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Proteomic Analysis of Pancreatic Zymogen Granules: Identification of New Granule Proteins

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Abstract

The composition of zymogen granules from rat pancreas was determined by LC-MS/MS. Enriched intragranular content, peripheral membrane and integral membrane protein fractions were analyzed after one-dimensional SDS/PAGE and tryptic digestion of gel slices. A total of 371 proteins were identified with high confidence, including 84 previously identified granule proteins. The 287 remaining proteins included 37 GTP-binding proteins and effectors, 8 tetraspan membrane proteins, and 22 channels and transporters. Seven proteins – pantophysin, cyclic nucleotide phosphodiesterase, carboxypeptidase D, ecto-nucleotide phosphodiesterase 3, aminopeptidase N, ral, and the potassium channel TWIK-2 – were confirmed by immunofluorescence microscopy or by immunoblotting to be new zymogen granule membrane proteins.

Keywords

proteomics; mass spectrometry; LC-MS/MS; pancreas; zymogen granules; acinar cells

Introduction

Pancreatic acinar cells are the sites of synthesis and storage of digestive enzymes released into the pancreatic duct for transport to the duodenum. 1 The enzymes reside in a storage organelle in the cell cytoplasm, the zymogen granule (ZG), and are released by exocytosis into the acinar lumen. The exocytosis process involves the fusion of the ZG membranes with the apical plasma membrane and occurs after acinar cells are stimulated by hormones such as cholecystokinin and acetylcholine. Despite the relevance of the ZG as a mediator of digestive function, its exocytosis is only beginning to be understood at the molecular level.

Exocytosis of zymogen granules at the acinar lumen is dependent in part upon granule membrane proteins such as the SNARE (N-ethylmaleimide-sensitive factor attachment protein receptor) components syntaxin 3 and vamp 8.^{2,3} Recently, other proteins playing a role in exocytosis have been documented in pancreas yet were never identified as being present in ZG membranes. One such protein is Noc2, a rab-interacting protein strictly required for ZG exocytosis⁴ and known to be present in endocrine and salivary gland granules.⁵ As a post-Golgi transport intermediate that can be purified in large quantities, the ZG membrane should be an abundant source of proteins involved in exocytosis and granule biogenesis in exocrine

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pancreas. Many of these proteins are likely to be involved in similar processes in other cell types as well.

Zymogen granule membranes also contain digestive enzymes such as GP-3/pancreatic lipase-related protein 2.^{6,7} Some of the membrane proteins are released into the acinar lumen and appear in the pancreatic juice. GP2, the major granule membrane protein, is anchored via a glycosylphosphatidyl inositol linkage and has both membrane and soluble forms⁸ as does ITMAP, a granule transmembrane protein.⁹ Membranes contain proteins that are thought to aid in granule formation. These include muclin, a sulfated glycoprotein in mouse pancreas; ¹⁰ ZG16, a lectin thought to help form a protein scaffold for attachment of granule content proteins to the membrane; ¹¹ and syncollin, which regulates granule size and release. ^{12,13} ZG membranes also have ion channels and transporters important for maintaining low pH and the ionic milieu in the granule lumen. ¹⁴

The major zymogen granule content proteins have been identified previously by purification of the proteins, conventional N-terminal peptide sequencing techniques and specific immunolocalization of granule components. The granules contain hydrolytic enzymes such as amylase, the most abundant protein, trypsinogens, elastases and chymotrypsinogen. ¹⁵ The importance of the granule content proteins for disease processes has been highlighted by the demonstration that individuals with mutations in trypsinogen are predisposed to pancreatitis because of the premature activation of the zymogen trypsinogen to trypsin. ¹⁶

Because of the importance of knowing the composition of the intragranular content as well as granule membrane proteins, we undertook a comprehensive identification of these proteins by LC-MS/MS. Methods for obtaining highly purified secretory granules and their membranes have been reported (summarized in ¹⁷). We prepared highly enriched content and membrane fractions and analyzed their protein composition. More than 500 proteins were identified in the preparation, including 371 with high confidence, of which 84 are known granule proteins. A number of these proteins potentially are important regulators of granule exocytosis. We confirmed seven of the newly identified proteins to be granule membrane proteins.

Materials and Methods

Isolation of Zymogen Granules. The purification of zymogen granules was performed as described previously in detail. ¹⁷ In brief, pancreas was removed from male and female Sprague Dawley or Brown Norway rats (for preparation of content fractions only) fed ad libitum, then anesthetized using CO2 narcosis in compliance with NIH animal care and use guidelines and decapitated. The pancreas was washed three times in homogenization buffer (HB: 0.27 M sucrose, 2 mM MOPS, 0.5 mM MgSO₄, pH 6.5–6.7). All solutions contained a protease inhibitor cocktail of 1 µg/ml each of leupeptin and pepstatin (Roche Applied Science, Indianapolis, IN), 10 U/ml aprotinin (Sigma-Aldrich, St. Louis, MO), and either 0.5 mM phenylmethanesulfonyl fluoride (PMSF) or benzamidine (Sigma-Aldrich). The mesentery was trimmed from the pancreas and the tissue minced with scalpels and fine scissors. After homogenization with three strokes of a Teflon-glass homogenizer (Wheaton, Milville, NJ), a post-nuclear supernatant was prepared after centrifugation at 600 g for 10 min. The pellet was rehomogenized and centrifuged again. The supernatants were combined and filtered through nylon mesh. An aliquot from the post-nuclear supernatant was saved. The granules were recovered either by centrifugation at 1750 g for 20 min. (content protein preparation 1 = C1) or by centrifugation at 3000 g for 30 min. through 5 ml cushions of 30% and 60% Percoll (GE Healthcare, Piscataway, NJ) in gradient buffer (GB: 0.26 M sucrose 20 mM MOPS, 1 mM EDTA pH 6.7) (all other preparations). Granule pellets were either washed twice in HB with 1 mM EDTA (HBE) added to remove mitochondria and gently resuspended in HB with 1 mM EDTA (C1) or the loose granule pellets in 60% Percoll were directed resuspended in HBE.

After homogenization (5 strokes in a Dounce homogenizer) the crude granule preparation was loaded onto 60% Percoll in GB and spun for 35 min. at 12,000 g. The white granules at the bottom of the gradient were gently resuspended in HBE, homogenized in a Dounce homogenizer and loaded onto 0.6-2 M sucrose gradients (10 mM MOPS, 5% Ficoll (Sigma-Aldrich), 1 mM EDTA pH 6.7). After centrifugation for 4 h at 100,000 g using an SW41 rotor and an Optima L-90K ultracentrifuge (Beckman Coulter, Fullerton, CA), the granule band near the bottom of the tube was collected and diluted with HBE. Granules were pelleted by centrifugation at 3000 g for 20 min.

After resuspension of the granule pellets in HBE, 5–6 volumes of 0.1 M NaHCO₃, pH 8.1 were added to lyse the granules. After 45 min. of incubation, the lysed granules were loaded onto 0.5-1.1 M sucrose gradients in gradient buffer (GB = 10 mM HEPES. 1 mM EDTA pH 7.0) and the gradients were centrifuged for 13 h at 80,000 g. The granule content was collected from the top of the gradient and concentrated by precipitation with trichloroacetic acid (TCA). The granule membrane band was collected and diluted with GB and recovered by centrifugation at 200,000 g for 20 min. using a TL100.3 rotor in a TI-100 ultracentrifuge (Beckman Coulter). The membranes were sonicated and washed 2 more times in 0.1 M NaHCO₃. Membranes from the post-nuclear supernatants and other steps in the fractionation procedure were collected and washed using the same methods.

To prepare peripheral and integral membrane fractions, the membranes were subjected to carbonate extraction as previously described. Membranes were sonicated in 0.1 M NaCO₃, pH 10.8, incubated at 4° C for 30 min. and then centrifuged at 200,000~g as described above. The extraction was repeated a second time. Membranes recovered after centrifugation were washed in 10~mM HEPES 1 mM EDTA. The carbonate washes (supernatants) were combined and the proteins recovered by TCA precipitation (peripheral membrane protein fraction). All fractions were frozen and stored at -80° C until use. Protein concentrations were determined using the Bradford method (Bio-Rad, Hercules, CA).

Bovine pancreatic granules were prepared by a modification of the procedure of Greene et al. 1 Fresh bovine pancreas was obtained from a local slaughterhouse, minced and homogenized as described above for the preparation of rat ZGs except the HB contained 0.8 M sucrose (HBH). Granules were isolated by centrifugation at $1000\,g$ for $10\,\text{min}$. This centrifugation was repeated a second time and the white granule pellets were washed to remove mitochondria then were slowly resuspended in HBH with $1\,\text{mM}$ EDTA (HBHE) and loaded on Percoll gradients as described above except with $0.7\,\text{M}$ sucrose. The loose granule pellets at the bottom of the Percoll gradients were resuspended in HBHE and the granules recovered by centrifugation at $3000\,g$ for $20\,\text{min}$. The granule pellets were resuspended in HBHE and lysed with NaHCO $_3$ as described above. The membrane and content fractions were also isolated as described above for rat pancreas.

LC-MS/MS Analysis. Four independent ZG preparations from rat pancreas were analyzed by LC-MS/MS. Proteins from two intragranular content preparations, one integral membrane and one peripheral membrane preparation were separated by SDS/PAGE on 10% gels after heating to 100° C. for 2 min. in the presence of 50 mM dithiothreitol. Fifty μg of protein was loaded on each of two adjacent lanes. Gels were fixed in 46 % methanol, 7 % acetic acid, and 0.1% Coomassie Blue R-250, destained in this solution without Coomassie, and stored in 1% acetic acid until use. Silver staining of parallel samples using the method of Wray et al 18 was used for documentation purposes only.

Twenty to 30 contiguous slices were excised from each gel. Each slice was digested using mass spectrometry grade trypsin (Promega, Madison, WI) at 12.5 to 25.0 ng/ μ L in 25mM NH₄HCO₃ buffer. For the peripheral membrane and integral membrane sample, 10% AcN was

added to the digestion buffer. The resulting peptides were extracted and dried under vacuum, then resuspended in 10 μl of 0.1% formic acid. Four to 6 μl of peptide mixtures were analyzed using nanoflow LC/ESI-MS/MS. The content extracts were analyzed with a CapLC HPLC coupled directly to a QTOF Micro MS (Waters, Milford, MA) and the membrane extracts were analyzed with a nanoAcquity UPLC coupled directly to a QTOF Premier MS (Waters).

For all preparations, a C18 pre-column was used to load the sample to a 75- μ m \times 15-cm fused silica C18 analytical column. In the case of CapLC, PepMap100 was used as the analytical column (LC Packings, Dionex, Sunnyvale, CA), whereas Atlantis columns (Waters) were used for UPLC. A gradient of 2–40 % ACN in 0.1% formic acid was delivered over 80 or 120 min at a flow rate of 200 nL/min through a fused silica distal end-coated tip nano-electrospray needle (New Objective, Woburn, MA). The data acquisition involved MS survey scans and automatic data-dependent MS/MS acquisitions, which were invoked after selected ions met preset parameters of minimum signal intensity of 8 counts per second, ion charge state 2+, 3 +, or 4+, and appropriate retention time. Survey scans of 1 s were followed by MS/MS of the three most intense ions for up to 6.6 s each, or until 6,000 total MS/MS ion counts per precursor peptide were obtained. The raw MS data were subsequently processed using ProteinLynx software (Waters), which generated DTA or PKL files from each MS/MS spectrum, which were merged into a single file containing all spectra from all of the gel bands from a single lane (i.e. one PKL file for each granule preparation).

Protein Identification Criteria. Stringent criteria for determining whether protein matches are genuine have been previously established and applied by us to the analysis of the neuronal post-synaptic density. ¹⁹ We used similar criteria in these studies. The DTA or PKL files were used to search the NCBI and Swissprot nonredundant protein databases (updated on June 7, 2006) using the Mascot search engine (Version 2.1.0, Matrix Science, Boston, MA). The search parameters included peptide mass tolerance of up to 1.5 Da, MS/MS mass tolerance of up to 0.5 Da, and variable oxidation of methionines with up to one missed tryptic cleavage allowed. The Mascot algorithm was used to determine peptide and protein expectation values. Each protein in the peptide summary report that met the probability-based Mowse threshold [p(x)]0.05] determined by Mascot were analyzed by a stricter set of criteria to determine the number of unique peptide matches. To pass our threshold, peptides had to have a minimum 6 residues, a Mascot probability-based score >15, an expectation value of <0.5, a precursor ion mass error of <0.5 Da, no missed cleavages and a rank of 1. In addition, the peptide could not appear in other proteins of higher score, and for each protein, only the highest scoring peptide (lowest expectation value) with a given amino acid sequence was considered. In general, each protein match was required to have at least two nonredundant unique peptides meeting these criteria, but not also found in other proteins identified unless they were isoforms of the same protein. Exceptions were made for proteins previously shown to be in ZGs, in pancreatic juice, or in granules of parotid gland, which are close relatives, or to be highly similar to known granule proteins. For proteins with closely related family members sharing peptides, one unique peptide and one shared peptide was considered sufficient for assignment purposes. Spectra of peptides from proteins scoring 50 or below were visually inspected to assure that the peptide assignments were reliable.

Functional annotation and organelle assignments were made using ProteinCenter (Proxeon Biosystems A/S, Odense, Denmark) together with the linked Uniprot, Genbank and Unigene (for tissue-specific mRNA expression) databases. Additional annotation was incorporated from literature searches, using the references provided in the tables in the text and Supplemental Information. Proteins localized to more than one organelle were assigned to the endoplasmic reticulum or endosomes/lysosomes categories if that was their predominant localization. Since some proteins whose predominant localization is to the plasma membrane or the Golgi

apparatus are known to be present in secretory granules, these proteins are not listed as separate categories. Otherwise, proteins are characterized as enzymes, membrane, or secreted proteins.

Antibodies. Monoclonal antibody directed against ral was purchased from BD Pharmingen. Rabbit anti-pantophysin was a gift of Dr. Rudolf Leube, (Johannes Gutenberg University, Mainz, Germany). Rabbit antibody to aminopeptidase M/N was a gift of Dr. Ann Hubbard (Johns Hopkins School of Medicine, Baltimore, MD) who together with Dr. Michele Maurice (INSERM Saint-Antoine Medical Faculty, Paris, France), also provided the monoclonal antiectonucleotide phosphodiesterase 3 (ENPP3). Rabbit antibodies to carboxypeptidase D and cyclic nucleotide phosphodiesterase were gifts of Drs. Lloyd Fricker (Albert Einstein College of Medicine, Bronx, NY) and David Colman (McGill Univ., Montreal, Canada), respectively. Affinity purified antibody to TWIK-2 was provided by Dr. Anant Mhatre (NYU School of Medicine). Antibody to ribophorin 1 was provided by Dr. Gert Kreibich (NYU School of Medicine). Antibody to ral was purchased from BD Biosciences, to mitochondrial hsp60 from Stressgen, and to amylase from Sigma. Antibody to GP2 was made by our laboratory as described previously.

Immunofluorescence Microscopy. Rat pancreas was cut into 2 mm blocks and fixed for 3 h in 8% paraformaldehyde in 60 mM PIPES, 25 mM HEPES, 2 mM MgCl₂, 10 mM EGTA, pH 6.9 (PHEM). The blocks were washed in PHEM buffer and PBS with 20 mM glycine. The blocks were infused sequentially in PBS containing 2% and 10% gelatin and then equilibrated with 2.3 M sucrose in PBS overnight at 4° C. After freezing at -80° C, thin (0.5μ) frozen sections were prepared on a Leica cryomicrotome (Bannockburn, IL) and bound to Superfrost Plus Gold slides (Electron Microscopic Sciences, Hatfield, PA) with silicone isolators. Sections were stored at 4° C in 2.3 M sucrose in PBS until use. After washing 5 times in PBS and once in PBS with 1% nonfat milk, antibodies were applied overnight (1:250–1:1000). After washing in PBS, Alexa 488 goat anti-rabbit or mouse secondary antibodies (Molecular Probes) were applied along with Texas-red conjugated phalloidin (Molecular Probes) to label actin filaments at the luminal surface of the acinar cells. DAPI was also present in the mounting medium (Prolong Gold DAPI, Invitrogen, Carlsbad, CA) for orientation purposes. Samples were photographed on a Zeiss LSM510 confocal microscope (Carl Zeiss, Thornwood, NY). Isolated granules were prepared from the Percoll gradients, diluted in HB and allowed to settle on polylysine-coated coverslips for 1 h at 4° C. They were fixed in 4% paraformaldehyde, 20 mM HEPES, 0.3 M sucrose for 30 min. After washing with Hank's PBS, they were stored at 4° C. Before use, the granules were permeabilized with 0.2% TX-100 for 1 min. Staining was otherwise conducted as described above for pancreatic sections. Samples were photographed on a Zeiss Axiophot microscope equipped with a Hamamatsu camera (Bridgewater, NJ).

Western Blotting. Immunoblotting was performed after SDS/PAGE of membrane samples from the post-nuclear supernatants and the granules. After transfer to nitrocellulose and blocking in 5% milk, 0.5% Tween-20 in PBS, antibodies were applied overnight (1:200–1:2000). Secondary antibodies directed against rabbit or mouse IgG and coupled to horseradish peroxidase (Jackson Immunoresearch, West Grove, PA) were used with a chemiluminescence substrate (Western Lightning Plus, Perkin Elmer, Boston, MA or ECL Advance, GE Healthcare, Piscataway, NJ) to detect the immunoradioactivity. The film was digitally scanned and processed using Adobe Photoshop. All quantitation was performed using NIH Image software.

Results

Zymogen granules were purified from rat pancreas. Based on quantification of Coomassie Blue and silver stained polyacrylamide gels of the preparation (Figure 1A) and amylase activity

measurements (data not shown), an increase of 4.7 fold of amylase specific activity and a similar increase in the levels of the other major granule proteins was obtained. This is comparable to the 4–4.6 fold purification previously reported by ourselves ¹⁷ and others. ²⁸ Since ZG proteins constitute as much as 30% of total acinar cell protein, our preparations are close to the theoretical limit of purity. ²⁹ The granules were substantially pure and visible contamination was minimal when the fraction was examined by electron microscopy. ¹⁷

Peripheral and integral membrane protein fractions were prepared from membranes incubated with sodium carbonate. Although there was some overlap in the protein patterns, for the most part the major peripheral and integral membrane proteins appeared distinct (Figure 1A). Using specific antibodies to other organelles, we determined that lysosomal membrane proteins were detectable in the preparation while mitochondria and endoplasmic reticulum were not detectable in granules when compared to equal amounts of the post-nuclear supernatant (Figure 1B). The presence of lysosomes was expected since some are similar in density and size to ZGs.

Proteins from intragranular content, peripheral membrane, and integral membrane protein fractions were separated by one-dimensional SDS/PAGE. The gels were cut into slices, the proteins digested with trypsin, and the resulting peptides were analyzed by LC/MS-MS. The resulting spectra were used to search NCBInr and Swissprot databases to identify the proteins present. From the four content and membrane preparations, a total of 371 proteins were identified with high confidence (see Methods for a discussion of criteria used in this analysis). Of these, 84 were known granule proteins (23% of the total). The functional distribution of the proteins is depicted in graphical form in Figure 2. Another 140 proteins were identified with less confidence based on a single unique peptide match (see Supplemental Table 1 for a complete list). To verify our database search criteria, we also searched a rat NCBI real/reverse combined database using the peptide sets from each ZG preparation. Even using our low stringency criteria, these searches yielded a total of only one false protein assignment, which was based on a single peptide match, confirming the validity of our methods. Moreover, this false positive result would not have survived the filter used to establish our high confidence identifications.

Table 1 includes a list of the 23 previously known granule content proteins that we identified. Many of these proteins (e.g., amylase, trypsinogens, chymotrypsinogen, elastases) are well-characterized ZG proteins. Others are not necessarily granule specific but have been shown to be present in granules. Among these is protein disulfide isomerase, a protein predominantly localized to the endoplasmic reticulum but present in granules as well. ³⁰ Presumably the appearance in granules occurs when molecules occasionally escape from the endoplasmic reticulum (ER) and traverse the secretory pathway.

We also identified 61 membrane proteins previously reported to be in pancreatic zymogen granule membranes (Table 1). Here again, some are predominantly localized to granules, such as GP2, the major granule membrane protein, ^{8,31} and ITMAP. ⁹ GP2, ITMAP, and some of the other proteins also appear in content. Proteins predominantly localized to the apical plasma membrane, such as dipeptidase I and gamma-glutamyl transpeptidase, were identified. These proteins have also been shown to be present in granule membranes. ^{32,33} Sixteen GTP binding proteins, both conventional G protein subunits and small ras-related GTPases, which had been previously detected in pancreatic ZGs, were also identified in our studies. The vacuolar H⁺-ATPase is known to acidify organelles. ZGs are acidic and several subunits have been previously shown to be present on their membranes. ³⁴ We identified 10 of the 14 known subunits. ³⁵

Other secreted proteins were identified in the preparation (Table 2). These include proteins that are likely to be present in rat pancreatic ZGs. For example, trypsinogen V (via a single unique peptide) and trypsinogens 8 and 9 were identified. Given the composition of ZGs, these are likely to be granule proteins. In addition four proteins found in the pancreatic juice – chymopasin, clusterin, cystatin C, and gamma-glutamyl hydrolase – are likely granule candidates. Among the other secreted enzymes identified was lipoprotein lipase, a secretory protein made in many tissues and whose mRNA is present in pancreas. ³⁶

Membrane proteins were also identified that had not previously been found in zymogen granules (Table 3). These include two proteins known to be present in parotid secretory granules -- rab26 and noc2. A number of transporters and channels were also identified. These included aquaporin-8, the potassium channel TWIK-2/KCNK6, ATPases, anion and cation channels, and amino acid transporters. In addition, GTP binding proteins, enzymes, and many other membrane proteins were identified. Some of the proteins are primarily found in other organelles, such as lysosomes, which are likely present in our ZG preparations, and the endoplasmic reticulum (Table 3 and Supplemental Tables 1 and 2 in Supporting Information). Despite the large number of proteins we identified, at least 19 proteins reported in the literature to be present in granules were not detected in our LC/MS-MS analysis (Supplemental Table 2).

Four of the new proteins in Table 3 were confirmed to be ZG proteins by immunofluorescence microscopy (Figure 3 and Figure 4). These included the membrane protein pantophysin, a tetraspan membrane protein and homolog of synaptophysin thought to be involved in vesicle trafficking. The Pantophysin was localized to ZGs on pancreatic sections (Figure 3) and on isolated granules (Figure 4). Similarly, cyclic nucleotide phosphodiesterase (CNP) was found in granules when sections or isolated granules were stained with a specific antibody (Fig. 3 & Fig. 4). Ecto-nucleotide pyrophosphatase 3 (ENPP3) was localized to the apical membrane of pancreatic acinar cells using a monoclonal antibody (Figure 3) that also labeled the regions where the granules are found and isolated granules (Figure 4). Carboxypeptidase D (CPD) is a protein known to be present in the trans Golgi network in other cell types. It localized primarily to regions deeper in the cell than most granules (Figure 3). Immunofluorescence labeling of isolated granules using antibodies to CPD revealed intense staining of large vesicle structures and a lower, but detectable level on some of the granules (Figure 4). This would be consistent with a scenario whereby some CPD enters immature granules from the TGN but is transported out as the granules mature.

Three additional proteins were found to be enriched in granule membrane fractions as determined by immunoblotting but had low levels of labeling by immunofluorescence microscopy (Figure 5). These included the small ras-related GTPase ral and the 2P domain K + channel TWIK-2 (rKCNK6), The antibody to aminopeptidase N, which is known to be an apical membrane protein in many cell types, including pancreatic duct and acinar cells, ³⁸ was observed to crossreact with rat GP2 (data not shown) and so bovine membranes were used for immunoblotting. Aminopeptidase was also enriched in the pancreatic membrane fractions as compared to total membranes from the post-nuclear supernatant (Figure 5).

Discussion

Of the 371 proteins that met our criteria for high confidence identification by mass spectrometry, 84 had been previously reported to be in secretory granules. Many of the new proteins identified are secreted proteins and proteins known or predicted to be membrane-associated (Table 2 and Table 3). There was considerable redundancy in the protein composition of the different fractions. This was expected because many of the integral

membrane proteins are also present in the content of the granules and the major granule content proteins are thought to be present in granule membranes as well.

Most of the secretory proteins identified by us were known zymogen granule proteins. However, a few are enzymes that had been identified in pancreas or pancreatic juice but never shown previously to be in granules, including gamma-glutamyl hydrolase^{39,40} and chymopasin, a chymotrypsin-like enzyme.⁴¹ Cystatin C is a small protein (14 kDa) made by the pancreas and also found in the pancreatic juice and in granules in endocrine glands.^{42,43} For this reason, it is listed in Table 2 as a good candidate for a ZG protein although only one unique peptide was detected. Clusterin, another protein that was identified, has been localized to apical region of pancreatic acinar cells undergoing regeneration,⁴⁴ which would be consistent with a ZG localization in these cells. It is reasonable to propose that a small minority of acinar cells are being renewed at any given time and therefore contain this protein in their granules. Transcobalamin 2 has been previously localized in rat pancreas where it was found primarily in pancreatic duct cells.⁴⁵ However, the investigators reported "irregular" staining for transcobalamin 2 over acinar cells, which would be consistent with a low level presence in ZGs.

Several proteins associated with the apical plasma membranes of epithelial cells were identified. It has already been established that some apical plasma membrane proteins, such as dipeptidase 1 and γ -glutamyl transpeptidase, are also found in ZGs. ^{32,33} Secretory granules are most likely the transport vehicle by which these proteins, but not all apical membrane proteins, are escorted to the plasma membrane. ⁴⁶ ENPP3, which we have shown to be on the apical membrane of acinar cells (Figure 3) and at lower levels in granules, also would be in this category as would aminopeptidase N, which was enriched in granule membranes (Figure 5). Among the other proteins identified, aquaporin-8 is also found at the lumen of pancreatic acinar cells ⁴⁷ and was identified in our ZG proteomic analysis. 5'-nucleotidase is potentially in this category as well. ⁴⁸

Very few Golgi apparatus-specific proteins were found in the preparation. Two proteins concentrated in the trans Golgi network (TGN), CPD⁴⁹ and syntaxin 16⁵⁰ were identified. Another Golgi protein, MG-160, is predominantly found in the medial Golgi but as a sialoglycoprotein is likely to be present as well in the trans-Golgi where sialylation is known to occur. ⁵¹ It was also identified in a proteomic analysis of adrenal chromaffin granules. ⁵² No other proteins specific for the cis and medial portions of the Golgi apparatus were detected. Granules form at the TGN and as they pinch off, it is believed that some membrane proteins of the TGN enter them. These TGN proteins are removed from the so-called immature granules (IZG) during their maturation.⁵³ This mechanism has been demonstrated to occur for TGN proteins, such as CPD and CALNUC (nucleobindin-1) in pituitary cells^{22,54} and the cationindependent mannose-6-phosphate receptor (M6PR) in pancreatic acinar cells. 22,55 Indeed, M6PR was also identified in our preparations (Table 1) as was nucleobindin-2, a close relative of CALNUC known to be secreted from cells. 56,57 Since IZG's would be expected to copurify with the mature granules, it is reasonable to propose that CPD, and possibly nucleobindin-2, syntaxin 16 and MG-160 are in IZGs in acinar cells as well. This would account for the staining we observed for CPD, which was primarily in regions near the Golgi apparatus but did show low level labeling of some granules as revealed by immunofluorescence microscopy (Figure 4).

A large cohort of ion and amino acid transporters were identified including the potassium channel protein TWIK-2/rKCNK6, a two-pore weak inward rectifying channel found in many epithelial cells. 58 This protein was shown to be present in granule membranes. The only cation channel previously reported to be present in granule membranes was the ATP-sensitive potassium channel subunit Kir6.1/IRK-8, 59 which was not detected in the current study. The

amino acid transporter Slc3a2 and its subunits (L-type amino acid transporters 1 and 2) were also found. While such amino acid transporters are generally associated with the plasma membrane, it has been shown that Slc3a1, the closest homolog, is localized in secretory granules of neurons. Thus Slc3a2 would be a good candidate for a ZG membrane amino acid transporter.

Small GTP binding proteins and their binding partners were found in the ZG membrane preparations. In particular, rab proteins, such as rab3 and rab27 family members are known to be regulators of secretory granule exocytosis. 61 A number of small GTPases had already been shown to be in ZGs (see Table 1). Rab26 is a candidate for a new ZG membrane protein. It is expressed in pancreas and it localizes to granules in parotid gland. 62 As mentioned previously, noc2, a rab-binding protein found in granule membranes of salivary gland cells, 5 plays a critical role in ZG release from pancreatic acinar cells. 3 It was identified by LC/MS-MS in the ZG membrane preparations as well.

In addition to the rab proteins, other proteins involved in exocytosis and vesicle trafficking were also detected. These included the SNARE proteins syntaxins 3, 6, and 7, vamps 2, 3 and 8, and SNAPS 23 and 29, which had already been detected in zymogen granules (Table 1). Syntaxins 12 and 16b were also identified, although it is not known if these are granule-specific, while syntaxins 3 and 8, which had been reported to be in zymogen granules, were not identified (see Supplementary Table 3). Other proteins in this category but never before identified in granules included synaptotagmin-like protein 1, which interacts with rab27 and is thought to be involved in granule exocytosis, ⁶³ and the related synaptotagmin-like protein 4, which regulates amylase secretion in parotid cells.⁶⁴ Annexin A13, part of the annexin family of calcium and phospholipid binding proteins that regulates vesicle fusion at the apical membrane of polarized epithelial cells, was also identified. ⁶⁵ Phosphatidylinositol lipids, including PtdIns4P, are important regulators of vesicle generation and vesicle fusion. ⁶⁶ We identified phosphatidylinositol 4-kinase type-II beta (PtdIns 4-kinase). In chromaffin granules, PtdIns 4kinase is present on secretory granules and in neuroendocrine PC12 cells, the type II form has been shown to be present in immature granules. 67,68 In addition, PtdIns 4,5-kinase regulates granule exocytosis in PC12 cells. ⁶⁹ Thus, PtdIns 4-kinase is a potential regulator of granule biogenesis and exocytosis in pancreatic acinar cells as well.

As was anticipated, lysosomal membrane proteins were identified in the preparation by LC-MS/MS. These included the major glycoproteins, LAMP-1 and LAMP-2. However, it should be noted that proteins primarily associated with lysosomes have been identified previously in secretory granules, including CD63 and cathepsin B, both of which were identified in this study as well. It is therefore an open question as to whether these and other proteins identified that have been in part localized to lysosomes and endosomes are present as well in pancreatic ZGs.

As shown in Supplemental Table 2, at least 19 proteins reported in the literature to be present in granules were not identified, in addition to the four subunits of the H⁺-ATPase that were not found, as noted above. Two of the other proteins, SPINK and hsp10 are very small (<11 kDa). Small proteins have a limited tryptic peptide repertoire and do not fix well after SDS/PAGE, making them more difficult to detect. Caveolin was reported to be released from acinar cells in a complex with apolipoproteins A1 and E.⁷⁰ This particle is large and would be removed from the content preparations during centrifugation after granule lysis. In addition, the serglycin core protein has no internal tryptic peptides. We speculate that the other proteins such as muclin, which is a major protein in mouse ZG membranes, ¹⁰ were not detected either because they are expressed at low levels in rat pancreas or because their peptides did not separate adequately from those of abundant proteins. Nevertheless, in our experiments, we did identify 79% of the ZG proteins that had been reported in the literature. This is comparable to the 80% coverage recently reported for the MS/MS analysis of synaptic vesicle proteins

separated using PAGE.⁷¹ Admittedly, the criteria we used to eliminate false positives may also result in our failing to identify some new granule proteins.

In a recent study using mass spectrometry, Chen et al⁷² reported identifying 73 new ZG proteins (along with 28 known proteins). Importantly, myosin Vc and SNAP-29, which had not been previously reported to be present in granules, were verified by immunocytochemistry to be new granule proteins. Rap1, a granule membrane protein in parotid gland secretory granules, ⁷³ was also shown to be in ZG membranes. In addition, these investigators confirmed the localization of three proteins (rab6, rab11, and rab27B) previously identified as ZG proteins. ^{74–76} All of these proteins were identified in our study as well (see Table 1). Of the other 67 proteins from the Chen et al⁷² study, one protein had been previously identified in granules, one is no longer in the rat database, 35 were also present in our preparations, and 31 were not detected by us. In summary, we identified with high confidence more than 300 proteins in our preparations that were not reported by Chen et al.⁷² We confirmed the identity and location of a subset of these by immunocytochemistry and Western blotting, increasing the probability that many or most of the proteins found by us in our experiments are indeed novel zymogen granule proteins.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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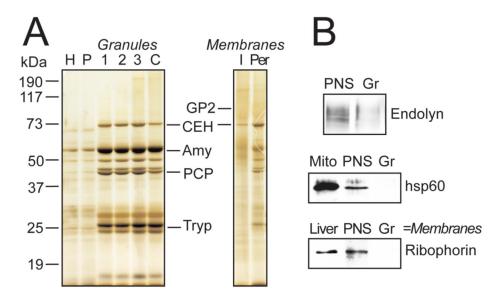


Figure 1.

Preparation of zymogen granules from rat pancreas. A) Granules were prepared as described in the Methods. 5 µg of the initial homogenate (H), the post-nuclear supernatant (PNS), the first granule pellet (1), the Percoll gradient fraction (2), and the final purified granules recovered from the sucrose gradient (3) were subjected to SDS/PAGE on 10% gels. The granule content fraction (C) as well as the integral (I) and peripheral (Per) membrane fractions isolated after treatment of the membranes with 0.1 M sodium carbonate are also depicted. Amylase and other content protein bands were enriched ~ 5 fold. B) 5 µg of protein from the indicated fractions was used in immunoblotting experiments after SDS/PAGE and transfer to nitrocellulose. Antibodies specific for the endosome/lyososome membrane marker endolyn, the mitochondrial protein hsp60 and the endoplasmic reticulum membrane protein ribophorin 1 were used as probes and the blots developed using the enhanced chemiluminescence method. Anti-endolyn samples were membranes from the homogenate, PNS, and granule fractions. Anti-hsp60 samples were a mitochondrial fraction prepared from rat pancreas (Mito.), PNS and purified granules (Gr). Anti-ribophorin samples consisted of total rat liver membranes, pancreas PNS membranes, and granule membranes. The data show that lysosomes are present in the granule preparation but not enriched while mitochondria and endoplasmic reticulum were not detected by this method, indicating that they were selectively depleted during zymogen granule purification. The intensity of the bands using these methods was linear over ~8 fold range (not shown).

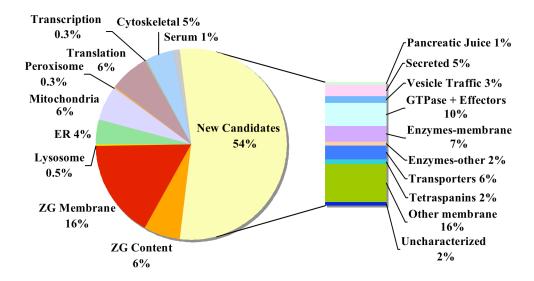


Figure 2. Diagram of the functional categories of the soluble and membrane proteins identified by LC-MS/MS. Based on annotations in the ProteinCenter, Uniprot and Genbank databases or predictions based on similarity to related proteins in the same databases, the 371 proteins identified with high confidence (see text) are grouped in the pie chart according to their functional and subcellular distribution. 23% were known zymogen granule proteins and 54% were candidates for new granule proteins. At right, the new candidates are broken out by category together with the percent of the total proteins identified (as listed in Table 3; also see Supplemental Table 2 for detailed annotation).

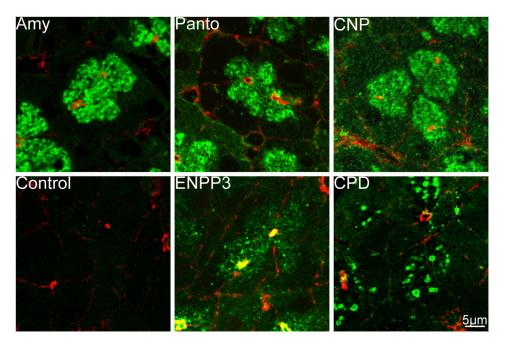


Figure 3. Immunofluorescence microscopy of pancreatic sections. Frozen thin sections of rat pancreas were incubated with rabbit antibodies to amylase (Amy), pantophysin (Panto), carboxypeptidase D (CPD), and cyclic nucleotide phosphodiesterase (CNP) as well as a monoclonal antibody to ecto-nucleoside pyrophosphatase 3 (ENPP3). The negative control was a nonimmune rabbit serum used at the same dilution (1:200). Controls performed using irrelevant mouse monoclonal antibodies gave even lower nonspecific background (data not shown). Alexa 488 - conjugated anti-mouse or anti-rabbit IgG was used in a second step along with TX-Red conjugated phalloidin, which binds strongly to actin at the acinar lumen. Pantophysin and CNP labeling was over the granule region and to some extent over other membranes of the cell. CPD labeling was primarily in regions deeper than the bulk of the granules and is consistent with its presence in the trans Golgi network. ENPP3 was localized predominantly over the lumenal membranes of the acinar cells but also at a low level over the granule region beneath it. By comparison, amylase labeling, as expected, was over the ZG's surrounding the acinar lumens.

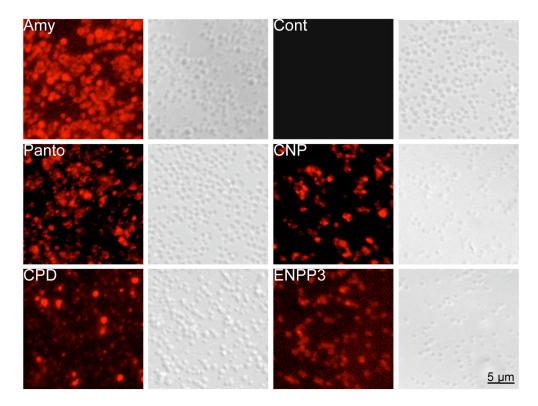


Figure 4. Immunofluorescence microscopy on isolated granules. Zymogen granules on coverslips were stained for immunofluorescence microscopy using antibodies against amylase (Amy), pantophysin (Panto), CPD, CNP, and ENPP3. Rhodamine-conjugated anti-mouse or antirabbit IgG was used in a second step. Depicted in parallel are representative fields using fluorescent and differential interference contrast filters. All of the antibodies gave specific signal although anti-CPD labeled some large vesicles very intensely with low level labeling over the bulk. ENPP3 staining was weak compared to pantophysin or CNP, as expected (see Figure 3). Control coverslips were incubated in a nonimmune rabbit serum and rhodamine-conjugated anti-rabbit IgG. They were photographed at the longest exposure used for the antibody-stained coverslips and processed similarly using Adobe Photoshop.

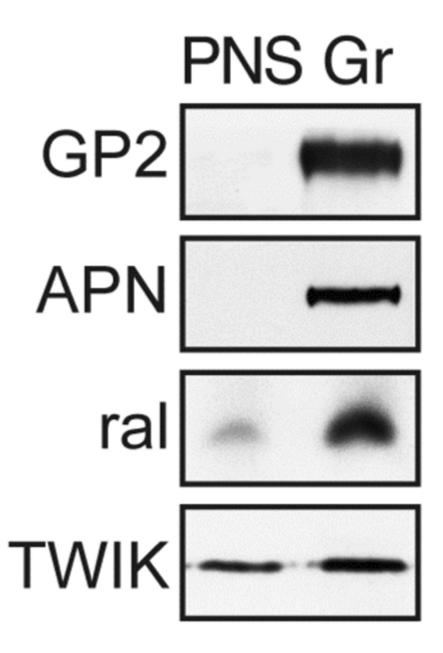


Figure 5.

Immunoblotting of purified zymogen granule fractions. Granules and their membranes were prepared from bovine pancreas (top 2 panels) or rat pancreas (bottom 2 panels). 3 µg of membranes from the PNS or purified granules were subjected to SDS/PAGE and transferred to nitrocellulose. Immunoblotting was conducted using enhanced chemiluminescence and antibodies to GP2, aminopeptidase N, ral and TWIK-2/rKCNK6. All of these proteins were enriched in granule membranes (Gr) as compared to total PNS membranes.

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Table

Methods for criteria) and had been previously reported in the literature (Ref) to be in zymogen granules (ZG). The ZG preparations where 2 or both (C), Integral or Peripheral membranes]. The database (Swiss or NCBI) that yielded the Mascot score is also given. Proteins List of Known Zymogen Granule Proteins Identified by LC-MS/MS. Proteins listed were identified in our LC-MS/MS experiments (see the protein was identified by us are listed and the preparation with the most unique peptides and highest score is in bold [= Content1 or of salivary gland granules, which are related to pancreatic ZG are also included. Numbers of identified total, unique (Uni) and shared (Sh) peptides are listed, as are the previously reported major subcellular locations in addition to granules (Other Location).

Protein Name	NCBI Access #	Mass	Mascot Score	Fotal	Peptides Uni(Sh)	Prep	Ref
Content Proteins							
alpha-amylase, pancreatic	67373	56522	30828	1198	5.	LP.C	
caldecrin (chymotrypsin C/elastase IV)	1246029	29355	1298	08	9	1.P.C	
carboxynentidase A1	1345702	47168	5614	277	14(2)	I.P.C	
carboxynentidase A2	61556903	46883	0099	245	7	1 P C	
carboxypepuuse 122	6078607	47485	7618	263	† <u>C</u>	1,1,0	
carboxypetrase D1	1205620	01710	010/	507	77 (۲ ٬ ۲	ו
camepsin D	1/03630	3/4/0	00	7 6	4 2	7 5	//
cholesterol esterase	55943	/6699	47/17	8877	4 7	1, r ,C	
chymotrypsinogen B	6978717	27831	9666	317	w	I,P,C	
colipase	203503	12272	139	32	2	P,C	
elastase 1	6978801	28979	3184	103	33	I,P,C	
elastase 2	6978803	28866	9192	258	7	I,P,C	
elastase 3B	62649890	28767	1042	53	7	I.P.C	
heat shock protein (hsn60)	56383	72609	102	"	_	C2	30
kallikrein tissue	818030	23515	419	20	· (**)	CZ	78
nancreatic linase	1865646	51407	5931	430	71	190)
pointed in the state of protein 1	14001	57375	1001	120	7 -	, i, i	
paneteauc npase-related protein i	14091//2	04040	130	27.5	ţ,	ر د ر	
phosphoupase A.2	129416	16413	<u>6</u> :	25	ν,	، د	Î
phospholipase c, betal	117647200	133309	47	9	- :	4	6/
protein disulfide-isomerase A3	1352384	56588	196	21	10	ľЪ	30
reg-1(pancreatic stone protein)	6981470	18660	77	cs	2	ပ	80
trypsinogen I	6981420	25943	3632	180	8	I,P,C	
trypsinogen II, anionic	6981422	26211	1091	26	2	P,C	
trypsinogen III, cationic	27465583	26252	2747	110	5	I,P,C	
Membrane Proteins							
beta-actin	13592133	41724	46	9	S	I, P ,C2	81
annexin II; calpactin 1	9247200	38951	66	S	3	Ϊ́Ρ	82
annexin A4/ZÂP36	37999910	35826	187	∞	4	I,P,C2	83
cation-independent man-6-PO4 receptor	6981078	273222	09	2	2	Ь	55
CD63/granulophysin	5929904	13830	213	24	2	I,P	84
chloride channel protein 3 (CLC-3)	4762023	96206	75	6	4(1)	ı	82
cysteine string protein	1095322	22086	276	35	4	ΙΡ	98
dipeptidase 1	400240	45477	1852	204	18	I,P,C2	33
dynactin 2	50926127	44121	70	S	33	Ь	87
dynein cytoplasmic heavy chain	294543	53174	174	26	7	I,C2	87
gamma-glutamyltranspeptidase 1	121150	61517	5772	491	17	I,P,C	32
GP2/ZG membrane glycoprotein 2	19705557	58707	16175	1005	14	I,P,C	8,31
integral membrane-associated protein ITMAP	2460316	96289	1070	66	10	I, P ,C2	6
myosin Ic heavy chain	400429	118017	52	6	2	I, P ,C2	88
myosin Vc	62653910	234186	2171	132	34(4)	Ϊ́Ρ	72
pancreatic lipase-related protein 2 (GP-3)	1708841	52501	10973	1010	20	I ,P ,C	68
peptidylglycine α-amidating monooxygenase	56841	94745	116	6	4	Н	06
secretory carrier membrane protein 1	34853043	37974	1024	20	5	I,P	28,91
secretory carrier membrane protein 2	10764633	34318	499	26	3	I,P	28,91
secretory carrier membrane protein 3	10764631	38344	453	30	4	ΙΡ	28,91

Protein Name NCBI Mass None Peptids Reptids Re								
ye curier membrane protein 4 13929018 25495 1127 7 1 1 11P 2	Protein Name	NCBI Access #	Mass	Mascot Score			Prep	Ref
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19705578 56515 535 65 13 1,P 5865560 50827 350 26 8 1,P 38648872 2891 143 9 4 1,P 37589624 26112 150 22 7 1,P 62078587 43873 170 23 6 1,P	H+ATPase V1 subunit A1	34869154	68222	388	30	6	т;	102
38648872 28291 143 9 4 I.P. 3789624 26112 150 22 7 I.P. 3789624 43873 170 23 6 I.P.	H+ATPase V1 subunit B2	19705578	56515	535	65	13	ď.	
1 3789624 26112 150 22 7 1. P 1. P 62078587 43873 170 23 6 1. P	H+A1Fase V1 subunit C1 H+ATPase V1 subunit D	38803300	2826/	050 143	9 ₇ o	% 4	I,F	
62078587 43873 170 23 6 I. P	H+ATPase V1 subunit E1	37589624	26271	150	22	+ 1	i, di	102
	H+ATPase V1 subunit H	62078587	43873	170	23	9	I,P	

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Table 2

List of Putative Novel Zymogen Granule Content Proteins Identified by LC-MS/MS. Secreted proteins identified but not previously reported in zymogen granules are listed. The protein identification and classification criteria were as described in the Methods

section. ** also reported by Chen et al. 72

Protein Name	NCBI Access #	Mass	Mascot	Total	Peptides Uni(Sh)	Prep
Pancreatic Juice Proteins chymopasin clusterin cystatin C gamma-glutamyl hydrolase gamma-glutamyl hydrolase Other Secreted Proteins 17-beta hydroxysteroid dehydrogenase 13 17-beta hydroxysteroid dehydrogenase 11 17-beta hydroxysteroid dehydrogenase 11 17-beta hydroxysteroid dehydrogenase 11 18-serine protease precursor (predicted) cyi67 serine protease precursor (predicted) eosinophil peroxidase (predicted) epidemnal growth factor precursor granzyme A ipoprotein lipase metalloproteinase inhibitor 3 (TIMP-3) nucleobindin-2 peroxitedoxin-4 prostatic acid phosphatase semaphorin 3C (predicted) sphingomyelin phosphodiesterase, acid-like 3B trypsinogen Vb trypsinogen Vb trypsinogen Vb trypsinogen V (shares with 8)	16758930 57241 83301921 6978890 77416416 51948390 58293772 73620083 5092773 73620083 5092773 7362083 50927378 62656751 38303863 564671 17367404 37490233 576258 62646703 71043890 5910985 57415 34855584	28098 51342 14012 35807 33473 33473 32917 58792 25746 32180 98656 123870 28545 53049 24210 58059 30988 39620 112085 51613 47390 26249	1077 220 335 287 287 140 5110 28 116 63 116 63 195 74 74 74 77 201 20 39 39 47 218 218 218 228 28 29 20 20 20 20 20 20 20 20 20 20 20 20 20	25 18 18 18 19 21 10 10 27 27 27	2.1. 2.1. 2.1. 2.1. 2.1. 2.1. 3.4. 4.2. 5.2. 5.3. 5.4. 5.4. 5.4. 5.4. 5.4. 5.4. 5.4	1. P. C.

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identification were as described in the Methods section. Abbreviations are the same as in Table 1. $^{\$\$}$ shown in this study to be present in ZG; *** also reported by Chen et al. 70 List of Putative Novel Zymogen Granule Membrane-Associated and Soluble Proteins Identified by LC-MS/MS. The criteria for protein

	MON		i i			
Protein Name	Access #	Mass	score	Total	repuaes Uni(Sh)	Prep
Transporters and Channels						
aquaporin 8	9506395	28036	46	∞	2	Ι
ATPase, aminophospholipid transporter class I, type 8A	109499663	134677	1261	99	15	ď.
At Fase, anniophosphonplu dansponer class 1, type ob	51850114	143/47	2/1	0 0	3(1)], _
cation-chloride cotransporter 0	21629114 24899633	77077	. 138	o <u>1</u>	4	- I
catour-carrier family 7 member 4	34869937	68335	82	<u> </u>	+ 0	1 D
chloride channel protein 5 (Cl C-5)	1122330	83014	41	9	7 []	1,1
choline transporter-like protein 1/CD9?	73918925	78685	30	o (2)	-
ligand gated ATP recentor P2X4	51260025	43487	3 =	1 7	1 v	d I
L-type amino acid transporter 1(4F2 light chain)	12643400	55867	56	7	2(1)	I.P
L-type amino acid transporter 2	16758188	58153	61	8	က်	I,P
Na,K-ATPase alpha-1 subunit	205632	113192	140	6	4	I,P
P-type ATPase class II 9b	62664679	129095	614	37	9	I,P
similar to R13A5.9	27683291	87947	934	51	9	I ,P
Slc3a2/CD98hc (L-type amino acid transporter)	38303937	58036	1147	109	14	I,P,C2
solute carrier family 1 member 3/Slc1a3	9507115	59659	62	∞	က	I,P
solute carrier family 16, member 1	6981542	53203	161	9	5	I,P
solute carrier family 35, member C2	62646377	40306	39	m ;	2	I,P
solute carrier family 36, member 1	18426842	52535	575	23	9	I,P
solute carrier family 38, member 5	20302002	51669	06	so :	m	I ,P
transient receptor potential cation channel, subfamily M4	109458719	144038	127	10	3(1)	 •
I W IN-2/2F domain K+ channel (rKCINKb)	9971949	34193	293	97	ç	-
Vesicular Trafficking	21,42,506	22150	10.	-	-	-
u-soluble INSF attachment protein (u-SiNAF)	2143380	33130	721	4	4 v	1, T
alillexiii A13 ohomaa muliivaaioular hodu motain 2/ma9/	109460196	45/50 25046	177	1.1	o c	1,r I D
charged multivesicallar body protein 5/8NF7DC2	7391777	24560	121	CI V	10	; ;
myosin Va	11559935	211630	397	22	1(4)	Î.P
phosphatidylinositol 4-kinase type-II beta	54400734	54430	17	10	<u>,</u> v	<u>.</u>
synaptotagmin-like 1	71043698	59435	474	47	12	I.P
synaptotagmin-like 4 (granuphilin-a)	17939356	75853	154	14	9	I,P
syntaxin 16b	109469301	80889	96	4	3	І ,Р
syntaxin 12	77695930	31168	220	13	4	Ι
vacuolar protein sorting-associated protein 45	23396892	64853	32	4	2	-
Vesicular Trafficking GTP ases and Effectors			i	,	,	
ADP ribosylation factor ARF-4	6680720 8633561	20384	58	9 0	m 1	7. 1.
ADF fidosylation factor-related Aff80	34637541	21323	103	٧	- c	1,F
Cdc+2 G(j)ot	6980962	40119	196	C 1 C	2(2)	1, L
G(1)01 G(j)02	13591955	40473	224	; -	2(3)	1,1 I P
G(1)02 G protein alpha 13 (GNA13)	61557003	43984	142	. 82	2(1)	; I
MAP-kinase activating death domain	16758360	177880	120	13	5	I,P
noc2/rabphilin 3A-like without C2 domains	19424292	33412	29	4 :	5	I,P
rabla	32527715	22663	788	/8/	(<u>)</u>	1,P,C2
rab1b (shares with 1a)	52138628 13020006	22176	436 586	9,6	7(p) 7	1,F
rab2b	83415090	24070	286	38.	1(4)	7), 1; 1
rab3a	61098195	24954	865	81	1(5)	I

Protein Name	NCBI Access #	Mass	Mascot	Pepi Total	Peptides Uni(Sh)	Pren
						Jack
rahAa	38303943	73877	7.6	1.2	2(1)	۵
rab4b	21313012	23614	121	1 =	2(1) 2(1)	Ţ.
rab7	92022	22789	153	11	7	I,P
rab8a**	49522647	23522	346	35	4(3)	I,P
rabsb	23463313 420269	23588	253	35	3(5)	4, I
rab13	21952483	22887	133	17	1(2)	<u>-</u>
rab14**	420272	23850	335	20	5(1)	I,P
rab18	27685547	22962	% ⁷ %	ο (4 5	I,P
rab26 rab37a	1083775 8394142	28186	1777	77 77 77	3(1) 4(3)	т, <u>г</u>
1402/a rab35	62900797	23052	397	33	4(3) 4(2)	I'H
rac1 **	54607147	21436	272	35	, m	I,P
ralA	13592039	23538	286	41.	2(4)	I,P
ralb	4/939184	23303	159 60		2(4) 2	7, <u>-</u>
14/20 h-ras	131873	21301	73	701	4 W	I,I
k-ras2 protein	13928698	21481	105	∞	8	I,P
n-ras	18158431	21230	62	7	1(2)	Д ;
r-ras	34856057	23894	84 <u>7</u>	7.5	7 (d.E
rhof	79152381	22109	C 25	11 %	1 C	7,7 I P
rno activating protein 1 (p50-rhoGAP)	62645722	53024	561	. 1	ı v	I.P
rho-GDI3	34870596	25295	92	10	S	I,P
Tetraspan Membrane Proteins						
CD151 antigen	11968106	28336	46	7.	61 (ď,
CD81 antigen	69/8639	258/1	887	4 1	71 (J., -
Claudin domain containing 1	35/41538	36000	/ 6	~ <	7 0	- -
partophysin \$\frac{1}{2}\$	62079261	28610	378	45	14	I.P
tetraspanin-7	62666547	32122	323	29	æ	I,P
tetraspanin-8/transmembrane 4 member 3	38197346	25528	94	7	2	I,P
transmembrane 4 superfamily member 6 Tspan6	27674865	27517	228	16	4	I,P
Enzymes – Membrane-associated 2.3 3-cyclic nucleotide 3-nhomhodiecterases.	203493	47239	200	19	œ	1 D
5,5 cycuc macronac 5 prospinomearanae 5'-nucleotidase	11024643	63928	112	5 ∞	9	I.P
aminopeptidase M/N ^{\$\$}	601865	109249	2752	140	23	I,P
aminopeptidase Vp165	19424264	104503	37	4 /	61.	<u>.</u>
beta Klotho protein	109500603	86988	96	9 (4 (- <u>-</u> -
carbonic annydrase ALV	62043907	57502 152520	671	3 C	√ ∑	1,r 1
DHHC24 zinc finger protein RGD 1305755	86129558	42604	167	11	2 67	i I
ectonucleoside triphosphate diphosphohydrolase/CD39	12018242	57371	244	12	4	I,P
ectonucleotide pyrophosphatase/phosphodiesterase 3****	1526949	99024	5554	357	27	Т,Р
glycerophosphodiester phosphodiesterase domain containing 5 berein	62640954 57929	68644 44898	151 137	13	m v	4, I
hypothetical protein LOC304325 (putative kinase)	70794760	46848	375	37	0.4	ΙΉ
interferon gamma induced GTPase	32527749	161531	140	9	4	Ā
itchy homolog E3 ubiquitin protein ligase	54312102	97685	126	∞ (m (- ;
leukocyte common antigen-related protein Ivn B protein tyrosine kinase	249840 294581	58492	805 41	£ 4	2(1)	- - -
metallo-beta-lactamase superfamily protein like	34853071	31170	58	- w	3	·I
nicastrin	27819651	78350	1499	59	27	I.P,C2
phogrin/LAZ-beta phospholinid scramblase 1	17105346	36687	677 75	73 10	10 10 10 10 10 10 10 10 10 10 10 10 10	7, I
			2	2	,	i

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Destein Name	NCBI	Mass	Mascot	Pep	Peptides Timi(Sh)	Pros
	I GGGGGG	CONTACT	1000			dari
presenilin-1	6174931	52756	33	9	2	I.P
protease, serine, 8 (prostasin)	20301968	36820	131	7	2	I,P
protein tyrosine phosphatase non-receptor type 9	61556770	61619	300	26	S	I,P
protein tyrosine phosphatase receptor type D	109475037	200136	177	24	5(2)	-
aldehyde dehydrogenase 1	109480409	107333	91	v	"	7.7
glutathione S-transferase pi	25453412	23424	119	o vo	n m	38
heat shock cognate 71 kDa protein	13242237	70884	422	22	11	I,P
heat shock protein hsp 90-beta	1346320	83264	106	2	2	I,C2
peroxiredoxin-1	2499470	22095	28	4 (4 (P,C2
pyrroline-5-carboxylate reductase 1	109489508	48113	100	ب د د	<i>r</i> 0 (- :
Vesicle amine transport protein 1 nomolog Other Membrane accordated Proteins	/6096306	43091	312	7.3	o	I,F
Other Membrane-associated Froteins alpha catenin	55700755	100174	40	œ	C	_
alpha catellii Alzhaimar's pracursor protain (ADD)	55/42/33	86649	367	o <u>7</u>	1 1-	IPC
R-hox and SPRY domain containing protein	38541109	49153	107	ું ∝	- 4	1,1,2,2 I P
beta-2-microglobulin	7549746	13711	65	0 4	2	<u>;</u> –
beta-filamin	109501396	291287	154	∙ ∞	ıν	ΙΡ
cation-dependent man-6-PO4 receptor	56090485	31075	78	9	2	Ā
CD166	47605356	64981	62	3	2	I
CD1d**	2118857	38616	754	74	6	I,P,C2
CD47 integrin-associated signal transducer	9506469	32974	156	20	4	I,P
c-met/hepatocyte growth factor receptor	1771558	153843	95	7	3	I,P
coxsackie-adenovirus-receptor	6013133	39923	89	4	3	I
Fras1 related extracellular matrix protein 2	109464881	378472	108	14	vo i	I,P
glypican 4 heparan sultate proteoglycan	620/8949	62522	245	Ξ τ	n o	J
Golgi sialoglycoprotein MG-160	8393450	133469	85 53	~ 5	7 -	7, I
Inppocarcin-like protein 1 hymothatical motoria DVEZ-666N024	0393804	55030	32 118	2 ∨	4 "	T, L
iiybouicticai protein Dari Zboomoo4 imminoolohilin sinerfamily member 3	109497812	159874	91	n =	o c	-
insulin recentor	8393621	15656	205	7	1 (r	ď
integral membrane protein 2B	55741681	30294	252	· <u>1</u>	o ve	I. J.
integrin alpha 5	299145	27655	138	6	4	ī
integrin alpha 6	109468286	108731	422	24	14	I,P
integrin alpha FG-GAP repeat containing 3	57527508	60209	156	S	3	I,P
integrin beta 1	8393636	88436	238	15	∞ :	I,P
integrin beta 4	6981108	200462	318	<u>8</u>	Ξ,	Т,Р
integrin beta-5	10949441/	53410	130	4 (7 (- -
interleukin 1 receptor accessory protein	720835	05550	370	7 <u>C</u>	7 0	7 <u>1</u>
KIAA0152	62600386	32398	121	; ∝	o v	; -
LDL recentor-related protein 5	62641684	178866	56	2 0	2	
leukemia inhibitory factor receptor	13591979	122317	306	17	12	ΙΡ
low density lipoprotein receptor	28461161	96559	87	2	2	–
MARCKS-related protein	76363234	19704	28	2	2	Ι
membrane targeting tandem C2 domain containing	68342017	55019	195	35	7	I,P
mucin 1	62643778	176643	235	14	ε,	I,P
myeloid-associated differentiation marker	33590376	35125	258	8 5	4 (J, I
neogenin	10/20132	159959	18/	, 10	~ c	7 <u>.</u>
occludin	81885777	10329	67 05	o r	10	
osteoclast inhibitory lectin	13958626	25670	218	- ∞	1 6	·
phosphatidylethanolamine binding protein	8393910	20788	146	3	3	$^{\rm C}$
plexin-B2	109481135	215981	131	10	9	I
polymeric immunoglobulin receptor	27151742	84745	1553	63	10	I,P,C2

Protein Name	NCBI	Mass	Mascot	Total	Peptides Uni(Sh)	Pren
		CONTA	3			darr
polyubiquitin**	1050930	8560	247	23	3	I,P
prostaglandin F2 receptor negative regulator	9507007	69986	141	10	6	I.P
similar to CG8841-PÅ, isoform A	109489377	86988	9/	9	3	I,P
similar to RAS and EF-hand containing	109472665	127613	913	62	11	I,P
similar to Y73F8A.5	109467419	110513	72	∞	2(1)	Ϊ́Ρ
single Ig IL-1-related receptor	76363407	46142	06	6	. 60	П
sushi domain containing 2	109509348	95414	383	24	7	I,P
syndecan 4	6981522	21948	236	4	3	I,P
syndecan binding protein/syntenin-1	14010891	32403	92	16	2	Ь
T-cell immunomodulatory protein	19424236	67294	359	33	S	I,P
transmembrane protein 16Å	109459694	146996	41	5	2	I,P
transmembrane protein 16F	62652993	138377	603	29	7	I,P
transmembrane protein 2	62642028	153857	99	5	2	П
transmembrane protein 30A	50925775	37149	63	5	4	I,P
transmembrane protein 63A	109498279	105429	1763	121	13	Ι
transmembrane protein 63B	109486727	123841	82	6	3	I,P
tumor-associated calcium signal transducer 1	49117328	35185	78	3	2	Ι,Ρ
very low density lipoprotein receptor	6981706	96479	643	31	10	I,P
V-set and immunoglobulin domain containing 1	83649788	43f910	57	4	2	Ь
Uncharacterized Proteins						
hypothetical protein LOC290303	57526900	21667	125	∞	2	I,P
hypothetical protein LOC307833	62945264	39917	49	S	2	Ь
hypothetical protein NipSnap2	62945328	32921	49	9	2	Ь
similar to CG5149-PA	109508213	73536	119	∞	3	Ь
uncharacterized protein family UPF0227 member	109459017	51511	114	6	က	П
uncharacterized protein family UPF0227 member	55741536	33972	88 88	9	2	I,P