-CoA reductase	36 kDa	0.5593
297	PREDICTED: growth hormone-inducible transmembrane protein	36 kDa	0.5566
298	mitochondrial Rho GTPase 2	70 kDa	0.5565
299	PREDICTED: actin, aortic smooth muscle	18 kDa	0.5559
300	ubiquinol-cytochrome c reductase complex assembly factor 1	33 kDa	0.5468
301	vesicle-associated membrane protein-associated protein A	30 kDa	0.5381
302	PREDICTED: ornithine aminotransferase, mitochondrial	49 kDa	0.5359
303	ras-related protein Rab-5C	37 kDa	0.534
304	mitochondrial carnitine/acylcarnitine carrier protein CACL	34 kDa	0.5278
305	NADH dehydrogenase	27 kDa	0.5141
306	PREDICTED: succinate dehydrogenase cytochrome b560 subunit, mitochondrial isoform X1	19 kDa	0.5124
307	phosphatidate cytidylyltransferase, mitochondrial precursor	15 kDa	0.511
308	PREDICTED: transmembrane protein C9orf123 homolog	11 kDa	0.5014
309	coiled-coil domain-containing protein 51	47 kDa	0.4994
310	40S ribosomal protein S25	15 kDa	0.4948
311	E3 ubiquitin-protein ligase MARCH5	31 kDa	0.4904
312	mitochondrial import inner membrane translocase subunit TIM44	52 kDa	0.4864
313	PREDICTED: ras-related protein Rab-7a isoform X1	24 kDa	0.4851
314	transmembrane protein 65	24 kDa	0.4851
315	traB domain-containing protein	40 kDa	0.4835
316	carnitine O-palmitoyltransferase 2, mitochondrial	20 kDa	0.4829
317	RAB1A, member RAS oncogene family	28 kDa	0.4809
318	solute carrier family 25 member 47-B	12 kDa	0.4679
319	serine hydroxymethyltransferase, mitochondrial	57 kDa	0.4676
320	protein QIL1	12 kDa	0.4617
321	nucleoside diphosphate kinase A	20 kDa	0.46
322	sodium/potassium-transporting ATPase subunit alpha-3	113 kDa	0.46
323	PREDICTED: ras-related protein Rab-11B	25 kDa	0.4566
324	PREDICTED: FUN14 domain-containing protein 2 isoform X1	16 kDa	0.4517
325	PREDICTED: mitochondrial ubiquitin ligase activator of nfkb 1-A	33 kDa	0.4502
326	PREDICTED: saccharopine dehydrogenase-like oxidoreductase-like	12 kDa	0.4498
327	LIM domain and actin-binding protein 1	20 kDa	0.4494
328	60 kDa heat shock protein, mitochondrial	29 kDa	0.4492
329	synaptojanin-2-binding protein	16 kDa	0.4474
330	39S ribosomal protein L43, mitochondrial	16 kDa	0.4474
331	PREDICTED: mitochondrial dicarboxylate carrier	29 kDa	0.4467
332	PREDICTED: solute carrier family 25 member 51-like	34 kDa	0.4416
333	acyl-CoA dehydrogenase family member 9, mitochondrial	69 kDa	0.4368
334	PREDICTED: heat shock cognate 71 kDa protein, partial	30 kDa	0.4256
335	PREDICTED: sarcolemmal membrane-associated protein isoform X4	92 kDa	0.4246
336	mitochondrial import inner membrane translocase subunit TIM14	13 kDa	0.4225
337	PREDICTED: magnesium transporter MRS2 homolog, mitochondrial isoform X1	48 kDa	0.4222
338	cytosolic 5'-nucleotidase 3	39 kDa	0.4201
339	outer dense fiber of sperm tails 2b	22 kDa	0.4201
340	60S ribosomal protein L18	22 kDa	0.417
341	uncharacterized protein LOC556781	13 kDa	0.4125
342	mitochondrial carnitine/acylcarnitine carrier protein	22 kDa	0.4111

343	metaxin-2	31 kDa	0.4105
344	PREDICTED: LETM1 domain-containing protein LETM2, mitochondrial	54 kDa	0.4099
345	PREDICTED: ADP-dependent glucokinase isoform X2	58 kDa	0.4098
346	heat shock protein 75 kDa, mitochondrial	82 kDa	0.4056
347	PREDICTED: mitochondrial glutamate carrier 1-like	22 kDa	0.4053
348	solute carrier family 25 member 46	45 kDa	0.4015
349	epimerase family protein SDR39U1	36 kDa	0.3997
350	PREDICTED: malate dehydrogenase 1Aa, NAD (soluble) isoform X1	36 kDa	0.3979
351	PREDICTED: 40S ribosomal protein S9-like	22 kDa	0.3969
352	surfeit locus protein 1	32 kDa	0.3945
353	PREDICTED: succinate dehydrogenase	32 kDa	0.3945
354	PREDICTED: multiple PDZ domain protein isoform X1	93 kDa	0.3942
355	PREDICTED: ras-related protein Rab-10	23 kDa	0.3915
356	hydroxysteroid dehydrogenase-like protein 2	51 kDa	0.391
357	COX15 homolog	51 kDa	0.3898
358	mpv17-like protein 2	23 kDa	0.3863
359	PREDICTED: uncharacterized protein LOC571872 isoform X1	32 kDa	0.385
360	1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon	42 kDa	0.3843
361	PREDICTED: 60S ribosomal protein L23a	18 kDa	0.3842
362	very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 2	28 kDa	0.3834
363	delta-1-pyrroline-5-carboxylate synthase	85 kDa	0.381
364	PREDICTED: mitochondrial Rho GTPase 1 isoform X4	71 kDa	0.38
365	mitochondrial dynamics protein MID51	52 kDa	0.377
366	fatty aldehyde dehydrogenase	28 kDa	0.3751
367	PREDICTED: LOW QUALITY PROTEIN: 40S ribosomal protein S13-like	19 kDa	0.3748
368	PREDICTED: 40S ribosomal protein S14 isoform X1	19 kDa	0.3717
369	RAB5A, member RAS oncogene family, a	24 kDa	0.3713
370	ras-related protein Rab-1B	19 kDa	0.3687
371	PREDICTED: paraplegin	92 kDa	0.3682
372	PREDICTED: 40S ribosomal protein S8	24 kDa	0.3596
373	alpha/beta hydrolase domain-containing protein 11	34 kDa	0.3592
374	chaperone activity of bc1 complex-like, mitochondrial	70 kDa	0.3546
375	coiled-coil domain-containing protein 90B, mitochondrial	29 kDa	0.3538
376	PREDICTED: tubulin beta-2B chain-like isoform 1	55 kDa	0.3527
377	PREDICTED: reticulon-3-B-like isoform X2	25 kDa	0.3487
378	dynamin-like 120 kDa protein, mitochondrial precursor	112 kDa	0.3475
379	uncharacterized protein LOC100135257	35 kDa	0.3467
380	calmegin precursor	66 kDa	0.3453
381	electron transfer flavoprotein subunit alpha, mitochondrial	35 kDa	0.3437
382	PREDICTED: mitochondrial 2-oxodicarboxylate carrier isoform X2	15 kDa	0.3427
383	retinol dehydrogenase 8a	35 kDa	0.3408
384	NADH dehydrogenase 1 beta subcomplex subunit 10	20 kDa	0.3362
385	PREDICTED: 40S ribosomal protein S15a isoform X1	15 kDa	0.3359
386	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 precursor	67 kDa	0.3337
387	PREDICTED: regulator of microtubule dynamics protein 2 isoform X1	47 kDa	0.3333
388	acyl-CoA synthetase long-chain family member 3b	79 kDa	0.3283
389	succinate dehydrogenase	32 kDa	0.3221
390	arginase-1	37 kDa	0.3216
391	cytosol aminopeptidase	21 kDa	0.3174
392	PREDICTED: succinyl-CoA ligase	16 kDa	0.3172
393	PREDICTED: LOW QUALITY PROTEIN: metalloendopeptidase OMA1, mitochondrial	16 kDa	0.3172
394	transmembrane protein 11, mitochondrial	27 kDa	0.3158
395	ATP synthase subunit s, mitochondrial	27 kDa	0.3123
396	calcium-binding mitochondrial carrier protein SCaMC-1	16 kDa	0.3114
397	retinol dehydrogenase 14	32 kDa	0.3104
398	peptidyl-prolyl cis-trans isomerase FKBP8	44 kDa	0.3101
399	PRA1 family protein 3	22 kDa	0.3067
400	PREDICTED: sterol 26-hydroxylase, mitochondrial	27 kDa	0.3056
401	mitochondrial import inner membrane translocase subunit TIM50 precursor	44 kDa	0.3049

402	PREDICTED: NADH dehydrogenase (ubiquinone) complex I, assembly factor 6	33 kDa	0.3048
403	ubiquinone biosynthesis protein COQ7 homolog	22 kDa	0.2986
404	rho-related gtp-binding protein rhoc	22 kDa	0.2986
405	ATPase family AAA domain-containing protein 1-B	22 kDa	0.2986
406	carnitine O-palmitoyltransferase 2, mitochondrial	22 kDa	0.2986
407	PREDICTED: enoyl-CoA delta isomerase 1, mitochondrial	33 kDa	0.2981
408	L-lactate dehydrogenase A chain	39 kDa	0.2963
409	G-protein-coupled receptor kinase 7A	62 kDa	0.2953
410	cytochrome c-type heme lyase	34 kDa	0.2943
411	PREDICTED: 10 kDa heat shock protein, mitochondrial isoform X2	11 kDa	0.2923
412	uncharacterized protein LOC553782	11 kDa	0.2923
413	uncharacterized protein LOC100127828	34 kDa	0.288
414	solute carrier family 25 member 33	34 kDa	0.2868
415	mitochondrial ubiquitin ligase activator of nfkb 1-A	23 kDa	0.2854
416	PREDICTED: pyruvate dehydrogenase kinase, isozyme 3 isoform X2	46 kDa	0.2848
417	DDRGK domain-containing protein 1 precursor	35 kDa	0.2844
418	trifunctional enzyme subunit alpha, mitochondrial	47 kDa	0.2839
419	renalase	41 kDa	0.2816
420	phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	11 kDa	0.2813
421	40S ribosomal protein S7	17 kDa	0.2805
422	40S ribosomal protein S4, X isoform	29 kDa	0.2799
423	uncharacterized protein LOC449549	23 kDa	0.2784
424	phosphatidate cytidylyltransferase, mitochondrial precursor	11 kDa	0.2779
425	uncharacterized protein LOC556781	23 kDa	0.2767
426	PREDICTED: 60S ribosomal protein L9 isoform X2	17 kDa	0.2759
427	band 3 anion transport protein	11 kDa	0.2745
428	PREDICTED: pyruvate dehydrogenase protein X component, mitochondrial	54 kDa	0.2734
429	NAD-dependent protein deacetylase sirtuin-3, mitochondrial	18 kDa	0.2715
430	lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	54 kDa	0.2712
431	60S ribosomal protein L14	18 kDa	0.2694
432	40S ribosomal protein S19	18 kDa	0.2694
433	60S ribosomal protein L7a	30 kDa	0.2692
434	PREDICTED: glycerol kinase-like isoform X4	30 kDa	0.2692
435	glycerophosphodiester phosphodiesterase domain-containing protein 1	36 kDa	0.2686
436	mitofusin-2	80 kDa	0.268
437	PREDICTED: syntaxin-12 isoform X1	30 kDa	0.2679
438	60S ribosomal protein L4	43 kDa	0.2673
439	PREDICTED: ferrochelatase, mitochondrial isoform X1	43 kDa	0.2673
440	60S ribosomal protein L24	18 kDa	0.2672
441	protein THEM6 precursor	24 kDa	0.2668
442	solute carrier family 25 member 47-B	24 kDa	0.2668
443	PREDICTED: calnexin isoform X1	67 kDa	0.2661
444	protein THEM6 precursor	24 kDa	0.2653
445	60S ribosomal protein L27a	18 kDa	0.2651
446	guanine nucleotide binding protein (G protein), beta polypeptide 3b	37 kDa	0.2644
447	probable 28S ribosomal protein S10, mitochondrial	12 kDa	0.2617
448	electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	69 kDa	0.2605
449	G-protein-coupled receptor kinase 7A	62 kDa	0.26
450	phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	12 kDa	0.2587
451	PREDICTED: ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	44 kDa	0.2577
452	40S ribosomal protein S18	18 kDa	0.257
453	40S ribosomal protein S5	25 kDa	0.2562
454	peptidyl-prolyl cis-trans isomerase FKBP8	44 kDa	0.256
455	eukaryotic translation elongation factor 1 alpha 1-like	50 kDa	0.2557
456	PREDICTED: epoxide hydrolase 1, partial	38 kDa	0.2554
457	PREDICTED: von Willebrand factor A domain-containing protein 1	25 kDa	0.2548
458	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex 1-like	19 kDa	0.2532
459	uncharacterized protein LOC723999	19 kDa	0.2532

460	PREDICTED: vesicle-associated membrane protein 2-like	12 kDa	0.2529
461	long-chain fatty acid transport protein 4	25 kDa	0.2519
462	dynamin-1-like protein	77 kDa	0.2503
463	PREDICTED: 60S ribosomal protein L36	12 kDa	0.2501
464	PREDICTED: 60 kDa heat shock protein, mitochondrial-like, partial	12 kDa	0.2501
465	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial precursor	38 kDa	0.2497
466	PREDICTED: lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial-like	45 kDa	0.2495
467	NADH dehydrogenase	19 kDa	0.2494
468	PRELI domain containing 1b	25 kDa	0.2491
469	green-sensitive opsin-4	39 kDa	0.2479
470	mimitin, mitochondrial	19 kDa	0.2476
471	solute carrier family 25 member 40	39 kDa	0.247
472	PREDICTED: glutaminase kidney isoform, mitochondrial isoform X3	26 kDa	0.245
473	PREDICTED: NADPH:adrenodoxin oxidoreductase, mitochondrial	12 kDa	0.2446
474	erlin-1 precursor	39 kDa	0.2434
475	bcl-2-like protein 13	52 kDa	0.2432
476	isovaleryl-CoA dehydrogenase, mitochondrial	46 kDa	0.2426
477	uncharacterized protein LOC100127834	33 kDa	0.2425
478	PREDICTED: NCK-interacting protein with SH3 domain-like	19 kDa	0.2423
479	PREDICTED: UPF0562 protein C7orf55 homolog	13 kDa	0.242
480	pancreatic progenitor cell differentiation and proliferation factor A	13 kDa	0.242
481	PREDICTED: OCIA domain-containing protein 1 isoform X1	26 kDa	0.2398
482	PREDICTED: dnaJ homolog subfamily C member 30-like isoform X1	26 kDa	0.2385
483	probable glutamate--tRNA ligase, mitochondrial precursor	40 kDa	0.2374
484	PREDICTED: apoptosis-inducing factor 1, mitochondrial isoform X1	13 kDa	0.2369
485	PREDICTED: red-sensitive opsin-1 isoform X1	41 kDa	0.2325
486	PREDICTED: NADH dehydrogenase	20 kDa	0.2306
487	PREDICTED: protein phosphatase 1K, mitochondrial isoform X1	41 kDa	0.2293
488	PREDICTED: 40S ribosomal protein S2	20 kDa	0.2291
489	PREDICTED: cytochrome c oxidase assembly factor 1 homolog isoform X3	20 kDa	0.2291
490	PREDICTED: transmembrane emp24 domain-containing protein 9 isoform X1	27 kDa	0.2288
491	NADH dehydrogenase	48 kDa	0.2278
492	PREDICTED: epoxide hydrolase 1-like, partial	20 kDa	0.2245
493	40S ribosomal protein S10	20 kDa	0.2245
494	carnitine O-acetyltransferase b	70 kDa	0.2237
495	acyl-CoA dehydrogenase-like	49 kDa	0.2232
496	PREDICTED: proteoglycan 4-like isoform X1	13 kDa	0.2228
497	PREDICTED: phosphatidylserine decarboxylase proenzyme-like isoform X2	42 kDa	0.2225
498	mitochondrial folate transporter/carrier	35 kDa	0.2205
499	ras-related protein Rap-1b precursor	21 kDa	0.22
500	probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial	107 kDa	0.2195
501	PREDICTED: T-cell activation inhibitor, mitochondrial	57 kDa	0.2183
502	ras-related protein Rap-1b-like	21 kDa	0.2172
503	60S ribosomal protein L7	29 kDa	0.2145
504	PREDICTED: coiled-coil domain containing 127a isoform X1	36 kDa	0.2138
505	uncharacterized protein LOC100302470 precursor	21 kDa	0.2131
506	NADH dehydrogenase	21 kDa	0.2131
507	60S ribosomal protein L30	14 kDa	0.2122
508	S-adenosylmethionine mitochondrial carrier protein	29 kDa	0.2095
509	protoporphyrinogen oxidase	52 kDa	0.2089
510	ADP-ribosylation factor-like 3, like 1	22 kDa	0.2078
511	PREDICTED: mitochondrial calcium uniporter regulator 1	22 kDa	0.2078
512	PREDICTED: choline dehydrogenase, mitochondrial	29 kDa	0.2066
513	recoverin-like	22 kDa	0.2065
514	28S ribosomal protein S23, mitochondrial	22 kDa	0.2065
515	28S ribosomal protein S5, mitochondrial precursor	45 kDa	0.2054
516	calcium-binding mitochondrial carrier protein SCaMC-2-A	52 kDa	0.2051
517	PREDICTED: uncharacterized aarF domain-containing protein kinase 2	14 kDa	0.2044
518	PREDICTED: cytochrome c oxidase subunit 5B, mitochondrial-like	14 kDa	0.2044

519	PREDICTED: transmembrane protein 70, mitochondrial	30 kDa	0.2028
520	PREDICTED: 60S ribosomal protein L6	30 kDa	0.2019
521	CAAX prenyl protease 1 homolog	53 kDa	0.2003
522	ras-related protein Rab-18	23 kDa	0.1979
523	synaptosomal-associated protein 25-B	23 kDa	0.1979
524	PREDICTED: transmembrane emp24 domain-containing protein 2	23 kDa	0.1968
525	uncharacterized protein LOC492355	23 kDa	0.1945
526	methyltransferase like 7A precursor	31 kDa	0.194
527	saccharopine dehydrogenase b	47 kDa	0.1935
528	opsin-1, short-wave-sensitive 2	39 kDa	0.1924
529	transcription factor A, mitochondrial	31 kDa	0.1907
530	dnaJ homolog subfamily C member 2	48 kDa	0.1902
531	78 kDa glucose-regulated protein precursor	72 kDa	0.1892
532	elongation factor 1-alpha	48 kDa	0.1891
533	rhodopsin	40 kDa	0.1891
534	HIG1 domain family member 2A, mitochondrial	15 kDa	0.1888
535	39S ribosomal protein L14, mitochondrial precursor	15 kDa	0.1888
536	guanine nucleotide-binding protein G(o) subunit alpha	40 kDa	0.1878
537	PREDICTED: required for meiotic nuclear division protein 1 homolog isoform X1	48 kDa	0.1875
538	60S ribosomal protein L31	16 kDa	0.1872
539	PREDICTED: multiple PDZ domain protein isoform X3	16 kDa	0.1872
540	ras-related protein Rab-14	24 kDa	0.1858
541	CDP-diacylglycerol--inositol 3-phosphatidyltransferase	24 kDa	0.1848
542	PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP8 isoform X1	57 kDa	0.1842
543	PREDICTED: ADP-ribosylation factor 2	16 kDa	0.1841
544	mitochondrial folate transporter/carrier	33 kDa	0.1828
545	transmembrane emp24 domain-containing protein 10 precursor	24 kDa	0.1818
546	60S ribosomal protein L10	25 kDa	0.1798
547	uncharacterized protein LOC560648	16 kDa	0.1797
548	PREDICTED: protein CCSMST1	16 kDa	0.1797
549	60S ribosomal protein L10a	25 kDa	0.1769
550	UMP-CMP kinase	25 kDa	0.1769
551	PREDICTED: probable palmitoyltransferase ZDHHC14 isoform X1	16 kDa	0.1754
552	PREDICTED: protein CCSMST1	16 kDa	0.1754
553	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	68 kDa	0.175
554	enoyl-CoA delta isomerase 2, mitochondrial	42 kDa	0.1748
555	PREDICTED: carnitine palmitoyltransferase 1A isoform X2	69 kDa	0.174
556	PREDICTED: AFG3-like protein 1	60 kDa	0.1739
557	succinyl-CoA ligase	34 kDa	0.1729
558	polymerase delta-interacting protein 2	43 kDa	0.1721
559	60S acidic ribosomal protein P0	34 kDa	0.1715
560	ATP synthase subunit delta, mitochondrial	17 kDa	0.1714
561	solute carrier family 25 member 33	34 kDa	0.1709
562	mitochondrial dynamics protein MID49	52 kDa	0.1703
563	PREDICTED: mitochondrial fission 1 protein	17 kDa	0.17
564	Probable saccharopine dehydrogenase	26 kDa	0.1689
565	probable D-lactate dehydrogenase, mitochondrial	53 kDa	0.1681
566	probable asparagine--tRNA ligase, mitochondrial	26 kDa	0.168
567	PREDICTED: 40S ribosomal protein S24	17 kDa	0.1638
568	28S ribosomal protein S14, mitochondrial	17 kDa	0.1638
569	flavin containing monooxygenase 5	27 kDa	0.1631
570	microsomal glutathione S-transferase 1.1	18 kDa	0.1626
571	mitochondrial peptide methionine sulfoxide reductase	27 kDa	0.1623
572	PREDICTED: l-isoaspartyl protein carboxyl methyltransferase, like isoform X2	27 kDa	0.1623
573	mitochondrial folate transporter/carrier	36 kDa	0.161
574	protein SCO2 homolog, mitochondrial	36 kDa	0.1604
575	DnaJ (Hsp40) homolog, subfamily A, member 3B	36 kDa	0.1604
576	28S ribosomal protein S9, mitochondrial	46 kDa	0.1602
577	dihydroorotate dehydrogenase (quinone), mitochondrial	46 kDa	0.1593

578	39S ribosomal protein L20, mitochondrial	18 kDa	0.1591
579	PREDICTED: biotin--protein ligase isoform X1	93 kDa	0.1587
580	cytosol aminopeptidase	37 kDa	0.1575
581	PREDICTED: 60S ribosomal protein L27-like	18 kDa	0.1557
582	succinate dehydrogenase	18 kDa	0.1557
583	PREDICTED: dnaJ homolog subfamily C member 30	47 kDa	0.1557
584	aminomethyltransferase, mitochondrial	38 kDa	0.1542
585	40S ribosomal protein S16	18 kDa	0.1536
586	solute carrier family 3 (amino acid transporter heavy chain), member 2b	57 kDa	0.1534
587	PREDICTED: uncharacterized protein At5g50100, mitochondrial-like isoform X1	19 kDa	0.1525
588	ras-related protein Rab-3A	28 kDa	0.1519
589	uncharacterized protein LOC794398	28 kDa	0.1519
590	phosphatidylinositide phosphatase SAC1-B	67 kDa	0.1512
591	PREDICTED: 40S ribosomal protein S3-like isoform X1	28 kDa	0.1512
592	PREDICTED: sphingomyelin phosphodiesterase 2 isoform X1	48 kDa	0.1506
593	PREDICTED: serine/threonine-protein kinase DCLK1 isoform X1	38 kDa	0.1501
594	erlin-1 precursor	39 kDa	0.1481
595	mitoferrin-1	19 kDa	0.1464
596	dehydrogenase/reductase SDR family member 4	29 kDa	0.1453
597	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 precursor	70 kDa	0.1445
598	ras-related protein Rab-8B	20 kDa	0.1427
599	ATPase family AAA domain-containing protein 1-B	20 kDa	0.1427
600	peripherin-2	20 kDa	0.1418
601	complement component 1 Q subcomponent-binding protein, mitochondrial	30 kDa	0.1415
602	mitochondrial ubiquitin ligase activator of NFKB 1	40 kDa	0.1414
603	PREDICTED: NADH dehydrogenase	20 kDa	0.14
604	signal peptidase complex subunit 3	20 kDa	0.1391
605	actin-like protein 6A	31 kDa	0.138
606	PREDICTED: 60S ribosomal protein L11 isoform X2	20 kDa	0.1373
607	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	52 kDa	0.1372
608	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	42 kDa	0.135
609	PREDICTED: protein TsetseEP-like	21 kDa	0.1348
610	ADP-ribosylation factor-like protein 2	21 kDa	0.134
611	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	21 kDa	0.1332
612	39S ribosomal protein L12, mitochondrial	21 kDa	0.1316
613	solute carrier family 25 member 35	32 kDa	0.1309
614	PREDICTED: bcl10-interacting CARD protein isoform X2	21 kDa	0.1308
615	guanine nucleotide-binding protein subunit beta-5	43 kDa	0.1302
616	uncharacterized protein LOC393228	21 kDa	0.1301
617	PREDICTED: ras-related C3 botulinum toxin substrate 1	22 kDa	0.1286
618	PREDICTED: oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) isoform X2	44 kDa	0.1279
619	dnaJ homolog subfamily A member 3, mitochondrial	44 kDa	0.1272
620	peroxiredoxin-2	22 kDa	0.1271
621	Bcl-2/adenovirus E1B 19kD interaction protein XR	22 kDa	0.1271
622	PREDICTED: uncharacterized aarF domain-containing protein kinase 1 isoform X1	22 kDa	0.1271
623	60S ribosomal protein L9	22 kDa	0.1264
624	abhydrolase domain-containing protein 4	22 kDa	0.1264
625	RPE-retinal G protein-coupled receptor	33 kDa	0.1259
626	trifunctional enzyme subunit alpha, mitochondrial	33 kDa	0.1255
627	elongation factor Ts, mitochondrial	34 kDa	0.125
628	transmembrane protein 14A	11 kDa	0.1247
629	PREDICTED: G-rich sequence factor 1 isoform X1	45 kDa	0.1247
630	ATP synthase mitochondrial F1 complex assembly factor 2	34 kDa	0.1245
631	PREDICTED: 2-oxoglutarate dehydrogenase-like, mitochondrial	115 kDa	0.1238
632	protein-S-isoprenylcysteine O-methyltransferase	34 kDa	0.1236
633	PREDICTED: aarF domain-containing protein kinase 4	11 kDa	0.1233
634	28S ribosomal protein S27, mitochondrial	46 kDa	0.1233
635	40S ribosomal protein SA	34 kDa	0.1231
636	succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	57 kDa	0.1231

637	PREDICTED: 2-oxoglutarate dehydrogenase, mitochondrial	93 kDa	0.1223
638	mitochondrial-processing peptidase subunit alpha	58 kDa	0.1223
639	PREDICTED: cytochrome b-c1 complex subunit 6, mitochondrial-like	23 kDa	0.1222
640	PREDICTED: potassium voltage-gated channel subfamily B member 2	93 kDa	0.1215
641	PREDICTED: glycerol-3-phosphate acyltransferase 1, mitochondrial	93 kDa	0.1215
642	electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	23 kDa	0.1202
643	PREDICTED: mitochondrial thiamine pyrophosphate carrier isoform X1	35 kDa	0.12
644	adipocyte plasma membrane-associated protein	47 kDa	0.1199
645	PREDICTED: glycerol kinase isoform X4	59 kDa	0.1196
646	flotillin 2	47 kDa	0.1193
647	ras-related protein Rab-18-B	23 kDa	0.1189
648	flotillin-2a	47 kDa	0.1183
649	surfeit gene 4, like	23 kDa	0.1176
650	long-chain fatty acid transport protein 1	72 kDa	0.1173
651	PREDICTED: heme oxygenase 2	36 kDa	0.1166
652	ras-related protein Rab-5B	24 kDa	0.1157
653	long-chain fatty acid transport protein 4	73 kDa	0.1157
654	lysine--tRNA ligase	60 kDa	0.1156
655	L-2-hydroxyglutarate dehydrogenase, mitochondrial	12 kDa	0.1144
656	coiled-coil domain containing 56-like	12 kDa	0.1144
657	PREDICTED: mitochondrial coenzyme A transporter SLC25A42 isoform X1	36 kDa	0.1138
658	PREDICTED: ER membrane protein complex subunit 1 isoform X1	111 kDa	0.1134
659	PREDICTED: 3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial-like isoform X2	12 kDa	0.1132
660	PREDICTED: regulator of G-protein signaling 9 isoform X2	62 kDa	0.113
661	PREDICTED: multiple PDZ domain protein isoform X1	37 kDa	0.1126
662	PREDICTED: sialic acid-binding Ig-like lectin 6	24 kDa	0.1122
663	protein FAM173A	24 kDa	0.1122
664	PREDICTED: patatin-like phospholipase domain-containing protein 4	12 kDa	0.112
665	adenylyl cyclase-associated protein 1	50 kDa	0.112
666	PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP8 isoform X1	37 kDa	0.1111
667	PREDICTED: ammonium transporter Rh type A isoform X1	12 kDa	0.1109
668	ubiquitin-60S ribosomal protein L40	12 kDa	0.1109
669	PREDICTED: SRA stem-loop-interacting RNA-binding protein, mitochondrial	12 kDa	0.1098
670	PREDICTED: uncharacterized protein NCBP2-AS2-like	12 kDa	0.1098
671	superoxide dismutase	25 kDa	0.1094
672	guanylate kinase 1b	25 kDa	0.1094
673	GTP:AMP phosphotransferase AK3, mitochondrial	25 kDa	0.1089
674	PREDICTED: ER membrane protein complex subunit 6	12 kDa	0.1087
675	PREDICTED: 39S ribosomal protein L53, mitochondrial-like	12 kDa	0.1087
676	PREDICTED: glutaminase kidney isoform, mitochondrial isoform X2	38 kDa	0.1086
677	serine/threonine-protein kinase DCLK2 isoform 1	90 kDa	0.1084
678	cytochrome c oxidase assembly factor 3 homolog, mitochondrial	12 kDa	0.1077
679	dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit precursor	51 kDa	0.1074
680	28S ribosomal protein S34, mitochondrial	25 kDa	0.1073
681	apolipoprotein O	25 kDa	0.1063
682	propionyl-CoA carboxylase alpha chain, mitochondrial	79 kDa	0.1058
683	PREDICTED: 40S ribosomal protein S2	12 kDa	0.1056
684	PREDICTED: cytochrome c oxidase subunit 7A-related protein, mitochondrial-like	12 kDa	0.1056
685	60S ribosomal protein L35a	13 kDa	0.1046
686	NADH dehydrogenase (ubiquinone) iron-sulfur protein 5	13 kDa	0.1046
687	28S ribosomal protein S33, mitochondrial	13 kDa	0.1046
688	solute carrier family 2, facilitated glucose transporter member 1	53 kDa	0.1043
689	PREDICTED: fatty aldehyde dehydrogenase isoform X2	40 kDa	0.1038
690	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	26 kDa	0.1038
691	PREDICTED: LOW QUALITY PROTEIN: lysosome membrane protein 2	26 kDa	0.1038
692	pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	13 kDa	0.1036
693	uncharacterized aarF domain-containing protein kinase 1	13 kDa	0.1036
694	PREDICTED: LOW QUALITY PROTEIN: lysosome membrane protein 2	53 kDa	0.1029

695	diablo, IAP-binding mitochondrial protein a	13 kDa	0.1026
696	bcl-2-like protein 1	26 kDa	0.1023
697	PREDICTED: oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) isoform X3	26 kDa	0.1023
698	peroxisomal biogenesis factor 3	26 kDa	0.1023
699	BRI3-binding protein precursor	26 kDa	0.1023
700	coenzyme Q-binding protein COQ10 homolog, mitochondrial	27 kDa	0.1014
701	39S ribosomal protein L17, mitochondrial	13 kDa	0.1008
702	flotillin-1	41 kDa	0.1006
703	PREDICTED: sodium/potassium/calcium exchanger 2-like isoform X2	68 kDa	0.1006
704	PREDICTED: ceroid-lipofuscinosis, neuronal 6a isoform X1	19 kDa	0.0999
705	PREDICTED: fatty aldehyde dehydrogenase-like	55 kDa	0.0998
706	PREDICTED: aarF domain-containing protein kinase 4	70 kDa	0.0986
707	band 3 anion transport protein	27 kDa	0.0982
708	PREDICTED: transmembrane emp24 domain-containing protein 7 isoform X2	27 kDa	0.0982
709	PREDICTED: 40S ribosomal protein S20	13 kDa	0.0981
710	PREDICTED: transmembrane protein 186 isoform X1	13 kDa	0.0981
711	FAM82B	13 kDa	0.0981
712	cone cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha'	98 kDa	0.098
713	phosphofructokinase, muscle b	70 kDa	0.0978
714	PREDICTED: prostate stem cell antigen-like	13 kDa	0.0972
715	PREDICTED: small integral membrane protein 8 isoform X2	13 kDa	0.0972
716	UPF0545 protein C22orf39 homolog	14 kDa	0.0964
717	PREDICTED: sideroflexin-2 isoform X3	14 kDa	0.0964
718	PREDICTED: renin receptor isoform X1	42 kDa	0.096
719	60S ribosomal protein L8	28 kDa	0.0956
720	PREDICTED: ubiquitin carboxyl-terminal hydrolase 30 isoform X1	57 kDa	0.0953
721	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	43 kDa	0.0951
722	PREDICTED: cytochrome c oxidase subunit 5B, mitochondrial-like	14 kDa	0.0947
723	transmembrane protein 33	29 kDa	0.094
724	heat shock cognate 71 kDa protein	29 kDa	0.094
725	PREDICTED: 60S ribosomal protein L36a-like	14 kDa	0.0939
726	probable carboxypeptidase PM20D1.2 precursor	58 kDa	0.0935
727	monoacylglycerol lipase ABHD12	44 kDa	0.0932
728	tyrosine--tRNA ligase, mitochondrial	14 kDa	0.0931
729	acyl-coenzyme A thioesterase THEM4	29 kDa	0.0928
730	ATPase family AAA domain-containing protein 1-A isoform 1	44 kDa	0.0922
731	ATP-dependent Clp protease proteolytic subunit, mitochondrial	29 kDa	0.092
732	peroxisomal biogenesis factor 3	14 kDa	0.0915
733	28S ribosomal protein S2, mitochondrial	29 kDa	0.0909
734	PREDICTED: anoctamin-8	14 kDa	0.0908
735	PREDICTED: 40S ribosomal protein S26-like	14 kDa	0.0908
736	protein kinase, cAMP-dependent, regulatory, type II, alpha A	45 kDa	0.0904
737	glutamate dehydrogenase 1b	60 kDa	0.0902
738	ER membrane protein complex subunit 3	30 kDa	0.0898
739	methylmalonic aciduria type A protein, mitochondrial	30 kDa	0.0898
740	1-acyl-sn-glycerol-3-phosphate acyltransferase gamma	45 kDa	0.0895
741	alpha-1,3/1,6-mannosyltransferase ALG2	46 kDa	0.0887
742	PREDICTED: ATP synthase-coupling factor 6, mitochondrial isoform X1	15 kDa	0.0886
743	uncharacterized protein C19orf52 homolog	30 kDa	0.0883
744	putative hexokinase HKDC1	61 kDa	0.0882
745	F-box/LRR-repeat protein 2	46 kDa	0.088
746	membrane magnesium transporter 1 precursor	15 kDa	0.0879
747	28S ribosomal protein S6, mitochondrial	15 kDa	0.0879
748	cytochrome P450, family 27, subfamily C, polypeptide 1	62 kDa	0.0877
749	40S ribosomal protein S6	31 kDa	0.0866
750	39S ribosomal protein L51, mitochondrial precursor	15 kDa	0.0858
751	PREDICTED: neuronal migration protein doublecortin isoform X2	31 kDa	0.0849
752	holocytochrome c synthetase a	32 kDa	0.084
753	iron-sulfur cluster assembly 1 homolog, mitochondrial precursor	15 kDa	0.0839

754	uncharacterized protein LOC541327	15 kDa	0.0839
755	PREDICTED: histidine triad nucleotide-binding protein 2, mitochondrial-like isoform X1	15 kDa	0.0839
756	PREDICTED: serine/threonine-protein phosphatase PGAM5, mitochondrial isoform X1	32 kDa	0.0833
757	PREDICTED: carnitine O-palmitoyltransferase 1, liver isoform isoform X2	48 kDa	0.0827
758	protein phosphatase PTC7 homolog	32 kDa	0.0821
759	3-hydroxyisobutyrate dehydrogenase, mitochondrial	33 kDa	0.0815
760	60S ribosomal protein L28	16 kDa	0.0814
761	40S ribosomal protein S3a	33 kDa	0.0812
762	c3orf33 homolog	16 kDa	0.0808
763	PREDICTED: aspartate beta-hydroxylase isoform X2	33 kDa	0.0806
764	citrate lyase subunit beta-like protein, mitochondrial	33 kDa	0.0803
765	PREDICTED: mitofusin-1-like	84 kDa	0.08
766	PREDICTED: uncharacterized protein LOC323326 isoform X1	33 kDa	0.0797
767	transmembrane protein 177	34 kDa	0.0786
768	ubiquitin-conjugating enzyme E2Nb	16 kDa	0.0785
769	glutathione peroxidase 1	16 kDa	0.0785
770	PREDICTED: kynurenine--oxoglutarate transaminase 1 isoform X1	51 kDa	0.078
771	exonuclease 3'-5' domain-containing protein 2	69 kDa	0.0775
772	cytochrome P450, family 20, subfamily A, polypeptide 1	52 kDa	0.0773
773	PREDICTED: phosphatidate cytidylyltransferase 1	52 kDa	0.0768
774	evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	52 kDa	0.0768
775	band 3 anion transport protein	35 kDa	0.0761
776	PREDICTED: metal transporter CNNM4	35 kDa	0.0751
777	uncharacterized protein C15orf61 homolog	17 kDa	0.0747
778	2,4-dienoyl-CoA reductase, mitochondrial	35 kDa	0.0746
779	transitional endoplasmic reticulum ATPase	89 kDa	0.0745
780	PREDICTED: 40S ribosomal protein S23-like	17 kDa	0.0742
781	dnaJ homolog subfamily C member 15	17 kDa	0.0742
782	PREDICTED: 60S ribosomal protein L23	17 kDa	0.0737
783	microsomal glutathione S-transferase 1.2	17 kDa	0.0737
784	PREDICTED: creatine kinase S-type, mitochondrial isoform X2	17 kDa	0.0737
785	glutaredoxin-related protein 5, mitochondrial	17 kDa	0.0737
786	PREDICTED: syntaxin-18 isoform X1	36 kDa	0.0736
787	3-hydroxyisobutyrate dehydrogenase a	36 kDa	0.0733
788	hexaprenyldihydroxybenzoate methyltransferase, mitochondrial	36 kDa	0.0733
789	putative Ras-related protein Rab-42	18 kDa	0.0732
790	ragulator complex protein LAMTOR1	18 kDa	0.0732
791	PREDICTED: 60S ribosomal protein L12	18 kDa	0.0728
792	PREDICTED: tubulin beta-1 chain	18 kDa	0.0728
793	glycerophosphodiester phosphodiesterase 1	36 kDa	0.0726
794	PREDICTED: acyl carrier protein, mitochondrial	18 kDa	0.0723
795	mitoferrin-1	18 kDa	0.0723
796	fumarate hydratase, mitochondrial precursor	55 kDa	0.0721
797	mitochondria-eating protein	55 kDa	0.0719
798	uncharacterized protein LOC768289	37 kDa	0.0709
799	PREDICTED: calcium-binding mitochondrial carrier protein SCaMC-1 isoform X1	37 kDa	0.0707
800	protein SERAC1	18 kDa	0.0704
801	PREDICTED: protein SERAC1 isoform X2	18 kDa	0.0704
802	PREDICTED: histidine triad nucleotide-binding protein 3 isoform X1	18 kDa	0.07
803	PREDICTED: ATP-binding cassette sub-family B member 10, mitochondrial	18 kDa	0.07
804	arginase-2, mitochondrial	38 kDa	0.0694
805	PREDICTED: sodium/potassium-transporting ATPase subunit beta-2-like	19 kDa	0.0691
806	PREDICTED: 60S ribosomal protein L21	19 kDa	0.0691
807	complexin 4b	19 kDa	0.0682
808	eukaryotic translation initiation factor 4A, isoform 1A	39 kDa	0.0668
809	PREDICTED: DNA polymerase subunit gamma-2, mitochondrial	39 kDa	0.0668
810	fatty-acid amide hydrolase 2-A	59 kDa	0.0664
811	polyribonucleotide nucleotidyltransferase 1, mitochondrial	60 kDa	0.0653
812	28S ribosomal protein S22, mitochondrial	40 kDa	0.0652

813	keratin, type II cytoskeletal 8	61 kDa	0.0651
814	PREDICTED: armadillo repeat-containing protein 10	20 kDa	0.0646
815	cAMP-dependent protein kinase catalytic subunit beta	41 kDa	0.0643
816	abhydrolase domain-containing protein 16A	20 kDa	0.0642
817	methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	62 kDa	0.0638
818	PREDICTED: clathrin coat assembly protein AP180 isoform X5	41 kDa	0.0637
819	reticulon-1 isoform 1	83 kDa	0.0633
820	synembryn-A	62 kDa	0.0632
821	PREDICTED: coenzyme Q-binding protein COQ10 homolog A, mitochondrial	20 kDa	0.0631
822	minor histocompatibility antigen H13	20 kDa	0.0631
823	ADP-ribosylation factor-like protein 1	20 kDa	0.0628
824	PREDICTED: synembryn-A isoform X1	63 kDa	0.0625
825	L-threonine 3-dehydrogenase, mitochondrial	42 kDa	0.0625
826	PREDICTED: signal peptidase complex catalytic subunit SEC11A-like	21 kDa	0.0621
827	leucine-rich repeat, immunoglobulin-like and transmembrane domains 1 precursor	64 kDa	0.0613
828	brain creatine kinase b	43 kDa	0.0606
829	PREDICTED: translocon-associated protein subunit gamma	21 kDa	0.0603
830	valacyclovir hydrolase	21 kDa	0.0597
831	reticulon-1 isoform 1	88 kDa	0.0596
832	PREDICTED: neuroplastin-like	44 kDa	0.0596
833	PREDICTED: transmembrane and coiled-coil domains protein 1-like	21 kDa	0.0594
834	phosphatidylserine synthase 1	21 kDa	0.0594
835	isochorismatase domain-containing protein 2, mitochondrial	21 kDa	0.0594
836	heat shock protein HSP 90-beta	89 kDa	0.0591
837	ADP-ribosylation-like factor 6 interacting protein 5	22 kDa	0.059
838	ADP-ribosylation factor-like 7	22 kDa	0.059
839	PREDICTED: BCL2/adenovirus E1B 19 kDa protein-interacting protein 3 isoform X1	22 kDa	0.0587
840	lactation elevated protein 1 homolog B	22 kDa	0.0581
841	immunoglobulin superfamily member 8 precursor	68 kDa	0.0578
842	tyrosine-protein phosphatase non-receptor type 1	22 kDa	0.0572
843	PREDICTED: branched-chain-amino-acid aminotransferase, mitochondrial isoform X2	45 kDa	0.0569
844	PREDICTED: probable arginine--tRNA ligase, mitochondrial isoform X1	22 kDa	0.0569
845	PREDICTED: GTP-binding protein SAR1b	22 kDa	0.0569
846	28S ribosomal protein S29, mitochondrial	46 kDa	0.0567
847	PREDICTED: peptide chain release factor 1, mitochondrial-like	46 kDa	0.0565
848	PREDICTED: 60S ribosomal protein L18a-like	23 kDa	0.0563
849	solute carrier family 7, member 3	70 kDa	0.056
850	bcl2-associated X protein, b	23 kDa	0.0557
851	transmembrane protein 160	23 kDa	0.0557
852	synaptotagmin II	47 kDa	0.0555
853	ras-related protein Rab-24	23 kDa	0.0555
854	PREDICTED: short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	47 kDa	0.0552
855	lamin-B2	23 kDa	0.0549
856	PREDICTED: carbonyl reductase family member 4 isoform X1	23 kDa	0.0544
857	PREDICTED: acyl-CoA thioesterase 9, tandem duplicate 1 isoform X1	23 kDa	0.0541
858	60S ribosomal protein L3	48 kDa	0.054
859	methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	72 kDa	0.0538
860	PREDICTED: NADPH--cytochrome P450 reductase isoform X1	48 kDa	0.0536
861	uncharacterized protein LOC100005854	24 kDa	0.0536
862	acylpyruvase FAHD1, mitochondrial	24 kDa	0.0536
863	keratin, type I cytoskeletal 18	49 kDa	0.0528
864	PREDICTED: neural cell adhesion molecule 1 isoform X1	74 kDa	0.0527
865	PREDICTED: protein TBRG4	74 kDa	0.0526
866	28S ribosomal protein S18a, mitochondrial	24 kDa	0.0525
867	PREDICTED: probable protein-cysteine N-palmitoyltransferase porcupine isoform X1	25 kDa	0.0513
868	PREDICTED: 60S ribosomal protein L13a, partial	25 kDa	0.0506
869	PREDICTED: phosphofructokinase, muscle b isoform X1	25 kDa	0.0506
870	oxidase (cytochrome c) assembly 1-like	51 kDa	0.0503
871	PREDICTED: V-type proton ATPase subunit S1	52 kDa	0.0497

872	60S ribosomal protein L17	25 kDa	0.0497
873	adenylate kinase 4, mitochondrial	25 kDa	0.0497
874	PREDICTED: mitochondrial antiviral-signaling protein isoform X1	52 kDa	0.0496
875	epoxide hydrolase 1	52 kDa	0.0493
876	PREDICTED: protein transport protein Sec61 subunit alpha-like 1	52 kDa	0.0491
877	cardiolipin synthase	26 kDa	0.049
878	squalene synthase	53 kDa	0.0486
879	glutathione S-transferase kappa 1	26 kDa	0.0486
880	bifunctional coenzyme A synthase precursor	53 kDa	0.0484
881	putative hexokinase HKDC1	26 kDa	0.0484
882	PREDICTED: phospholipid scramblase 2	26 kDa	0.0477
883	BRI3-binding protein precursor	26 kDa	0.0477
884	PREDICTED: ATP synthase subunit s-like protein isoform X1	27 kDa	0.0473
885	PREDICTED: translation initiation factor IF-3, mitochondrial	27 kDa	0.0473
886	phosducin	27 kDa	0.0467
887	PREDICTED: succinate-semialdehyde dehydrogenase, mitochondrial isoform X1	55 kDa	0.0464
888	von Willebrand factor A domain-containing protein 8	27 kDa	0.0463
889	PREDICTED: tudor and KH domain-containing protein isoform X1	56 kDa	0.046
890	diablo homolog, mitochondrial	27 kDa	0.0459
891	4-aminobutyrate aminotransferase, mitochondrial	56 kDa	0.0457
892	PREDICTED: reticulon-1 isoform X1	85 kDa	0.0455
893	HCLS1-associated protein X-1	28 kDa	0.0454
894	dol-P-Man:Man(7)GlcNAc(2)-PP-Dol alpha-1,6-mannosyltransferase precursor	56 kDa	0.0453
895	syntaxin binding protein 1b	57 kDa	0.045
896	dolichol-phosphate mannosyltransferase subunit 1	28 kDa	0.045
897	apoptogenic protein 1, mitochondrial	28 kDa	0.045
898	melanoregulin	28 kDa	0.045
899	PREDICTED: vesicle-fusing ATPase isoform X1	86 kDa	0.0447
900	acyl-CoA thioesterase 9, tandem duplicate 1	28 kDa	0.0446
901	PREDICTED: Golgi SNAP receptor complex member 1 isoform X1	28 kDa	0.0444
902	39S ribosomal protein L9, mitochondrial	28 kDa	0.0443
903	phosducin 2	29 kDa	0.0441
904	PREDICTED: alpha-aminoadipic semialdehyde dehydrogenase	59 kDa	0.0432
905	internexin neuronal intermediate filament protein, alpha	59 kDa	0.0432
906	glutamyl-tRNA(Gln) amidotransferase subunit A, mitochondrial	59 kDa	0.0432
907	PREDICTED: ATP-binding cassette sub-family B member 10, mitochondrial	29 kDa	0.043
908	probable tRNA N6-adenosine threonylcarbamoyltransferase, mitochondrial	29 kDa	0.043
909	39S ribosomal protein L10, mitochondrial precursor	29 kDa	0.043
910	ES1 protein homolog, mitochondrial	29 kDa	0.0429
911	PREDICTED: E3 ubiquitin-protein ligase RNF170-like	29 kDa	0.0427
912	PREDICTED: mitochondrial 10-formyltetrahydrofolate dehydrogenase	90 kDa	0.0426
913	uncharacterized protein LOC619266 precursor	60 kDa	0.0426
914	catechol O-methyltransferase	30 kDa	0.0424
915	PREDICTED: calcium signal-modulating cyclophilin ligand isoform X1	30 kDa	0.0419
916	uncharacterized protein LOC447917 precursor	30 kDa	0.0416
917	28S ribosomal protein S15, mitochondrial	30 kDa	0.0414
918	PREDICTED: outer dense fiber protein 2	96 kDa	0.04
919	phosphatidylinositol transfer protein beta isoform	32 kDa	0.0396
920	thioredoxin-related transmembrane protein 1 precursor	32 kDa	0.0392
921	PREDICTED: ethylmalonyl-CoA decarboxylase isoform X1	32 kDa	0.0392
922	PREDICTED: enoyl-CoA hydratase domain-containing protein 3, mitochondrial-like	32 kDa	0.0392
923	PREDICTED: trimethyllysine dioxygenase, mitochondrial	32 kDa	0.0392
924	PREDICTED: proline-rich protein 18-like	32 kDa	0.0388
925	PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform X1	65 kDa	0.0387
926	PREDICTED: ATP-dependent (S)-NAD(P)H-hydrate dehydratase isoform X10	32 kDa	0.0386
927	PREDICTED: pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial-like	99 kDa	0.0385
928	PREDICTED: translocon-associated protein subunit alpha-like isoform X3	32 kDa	0.0385
929	synaptophysin b isoform 1	33 kDa	0.0384

930	PREDICTED: ATP-binding cassette sub-family B member 10, mitochondrial	33 kDa	0.0382
931	PREDICTED: LOW QUALITY PROTEIN: metalloendopeptidase OMA1, mitochondrial	33 kDa	0.038
932	3-mercaptopyruvate sulfurtransferase	33 kDa	0.0378
933	PREDICTED: translation factor GUF1, mitochondrial	33 kDa	0.0378
934	PREDICTED: protein FAM134C	33 kDa	0.0377
935	carnitine O-acetyltransferase	68 kDa	0.0375
936	PREDICTED: protein CLN8 isoform X1	34 kDa	0.0372
937	NAD-dependent protein deacylase sirtuin-5, mitochondrial	34 kDa	0.0372
938	acyl-CoA synthetase long-chain family member 1	68 kDa	0.037
939	malonyl-CoA decarboxylase, mitochondrial	34 kDa	0.0368
940	uncharacterized protein LOC100001340	34 kDa	0.0366
941	enoyl-CoA hydratase domain-containing protein 2, mitochondrial	35 kDa	0.0361
942	heme oxygenase 2	35 kDa	0.036
943	PREDICTED: CAAX prenyl protease 2	35 kDa	0.0354
944	PREDICTED: stromal interaction molecule 1 isoform X3	72 kDa	0.0352
945	PREDICTED: lon protease homolog, mitochondrial	108 kDa	0.0352
946	iron-sulfur protein NUBPL	36 kDa	0.0351
947	thioredoxin-related transmembrane protein 2-B precursor	36 kDa	0.0349
948	isoleucine--tRNA ligase, mitochondrial	110 kDa	0.0345
949	PREDICTED: transmembrane protein 43-like	37 kDa	0.0341
950	glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial	37 kDa	0.0339
951	PREDICTED: protein angel homolog 1	37 kDa	0.0337
952	UDP-xylose and UDP-N-acetylglucosamine transporter	37 kDa	0.0335
953	uncharacterized protein LOC559844	37 kDa	0.0334
954	casein kinase 1, alpha 1	38 kDa	0.0332
955	39S ribosomal protein L39, mitochondrial	38 kDa	0.0332
956	neurotrimin isoform 1 precursor	38 kDa	0.0328
957	PREDICTED: monoacylglycerol lipase abhd6-A	38 kDa	0.0327
958	ATPase asna1	38 kDa	0.0326
959	threonine aldolase 1	38 kDa	0.0325
960	protein phosphatase methylesterase 1	39 kDa	0.0324
961	PREDICTED: tectonic-2	39 kDa	0.0322
962	peripherin 2b (retinal degeneration, slow)	39 kDa	0.0321
963	heterogeneous nuclear ribonucleoprotein K	39 kDa	0.0321
964	PREDICTED: nucleolin isoform X5	79 kDa	0.032
965	PREDICTED: striatin-3 isoform X1	79 kDa	0.032
966	PREDICTED: ATP-dependent RNA helicase DDX3X isoform X6	79 kDa	0.0319
967	opsin-1, short-wave-sensitive 1	39 kDa	0.0318
968	protein phosphatase 1 regulatory subunit 7 isoform 1	40 kDa	0.0315
969	lectin, mannose-binding 2-like b precursor	40 kDa	0.0314
970	PREDICTED: ATP-dependent zinc metalloprotease YME1L1-like isoform X1	81 kDa	0.0312
971	PREDICTED: KH domain containing, RNA binding, signal transduction associated 1a isoform X2	41 kDa	0.0307
972	UPF0554 protein C2orf43 homolog	41 kDa	0.0303
973	elongation factor G, mitochondrial	83 kDa	0.0302
974	major histocompatibility complex class I UEA precursor	41 kDa	0.0301
975	PREDICTED: 11-cis retinol dehydrogenase isoform X1	41 kDa	0.0301
976	cytosolic 5'-nucleotidase 1A	41 kDa	0.0301
977	methylmalonyl-CoA mutase, mitochondrial	84 kDa	0.03
978	eukaryotic translation initiation factor 3 subunit H-A	42 kDa	0.0298
979	immunity-related GTPase family, q2	42 kDa	0.0297
980	LETM1 domain-containing protein 1	42 kDa	0.0296
981	PREDICTED: protein XRP2 isoform X1	42 kDa	0.0296
982	NAD-dependent protein deacetylase sirtuin-2	42 kDa	0.0296
983	ATP-dependent RNA helicase SUPV3L1, mitochondrial precursor	86 kDa	0.0293
984	nucleoside diphosphate-linked moiety X motif 8, mitochondrial	43 kDa	0.0292
985	4-hydroxybenzoate polyprenyltransferase, mitochondrial	43 kDa	0.029
986	solute carrier family 43 member 3	43 kDa	0.0287
987	acyl-CoA:lysophosphatidylglycerol acyltransferase 1	43 kDa	0.0287
988	mitoferrin-2	44 kDa	0.0283

989	abhydrolase domain-containing protein 4	44 kDa	0.0283
990	basigin precursor	45 kDa	0.0278
991	isobutyryl-CoA dehydrogenase, mitochondrial	45 kDa	0.0274
992	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2b isoform X1	92 kDa	0.0274
993	endoplasmin precursor	92 kDa	0.0274
994	striatin	92 kDa	0.0273
995	casein kinase 2, alpha 1 polypeptide	46 kDa	0.0272
996	PREDICTED: vacuole membrane protein 1 isoform X1	46 kDa	0.0271
997	glycosaminoglycan xylosylkinase	46 kDa	0.0271
998	PREDICTED: protein NDRG3 isoform X1	46 kDa	0.0269
999	prominin-1 precursor	94 kDa	0.0268
1000	cytochrome P450 2U1	46 kDa	0.0268
1001	PREDICTED: heterogeneous nuclear ribonucleoprotein Q isoform X2	47 kDa	0.0265
1002	PREDICTED: serine protease HTRA2, mitochondrial	47 kDa	0.0263
1003	tapasin-like	48 kDa	0.0261
1004	PREDICTED: ubiquitin associated protein 2b isoform X1	48 kDa	0.0261
1005	26S proteasome non-ATPase regulatory subunit 3	48 kDa	0.026
1006	PREDICTED: poly(A) RNA polymerase, mitochondrial	48 kDa	0.026
1007	uncharacterized protein C6orf136 homolog	48 kDa	0.0258
1008	sarcolemma associated protein b	48 kDa	0.0257
1009	uncharacterized protein LOC405817	49 kDa	0.0254
1010	PREDICTED: uncharacterized protein LOC557028 isoform X2	49 kDa	0.0253
1011	PREDICTED: ATP-binding cassette sub-family B member 6, mitochondrial isoform X1	99 kDa	0.0253
1012	PREDICTED: mannosyl-oligosaccharide glucosidase isoform X1	49 kDa	0.0253
1013	39S ribosomal protein L37, mitochondrial	49 kDa	0.0252
1014	TLD domain-containing protein 1	50 kDa	0.025
1015	PREDICTED: uncharacterized aarF domain-containing protein kinase 2	50 kDa	0.0248
1016	PREDICTED: drebrin isoform X2	50 kDa	0.0248
1017	PREDICTED: uncharacterized protein si:ch211-11k18.4	51 kDa	0.0245
1018	elongation factor 1-gamma	51 kDa	0.0244
1019	UBX domain-containing protein 4	52 kDa	0.024
1020	protein disulfide-isomerase TMX3 precursor	52 kDa	0.0238
1021	N-acylneuraminate cytidylyltransferase	53 kDa	0.0236
1022	F-box/LRR-repeat protein 4	53 kDa	0.0232
1023	PREDICTED: protein LYRIC isoform X1	53 kDa	0.0231
1024	protein crumbs homolog 2	54 kDa	0.0229
1025	phosphatidate cytidylyltransferase 2	54 kDa	0.0227
1026	coiled-coil domain-containing protein 47 precursor	56 kDa	0.0221
1027	aldehyde dehydrogenase 2 family (mitochondrial), tandem duplicate 2	57 kDa	0.0218
1028	pyruvate dehyrogenase phosphatase catalytic subunit 1	57 kDa	0.0218
1029	PREDICTED: lysophosphatidylcholine acyltransferase 1-like	59 kDa	0.021
1030	amine oxidase	59 kDa	0.021
1031	prenylcysteine oxidase 1 precursor	59 kDa	0.0208
1032	PREDICTED: pyruvate kinase PKM isoform X1	60 kDa	0.0206
1033	retinoid isomerohydrolase	61 kDa	0.0203
1034	PREDICTED: GPI transamidase component PIG-S isoform X2	63 kDa	0.0197
1035	T-complex protein 1 subunit gamma	63 kDa	0.0196
1036	PREDICTED: serine beta-lactamase-like protein LACTB, mitochondrial isoform X1	64 kDa	0.0192
1037	transmembrane anterior posterior transformation protein 1 homolog	66 kDa	0.0188
1038	protein FAM73B	66 kDa	0.0188
1039	PREDICTED: long-chain fatty acid transport protein 6-like isoform X1	69 kDa	0.0179
1040	PREDICTED: proline dehydrogenase 1, mitochondrial-like	69 kDa	0.0178
1041	polyadenylate-binding protein 1	71 kDa	0.0174
1042	membrane protein, palmitoylated 5b (MAGUK p55 subfamily member 5)	71 kDa	0.0174
1043	PREDICTED: gamma-glutamyltransferase 7 isoform X1	72 kDa	0.0171
1044	PREDICTED: TBC1 domain family member 17 isoform X1	73 kDa	0.0168
1045	PREDICTED: caseinolytic peptidase B protein homolog	74 kDa	0.0166
1046	lipase maturation factor 2	76 kDa	0.0161
1047	transferrin receptor protein 1	77 kDa	0.0161

1048	PREDICTED: probable threonine--tRNA ligase 2, cytoplasmic-like	78 kDa	0.0158
1049	PREDICTED: reticulon-4 isoform X1	80 kDa	0.0153
1050	protein crumbs homolog 2	162 kDa	0.0153
1051	PREDICTED: cyclic nucleotide-gated channel rod photoreceptor subunit alpha-like	82 kDa	0.0151
1052	PREDICTED: amyloid beta A4 protein-like isoform X2	84 kDa	0.0146
1053	PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	91 kDa	0.0135
1054	importin subunit beta-1	97 kDa	0.0126
1055	PREDICTED: dynamin 1a isoform X5	99 kDa	0.0124
1056	PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1	102 kDa	0.0121
1057	alpha-aminoadipic semialdehyde synthase, mitochondrial	105 kDa	0.0117
1058	PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2	116 kDa	0.0106
1059	von Willebrand factor A domain-containing protein 8	126 kDa	0.0097
1060	PREDICTED: pyruvate carboxylase, mitochondrial-like	130 kDa	0.0094
1061	insulin-like growth factor 1b receptor precursor	158 kDa	0.0078
1062	PREDICTED: crumbs family member 2b isoform X1	160 kDa	0.0076
1063	PREDICTED: rootletin isoform X1	226 kDa	0.0054
1064	PREDICTED: midasin	512 kDa	0.0024

Achievements

<投稿論文>
"Purification of cone outer segment for proteomic analysis on its membrane proteins in carp retina"
Takashi Fukagawa, Kazuaki Takafuji, Shuji Tachibanaki and Satoru Kawamura
PLoS One 2017; 12(3):e0173908

"Substrate Specificity and Subcellular Localization of Aldehyde-Alcohol Redox (AL-OL)-Coupling Reaction in Carp Cones"
Shinya Sato, Takashi Fukagawa, Shuji Tachibanaki, Yumiko Yamano, Akimori Wada and Satoru Kawamura
The Journal of Biological Chemistry 2013; 288(51):36589-97.

＜学会発表＞
ポスター発表
「Substrate Specificity and Localization of　AL-OL Coupling Reaction in Carp Cones」
Satoru Kawamura, Shinya Sato, Shuji Tachibanaki and Takashi Fukagawa
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「桿体・錐体視細胞の外節膜に発現している蛋白質の比較」
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