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Glypican1 identifies cancer exosomes and facilitates early detection of cancer

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Summary

Exosomes are lipid bilayer-enclosed extracellular vesicles (EVs) that contain proteins and nucleic acids. They are secreted by all cells and circulate in the blood. Specific detection and isolation of cancer cell-derived exosomes in circulation is currently lacking. Using mass spectrometry analyses, we identified a cell surface proteoglycan, glypican-1 (GPC1), specifically enriched on cancer cell-derived exosomes. GPC1$^+$ circulating exosomes (crExos) were monitored and isolated

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using flow cytometry from the serum of cancer patients and mice with cancer. GPC1$^+$ crExos were detected in the serum of patients with pancreas cancer with absolute specificity and sensitivity, distinguishing healthy subjects and patients with a benign pancreas disease from patients with early and late stage pancreas cancer. Levels of GPC1$^+$ crExos correlate with tumor burden and survival in patients pre- and post-surgical tumor resection. GPC1$^+$ crExos from patients and from mice with spontaneous pancreas tumors driven by oncogenic KRAS contained RNA with specific KRAS mutation, and it emerges as a reliable biomarker for the detection of PanIN lesions despite negative signal by MRI in mice. GPC1$^+$ crExos may serve as a potential non-invasive diagnostic and screening tool to detect early stages of pancreas cancer to facilitate possible curative surgical therapy.

Introduction

Exosomes are secreted membrane enclosed vesicles (extracellular vesicles or EVs) of a size range of 50 to 150 nm diameter[1]. Formed during the inward budding of late endosomes, they develop into intracellular multivesicular endosomes (MVEs)[2]. During this process, nucleic acids and proteins are encapsulated into exosomes[3–6]. Exosomes are released into the extracellular space and enter the circulation[7,8]. Various cell types such as immune cells[8], platelets[9] or endothelial cells[10], release exosomes into the blood stream. Several exosomes-enriched proteins have been described and include members of the tetraspanin family (CD9, CD63 and CD81), members of the endosomal sorting complexes required for transport (ESCRT; TSG101, Alix) and heat shock proteins (Hsp60, Hsp70, Hsp90)[11]. Epithelial tumor cells secrete exosomes carrying the epithelial cell adhesion molecule (EpCAM)[12–14]. Melanoma-derived exosomes contain the tumor-associated antigen Mart-1 and tyrosinase-related protein-2 (TYRP2)[15–17]. Exosomes from gastric, breast and pancreas cancer carry members of the human epidermal growth factor receptor (HER) family[18–20]. None of these markers are however specific to cancer-derived exosomes. Identification and isolation of cancer specific exosomes in body fluids would aid in the detection and monitoring of cancer and enable specific identification of DNA, RNA and protein content without contamination from non-cancer exosomes. Such possibility could enable the early monitoring of cancer and aid therapy decision.

GPC1 is a cancer exosomes specific protein

EVs from cancer cells (MDA-MB-231, triple negative human metastatic breast carcinoma), fibroblasts (HDF, human dermal fibroblasts; NIH/3T3, mouse embryonic fibroblasts) and non-tumorigenic epithelial cells (MCF10A, human mammary epithelial cells; E10, mouse lung epithelial cells) were isolated using established ultracentrifugation methods[21,22], and called exosomes based on the following observations. NanoSight® nanoparticle tracking analysis and transmission electron microscopy (TEM) revealed a range of 105±5 nm and 112±4 nm in diameter, respectively (Extended Data Fig. 1a,b)[23]. Presence of CD9 on exosomes was shown by immunogold and TEM (Extended Data Fig. 1c) and of flotillin1 and CD81 by immunoblot (Extended Data Fig. 1d, Extended Data Fig. 8)[23]. The exosomes proteome was evaluated using ultra performance liquid chromatography – mass spectrometry (UPLC-MS) (Extended Data Table 1)[24]. Proteins were identified in exosomes derived from different cell types (HDF, NIH/3T3, E10, MCF10A and MDA-MB-231), including the exosomes markers such as TSG101, CD9 and CD63 (total number of proteins identified in exosomes from different cell types were: HDF: 261, NIH/3T3: 171, E10: 232, MCF10A: 214 and MDA-MB-231: 242; Extended Data Table 2). Bioinformatic analyses revealed 48 proteins (25 cytoplasmic, 7 nuclear, 5 transmembrane, 1 membrane-anchored and 7 secreted) as exclusively present in the cancer cell-derived exosomes (MDA-MB-231; Fig. 1a, Extended Data Table 1). Glypican-1 (GPC1) is a membrane anchored protein reported previously as overexpressed in a variety of cancers, including breast and pancreas cancer[25,26,27]. GPC1 transcripts and protein levels were elevated in several breast and pancreas cancer cell lines compared to non-tumorigenic cells (Extended Data Fig. 1e,f & Extended Data Fig. 8). Therefore, in this study we focused on probing the utility of GPC1 as marker of cancer exosomes. In contrast to exosomes derived from non-tumorigenic cell lines, GPC1 protein was only detected in cancer cell-derived exosomes by immunoblot (Extended Data Fig. 1g & Extended Data Fig. 8). Additionally, GPC1$^+$ exosomes were detected by immunogold TEM in cancer exosomes (T3M4 pancreas cancer line) but not in non-cancer exosomes (HMLE; Fig. 1b).

We performed FACS analysis of exosomes coupled to aldehyde/sulphate beads to detect GPC1 protein on their surface (Fig. 1c). Immunogold and TEM identified cancer exosomes at the surface of beads with GPC1 expression while non-tumorigenic exosomes did not exhibit GPC1 expression (Fig. 1d). Exosomes purified using sucrose gradients or ultracentrifugation from cell lines showed GPC1 expression specifically when derived from cancer cell lines (Fig. 1c, e–f; Extended Data Fig. 1h & Extended Data Fig. 8).

To determine whether GPC1$^+$ exosomes could be isolated from the blood of tumor-bearing mice, we implanted MDA-MB-231 human breast cancer cells in the mammary fat pads of nude mice. The mice were bled prior to cancer cell inoculation, and repeatedly again when tumors reached an average volume of 300, 550, 1000 and 1350 mm^3, and circulating exosomes (crExos) were isolated and assessed for the presence of GPC1 (Fig. 2a). The relative percentage of GPC1$^+$ crExos increased proportionally with tumor growth and correlated with tumor burden (Fig. 2b–c; r=0.98, P=0.004). To further confirm the cancer cell origin of GPC1$^+$ crExos, we engineered MDA-MB-231 cells to stably express CD63-GFP fusion protein. CD63 is an established exosomal marker[22] and exosomes from these cells (MDA-MB-231-CD63GFP) in culture were uniformly positive for GFP (Fig. 2d). crExos were also collected from mice with orthotopic MDA-MB-231-CD63GFP tumors (~1500 mm^3 in size), and a subpopulation of the crExos were GFP$^+$ (Fig. 2e). GPC1 expression was exclusively detected in the GFP$^+$ crExos fraction but not in the GFP$^-$ crExos (Fig. 2f).

GPC1$^+$ circulating exosomes as a biomarker

Exosomes derived from cancer cell lines and circulating cancer cell-derived exosomes from tumor-bearing mice were almost exclusively positive for GPC1 (Fig. 1e and Fig. 2f). Next, we isolated crExos from patients with breast cancer (n=32), pancreatic ductal adenocarcinoma (PDAC, n=190) and healthy donors (n=100) (Patient data is shown in Extended Data Table 3). TEM of crExos isolated from the serum revealed a lipid bilayer and

CD9 positivity (Extended Data Fig. 2a–b). crExos isolated using sucrose gradient also showed expression of exosomes marker, flotillin1 (Extended Data Fig. 2c & Extended Data Fig. 8)[23,22]. The relative concentration of crExos was significantly higher in the sera of cancer patients compared to healthy individuals (Extended Data Fig. 2d), and the average size of PDAC crExos was significantly smaller compared to all other crExos (Extended Data Fig. 2e). Analyses of sera from healthy individuals revealed baseline positivity for GPC1 in crExos, ranging from 0.3 to 4.7% (average of 2.3%; Fig. 3a). We observed that 24 out of 32 (75% of patients) breast cancer patients demonstrated crExos GPC1$^+$ level higher that healthy individuals ($P<0.0001$; Fig. 3a). Any specific correlation between the level of GPC1$^+$ crExos and breast cancer subtypes was not appreciated in this patient cohort (Luminal A, Luminal B or Triple Negative subtypes; Extended Data Fig. 2f), albeit group size may be too small to conclusively probe such correlation. In contrast, all 190 PDAC crExos revealed levels of GPC1$^+$ crExos higher than levels noted in serum of healthy individuals ($P<0.0001$; Fig. 3a, Extended Data Fig. 7a–b). These results indicated a strong correlation between GPC1$^+$ crExos and cancer, particularly for PDAC in this analysis. These results encouraged us to perform further analyses to potentially inform on the utility of GPC1$^+$ crExos as a detection and monitoring tool for PDAC.

GPC1$^+$ crExos contain oncogenic Kras^{G12D}

Exosomes contain DNA and RNA[28]. *KRAS* is a frequently mutated gene in pancreas cancer and mutant transcripts have been found in circulation[3,29,30]. Primary tumor samples of 47 patients with PDAC were sequenced to assess oncogenic *KRAS* status. Sixteen PDAC tumors contained wild-type *KRAS* allele, 14 revealed *KRAS*^{G12D}mutation, 11 with *KRAS*^{G12V}allele, 5 with *KRAS*^{G12R} allele and 1 with *KRAS*$^{G12V/C}$ mutation (Fig. 3b). Sufficient amount of corresponding serum was available from 10 patients with Kras^{G12D} mutations and 5 with Kras^{G12V} mutation. GPC1$^+$ crExos and GCP1$^-$ crExos from the same patient were subjected to immunogold TEM to confirm specific GPC1 expression (Fig. 3c). All 15 GPC1$^+$ crExos with tumor validated oncogenic Kras mutation revealed identical mutation by qPCR analysis of exosomal mRNA using specific primers (Fig. 3d). Wild-type Kras mRNA was found both in GPC1$^+$ and GPC1$^-$ crExos, while mutant Kras transcript was only detected in the GPC1$^+$ crExos (Fig. 3d). These results provide further support for the cancer cell origin of the GPC1$^+$ crExos and highlight their potential utility identifying cancer specific genetic defects.

GPC1$^+$ crExos detect early stage pancreas cancer

Further analysis of sera from the discovery cohort of patients revealed that the levels of GPC1$^+$ crExos could distinguish patients with histologically validated pancreatic cancer precursor lesions (PCPL, n=5; Extended Data Table 3) from healthy individuals and patients with benign pancreatic disease (BPD, n=26; Extended Data Table 3, Extended Data Table 4, Fig. 3e). Specifically, the levels of GPC1$^+$ crExos in the PCPL group (intraductal papillary mucinous neoplasm, IPMN n=5) was consistently higher than the levels of GPC1$^+$ crExos in the healthy donor group, as well as in the BPD group (which includes 18 patients with pancreatitis and 8 with cystic adenomas; Fig. 3e). All patients in PCPL group presented with specific clinical symptoms and exhibited a macroscopic mass imaging using MRI or CT.

The BPD group exhibited similar GPC1$^+$ crExos levels (average 2.1% GPC1$^+$ crExos) as healthy individuals (Fig. 3e).

We compared the specificity and sensitivity of GPC1$^+$ crExos detection levels to CA 19-9 levels, a circulating protein currently used as a tumor biomarker for patients with pancreatic adenocarcinoma[31]. CA 19-9 levels were elevated in the serum of patients with PDAC when compared to healthy donors, but CA 19-9 levels were also significantly elevated in the serum of patients with BPD ($P<0.0001$; Extended Data Fig. 2g). Importantly, CA 19-9 serum levels failed to distinguish patients with PCPL from healthy donors (Extended Data Fig. 2g). When comparing patients with pancreatic cancer from stage I to stage IV, to healthy individuals and patients with BPD, the receiver operating characteristic (ROC) curves show that GPC1$^+$ crExos revealed a near perfect classifier with an AUC of 1.0 (95% CI: 0.988 – 1.0) exhibiting a sensitivity of 100% (95% CI: 98.1–100%) and specificity of 100% (95% CI: 97.1–100%); with a positive predictive value of 100% (95% CI: 98.1–100%) and a negative predictive value of 100% (95%: 86.8–100%; Fig. 3f and Extended Data Fig. 3a–f). In contrast, CA 19–9 was inferior in distinguishing between patients with pancreas cancer and healthy controls (AUC of 0.739, 95% CI: 70.2–82.6%, $P<0.001$; Fig. 3f and Extended Data Fig. 3a–f). Of note, neither the concentration of exosomes nor the size of exosomes was a valid parameter to stratify patients with pancreas cancer versus control (Fig. 3f and Extended Data Fig. 3a–f). GPC1$^+$ crExos showed a sensitivity and specificity of 100% in each stage of pancreas cancer (carcinoma-in-situ, stage I as well as stages II–IV), supporting its utility as a biomarker for all stages of pancreas cancer progression and its potential use for early detection of pancreas cancer.

Next, the discovery findings were validated using an independent patient cohort, composed of 6 patients with histologically validated BPD (chronic pancreatitis), 56 patients with PDAC and 20 healthy individuals (Extended Data Table 3). GPC1$^+$ crExos distinguished patients with PDAC from healthy individuals and patients with BPD (Fig. 3g). The BPD group exhibited similar GPC1$^+$ crExos levels as healthy individuals (Fig. 3g). In complete agreement with the discovery cohort, receiver operating characteristic (ROC) curves indicated that GPC1$^+$ crExos (from PDAC, BPD patients and healthy individuals) revealed a near perfect classifier with an AUC of 1.0 (95% CI: 0.956 – 1.0) a sensitivity of 100% (95% CI: 93.6–100%), a specificity of 100% (95% CI: 86.8–100%), a positive predictive value of 100% (95% CI: 93.6–100%), and a negative predictive value of 100% (95%: 86.3–100%; Fig.3h, Extended Data Fig. 3g).

GPC1$^+$ crExos inform pancreas cancer burden

GPC1$^+$ crExos levels correlated with tumor burden in mice (Fig. 2b–c). We next sought to evaluate whether GPC1$^+$ crExos levels could inform on metastatic disease burden of patients with PDAC (Extended Data Table 3). GPC1$^+$ crExos of PDAC patients with distant metastatic disease showed significantly higher levels of bead bound-GPC1$^+$ crExos (average 58.5%) when compared to patients with metastatic disease restricted to lymph nodes (average 50.5%) or no metastases (average 39.9%; Extended Data Fig. 4a). Further, we evaluated GPC1$^+$ crExos in serum of PDAC patients at pre- and post surgery stages (post operative day 7; PDAC n=29, PCPL n=4 and BPD n=4; Fig. 4a). Twenty-eight out of 29

PDAC patients and all PCPL patients with longitudinal blood collections showed a significant decrease in GPC1$^+$ crExos levels following surgical resection (PDAC: $P<0.0001$; PCPL: $P<0.001$; Fig. 4b). In contrast, CA 19-9 levels decreased in only 19 out of 29 PDAC patients and in none of the PCPL patients (PDAC: $P=0.003$; PCPL: $P=0.81$; Extended Data Fig. 4b). In 4 BPD patients, the levels of neither GPC1$^+$ crExos nor CA 19-9 showed a difference (Fig. 4b and Extended Data Fig. 4b).

To determine the prognostic relevance of GPC1$^+$ crExos in this longitudinal study cohort (Fig. 4a), patients were dichotomized into 2 groups. Group 1 was defined by a decrease of GPC1$^+$ crExos greater or equal (≥) to the median decrease in GPC1$^+$ crExos, and group 2 was defined by a decrease of GPC1$^+$ crExos less (<) than the median decrease of GPC1$^+$ crExos. Group 1 presented with improved overall (26.2 months) and disease specific (27.7 months) survival when compared to group 2 (15.5 months for both overall and disease specific), indicating that a greater decrease in GPC1$^+$ crExos levels after surgery is associated with increased survival (Fig. 4c–d). While a decrease in CA 19-9 levels is noted when comparing pre- and post-resection blood draws, this decrease did not significantly associate with overall and disease-specific survival (Fig. 4e–f and Extended Data Fig. 4b). Using a Cox regression model for a multivariate test to include the decrease in GPC1$^+$ crExos, median age, AJCC stage, tumor grade and CA 19-9 levels, only GPC1$^+$ crExos revealed to be an independent prognostic and predictive marker for disease-specific survival (hazard ratio: 5.353, CI: 1.651–17.358, $P=0.005$; Extended Data Fig. 4c–d).

Next, we evaluated whether an ELISA for circulating GPC1 could function with the same specificity and sensitivity as GPC1$^+$ crExos. Serum samples of the validation cohort (20 healthy individuals, 6 BPD patients and 56 PDAC patients) were analyzed for circulating GPC1. While GPC1 levels were significantly higher in the PDAC patients when compared to BPD patients and healthy individuals, the sensitivity and specificity of the assay was lower when compared to GPC1$^+$ crExos. The GPC1 ELISA was similar to circulating CA 19-9 assay. Receiver operating characteristic curve (ROC) indicated that GPC1 circulating protein shows an AUC of 0.781 (95% CI: 0.675–0.865) a sensitivity of 82.14% (95% CI: 69.6–91.9%), a specificity of 75% (95% CI: 54.9–90.6%), a positive predictive value of 0.04 (95% CI: 0 – 17.4%), and a negative predictive value of 100% (95%: 94.2 – 100%; Extended Data Fig. 4e–f).

GPC1$^+$ crExos to detect early PanIN lesions

In light of the highly specific and sensitive detection of GPC1$^+$ crExos in pancreas cancer, we next evaluated time course of GPC1$^+$ crExos appearance in the serum relative to pancreas tumor burden. To this end, we employed a genetically engineered mouse model (GEMM) for PDAC. The Ptf1a$^{cre/+}$; LSL-Kras$^{G12D/+}$; Tgfbr2$^{L/L}$ mice (PKT mice)[32] develop PDAC with full penetrance that reliably recapitulates the clinical and histopathological features of the human disease[32,33]. The PKT mice consistently progress from pancreatic intraepithelial neoplasia (PanIN) at 4.5 weeks of age and die at 8 weeks of age due to PDAC[32,33] (Extended Data Fig. 5a). In a longitudinal study, we bled PKT and littermate control mice repeatedly at 4, 5, 6, 7 and 8 weeks of age (n=7 PKT mice and n=6 control mice; Fig. 5a). Three out of 7 PKT mice were euthanized by week 7 along with 4 out of 6 controls, while the remaining 3 PKT mice and 2 controls were euthanized at week 8. At 4 weeks of age PKT mice showed on average an 8.4% GPC1$^+$ crExos, and this increased proportionally with time (and tumor burden) and severity of disease (histopathology), whereas control mice showed an average of 1.2% GPC1$^+$ crExos and this level remained constant with time (Fig. 5b). crExos sizes and concentration did not consistently correlate with disease over time (Extended Data Fig. 5b,c). Magnetic resonance imaging (MRI), an established imaging modality used for the evaluation of PDAC[34], was performed at the same time points when mice were bled to measure GPC1$^+$ crExos (Fig. 5c). When evaluated as a group, GPC1$^+$ crExos levels appeared prior to MRI detectable pancreatic masses (Fig. 5c–d and Extended Data Fig. 5d). GPC1$^+$ crExos size and concentration minimally correlated with pancreas cancer (Extended Data Fig. 5b–c), whereas GPC1$^+$ crExos levels correlated with tumor volume determined by MRI, and appeared to lead the growth of the tumor (Pearson correlation test, r=0.67, P=0.0005, 95% CI: 0.3504–0.8462; Fig. 5c,d and Extended Data Fig. 5d). Importantly, no elevation of GPC1$^+$ crExos was noted in mice cerulein-induced acute pancreatitis, supporting GPC1$^+$ crExos is elevation is pancreas cancer specific (Extended Data Fig. 5e). ROC curve analysis for GPC1$^+$ crExos showed an AUC of 1.0 (95% CI: 0.75–1.0) in PKT mice compared to healthy littermate control mice at all ages evaluated (Fig. 5e and Extended Data Fig. 5f).

A cross-sectional study was also initiated to assay tumor burden and GPC1$^+$ crExos in PKT mice, as early as 16 and 20 days of age (Fig. 5f). Mice were imaged by MRI, bled and euthanized at these early time points, when mice present with pre-PanIN to early PanIN lesions (Fig. 5f, Extended Data Fig. 6a and Extended Data Table 5). GPC1$^+$ crExos were detected in all PKT mice (PKT: 8.3% average, control: 1.8% average; Fig. 5g and Extended Data Table 5). Histological analysis of PKT mice confirmed pre-PanIN lesions in 4 out of 7 PKT mice, and despite no observed histological lesions in 3 out of 7 PKT mice, GPC1$^+$ crExos predicted future pancreas cancer emergence (Extended Data Table 5). Moreover, we did not observe pancreas-associated masses by MRI in 16 and 20 days old PKT mice. Both histopathological score and age of PKT mice correlated with GPC1$^+$ crExos levels (Fig. 5h–i). Of note, in 4 out of 7 PKT mice with no observed histological lesions, downstream signals for Kras activation, such as phosphorylated ERK (pERK), was detected in the pancreas tissue (Fig. 5j and Extended Data Fig. 6a). We also observed exclusive detection of mutant Kras^{G12D} mRNA in GPC1$^+$ crExos compared to GPC1$^-$ crExos (Extended Data Fig. 6b).

Discussion

Tumor-derived exosomes are enriched in GPC1, and GPC1$^+$ crExos exclusively carry mutant Kras mRNA. We show that GPC1$^+$ crExos is a reliable biomarker for detection of early pancreas cancer. GPC1$^+$ crExos are a prognostic marker superior to CA 19-9, the currently employed serum biomarker in pancreas cancer. GPC1$^+$ crExos lead MR imaging as they can be detected in circulation prior to MRI-detectable lesions in GEMM of pancreas cancer.

Routine screening of the general population for a rare cancer such as PDAC using MRI or CT would be prohibitively expensive and associated with a high false positive rate[35]. GPC1$^+$

crExos detect possibility of pancreas cancer in 16-day-old mice with unremarkable pancreas histology and negative MRI. These results suggest the utility of GPC1$^+$ crExos as a detection and monitoring tool for pancreas cancer, with an emphasis on its application in early detection, a clinical challenge that remains to be addressed.

While oncogenic KRAS mutations are likely driver mutations for pancreas cancer and are detected in early PanIN-1 lesions, it is still estimated that 15 to 20 years may lapse before early PanIN lesions become metastatic PDAC[36–38]. While this could offer a window for early detection of this disease, PDAC currently presents late with rather non-specific clinical symptoms. Therefore, as many as 80% of patients present with regional and distant metastasis at diagnosis[39]. Although our understanding of the molecular and genetic details associated with the progression of non-malignant precursor lesions to PDAC is steadily increasing, such knowledge has yet to translate into the development of biomarkers that do not require invasive biopsies. Patients with pancreas cancer exhibit elevated serum levels of CA 19-9, CEA, CA-50, SPan-1, peanut agglutinin, DU-PAN-2, a-fetoprotein, tissue polypeptide antigen and pancreatic oncofetal antigen[40]. While each of these markers exhibits some utility in tracking biopsy-diagnosed disease they are not tumor specific because they are also elevated in patients with benign diseases of the pancreas. The lack of specific serum-based biomarkers with high degree of sensitivity and specificity and retroperitoneal position of the pancreas further challenges the early detection of pancreas cancer[41,42]. Pancreatico-duodenectomy (Whipple procedure) can be curative for PDAC patients if tumors are detected early with clear surgical margins[43]. Due to the late diagnosis of pancreas cancer, only around 15% of patients present with surgically resectable tumors[44]. Studies comparing stage of disease with outcome following surgery suggests that death rates for PDAC would be reduced if the disease were diagnosed at an earlier stage[45].

Specific isolation of exosomes from the serum of cancer patients remains a challenge due to the lack of specific markers that can be used to identify and distinguish cancer exosomes from exosomes produced by other cells. Genetic profiling studies on circulating DNA from cancer patients are cofounded by the fact that the isolated DNA represents all cells of the body, thus making mutation and genetic defects challenging[46,47]. We previously demonstrated that the DNA in circulation is mainly contained in exosomes[6]. Therefore a marker for cancer-derived exosomes will significantly increase the sensitivity of detection for low frequency mutations in the circulation. Such mutations are frequently associated with tumor complexity and therapy resistance and relapse, providing a highly specific and sensitive non-invasive tool for genetic monitoring of a tumor. As a proof of concept GPC1$^+$ crExos identified KRAs mutations with 100% correlation with KRAS mutations in the tumor.

Our results provide evidence for GPC1 as a pan-specific marker of cancer exosomes. GPC1 is a cell surface proteoglycan that interacts with many proteins and has diverse functions[48]. Many cancer cells overexpress glypican-1 with most abundant increase observed in pancreas cancer cells lines and tissue[25–27]. Many studies have suggested a role of GPC1 as a positive regulator of cancer progression using orthotopic and GEMMs of PDAC[49,50]. GPC1$^+$ crExos is an attractive candidate for detection and isolation of exosomes in circulation of cancer patients for further genetic analysis of cancer specific alterations in DNA, microRNA, RNA and proteins. Such opportunity offers an unprecedented opportunity for informative early detection of pancreas cancer and help design potential curative surgical options.

Methods

Patient samples and tissue collection

The study was conducted according to the Reporting Recommendations for Tumor Marker Prognostic Studies (REMARK) criteria. The studies using human samples were designed as an explorative study. As there was no interventional approach in this study, a priori power calculation was not applicable. Instead, the number of patients included was assessed based on previous studies investigating the diagnostic relevance of circulating biologicals in pancreatic cancer[51].

Serum samples and tissue samples from patients with pancreas cancer, serum samples only from patients with a benign pancreas disease and from healthy donors, who had no evidence of acute or chronic or malignant disease and had no surgery within the past 12 months, were received from the department of General, Visceral and Transplantation Surgery from the University of Heidelberg and from the University Hospital of Dresden after approval by the local institutional review board (Heidelberg: 323/2004, Dresden: EK357112012). The cases were obtained under an IRB-exempt protocol of the MD Anderson Cancer Center (IRB no. PA14-0154). Serum samples from patients with breast cancer were collected at the MD Anderson Cancer Center after approval of the institutional review board (IRB no. LAB10-0690). A written consent for the serum sampling and tumor sampling was obtained pre-operatively from all patients and prior to serum collection from each healthy donor with disclosure of planned analyses regarding potential prognostic markers. The patients included in this study were all consecutive patients who underwent a surgical procedure at the University Hospital of Heidelberg, Germany, at the University Hospital of Dresden, Germany (pancreas disease) or at the MD Anderson Cancer Center (breast cancer). All samples were randomly selected from larger cohorts and were analyzed in a blinded fashion. Unblinding of clinical parameters and corresponding experimental data was performed only after finishing all experiments. Inclusion criteria of patients were a minimum of 18 years of age, histologically verified pancreas cancer (pancreatic ductal adenocarcinoma), histologically verified benign pancreas disease or breast cancer in a resection specimen, and a negative medical history for any other malignant disease. All blood samples were taken before treatment. Inclusion criteria for healthy control donors were a negative medical history for any malignant disease.

On the day of surgery, 10 ml serum separator tubes were used to collect blood samples before surgical incision. The blood samples were then centrifuged at 2,500g for 10 min to extract the serum, and the serum was stored at −80°C until analyzed. Likewise, blood samples were collected on day 7 after surgery for 29 patients with an adenocarcinoma of the pancreas (PDAC), 4 patients with chronic pancreatitis and 4 patients with an intraductal papillary mucinous neoplasm (IPMN).

Patient characteristics and clinical specimens

The pancreatic discovery cohort from the University Hospital of Heidelberg included 190 patients with an adenocarcinoma of the pancreas (PDAC), 18 patients with pancreatitis, 8 patients with a benign serous cystadenoma and 5 patients with an intraductal papillary mucinous neoplasm (IPMN). Patients were subjected to surgery between 2006 and 2012 at the Department of General, Visceral, and Transplantation Surgery, University of Heidelberg. Clinical information included age, gender, AJCC tumor stage, tumor size (pT), presence and number of lymph node metastases (pN), tumor grade (G), and treatment with (neo-)/adjuvant chemotherapy. The pancreatic cohort from the University Hospital of Dresden included 56 patients with an adenocarcinoma of the pancreas (PDAC), 6 patients with chronic pancreatitis, and 20 healthy donors. Patients were subjected to surgery between 2007 and 2013 at the Department of Gastrointestinal, Thoracic and Vascular Surgery, University of Dresden. Clinical information included age, gender, AJCC tumor stage, tumor size (pT), presence and number of lymph node metastases (pN), tumor grade (G), and treatment with (neo-)/adjuvant chemotherapy. The breast cancer cohort consisted of 32 women with breast cancer. All breast cancer patients were treated at the MD Anderson Cancer Center, Houston, Texas. Clinical information included age, gender, AJCC tumor stage, tumor size (pT), presence and number of lymph node metastases (pN), tumor grade, and treatment with (neo-)/adjuvant chemotherapy.

Animal Studies

Nude mice (nu/nu) (purchased from Jackson Laboratory) underwent breast pad injections with 0.5 million MDA-MB-231 cells or MDA-MB-231-CD63GFP cells in 20 µl of PBS injected per breast pad. Blood was collected retro-orbitally and exosomes were isolated prior to injection and at tumor volumes of 300, 550, 1000 and 1350mm^3. Mice were euthanized when the tumor size reached 1500 mm^3 or when severe disease symptoms were present.

The disease progression and genotyping for the Ptf1a$^{cre/+}$; LSL-Kras$^{G12D/+}$; Tgfbr2$^{L/L}$ (PKT) and the Pdx1$^{cre/+}$; LSL-Kras$^{G12D/+}$; p53$^{R172H/+}$ (KPC) mice was previously described[32,33,52]. In the PKT longitudinal cohort, retro-orbital blood collections were performed at 4, 5, 6, 7 and 8 weeks of age. Mice were euthanized at 8 weeks of age or sooner if severe disease symptoms were noted. Histopathological analysis of mouse pancreas specimen was performed following previously defined criteria[4]. Four C57BL/6 adult mice were subjected to repeated cerulean injection to induce acute pancreatitis (five hourly repeated i.p. injections of 50 µg cerulein per kg of body weight) and euthanized 24 hrs after injection the last injection. Histological analyses of pancreas of mice was performed according to Hingorani SR et al.[52], and an histological score was attributed according to the type of lesions detected: Score 1: PanIN1a, Score 2: PanIN1 a/b, Score 3: PanIN2, Score 4: PanIN3, Score 5: Ductal adenocarcinoma. All mice were housed under standard housing conditions at the MD Anderson Cancer Center (MDACC) animal facilities, and all animal procedures were reviewed and approved by the MDACC institutional animal care and use committee.

Cell lines

The following human cells lines were used: HMLE (American Type Culture Collection – ATCC, Manassas, VA), BJ (ATCC), HDF (ATCC), HMEL (ATCC), MCF-7 (ATCC), MDA-MB-231 (ATTC), Panc-1 (ATTC), SW480 (ATCC), HCT-116 (ATCC), MIA Paca2 (ATCC) and T3M4 cells (Cell Bank, RIKEN BioResource Centre, Japan). The following murine cells lines were used: NIH/3T3 (ATCC), E10 (ATCC), NMuMG (ATTC), 4T1 (ATTC) and B16F10 cells (ATTC). HDF cells were cultured in DMEM supplemented with 20% (v/v) fetal bovine serum (FBS), 100 $U.ml^{-1}$ penicillin and 100 $\mu g.ml^{-1}$ streptomycin. HMLE cells and MCF10A cells were grown in DMEM/F12 supplemented with 5% (v/v) horse serum, 100 $U.ml^{-1}$ penicillin, 100 $\mu g.ml^{-1}$ streptomycin, 20 $ng.ml^{-1}$ EGF, 0.5 $mg.ml^{-1}$ hydrocortisone, 100 $ng.ml^{-1}$ cholera toxin and 10 $\mu g.ml^{-1}$ insulin. HMEL, MCF-7, MDA-MB-231, HCT-116, SW480, 4T1, NIH/3T3, E10, U87 and B16F10 cells were maintained in DMEM supplemented with 10% (v/v) FBS, 100 $U.ml^{-1}$ penicillin and 100 $\mu g.ml^{-1}$ streptomycin. Panc-1, MIA Paca2 and T3M4 cells were cultured in RPMI-1640 supplemented with 10% (v/v) FBS, 100 $U.ml^{-1}$ penicillin and 100 $\mu g.ml^{-1}$ streptomycin. NMuMG cells were grown in DMEM supplemented with 10% (v/v) FBS, 100 $U.ml^{-1}$ penicillin, 100 $\mu g.ml^{-1}$ streptomycin and 10 $\mu g.ml^{-1}$ insulin. All cell lines were kept in a humidifying atmosphere at 5% CO_2 at 37°C. MDA-MB-231-CD63GFP cells were engineered by transfection with a plasmid encoding a CD63-GFP fusion protein expressed under the control of a CMV promoter (p-CMV6-CD63-GFP from Origene, RG217238). Transfections were performed using Lipofectamine 2000 reagent (Invitrogen).

Exosomes isolation from cells

Exosomes were obtained from supernatant of cells as previously described with some modifications[6]. Briefly, cells were grown in T225 cm^2 flasks in FBS-depleted of exosomes RPMI media until they reached a confluency of 80–90%. Next, the media was collected and centrifuged at 800g for 5 min, followed by a centrifugation step of 2,000g for 10 min to discard cellular debris. Then, the media was filtered using a 0.2 μm pore filter (Syringe filter, Cat. No. 6786-1302, GE Healthcare, UK). The collected media was then ultracentrifuged at 100,000g for 2 hrs at 4°C. The exosomes pellet was washed with 35 ml 1X PBS, followed by a second step of ultracentrifugation at 100,000g for 2 hrs at 4°C. Afterwards, the supernatant was discarded. Exosomes used for RNA extraction were resuspended in 500 μl of Trizol; exosomes used for protein extraction were resuspended in 250 μl of lysis buffer (8M Urea/2.5%SDS, 5 $\mu g.ml^{-1}$ leupeptin, 1 $\mu g.ml^{-1}$ pepstatin and 1mM phenylmethylsulphonyl fluoride). Exosomes used for flow cytometry analysis (FACS), transmission electron microscopy (TEM; see sections below) and immunogold staining were resuspended in 100 μl 1X PBS. Ten microliters of these exosomes sample were used for NanoSight LM10 (NanoSight Ltd., Minton Park, Amesbury, UK) analysis after dilution 1:100 in 1X PBS.

Exosomes isolation from human serum samples

As previously described, 250 μl of cell-free serum samples were thawed on ice[6]. Serum was diluted in 11 ml 1X PBS and filtered through a 0.2 μm pore filter. Afterwards, the samples were ultracentrifuged at 150,000g overnight at 4°C. Next, the exosomes pellet was washed in 11 ml 1X PBS followed by a second step of ultracentrifugation at 150,000g at 4°C for 2 hrs. The supernatant was discarded and pelleted exosomes were resuspended in 500 µl of Trizol for RNA analyses; or in 250 µl of lysis buffer (8M Urea/2.5%SDS, 5 µg.ml^{-1} leupeptin, 1 µg.ml^{-1} pepstatin and 1mM phenylmethylsulphonyl fluoride) for protein analyses. Exosomes used for flow cytometry analysis (FACS), transmission electron microscopy (TEM; see sections below) and immunogold staining were resuspended in 100 µl 1X PBS. Ten microliters of this exosomes sample were used for NanoSight LM10 (NanoSight Ltd., Minton Park, Amesbury, UK) analysis after Nano dilution 1:100 in 1X.

Immunogold Labeling and Electron Microscopy

Fixed specimens at an optimal concentration were placed onto a 400 mesh carbon/formvar coated grids and allowed to absorb to the formvar for a minimum of 1 minute. For immunogold staining the grids were placed into a blocking buffer for a block/permeabilization step for 1 hr. Without rinsing, the grids were immediately placed into the primary antibody at the appropriate dilution overnight at 4°C (1:300 anti-CD9 ab92726, Abcam and anti-GPC1 PIPA528055, Thermo Scientific). As controls, some of the grids were not exposed to the primary antibody. The following day, all the grids were rinsed with PBS then floated on drops of the appropriate secondary antibody attached with 10 nm gold particles (AURION, Hatfield, PA) for 2 hrs at room temperature. Grids were rinsed with PBS and were placed in 2.5% Glutaraldehyde in 0.1M Phosphate buffer for 15 min. After rinsing in PBS and distilled water the grids were allowed to dry and stained for contrast using uranyl acetate. The samples were viewed with a Tecnai Bio Twin transmission electron microscope (FEI, Hillsboro, OR) and images were taken with an AMT CCD Camera (Advanced Microscopy Techniques, Danvers, MA).

Sucrose gradient

Sucrose density gradients were performed to purify exosomes. Exosomes were resuspended in 2 ml of HEPES/sucrose stock solution (2.5M sucrose, 20mM HEPES/NaOH solution, pH 7.4). The exosomes suspension was overlaid with a linear sucrose gradient (2.0-0.25M sucrose, 20mM HEPES/NaOH, pH 7.4) in a SW41 tube (Beckman). The gradients were ultracentrifuged for 16 hrs at 210,000g at 4°C. Gradient fractions of 1 ml were collected from top to bottom and densities of each fractions were evaluated using a refractometer. Next, the exosomes pellets were washed in 1X PBS followed by a second step of ultracentrifugation at 150,000g at 4°C for 2 hrs. Exosomes pellets were resuspended in Laemmli buffer and/or PBS for further immunoblot and flow cytometry analysis.

Flow cytometry analysis of exosomes-bound beads

Exosomes were attached to 4 µm aldehyde/sulfate latex beads (Invitrogen, Carlsbad, CA, USA) by mixing 30 µg exosomes in a 10 µl volume of beads for 15 min at room temperature with continuous rotation. This suspension was diluted to 1 ml with 1X PBS and left for 30 min rotating at room temperature. The reaction was stopped with 100mM glycine and 2% BSA in 1X PBS and left 30 min rotating at room temperature. Exosomes-bound beads were washed 1 time in 1X PBS/2% BSA and centrifuge for 1 min at 10,000 rpm, blocked with 10% BSA with rotation at room temperature for 30 min, washed a second time in 1X PBS/2% BSA and centrifuged for 1 min at 10,000 rpm, and incubated with anti-GPC1

(PIPA528055, Thermo-Scientific, 3 μl of antibody in 20 μl of 2%BSA/1X PBS) during 30 min rotating at 4°C. Beads were centrifuged for 1 min at 10,000 rpm, the supernatant was discarded and beads were washed in 1X PBS/2% BSA and centrifuged for 1 min at 10,000 rpm. Alexa-488 or Alexa-594-tagged secondary antibodies (Life Technologies, NY 14072, USA, 3 μl of antibody in 20 μl of 2%BSA/1X PBS) were used during 30 min with rotation at 4°C. Secondary antibody incubation alone was used as control and to gate the beads with GPC1$^+$ bound exos. The percent positive bead was calculated relative to the total number of beads analyzed per sample (100,000 events). This percentage was therein referred to as the percent beads with GPC1$^+$ exosomes.

Ultra performance liquid chromatography – mass spectrometry (UPLC-MS)

Exosomes were mixed with 200 μl of methanol spiked with the Internal Standard tryptophan-d5. After brief vortex mixing, the samples were incubated for 1 hr at −20°C. After centrifugation at 16,000g for 15 min at 4°C, 190 μl of the supernatants was collected and the solvent removed. The dried extracts were then reconstituted in 15 μl of methanol, of which 10 μl were transferred to microtubes and derivatized. Chromatographic separation and mass spectrometric detection conditions employed are summarized below:

System	SQD
Column type	UPLC BEH C18, 1.0 x 100 mm, 1.7 μm
Flow rate	0.14 ml/min
Solvent A	H2O + 10mM Ammonium Bicarbonate (+NH4OH until pH: 8.8)
Solvent B	ACN
(%B), time	2%, 0 min
(%B), time	8%, 6.5 min
(%B), time	20%, 10 min
(%B), time	30%, 11 min
(%B), time	99.9%, 12 min
(%B), time	2%, 14 min
Column temperature	40°C
Injection volume	1 μl
Ionisation	ES+
Source temperature	120°C
Nebulisation N2 flow	600 l / hour
Nebulisation N2 temperature	350°C
Cone N2 flow	10 l / hour
Capillary voltage	3.2 kV
Cone voltage	30 V

The mass range, 50 – 1000 m/z, was calibrated with cluster ions of sodium formate. An appropriate test mixture of standard compounds was analyzed before and after the entire set of randomized duplicated sample injections, in order to examine the retention time stability and sensitivity of the LC/MS system throughout the course of the run. Data were processed using the TargetLynx application manager for MassLynx 4.1 software (Waters Corp., Milford, USA). A set of predefined retention time, mass-to-charge ratio pairs, Rt-m/z, corresponding to metabolites included in the analysis are fed into the program. Associated extracted ion chromatograms (mass tolerance window = 0.05 Da) are then peak-detected and noise-reduced in both the LC and MS domains such that only true metabolite related features are processed by the software. A list of chromatographic peak areas is then generated for each sample injection, using the Rt-m/z data pairs (retention time tolerance = 6 s) as identifiers. Normalization factors were calculated for each metabolite by dividing their intensities in each sample by the recorded intensity of the internal standard in that same sample. Visualization of disjoint and overlapping protein data sets was carried out by drawing a VennDiagram of the 5 protein data sets using an R package[53].

Cancer Antigen CA 19-9 Human and GPC1 ELISAs

Serum CA 19-9 and GPC1 protein levels in patients with pancreatic cancer, pancreatic cancer precursor lesion, or benign pancreatic disease, and in healthy donors were assessed using the Cancer Antigen CA 19-9 Human ELISA Kit (Abcam, ab108642) and the GPC1 Human ELISA kit (ABIN840422), according to the manufacturer's directions.

Western blot analyses

Cells were lysed in RIPA buffer containing 5 μg.ml^{-1} leupeptin, 1 μg.ml^{-1} pepstatin and 1mM phenylmethylsulphonyl fluoride. Exosomes were lysed in 8M Urea/2.5% SDS containing 5 μg.ml^{-1} leupeptin, 1 μg.ml^{-1} pepstatin and 1mM phenylmethylsulphonyl fluoride. Sample loading was normalized according to Bradford relative protein quantification and proteins separated following an electrophoretic gradient across polyacrylamide gels. Wet electrophoretic transfer was used to transfer the proteins in the gel onto PVDF membranes (ImmobilonP). The protein blot was blocked for 1hr at room temperature with 5% non-fat dry milk in PBS/0,05% Tween and incubated overnight at 4°C with the following primary antibodies: 1:300 anti-GPC1, PIPA528055 (Thermo-Scientific); 1:300 anti-β-Actin A3854 (Sigma-Aldrich); 1:300 anti-CD81 sc-166029 (Santa-Cruz); 1:300 anti-Flottilin1 sc-25506 (Santa-Cruz). Afterwards, HRP conjugated secondary antibodies were incubated for 1 hr at room temperature. Washes after antibody incubations were done on an orbital shaker, four times at 10 min intervals, with 1X PBS 0.05% Tween20. Blots were developed with chemiluminescent reagents from Pierce.

RNA extraction of cells and exosomes

RNA of cells and exosomes was isolated using Trizol Plus RNA purification kit (Life Technologies, 12183555) according to manufactures protocol. RNA was quantified using a Nanodrop® ND-1000 (Thermo Fischer Scientific).

Quantitative real-time-PCR (qRT-PCR)

qRT-PCR was performed on DNase treated RNA using the SuperScript® III Platinum® One-Step Quantitative RT-PCR System (Cat. no. 11732-088, Invitrogen, Life Technologies, Grand Island, NY 14072 USA) according to the manufacturer's directions on a 7300

Sequence Detector System (Applied Biosystems). 150 ng of RNA extracted from 2.5 × 10^8 exosomes was used as qPCR input. Primers for KRAS G12D mRNA and KRAS G12V mRNA (both Sigma-Aldrich Corp. St. Louis, MO, USA) were designed as reported previously[54]. Briefly, the altered base of KRAS G12D and KRAS G12V mutation was kept at the 3′ end of the forward primer. An additional base mutation was included two positions before the Kras mutation in order to increase the specificity of the amplification of the mutant Kras allele. Forward primer sequences for KRAS G12D mRNA: F-5′-ACTTGTGGTAGTTGGAGC*A*G*A*-3′. Forward primer sequences for KRAS G12V mRNA: F-5′-ACTTGTGGTAGTTGGAGC*A*G*T-3′.* Forward primer sequences for KRAS wild-type mRNA: F-5′-ACTTGTGGTAGTTGGAGCTGG-3′. Reverse primer for all KRAS: R-5′-TTGGATCATATTCGTCCACAA-3′. GPC1 mRNA primer pairs (Cat. No. PPH06045A) and 18S mRNA primer pairs (Cat. No. QF00530467) were purchased as ready specific primer pairs from Qiagen (Qiagen, Hilden, Germany). Threshold cycle[55] (C_t) the fractional cycle number at which the amount of amplified target reached a fixed threshold, was determined and expression was measured using the $2^{-\Delta Ct}$ formula, as previously reported[56].

DNA extraction from human primary pancreatic cancer tumors and crExos

Immediately after resection, pancreatic tumor samples were snap-frozen in liquid nitrogen and stored at −80°C until further processing. A 10 μm reference section of each sample was cut and stained with hematoxylin and eosin by standard methods to evaluate the proportion of tumor tissue and adjacent tumor stroma. Samples with a tumor stroma proportion > 30 % were excluded into this study. DNA isolation was performed using a commercial DNA Extraction Kit (DNeasy Blood & Tissue Kit, Cat. No. 69506, Qiagen, Germany) according to the manufacturer's protocol. The amount of DNA from tumor samples was quantified using a Nanodrop® 1000 Spectrophotometer (Thermo Fisher Scientific, Wilmington, DE 19810, USA).

Polymerase chain reaction (PCR) and Sanger Sequencing

PCR was performed in a 25 μl reaction tube consisting of 10 μl template DNA, 1 μM of each primer, 2.5mM dNTP, 2.5 10 x PCR Buffer, 25mM Mg solution, 0.5 μl H_2O and 2.5 μl Taq Polymerase. Amplification was carried out in a T100 ThermoCycler (Bio-Rad) under following conditions: 94°C for 1 min, 2 cycles of 94 °C for 10 s, 67°C for 30 s, 70 °C for 30 s; 2 cycles of 94 °C for 10 s, 64°C for 30 s, 70 °C for 30 s; 2 cycles of 94 °C for 10 s, 61°C for 30 s, 70 °C for 30 s; 35 cycles of 94 °C for 10 s, 59°C for 30 s, 70 °C for 30 s; endless 4 °C. KRAS amplicon were generated using the following primers: forward 5′-AAGGCCTGCTGAAAATGACTG-3′, 5′-AGAATGGTCCTGCACCAGTAA-3′. PCR products were purified using the QIAquick PCR purification kit (Qiagen, Hilden, Germany). Subsequently, sequencing reaction was performed using BigDye terminator kit (v3.1, Life Technologies, USA) according to the manufacturer's instructions. Sequencing products were separated on an ABI 3730 automated sequencer (Life Technologies, USA). KRAS mutation status was evaluated using Finch TV (Geospiza, Inc., Seattle, WA 98119, USA).

MRI imaging

MRI studies were conducted using a 7T small animal MR system, the Biospec USR70/30 (Bruker Biospin MRI, Billerica, MA) is based on an actively-shielded 7T magnet with a 30-

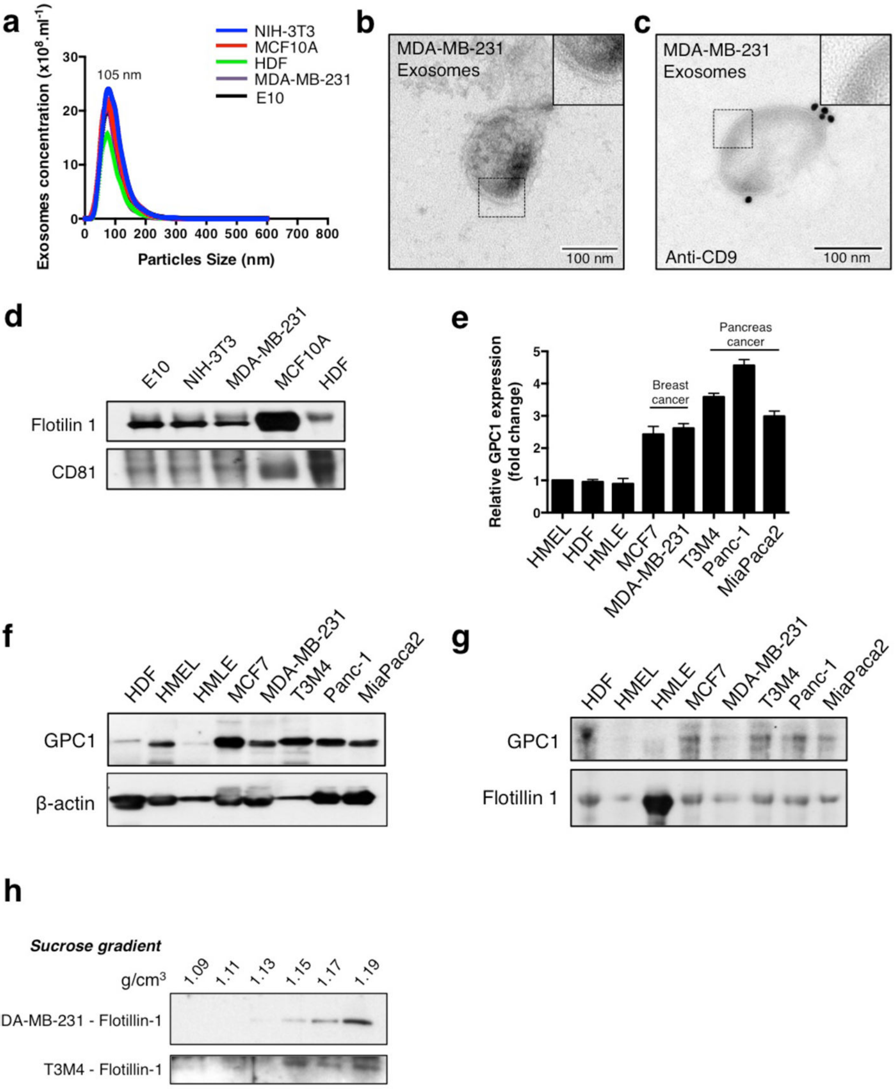
cm bore and cryo-refrigeration. The system is equipped with 6 cm inner-diameter gradients that deliver a maximum gradient field of 950 mT/m. A 3.5 cm inner-diameter linear birdcage coil transmits and receives the MR signal. For image acquisition, T2 weighted, respiratory gated, multi-slice imaging will be performed with respiration held to under 25 breaths per minute to minimize motion artifacts in the abdomen. For mice where fat signal might mask the T2 weighted image the fat-suppression pulse module will be utilized. Acquisition parameters were minimally modified from Schmid A et. Al.[57]. The RARE-T2 weighted pulse sequence was modified to include an effective Te of 56 ms with a total TR of 2265 ms. Between 18 and 20 coronal slices were acquired per mouse with a slice thickness of 0.75 mm and slice spacing of 1 mm. In plane, pixel sizes of 0.156 mm × 0.156 mm with a matrix size of 256×192 (40 mm × 30 mm FOV) was chosen to minimize in plane partial volume effects, maintain a FOV sufficient to cover the abdomen, while also providing sufficient throughput for the experiment.

To measure tumor burden, the region of suspected lesions are drawn blinded on each slice after images intensities were normalized. The volume is calculated by addition of delineated region of interest in mm^2 x 1 mm slice distance.

Statistical analysis

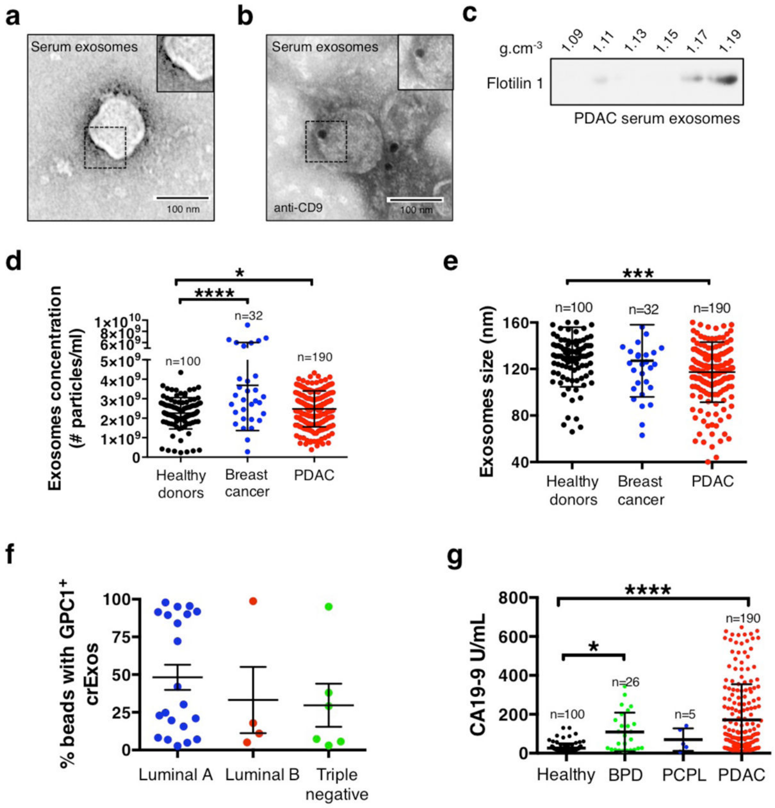
The GraphPad Prism version 6.0 (GraphPad Software, La Jolla, CA 92037 USA) and MedCalc statistical software version 13.0 (MedCalc Software bvba, Acacialaan 22, 8400 Ostend, Belgium) were used for all calculations. Unpaired Student's *t*-test was applied to calculate expression differences of the qPCR results (dCt-values). Analysis of variance (ANOVA) tests were performed to calculate differences of multiple serum factors in murine and human serum samples. As a post-hoc test, a Tukey-Kramer test was applied for pairwise comparison of subgroups when the ANOVA test was positive in case of equal variance. Tamhane T_2 test was applied for pairwise comparison of subgroups when the ANOVA test was positive in case of unequal variances. A paired two-tailed Student's *t*-test was applied to assay differences in percent bead with $GPC1^+$ crExos and CA 19-9 in the longitudinal cohort between pre-operative and postoperative blood samples. Receiver operating characteristic curves (ROC) were used to determine the sensitivity, specificity, positive and negative predictive value and to compare area under the curves (AUC) of serum factors using the Delong method[58]. The cut-off value was determined using the Youden-Index. Univariate analysis using the log-rank test was conducted to visualize (Kaplan Meier curves) and assess disease-specific survival (time from diagnosis to cancer-related death or last follow-up) in the longitudinal cohort of patients with pancreatic cancer. A multivariate analysis using the Cox proportional hazards regression model was performed to evaluate the effect of a decrease of percent bead with $GPC1^+$ crExos in addition to age (continuous variable), AJCC tumor stage, and tumor grade (G) and CA 19-9 levels ($U.ml^{-1}$). Correlation analysis between murine tumor burden and percent bead with $GPC1^+$ crExos was performed using the Spearman correlation test. Figures were prepared by using GraphPad Prism (GraphPad Software, La Jolla, CA 92037 USA) and MedCalc statistical software version 13.0 (MedCalc Software bvba, Acacialaan 22, 8400 Ostend, Belgium). All presented *P* values are two-sided and $P < 0.05$ was considered to be statistically significant.

Extended Data



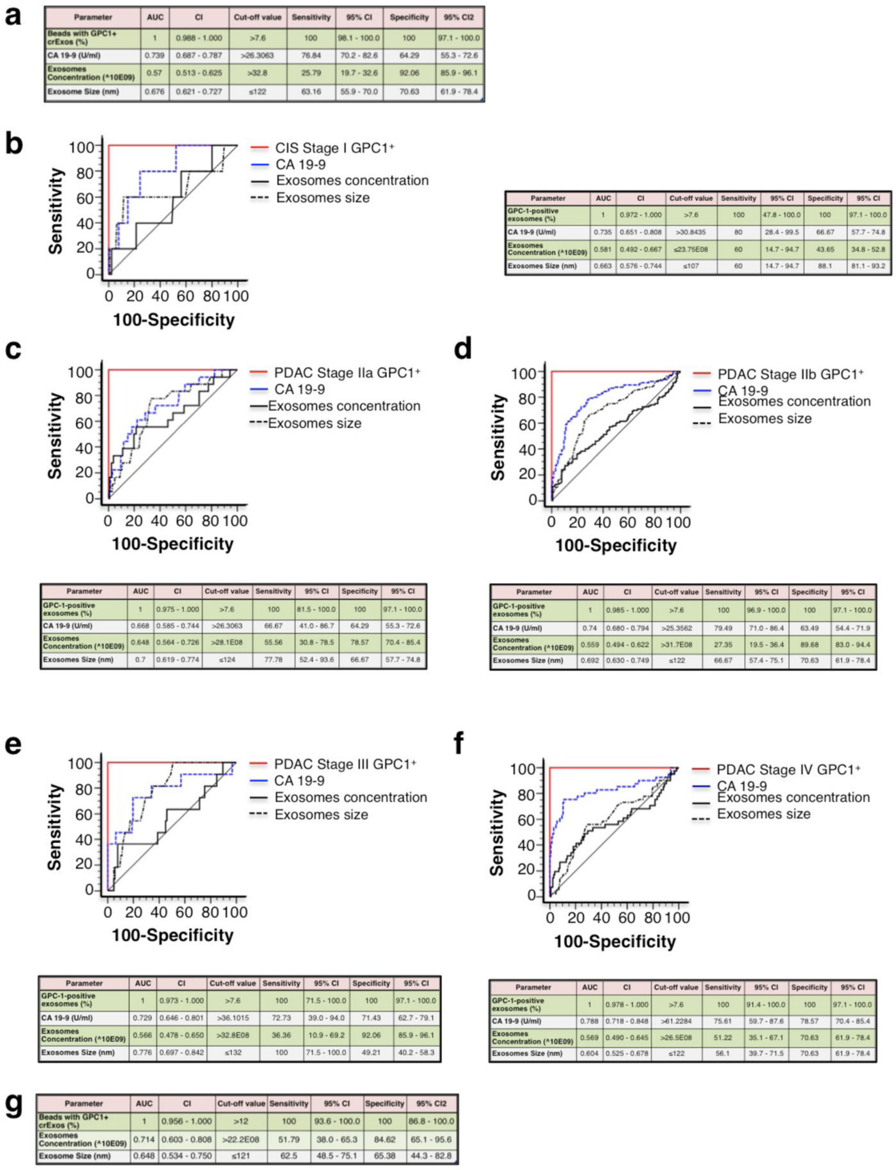
Extended Data Figure 1. Exosomes isolation

a, Exosomes concentration and size distribution by NanoSight® analysis of culture supernatant from NIH/3T3, MCF10A, HDF, MDA-MB-231 and E10 cells. Size mode: 105 nanometers (nm; 3 technical replicates). **b**, Transmission electron microscopy (TEM) micrograph of MDA-MB-231-derived exosomes. Upper right image shows a digitally zoomed inset. **c**, TEM micrograph of MDA-MB-231-derived exosomes following immunogold labeling for CD9. Gold particles are depicted as black dots. Upper right image shows a digitally zoomed inset. **d**, Immunoblot of flotillin1 and CD81 in exosomal proteins extracted from culture supernatant of E10, NIH/3T3, MDA-MB-231, MCF10A and HDF cells. **e**, RT–qPCR measurement of GPC1 mRNA levels in HMEL, HDF, HMLE, MCF7, MDA-MB-231, T3M4, Panc-1, MIA Paca2. Results are shown as mean ± standard deviation; n=3, 3 biological replicates, with 3 technical replicates each. **f**, Immunoblot of GPC1 in HMEL, HDF, HMLE, MCF7, MDA-MB-231, T3M4, Panc-1 and MIA Paca2 cell lysates (upper panel). β-actin was used as a loading control (lower panel). **g**, Immunoblot of GPC1 in exosomal protein lysates derived from the culture supernatant of 3 non-tumorigenic cell lines (HDF, HMEL, HMLE) and 5 tumorigenic cell lines (MCF7, MDA-MB-231, T3M4, Panc-1, MIA Paca2) (upper panel). Immunoblot of flotillin1 was used as loading control (lower panel). **h**, Immunoblot of flotillin1 in exosomal protein lysates from the culture supernatant of MDA-MB-231 and T3M4 following sucrose gradient purification. The protein content is assayed in each of the density layers listed.



Extended Data Figure 2. NanoSight® analysis in human serum samples

a, Transmission electron microscopy (TEM) micrograph of cancer patient serum-derived exosomes. Upper right image shows a digitally zoomed inset. **b**, TEM micrograph of cancer patient serum-derived exosomes following immunogold labeling for CD9. Gold particles are depicted as black dots. Upper right image shows a digitally zoomed inset. **c**, Immunoblot of flotillin1 of exosomal protein lysates from serum of cancer patient following exosomes purification by sucrose gradient. The protein content is assayed in each of the density layers listed. **d**, Exosomes concentration by NanoSight® analysis showing the number of exosomes per 1 ml of serum derived from healthy donors (n=100), from breast cancer patients (n=32) and from patients with a pancreatic ductal adenocarcinoma (PDAC, n=190). ANOVA, post-hoc Tamhane T_2, * $P<0.05$, **** $P<0.0001$; 3 technical replicates. **e**, Exosomes size distribution by NanoSight® analysis showing the mode size of exosomes in 1 ml of serum derived from healthy donors (n=100), from breast cancer patients (n=32) and from patients with a pancreatic ductal adenocarcinoma (PDAC, n=190). ANOVA, post-hoc Tukey-Kramer test, *** P<0.001; 3 technical replicates. **f**, Scatter dot plots depicting the percentage of beads with GPC1$^+$ bound exosomes purified from the serum of breast cancer patients. The patients are subdivided into three subtypes: Luminal A, Luminal B and Triple Negative breast cancer. **g**, Scatter plots depicting the serum CA 19-9 concentration (U/mL), evaluated by ELISA, in healthy donors (n=100), patients with benign pancreas disease (BPD, n=26), pancreas cancer precursor lesion (PCPL, n=5) and pancreatic ductal adenocarcinoma (PDAC, n=190). Discovery cohort, ANOVA, post-hoc Tamhane T2 * P<0.05; **** P<0.0001; 3 technical replicates. Data is presented as the mean ± standard deviation.



a

Parameter	AUC	CI	Cut-off value	Sensitivity	95% CI	Specificity	95% CI2
Beads with GPC1+ crExos (%)	1	0.988 - 1.000	>7.6	100	98.1 - 100.0	100	97.1 - 100.0
CA 19-9 (U/ml)	0.739	0.687 - 0.787	>26.3063	76.84	70.2 - 82.6	64.29	55.3 - 72.6
Exosomes Concentration (^10E09)	0.57	0.513 - 0.625	>32.8	25.79	19.7 - 32.6	92.06	85.9 - 96.1
Exosome Size (nm)	0.676	0.621 - 0.727	≤122	63.16	55.9 - 70.0	70.63	61.9 - 78.4

b

Parameter	AUC	CI	Cut-off value	Sensitivity	95% CI	Specificity	95% CI
GPC-1-positive exosomes (%)	1	0.972 - 1.000	>7.6	100	47.8 - 100.0	100	97.1 - 100.0
CA 19-9 (U/ml)	0.735	0.651 - 0.808	>30.8435	80	28.4 - 99.5	66.67	57.7 - 74.8
Exosomes Concentration (^10E09)	0.581	0.492 - 0.667	≤23.75E08	60	14.7 - 94.7	43.65	34.8 - 52.8
Exosomes Size (nm)	0.663	0.576 - 0.744	≤107	60	14.7 - 94.7	88.1	81.1 - 93.2

c

Parameter	AUC	CI	Cut-off value	Sensitivity	95% CI	Specificity	95% CI
GPC-1-positive exosomes (%)	1	0.975 - 1.000	>7.6	100	81.5 - 100.0	100	97.1 - 100.0
CA 19-9 (U/ml)	0.668	0.585 - 0.744	>26.3063	66.67	41.0 - 86.7	64.29	55.3 - 72.6
Exosomes Concentration (^10E09)	0.648	0.564 - 0.726	>28.1E08	55.56	30.8 - 78.5	78.57	70.4 - 85.4
Exosomes Size (nm)	0.7	0.619 - 0.774	≤124	77.78	52.4 - 93.6	66.67	57.7 - 74.8

d

Parameter	AUC	CI	Cut-off value	Sensitivity	95% CI	Specificity	95% CI
GPC-1-positive exosomes (%)	1	0.985 - 1.000	>7.6	100	96.9 - 100.0	100	97.1 - 100.0
CA 19-9 (U/ml)	0.74	0.680 - 0.794	>25.3562	79.49	71.0 - 86.4	63.49	54.4 - 71.9
Exosomes Concentration (^10E09)	0.559	0.494 - 0.622	>31.7E08	27.35	19.5 - 36.4	89.68	83.0 - 94.4
Exosomes Size (nm)	0.692	0.630 - 0.749	≤122	66.67	57.4 - 75.1	70.63	61.9 - 78.4

e

Parameter	AUC	CI	Cut-off value	Sensitivity	95% CI	Specificity	95% CI
GPC-1-positive exosomes (%)	1	0.973 - 1.000	>7.6	100	71.5 - 100.0	100	97.1 - 100.0
CA 19-9 (U/ml)	0.729	0.646 - 0.801	>36.1015	72.73	39.0 - 94.0	71.43	62.7 - 79.1
Exosomes Concentration (^10E09)	0.566	0.478 - 0.650	>32.8E08	36.36	10.9 - 69.2	92.06	85.9 - 96.1
Exosomes Size (nm)	0.776	0.697 - 0.842	≤132	100	71.5 - 100.0	49.21	40.2 - 58.3

f

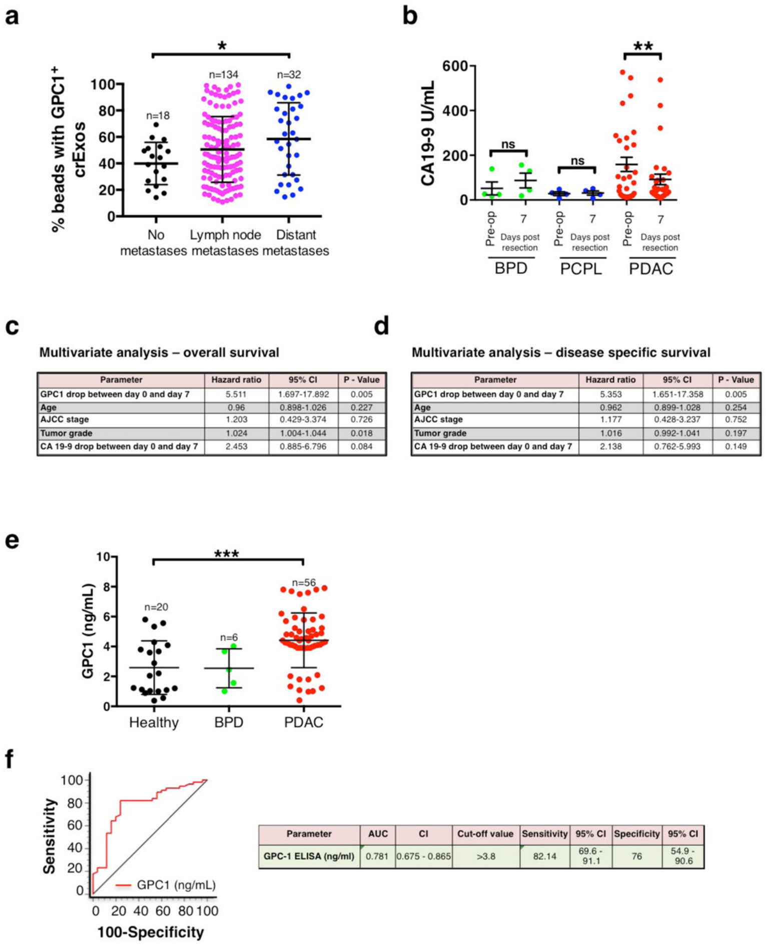
Parameter	AUC	CI	Cut-off value	Sensitivity	95% CI	Specificity	95% CI
GPC-1-positive exosomes (%)	1	0.978 - 1.000	>7.6	100	91.4 - 100.0	100	97.1 - 100.0
CA 19-9 (U/ml)	0.788	0.718 - 0.848	>61.2284	75.61	59.7 - 87.6	78.57	70.4 - 85.4
Exosomes Concentration (^10E09)	0.569	0.490 - 0.645	>26.5E08	51.22	35.1 - 67.1	70.63	61.9 - 78.4
Exosomes Size (nm)	0.604	0.525 - 0.678	≤122	56.1	39.7 - 71.5	70.63	61.9 - 78.4

g

Parameter	AUC	CI	Cut-off value	Sensitivity	95% CI	Specificity	95% CI2
Beads with GPC1+ crExos (%)	1	0.956 - 1.000	>12	100	93.6 - 100.0	100	86.8 - 100.0
Exosomes Concentration (^10E09)	0.714	0.603 - 0.808	>22.2E08	51.79	38.0 - 65.3	84.62	65.1 - 95.6
Exosome Size (nm)	0.648	0.534 - 0.750	≤121	62.5	48.5 - 75.1	65.38	44.3 - 82.8

Extended Data Figure 3. Tumor stage-specific analysis

a, Table associated with receiver Operating Characteristic (ROC) curve analysis depicted in Figure 1f. **b–f**, ROC curve analysis for percent GPC1$^+$ crExos (red line), CA 19-9 serum levels (blue scattered line), exosomes concentration (black line) and exosomes size (scattered black line) in patients with carcinoma in situ (CIS) or stage I pancreatic cancer (n=5) (a), stage IIa pancreatic cancer (n=18) (b), stage IIb pancreatic cancer (n=117) (c), stage III pancreatic cancer (n=11) (d), and stage IV pancreas cancer (n=41) (e), compared to control (healthy donors (n=100) and patients with a benign pancreatic disease (n=26), total n=126). **g**, Table associated with ROC curve analysis depicted in Figure 1h. AUC: Area under the curve, CI: confidence interval.



Multivariate analysis – overall survival

Parameter	Hazard ratio	95% CI	P - Value
GPC1 drop between day 0 and day 7	5.511	1.697-17.892	0.005
Age	0.96	0.898-1.026	0.227
AJCC stage	1.203	0.429-3.374	0.726
Tumor grade	1.024	1.004-1.044	0.018
CA 19-9 drop between day 0 and day 7	2.453	0.885-6.796	0.084

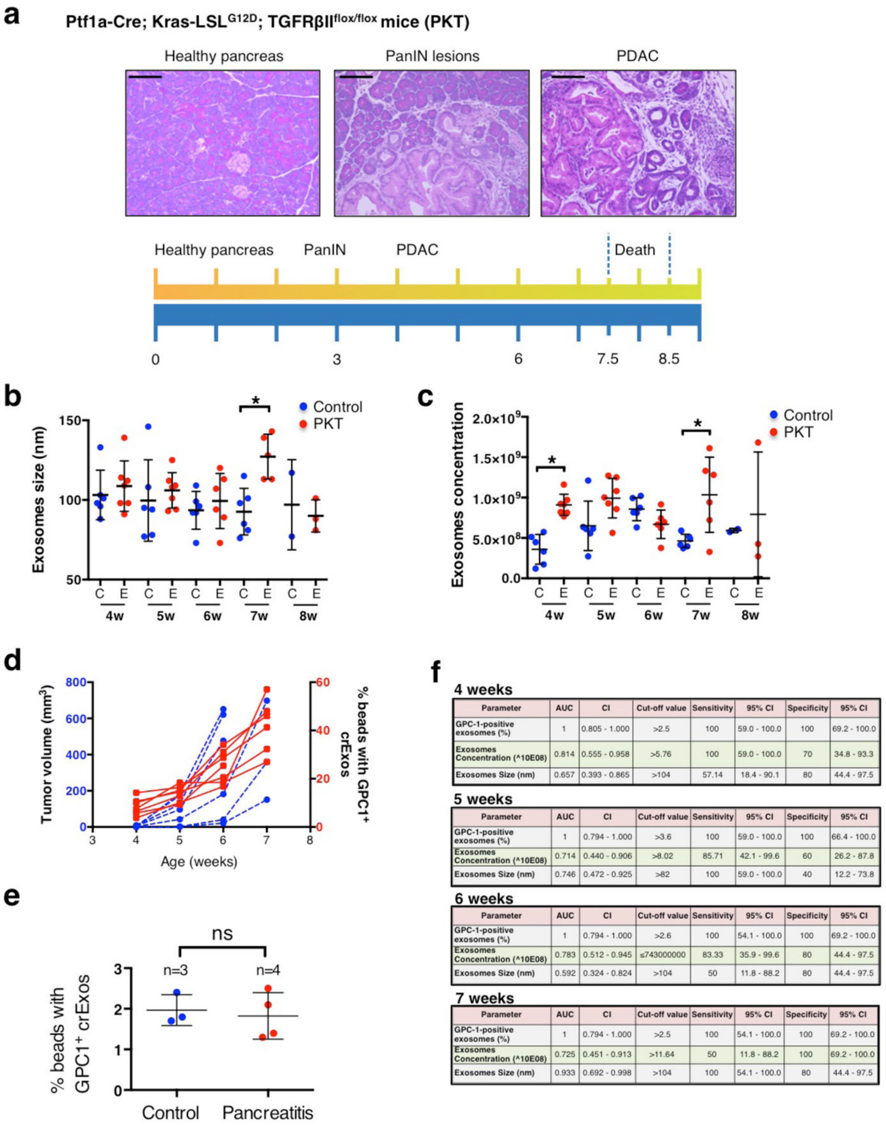
Multivariate analysis – disease specific survival

Parameter	Hazard ratio	95% CI	P - Value
GPC1 drop between day 0 and day 7	5.353	1.651-17.358	0.005
Age	0.962	0.899-1.028	0.254
AJCC stage	1.177	0.428-3.237	0.752
Tumor grade	1.016	0.992-1.041	0.197
CA 19-9 drop between day 0 and day 7	2.138	0.762-5.993	0.149

Parameter	AUC	CI	Cut-off value	Sensitivity	95% CI	Specificity	95% CI
GPC-1 ELISA (ng/ml)	0.781	0.675 - 0.865	>3.8	82.14	69.6 - 91.1	76	54.9 - 90.6

Extended Data Figure 4. Longitudinal human study

a, Scatter plots of percent beads with GPC1$^+$ crExos by flow cytometry in patients with pancreas cancer. Patients are divided based on metastatic disease (non-metastatic lesions, lymph node metastases and distant metastases). ANOVA, post-hoc Tukey-Kramer test, * P<0.05; 3 technical replicates. **b**, Scatter plots depicting serum CA 19-9 levels (U/ml) in patients with benign pancreas disease (BPD) (n=4), cancer precursor lesion (PCPL) (n=4), and pancreatic ductal adenocarcinoma (PDAC) (n=29) on the preoperative day and postoperative day 7 in patients. Paired two-tailed Student's *t*-test, ** P<0.01; 3 technical replicates. **c–d**, Multivariate analysis (Cox proportional hazards regression model) of prognostic parameters for overall (c) and disease-specific (d) survival of patients with pancreas cancer in the longitudinal cohort (n=29). **e**, Scatter plots depicting serum GPC1 (ng/ml) levels by ELISA in patients with benign pancreas disease (BPD, n=6), pancreatic ductal adenocarcinoma (PDAC, n=56) and healthy controls (n=20). ANOVA, post-hoc Tukey-Kramer test, **** P<0.0001; 3 technical replicates. **f**, ROC curve for circulating GPC1 protein (red line) in patients with pancreas cancer (n=56) vs. control (healthy donors (n=20) and patients with a benign pancreatic disease (n=26), total n=6). AUC: Area under the curve, CI: confidence interval.



4 weeks

Parameter	AUC	CI	Cut-off value	Sensitivity	95% CI	Specificity	95% CI
GPC-1-positive exosomes (%)	1	0.805 - 1.000	>2.5	100	59.0 - 100.0	100	69.2 - 100.0
Exosomes Concentration (^10E08)	0.814	0.555 - 0.958	>5.76	100	59.0 - 100.0	70	34.8 - 93.3
Exosomes Size (nm)	0.657	0.393 - 0.865	>104	57.14	18.4 - 90.1	80	44.4 - 97.5

5 weeks

Parameter	AUC	CI	Cut-off value	Sensitivity	95% CI	Specificity	95% CI
GPC-1-positive exosomes (%)	1	0.794 - 1.000	>3.6	100	59.0 - 100.0	100	66.4 - 100.0
Exosomes Concentration (^10E08)	0.714	0.440 - 0.906	>8.02	85.71	42.1 - 99.6	60	26.2 - 87.8
Exosomes Size (nm)	0.746	0.472 - 0.925	>82	100	59.0 - 100.0	40	12.2 - 73.8

6 weeks

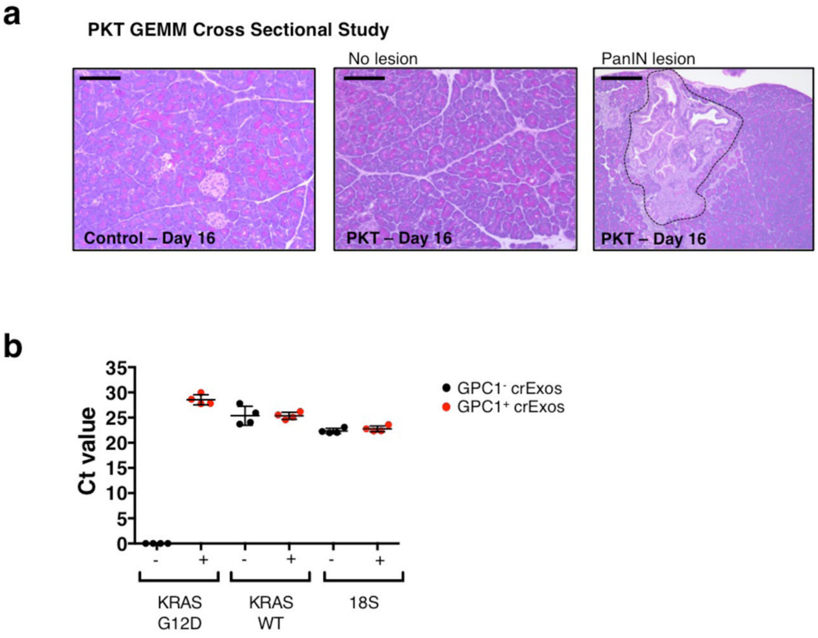
Parameter	AUC	CI	Cut-off value	Sensitivity	95% CI	Specificity	95% CI
GPC-1-positive exosomes (%)	1	0.794 - 1.000	>2.6	100	54.1 - 100.0	100	69.2 - 100.0
Exosomes Concentration (^10E08)	0.783	0.512 - 0.945	≤743000000	83.33	35.9 - 99.6	80	44.4 - 97.5
Exosomes Size (nm)	0.592	0.324 - 0.824	>104	50	11.8 - 88.2	80	44.4 - 97.5

7 weeks

Parameter	AUC	CI	Cut-off value	Sensitivity	95% CI	Specificity	95% CI
GPC-1-positive exosomes (%)	1	0.794 - 1.000	>2.5	100	54.1 - 100.0	100	69.2 - 100.0
Exosomes Concentration (^10E08)	0.725	0.451 - 0.913	>11.64	50	11.8 - 88.2	100	69.2 - 100.0
Exosomes Size (nm)	0.933	0.692 - 0.998	>104	100	54.1 - 100.0	80	44.4 - 97.5

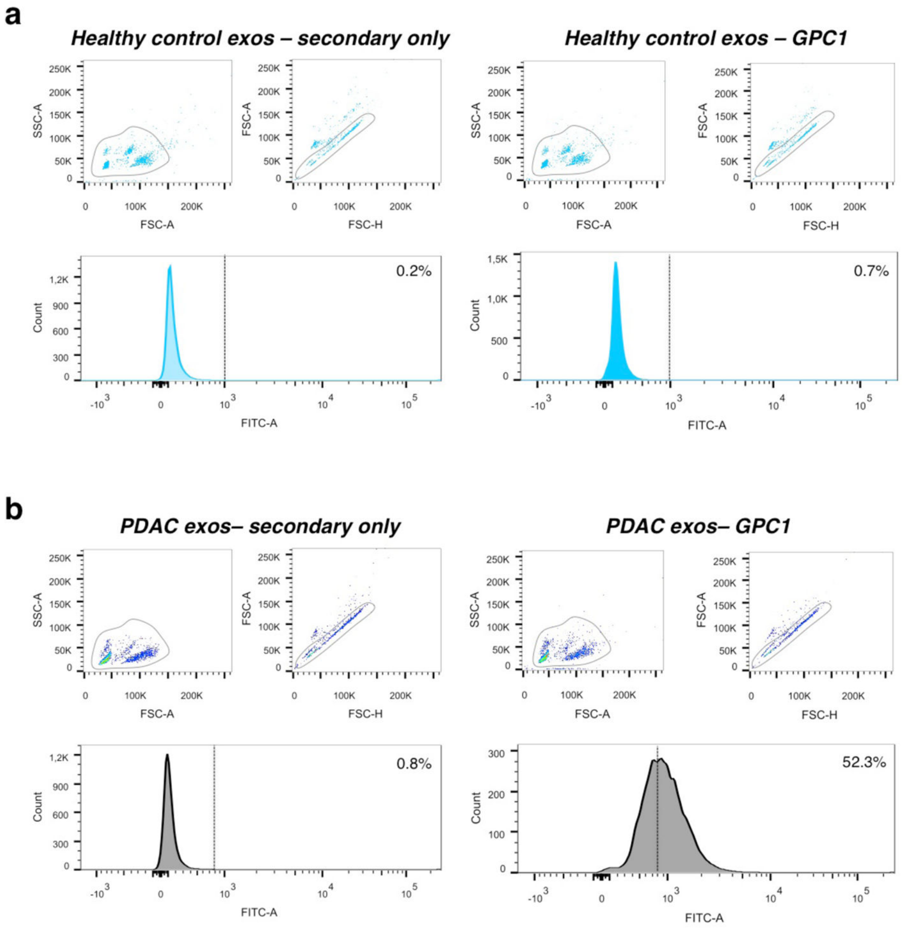
Extended Data Figure 5. PDAC GEMM longitudinal study

a, Schematic diagram depicting the spontaneous development and progression of pancreatic cancer in Ptf1a$^{cre/+}$;LSL-Kras$^{G12D/+}$;Tgfbr2$^{L/L}$ (PKT) mice and H&E of the pancreas at the indicated time points showing healthy pancreas, PanIN lesions, and PDAC lesions. Scale bars: 100 μm. **b–c**, Exosomes size (b) and concentration (c) assayed by NanoSight® analysis from the serum of PKT mice (E: experimental, red) and control mice (C: control, blue) at 4, 5, 6,7 and 8 weeks of age. ANOVA, post-hoc Tukey-Kramer test, * P<0.05; 3 technical replicates. **d**, Graph depicting the time wise progression of tumor volume measured by MRI and the % beads with GPC1$^+$ bound crExos in individual PKT mice (blue: tumor volume, red: % GPC1$^+$ crExos). **e**, Percent beads with GPC1$^+$ crExos on beads from control mice (n=3) and mice with cerulein-induced acute pancreatitis (n=4). Two-tailed Student's *t*-test, ns: not significant; 3 technical replicates. **f**, Results from ROC curves for percent beads with GPC1$^+$ bound crExos, exosomes concentration and exosomes size in 4, 5, 6 and 7 weeks old PKT mice (n=7) vs. control (including age-matched littermate healthy control (n=6) and mice with induced acute pancreatitis (n=4), n=10)). Data is presented as the mean ± standard deviation.



Extended Data Figure 6. PDAC GEMM cross sectional studies

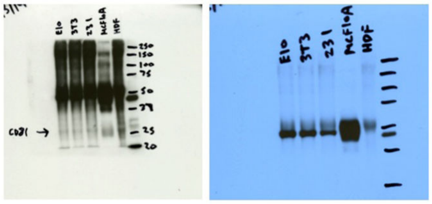
a, Representative micrographs of H&E stained pancreas from 16 days old control mice (left panel) and PKT mice presenting with (right panel, encircled) and without (middle panel) PanIN lesions. Scale bars: 100 μm. **b**, Ct values following qPCR analyses for oncogenic KRAS^{G12D}, wild-type KRAS and 18S internal control RNA from exosomes of 44–48 days old PKT mice serum segregated using FACS for GPC1$^+$ bead bound exos (red) and GPC1$^-$ bead bound exos (blue). Data is presented as the mean ± standard deviation.



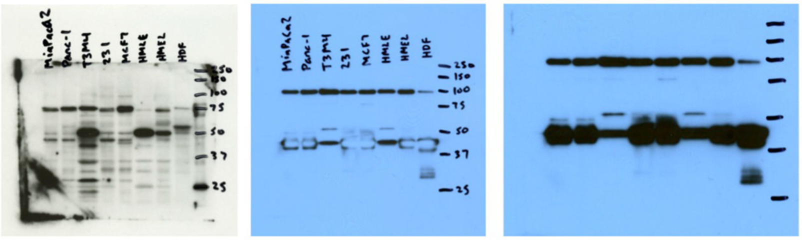
Extended Data Figure 7. Raw scatter dot plot depicting flow cytometry analyses of beads with GPC1$^+$ bound exosomes

a, Scatter plots and histogram of flow cytometry analyses of serum exosomes on beads of a representative healthy control (left panels are secondary antibody only; right panels are GPC1 antibody and secondary antibody). **b**, Scatter plots and histogram of flow cytometry analysis of serum exosomes on beads of a representative pancreas cancer sample (left panels are secondary antibody only; right panels are with GPC1 antibody and secondary antibody).

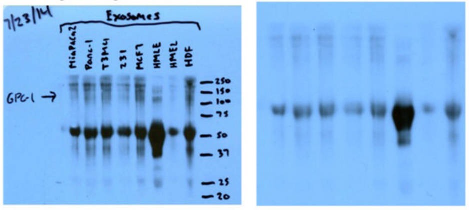
ED Figure 1d



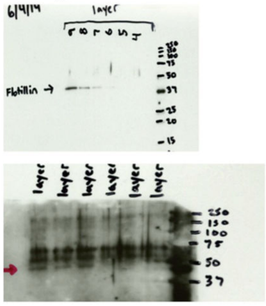
ED Figure 1f



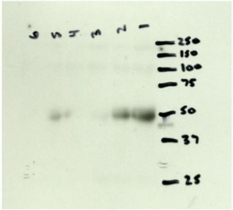
ED Figure 1g



ED Figure 1h



ED Figure 2c



Extended Data Figure 8.

Uncropped Western blots

Extended Data Table 1

List of the 48 proteins exclusive to MDA-MB-231 exosomes

Listing of the 48 proteins exclusively detected in exosomes from MDA-MB-231 cells determined by ultra performance liquid chromatography – mass spectrometry (UPLC-MS) and comparative analyses of exosomes derived from NIH/3T3, MCF 10A, HDF, E10 and MDA-MB-231 cells. The proteins are grouped based on cellular location.

Protein Name	Gene ID	Cellular Location
ATP-binding cassette sub-family A member 6	ABCA6	Transmembrane
Tetraspanin-4	TSPAN4	Transmembrane

Protein Name	**Gene ID**	**Cellular Location**
SLIT and NTRK-like protein 4	SLITRK4	Transmembrane
Putative protocadherin beta-18	PCDHB18	Transmembrane
Myeloid cell surface antigen CD33	CD33	Transmembrane
Glypican-1	**GPC1**	**Membrane anchored**

Protein Name	**Gene ID**	**Cellular Location**
Histone H2A type 2-A	HIST1H2AA	Nucleus
Histone H2A type 1-A	HIST1H1AA	Nucleus
Histone H3.3	H3F3A	Nucleus
Histone H3.1	HIST1H3A	Nucleus
Zinc finger protein 37 homolog	ZFP37	Nucleus
Hypermethylated in cancer 2 protein	HIC2	Nucleus
Zinc finger protein 12	ZSCAN12	Nucleus

Protein Name	**Gene**	**ID Cellular Location**
Laminin subunit beta-1	LAMB1	Secreted
Tubulointerstitial nephritis antigen-like	TINAGL1	Secreted
Peroxiredoxin-4	PRDX4	Secreted
Collagen alpha-2(IV) chain	COL4A2	Secreted
Putative protein C3P1	C3P1	Secreted
Collagen alpha-1(II) chain	COL2A1	Secreted
Hemicentin-1	HMCN1	Secreted

Protein Name	**Gene ID**	**Cellular Location**
Putative rhophilin-2-like protein	RHPN2P1	Not specified
Ankyrin repeat domain-containing protein 62	ANKRD62	Not specified
Tripartite motif-containing protein 42	TRIM42	Not specified !

Protein Name	**Gene ID**	**Cellular Location**
Junction plakoglobin	JUP	Cytoplasm
Tubulin beta-2B chain	TUBB2B	Cytoplasm
Endoribonuclease Dicer	DICER1	Cytoplasm
E3 ubiquitin-protein ligase TRIM71	TRIM71	Cytoplasm
Katanin p60 ATPase-containing subunit A-like 2	KATNAL2	Cytoplasm
Protein S100-A6	S100A6	Cytoplasm
5′-nucleotidase domain-containing protein 3	NT5DC3	Cytoplasm
Valine--tRNA ligase	VARS	Cytoplasm
Kazrin	KAZN	Cytoplasm
ELAV-like protein 4	ELAVL4	Cytoplasm
RING finger protein 166	RNF166	Cytoplasm
FERM and PDZ domain-containing protein 1	FRMPD1	Cytoplasm

Protein Name	**Gene ID**	**Cellular Location**
78 kDa glucose-regulated protein	HSPA5	Cytoplasm
Trafficking protein particle complex subunit 6A	TRAPPC6A	Cytoplasm
Squalene monooxygenase	SQLE	Cytoplasm
Tumor susceptibility gene 101 protein	TSG101	Cytoplasm
Vacuolar protein sorting 28 homolog	VPS28	Cytoplasm
Prostaglandin F2 receptor negative regulator	PTGFRN	Cytoplasm
Isobutyryl-CoA dehydrogenase, mitochondrial	ACAD8	Cytoplasm
26S protease regulatory subunit 6B	PSMC4	Cytoplasm
Elongation factor 1-gamma	EEF1G	Cytoplasm
Titin	TTN	Cytoplasm
Tyrosine-protein phosphatase type 13	PTPN13	Cytoplasm
Triosephosphate isomerase	TPI1	Cytoplasm
Carboxypeptidase E	CPE	Cytoplasm

Extended Data Table 2

Exosomes proteins assayed by ultra performance liquid chromatography – mass spectrometry (UPLC-MS) in indicated cell lines.

E10								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
1	P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	2721	65999	68	30	57.8	8.15
2	P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	2381	62027	59	24	68.2	5.14
3	P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	2146	58792	66	29	57.9	5.13
4	P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	2032	69321	104	9	13.5	5.92
5	P07996	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	1823	129300	57	29	37.9	4.71
6	P02765	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	1784	39300	50	3	8.7	5.43
7	P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	1719	163188	62	8	7.5	6.03
8	P20742	Pregnancy zone protein OS=Homo sapiens GN=PZP PE=1 SV=4	1562	163760	48	4	2.5	5.97
9	P02751	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	1186	262460	37	26	17.6	5.46
10	P12111	Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=5	1113	343457	51	39	20.2	6.26
11	P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	1057	65393	35	21	48.4	8.07
12	P01024	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	978	187030	43	18	14.7	6.02

E10								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
13	P00734	Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2	846	69992	21	6	8	5.64
14	P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	820	41710	23	12	47.5	5.29
15	P08779	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	762	51236	31	18	48	4.99
16	P19823	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2	708	106397	27	8	9.3	6.4
17	P02533	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	579	51529	25	15	37.1	5.09
18	P0C0L4	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1	492	192650	20	9	5.6	6.65
19	P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	446	60030	18	10	25.5	8.09
20	P12109	Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3	420	108462	11	7	11.3	5.26
21	P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	419	36030	12	6	28.4	8.57
22	Q07954	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2	419	504276	22	10	5.8	5.16
23	P02538	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	419	60008	18	10	27.1	8.09
24	P02788	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6	416	78132	16	3	4.8	8.5
25	P68032	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	408	41992	13	6	26.8	5.23
26	P02771	Alpha-fetoprotein OS=Homo sapiens GN=AFP PE=1 SV=1	395	68633	9	3	5.6	5.48
27	Q08380	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	392	65289	15	10	26.7	5.13
28	P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	364	50120	18	9	38.4	4.94
29	P13647	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	360	62340	17	11	23.4	7.59
30	Q04695	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	357	48076	20	10	32.6	4.97
31	Q9BYX7	Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1	347	41989	8	3	13.6	5.91
32	P06396	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	340	85644	11	7	12.5	5.9
33	P04114	Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	327	515283	16	12	2.4	6.58

E10

prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
34	P03956	Interstitial collagenase OS=Homo sapiens GN=MMP1 PE=1 SV=3	318	53973	15	11	33.5	6.47
35	Q06033	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2	298	99787	10	5	5.1	5.49
36	P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	297	15248	13	3	33.1	8.72
37	P24821	Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3	292	240700	12	10	9.4	4.79
38	P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	286	49639	12	7	34.2	4.78
39	P68371	Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1	278	49799	10	7	27.4	4.79
40	P02774	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1	273	52929	12	6	12	5.4
41	Q562R1	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	271	41976	8	3	16	5.39
42	P23142	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4	269	77162	10	5	7.4	5.07
43	P13646	Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4	256	49557	13	6	10.9	4.91
44	P02647	Apolipoprotein A–I OS=Homo sapiens GN=APOA1 PE=1 SV=1	255	30759	5	1	6	5.56
45	P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4	228	57900	9	6	20.3	7.96
46	P04004	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	215	54271	6	1	4.2	5.55
47	P19012	Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3	210	49181	14	6	10.3	4.71
48	Q15582	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1	196	74634	8	7	16.1	7.62
49	P36955	Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=4	188	46283	7	3	12	5.97
50	Q99715	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2	176	332941	8	5	4.9	5.38
51	P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	175	84607	8	4	12.8	4.94
52	P02675	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	174	55892	7	4	6.7	8.54
53	P02042	Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2	171	16045	9	2	12.9	7.85
54	P11717	Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=3	163	274199	5	2	0.8	5.64

E10

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55	P51884	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	161	38405	9	3	12.4	6.16
56	P08697	Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3	158	54531	2	1	2.2	5.87
57	P12259	Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4	153	251546	9	6	3.5	5.68
58	P08107	Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	147	70009	3	3	6.2	5.48
59	P17066	Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2	147	70984	3	3	6.2	5.81
60	P19013	Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4	146	57250	6	4	7.3	6.25
61	Q8TAA3	Proteasome subunit alpha type-7-like OS=Homo sapiens GN=PSMA8 PE=1 SV=3	144	28512	4	3	19.5	9.07
62	Q5XKE5	Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2	138	57800	7	3	6.9	6.75
63	P0C0S8	Histone H2A type 1 OS=Homo sapiens GN=HIST1H2AG PE=1 SV=2	136	14083	3	2	21.5	10.9
64	Q99816	Tumor susceptibility gene 101 protein OS=Homo sapiens GN=TSG101 PE=1 SV=2	135	43916	4	2	21.8	8.2
65	P23526	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	134	47685	3	2	9.5	5.92
66	P00747	Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2	132	90510	7	4	5.3	7.04
67	O95678	Keratin, type II cytoskeletal 75 OS=Homo sapiens GN=KRT75 PE=1 SV=2	132	59524	7	3	7.8	7.6
68	P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	132	95277	6	4	10.3	6.41
69	Q9UBG0	C-type mannose receptor 2 OS=Homo sapiens GN=MRC2 PE=1 SV=2	128	166568	2	2	1.6	5.54
70	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2	127	93255	6	3	10.3	7.27
71	P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	127	11360	5	4	38.8	11.36
72	P01008	Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1	126	52569	13	3	14.9	6.32
73	P19827	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3	124	101326	4	3	2.9	6.31
74	P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	123	70854	4	4	7.6	5.37
75	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5	123	51354	4	2	5.1	5.4

E10								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
76	P02794	Ferritin heavy chain OS=Homo sapiens GN=FTH1 PE=1 SV=2	122	21212	4	3	16.4	5.3
77	P05787	Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	122	53671	4	2	5.6	5.52
78	P01031	Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4	122	188186	5	3	2.6	6.11
79	Q5VTE0	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1	121	50153	4	3	14.1	9.15
80	P05452	Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=3	121	22522	5	3	28.7	5.52
81	P49327	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	119	273254	5	3	3.3	6.01
82	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	118	36615	2	2	6.9	5.71
83	Q9H4B7	Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1	112	50295	5	3	11.8	5.05
84	P15531	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1	111	17138	1	1	11.2	5.83
85	Q7Z3Y8	Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=2	109	49792	7	2	7.6	4.98
86	P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	109	83212	4	2	6.2	4.97
87	P08123	Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=7	105	129235	2	2	2.3	9.08
88	Q86YZ3	Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	101	282228	1	1	0.6	10.05
89	P02452	Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5	99	138857	4	2	3	5.6
90	P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	98	39395	2	2	6.9	8.3
91	P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3	97	77014	4	2	1.7	6.81
92	P02748	Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2	95	63133	3	2	3.8	5.43
93	Q8TEV9_REVERSED	Smith-Magenis syndrome chromosomal region candidate gene 8 protein OS=Homo sapiens GN=SMCR8 PE=1 SV=2 - REVERSED	91	104956	12	1	1.2	5.36
94	P02461	Collagen alpha-1(III) chain OS=Homo sapiens GN=COL3A1 PE=1 SV=4	90	138479	2	2	1.6	6.21
95	P00450	Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1	88	122128	3	3	2.9	5.44
96	P62979	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2	88	17953	4	3	19.9	9.68

E10								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
97	Q14697	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3	84	106807	2	2	3.9	5.74
98	Q08431	Lactadherin OS=Homo sapiens GN=MFGE8 PE=1 SV=2	83	43095	2	1	3.9	8.47
99	A6NMY6	Putative annexin A2-like protein OS=Homo sapiens GN=ANXA2P2 PE=5 SV=2	82	38635	2	2	6.2	6.49
100	P07355	Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	82	38580	3	2	10.3	7.57
101	Q9BYX7_REVERSED	Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1 - REVERSED	80	41989	4	1	3.5	5.92
102	Q8NI35	InaD-like protein OS=Homo sapiens GN=INADL PE=1 SV=3	79	196247	8	1	0.3	4.84
103	P15169	Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1	79	52253	1	1	3.3	6.86
104	P28074	Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3	79	28462	2	2	8.7	6.43
105	P49720	Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2	78	22933	3	2	16.6	6.14
106	Q04756	Hepatocyte growth factor activator OS=Homo sapiens GN=HGFAC PE=1 SV=1	77	70636	1	1	2.4	6.99
107	Q12931	Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3	76	80060	1	1	2	8.3
108	P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1	76	45031	4	2	7	6.68
109	P20618	Proteasome subunit beta type-1 OS=Homo sapiens GN=PSMB1 PE=1 SV=2	74	26472	2	2	13.3	8.27
110	Q14624	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4	73	103293	4	1	1.9	6.51
111	Q5D862	Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	72	247928	1	1	0.5	8.45
112	P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	71	47139	3	2	10.1	7.01
113	P02790	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	70	51643	7	1	5.4	6.55
114	P35442	Thrombospondin-2 OS=Homo sapiens GN=THBS2 PE=1 SV=2	70	129908	4	2	3.2	4.62
115	P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=4	69	46902	2	2	7.6	7.59
116	Q8WW52_REVERSED	Protein FAM151A OS=Homo sapiens GN=FAM151A PE=2 SV=2 - REVERSED	69	63987	2	1	1.4	6.2
117	P12110	Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4	69	108512	4	2	3.4	5.85

E10								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
118	P04083	Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	68	38690	1	1	3.8	6.57
119	P01009	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	68	46707	4	1	3.3	5.37
120	P22303	Acetylcholinesterase OS=Homo sapiens GN=ACHE PE=1 SV=1	67	67753	1	1	2.1	5.87
121	P55058	Phospholipid transfer protein OS=Homo sapiens GN=PLTP PE=1 SV=1	66	54705	1	1	2.2	6.53
122	P00488	Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4	66	83215	1	1	2.2	5.75
123	Q03692	Collagen alpha-1(X) chain OS=Homo sapiens GN=COL10A1 PE=1 SV=2	66	66117	1	1	1.9	9.68
124	P05546	Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3	65	57034	2	1	2.4	6.41
125	P01266	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5	65	304594	3	3	0.8	5.4
126	P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	63	36665	2	1	8.1	8.44
127	O15111_REVERSED	Inhibitor of nuclear factor kappa-B kinase subunit alpha OS=Homo sapiens GN=CHUK PE=1 SV=2 - REVERSED	63	84585	7	1	1.6	6.28
128	Q8NAV2_REVERSED	Uncharacterized protein C8orf58 OS=Homo sapiens GN=C8orf58 PE=2 SV=2 - REVERSED	63	39636	3	1	4.1	8.54
129	P28070	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4	62	29185	2	2	7.2	5.72
130	P07686	Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3	61	63071	1	1	2.9	6.29
131	P05543	Thyroxine-binding globulin OS=Homo sapiens GN=SERPINA7 PE=1 SV=2	61	46295	2	1	2.4	5.87
132	Q9HDC9	Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2	60	46451	3	1	1.7	5.82
133	P25787	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2	60	25882	1	1	6	6.92
134	P35125	Ubiquitin carboxyl-terminal hydrolase 6 OS=Homo sapiens GN=USP6 PE=1 SV=2	60	158557	12	1	0.4	7.87
135	A6NIZ1	Ras-related protein Rap-1b-like protein OS=Homo sapiens PE=2 SV=1	59	20912	1	1	6.5	5.37
136	B9A064	Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2	59	23049	2	1	3.7	9.08
137	Q99456	Keratin, type I cytoskeletal 12 OS=Homo sapiens GN=KRT12 PE=1 SV=1	58	53478	6	2	3.6	4.7

E10								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
138	Q86Y46	Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1	58	58887	5	4	6.7	6.93
139	P20774	Mimecan OS=Homo sapiens GN=OGN PE=1 SV=1	58	33901	2	2	9.7	5.46
140	Q9Y240	C-type lectin domain family 11 member A OS=Homo sapiens GN=CLEC11A PE=1 SV=1	57	35672	1	1	5.3	5.06
141	P10909	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	57	52461	2	1	7.8	5.89
142	Q9NPY3_REVERSED	Complement component C1q receptor OS=Homo sapiens GN=CD93 PE=1 SV=3 - REVERSED	57	68515	2	1	1.1	5.27
143	P81605	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	56	11277	2	2	22.7	6.08
144	P03973	Antileukoproteinase OS=Homo sapiens GN=SLPI PE=1 SV=2	55	14316	1	1	9.1	9.11
145	Q6YHK3	CD109 antigen OS=Homo sapiens GN=CD109 PE=1 SV=2	55	161587	2	2	1.8	5.59
146	P04180	Phosphatidylcholine-sterol acyltransferase OS=Homo sapiens GN=LCAT PE=1 SV=1	55	49546	1	1	2.5	5.71
147	Q9BXJ4	Complement C1q tumor necrosis factor-related protein 3 OS=Homo sapiens GN=C1QTNF3 PE=2 SV=1	55	26977	1	1	5.3	6.04
148	P16070	CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=3	53	81487	1	1	1.6	5.13
149	P02649	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	53	36132	1	1	2.8	5.65
150	P29353_REVERSED	SHC-transforming protein 1 OS=Homo sapiens GN=SHC1 PE=1 SV=4 - REVERSED	51	62782	6	1	1.4	6.01
151	P35580	Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3	51	228858	2	2	1.2	5.44
152	P28066	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	50	26394	1	1	4.1	4.74
153	O95445	Apolipoprotein M OS=Homo sapiens GN=APOM PE=1 SV=2	49	21239	4	1	6.9	5.66
154	P04745	Alpha-amylase 1 OS=Homo sapiens GN=AMY1A PE=1 SV=2	49	57731	1	1	2.3	6.47
155	Q13454	Tumor suppressor candidate 3 OS=Homo sapiens GN=TUSC3 PE=2 SV=1	49	39650	1	1	2	9.93
156	P49721	Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1	49	22822	3	1	19.9	6.51
157	P32119	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	49	21878	1	1	9.1	5.66
158	Q6ZU45	Putative C-type lectin domain-containing protein NCRNA00083 OS=Homo sapiens GN=NCRNA00083 PE=5 SV=1	49	25796	1	1	3.4	6.3
159	O43264_REVERSED	Centromere/kinetochore protein zw10 homolog	49	88773	1	1	0.8	5.89

E10								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
		OS=Homo sapiens GN=ZW10 PE=1 SV=3 - REVERSED						
160	Q9Y490	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	48	269599	2	2	1	5.77
161	Q96CD0_REVERSED	F-box/LRR-repeat protein 8 OS=Homo sapiens GN=FBXL8 PE=1 SV=1 - REVERSED	48	40490	11	1	1.9	7.03
162	P06702	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	47	13234	1	1	13.2	5.71
163	Q6P1X5_REVERSED	Transcription initiation factor TFIID subunit 2 OS=Homo sapiens GN=TAF2 PE=1 SV=3 - REVERSED	47	136883	1	1	0.5	8.46
164	Q16853	Membrane primary amine oxidase OS=Homo sapiens GN=AOC3 PE=1 SV=3	47	84568	1	1	1.2	6.05
165	P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	47	44586	3	1	8.4	8.3
166	P02749	Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3	46	38273	1	1	2.6	8.34
167	A8MPT4	Glutathione S-transferase theta-4 OS=Homo sapiens GN=GSTT4 PE=3 SV=2	45	27941	2	1	2.5	6.25
168	Q8N6V9_REVERSED	Testis-expressed sequence 9 protein OS=Homo sapiens GN=TEX9 PE=2 SV=1 - REVERSED	45	44798	2	1	1.5	6.2
169	Q9Y2U8_REVERSED	Inner nuclear membrane protein Man1 OS=Homo sapiens GN=LEMD3 PE=1 SV=2 - REVERSED	45	99935	2	1	0.7	7.31
170	P05154	Plasma serine protease inhibitor OS=Homo sapiens GN=SERPINA5 PE=1 SV=3	45	45646	2	1	1.5	9.3
171	Q8NDM7_REVERSED	WD repeat-containing protein 96 OS=Homo sapiens GN=WDR96 PE=2 SV=3 - REVERSED	45	191861	1	1	0.5	5.71
172	Q6NXT2	Histone H3.3C OS=Homo sapiens GN=H3F3C PE=1 SV=3	44	15204	1	1	5.2	11.1
173	O95248	Myotubularin-related protein 5 OS=Homo sapiens GN=SBF1 PE=1 SV=3	44	208184	1	1	0.4	6.46
174	Q9UK61_REVERSED	Uncharacterized protein C3orf63 OS=Homo sapiens GN=C3orf63 PE=1 SV=3 - REVERSED	44	188914	1	1	0.4	5.55
175	Q9Y6X9_REVERSED	MORC family CW-type zinc finger protein 2 OS=Homo sapiens GN=MORC2 PE=1 SV=2 - REVERSED	43	117750	2	1	1.6	8.6
176	P06746	DNA polymerase beta OS=Homo sapiens GN=POLB PE=1 SV=3	43	38154	1	1	1.8	9.01
177	Q92820	Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2	43	35941	1	1	4.1	6.67
178	Q9TNN7	HLA class I histocompatibility antigen, Cw-5 alpha chain OS=Homo sapiens GN=HLA-C PE=2 SV=1	43	40886	1	1	3.6	7.11

E10								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
179	Q12968_REVERSED	Nuclear factor of activated T-cells, cytoplasmic 3 OS=Homo sapiens GN=NFATC3 PE=1 SV=1 - REVERSED	41	115522	3	1	0.7	5.91
180	Q96M89	Coiled-coil domain-containing protein 138 OS=Homo sapiens GN=CCDC138 PE=1 SV=1	41	76171	2	1	2.3	8.75
181	Q9Y5E4_REVERSED	Protocadherin beta-5 OS=Homo sapiens GN=PCDHB5 PE=1 SV=1 - REVERSED	41	86369	2	1	1	4.87
182	Q9NU02_REVERSED	Ankyrin repeat domain-containing protein 5 OS=Homo sapiens GN=ANKRD5 PE=2 SV=2 - REVERSED	41	86610	2	1	1.8	8.51
183	Q7Z5M8	Abhydrolase domain-containing protein 12B OS=Homo sapiens GN=ABHD12B PE=2 SV=1	41	40750	4	1	1.7	8.57
184	Q15020_REVERSED	Squamous cell carcinoma antigen recognized by T-cells 3 OS=Homo sapiens GN=SART3 PE=1 SV=1 - REVERSED	41	109865	4	1	0.6	5.45
185	P10643	Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2	41	93457	2	1	2	6.09
186	P61769	Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1	40	13706	1	1	8.4	6.06
187	Q9BY43	Charged multivesicular body protein 4a OS=Homo sapiens GN=CHMP4A PE=1 SV=3	40	25083	2	1	6.3	4.65
188	O60312	Probable phospholipid-transporting ATPase VA OS=Homo sapiens GN=ATP10A PE=2 SV=2	40	167582	2	1	0.6	8.7
189	Q8NBM4	Ubiquitin-associated domain-containing protein 2 OS=Homo sapiens GN=UBAC2 PE=2 SV=1	40	38938	2	1	2.3	9.21
190	Q99798	Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2	40	85372	1	1	1	7.36
191	Q14849	StAR-related lipid transfer protein 3 OS=Homo sapiens GN=STARD3 PE=1 SV=2	40	50471	1	1	1.6	8.52
192	Q8NFY9	Kelch repeat and BTB domain-containing protein 8 OS=Homo sapiens GN=KBTBD8 PE=2 SV=2	39	68778	1	1	1.8	5.88
193	Q96K21	Zinc finger FYVE domain-containing protein 19 OS=Homo sapiens GN=ZFYVE19 PE=1 SV=3	39	51514	1	1	1.7	5.57
194	P02760	Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1	39	38974	1	1	2	5.95
195	P53675_REVERSED	Clathrin heavy chain 2 OS=Homo sapiens GN=CLTCL1 PE=1 SV=2 - REVERSED	39	186910	1	1	0.5	5.57
196	P0C869	Cytosolic phospholipase A2 beta OS=Homo sapiens GN=PLA2G4B PE=1 SV=2	39	87922	2	1	1	5.64
197	Q8WUM4	Programmed cell death 6-interacting protein	39	95963	1	1	1.6	6.13

E10								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
		OS=Homo sapiens GN=PDCD6IP PE=1 SV=1						
198	P05156	Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2	39	65707	1	1	1.2	7.72
199	P00736	Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2	39	80067	2	1	3.4	5.82
200	Q00535_REVERSED	Cyclin-dependent kinase 5 OS=Homo sapiens GN=CDK5 PE=1 SV=3 - REVERSED	38	33283	1	1	3.1	7.9
201	Q9ULT0	Tetratricopeptide repeat protein 7A OS=Homo sapiens GN=TTC7A PE=1 SV=3	38	96123	2	1	1.2	6.03
202	P25786	Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1	38	29537	1	1	4.6	6.15
203	Q9Y2C9_REVERSED	Toll-like receptor 6 OS=Homo sapiens GN=TLR6 PE=2 SV=2 - REVERSED	38	91820	1	1	1	6.83
204	Q14C86_REVERSED	GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 SV=2 - REVERSED	38	164876	2	1	0.5	5.09
205	Q5T1B0	Axonemal dynein light chain domain-containing protein 1 OS=Homo sapiens GN=AXDND1 PE=1 SV=1	38	117953	1	1	0.6	5.49
206	Q9P2G4_REVERSED	Uncharacterized protein KIAA1383 OS=Homo sapiens GN=KIAA1383 PE=1 SV=2 - REVERSED	38	100283	1	1	0.8	6.77
207	Q6NUP7	Serine/threonine-protein phosphatase 4 regulatory subunit 4 OS=Homo sapiens GN=PPP4R4 PE=1 SV=1	38	99389	2	1	0.7	7.96
208	Q16348	Solute carrier family 15 member 2 OS=Homo sapiens GN=SLC15A2 PE=2 SV=2	38	81730	3	1	1.5	8.4
209	Q9P2E9	Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4	38	152381	1	1	0.4	8.69
210	P04920	Anion exchange protein 2 OS=Homo sapiens GN=SLC4A2 PE=1 SV=4	38	136923	1	1	0.5	5.9
211	Q99819	Rho GDP-dissociation inhibitor 3 OS=Homo sapiens GN=ARHGDIG PE=2 SV=2	38	25082	1	1	2.7	5.45
212	O95071_REVERSED	E3 ubiquitin-protein ligase UBR5 OS=Homo sapiens GN=UBR5 PE=1 SV=2 - REVERSED	38	309158	2	1	0.3	5.59
213	P22352	Glutathione peroxidase 3 OS=Homo sapiens GN=GPX3 PE=1 SV=2	37	25537	1	1	5.3	8.26
214	P29401	Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3	37	67835	1	1	2.9	7.58
215	P35443	Thrombospondin-4 OS=Homo sapiens GN=THBS4 PE=1 SV=2	37	105802	1	1	1	4.44
216	Q14028_REVERSED	Cyclic nucleotide-gated cation channel beta-1 OS=Homo sapiens GN=CNGB1 PE=1 SV=2 - REVERSED	37	139590	2	1	0.6	4.76

E10

prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
217	Q14573_REVERSED	Inositol 1,4,5-trisphosphate receptor type 3 OS=Homo sapiens GN=ITPR3 PE=1 SV=2 - REVERSED	37	303912	2	1	0.4	6.05
218	Q9C0B2	Uncharacterized protein KIAA1751 OS=Homo sapiens GN=KIAA1751 PE=2 SV=2	37	86902	2	1	1.6	5.39
219	Q6ZUT9_REVERSED	DENN domain-containing protein 5B OS=Homo sapiens GN=DENND5B PE=1 SV=2 - REVERSED	37	144927	2	1	1	6.29
220	O94991	SLIT and NTRK-like protein 5 OS=Homo sapiens GN=SLITRK5 PE=1 SV=2	37	107418	2	1	1.4	6.48
221	O94868_REVERSED	FCH and double SH3 domains protein 2 OS=Homo sapiens GN=FCHSD2 PE=1 SV=3 - REVERSED	37	84224	2	1	1.9	5.55
222	Q4G0X9_REVERSED	Coiled-coil domain-containing protein 40 OS=Homo sapiens GN=CCDC40 PE=2 SV=2 - REVERSED	37	130033	1	1	0.5	5.21
223	Q9UC07_REVERSED	Zinc finger protein 69 OS=Homo sapiens GN=ZNF69 PE=2 SV=2 - REVERSED	37	65718	1	1	1.1	9.13
224	Q9Y496_REVERSED	Kinesin-like protein KIF3A OS=Homo sapiens GN=KIF3A PE=1 SV=4 - REVERSED	37	79991	1	1	0.9	6.16
225	Q14997	Proteasome activator complex subunit 4 OS=Homo sapiens GN=PSME4 PE=1 SV=2	37	211199	1	1	0.3	6.45
226	Q92841	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1	37	72326	1	1	0.9	8.82
227	Q8N6K7	Sterile alpha motif domain-containing protein 3 OS=Homo sapiens GN=SAMD3 PE=2 SV=2	37	61197	7	1	2.1	6.67
228	Q9NU22	Midasin OS=Homo sapiens GN=MDN1 PE=1 SV=2	36	632420	1	1	0.2	5.46
229	A8MW92_REVERSED	PHD finger protein 20-like protein 1 OS=Homo sapiens GN=PHF20L1 PE=1 SV=2 - REVERSED	36	114938	1	1	1.3	6.4
230	O95613	Pericentrin OS=Homo sapiens GN=PCNT PE=1 SV=4	36	377806	2	1	0.6	5.4
231	P10242_REVERSED	Transcriptional activator Myb OS=Homo sapiens GN=MYB PE=1 SV=2 - REVERSED	36	72296	3	1	1.3	6.35
232	Q7L8A9	Vasohibin-1 OS=Homo sapiens GN=VASH1 PE=1 SV=1	36	40931	1	1	1.9	9.5

HDF

prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
1	P02751	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	16183	262460	423	86	66	5.46
2	P07996	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	3990	129300	115	42	49.4	4.71
3	P12111	Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=5	3014	343457	118	59	33.3	6.26

HDF								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
4	P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	2557	69321	114	8	11.8	5.92
5	P02765	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	2385	39300	60	4	8.7	5.43
6	P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	2277	65999	62	25	51.1	8.15
7	P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	2109	58792	64	27	54.8	5.13
8	P03956	Interstitial collagenase OS=Homo sapiens GN=MMP1 PE=1 SV=3	1904	53973	57	20	60.8	6.47
9	P07093	Glia-derived nexin OS=Homo sapiens GN=SERPINE2 PE=1 SV=1	1820	43974	53	17	59.8	9.35
10	P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	1740	65393	52	23	56.2	8.07
11	P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	1729	163188	56	11	7.5	6.03
12	P24821	Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3	1664	240700	47	31	25.3	4.79
13	P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	1625	62027	36	20	62.6	5.14
14	P08253	72 kDa type IV collagenase OS=Homo sapiens GN=MMP2 PE=1 SV=2	1609	73835	50	24	60.5	5.26
15	P20742	Pregnancy zone protein OS=Homo sapiens GN=PZP PE=1 SV=4	1393	163760	42	5	4	5.97
16	P43235	Cathepsin K OS=Homo sapiens GN=CTSK PE=1 SV=1	1336	36942	26	9	53.5	8.72
17	P01024	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	1296	187030	53	13	15.4	6.02
18	P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	951	41710	31	14	47.5	5.29
19	P12109	Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3	940	108462	21	13	19.6	5.26
20	P98160	Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4	933	468532	48	30	13.6	6.06
21	P00734	Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2	818	69992	18	8	10.9	5.64
22	P19823	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2	799	106397	24	8	9.3	6.4
23	P06396	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	746	85644	26	11	14.3	5.9
24	P26022	Pentraxin-related protein PTX3 OS=Homo sapiens GN=PTX3 PE=1 SV=3	727	41949	16	8	30.2	4.94
25	P36955	Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=4	680	46283	23	5	12.2	5.97
26	Q08380	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	667	65289	21	12	30.3	5.13
27	Q15582	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1	604	74634	17	14	28.8	7.62
28	Q99715	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2	550	332941	23	19	11.7	5.38
29	Q14393	Growth arrest-specific protein 6 OS=Homo sapiens GN=GAS6 PE=1 SV=2	527	79625	16	10	19.4	5.84
30	P68032	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	521	41992	19	9	26.8	5.23
31	Q07954	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2	455	504276	16	13	4.5	5.16
32	P02771	Alpha-fetoprotein OS=Homo sapiens GN=AFP PE=1 SV=1	433	68633	13	4	6.7	5.48
33	P12110	Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4	430	108512	19	12	18.1	5.85

HDF								
prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
34	P02788	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6	429	78132	18	3	4.8	8.5
35	P0C0L4	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1	405	192650	15	8	5.6	6.65
36	P08254	Stromelysin-1 OS=Homo sapiens GN=MMP3 PE=1 SV=2	403	53943	15	9	24.9	5.77
37	P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	386	15248	18	5	34.5	8.72
38	P02533	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	376	51529	13	9	23.5	5.09
39	P35442	Thrombospondin-2 OS=Homo sapiens GN=THBS2 PE=1 SV=2	331	129908	13	8	9.2	4.62
40	P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	323	36030	9	5	26.3	8.57
41	P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1	323	45031	12	9	41.5	6.68
42	Q562R1	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	320	41976	11	4	13	5.39
43	Q8WUJ3	Protein KIAA1199 OS=Homo sapiens GN=KIAA1199 PE=1 SV=2	308	152900	13	9	12	7.98
44	O00391	Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3	301	82526	9	6	14.5	9.13
45	P07355	Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	298	38580	8	6	31	7.57
46	Q06033	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2	294	99787	11	4	8.8	5.49
47	P07339	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	282	44524	13	7	25.2	6.1
48	Q08431	Lactadherin OS=Homo sapiens GN=MFGE8 PE=1 SV=2	281	43095	12	8	26.6	8.47
49	P08123	Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=7	262	129235	7	7	8.4	9.08
50	P15144	Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4	254	109471	12	6	13	5.31
51	P08758	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2	249	35914	9	5	19.1	4.94
52	P13647	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	246	62340	14	7	14.6	7.59
53	P02774	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1	244	52929	9	5	12	5.4
54	P51884	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	239	38405	14	6	21.9	6.16
55	Q13219	Pappalysin-1 OS=Homo sapiens GN=PAPPA PE=1 SV=3	238	180856	6	4	6.1	5.76
56	P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4	238	57900	7	7	21.3	7.96
57	P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	234	70854	5	5	10.2	5.37
58	P04114	Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	231	515283	15	6	2.2	6.58
59	P98095	Fibulin-2 OS=Homo sapiens GN=FBLN2 PE=1 SV=2	221	126489	7	4	8.4	4.73
60	P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	216	60030	12	5	10.1	8.09
61	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2	215	93255	11	7	15.1	7.27
62	P00747	Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2	212	90510	9	5	8.5	7.04
63	P12259	Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4	210	251546	10	6	4.2	5.68
64	Q16363	Laminin subunit alpha-4 OS=Homo sapiens GN=LAMA4 PE=1 SV=4	210	202397	4	3	4.1	5.89
65	P04004	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	209	54271	4	1	3.1	5.55

HDF								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
66	P55268	Laminin subunit beta-2 OS=Homo sapiens GN=LAMB2 PE=1 SV=2	207	195854	11	6	6.4	6.07
67	P02647	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	204	30759	4	1	6	5.56
68	P23142	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4	202	77162	11	5	10.2	5.07
69	Q9Y6C2	EMILIN-1 OS=Homo sapiens GN=EMILIN1 PE=1 SV=2	198	106601	5	4	8.8	5.07
70	Q99816	Tumor susceptibility gene 101 protein OS=Homo sapiens GN=TSG101 PE=1 SV=2	60	43916	15	5	19.2	5.2
71	P05543	Thyroxine-binding globulin OS=Homo sapiens GN=SERPINA7 PE=1 SV=2	197	46295	6	3	8.2	5.87
72	Q13510	Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=1 SV=5	197	44631	5	5	18.5	7.52
73	P02452	Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5	188	138857	8	4	5.2	5.6
74	P11047	Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3	179	177489	6	4	3.8	5.01
75	P02042	Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2	176	16045	11	2	12.9	7.85
76	P35443	Thrombospondin-4 OS=Homo sapiens GN=THBS4 PE=1 SV=2	171	105802	6	5	7.3	4.44
77	P49747	Cartilage oligomeric matrix protein OS=Homo sapiens GN=COMP PE=1 SV=2	167	82808	6	5	7.1	4.36
78	P19827	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3	166	101326	3	3	2.9	6.31
79	P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	165	47139	4	3	12	7.01
80	P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=4	163	46902	2	2	7.6	7.59
81	P01031	Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4	162	188186	7	4	3	6.11
82	P02538	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	159	60008	9	4	9.9	8.09
83	P02100	Hemoglobin subunit epsilon OS=Homo sapiens GN=HBE1 PE=1 SV=2	159	16192	7	2	12.9	8.67
84	P07858	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3	159	37797	5	4	15	5.88
85	Q6YHK3	CD109 antigen OS=Homo sapiens GN=CD109 PE=1 SV=2	158	161587	6	5	5.3	5.59
86	P42785	Lysosomal Pro-X carboxypeptidase OS=Homo sapiens GN=PRCP PE=1 SV=1	155	55764	2	1	4.2	6.75
87	P02649	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	154	36132	6	3	9.1	5.65
88	P02794	Ferritin heavy chain OS=Homo sapiens GN=FTH1 PE=1 SV=2	154	21212	5	4	38.3	5.3
89	P02675	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	154	55892	3	2	3.9	8.54
90	Q92626	Peroxidasin homolog OS=Homo sapiens GN=PXDN PE=1 SV=2	153	165170	5	4	4.9	6.79
91	P08697	Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3	150	54531	2	1	2.2	5.87
92	P00736	Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2	150	80067	6	5	13	5.82
93	Q9Y4K0	Lysyl oxidase homolog 2 OS=Homo sapiens GN=LOXL2 PE=1 SV=1	148	86668	3	3	5.7	5.95
94	Q13103	Secreted phosphoprotein 24 OS=Homo sapiens GN=SPP2 PE=1 SV=1	147	24322	2	1	5.7	8.59
95	P34931	Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2	145	70331	3	3	7	5.76
96	P04083	Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	141	38690	3	3	16.2	6.57

HDF								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
97	Q9Y490	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	140	269599	7	4	4.2	5.77
98	P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	139	50120	8	4	19.7	4.94
99	P15169	Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1	139	52253	2	1	3.3	6.86
100	P07686	Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3	137	63071	8	3	15.8	6.29
101	P02748	Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2	135	63133	3	2	3.8	5.43
102	P19013	Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4	130	57250	8	4	7.3	6.25
103	P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	129	49639	6	4	18.5	4.78
104	Q9Y240	C-type lectin domain family 11 member A OS=Homo sapiens GN=CLEC11A PE=1 SV=1	128	35672	3	1	8	5.06
105	P51888	Prolargin OS=Homo sapiens GN=PRELP PE=1 SV=1	124	43782	6	4	15.2	9.47
106	Q9UBG0	C-type mannose receptor 2 OS=Homo sapiens GN=MRC2 PE=1 SV=2	123	166568	1	1	1.1	5.54
107	P00742	Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2	122	54697	5	3	7.6	5.68
108	Q86YZ3	Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	115	282228	1	1	0.7	10.05
109	P13646	Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4	112	49557	5	4	6.1	4.91
110	P09871	Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1	111	76635	5	4	6.8	4.86
111	P10619	Lysosomal protective protein OS=Homo sapiens GN=CTSA PE=1 SV=2	106	54431	4	3	12.5	6.16
112	P62979	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2	100	17953	7	3	28.2	9.68
113	Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2	98	83497	4	2	8.4	6.47
114	P07602	Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2	96	58074	4	3	7.6	5.06
115	P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	96	84607	5	2	5.9	4.94
116	P49746	Thrombospondin-3 OS=Homo sapiens GN=THBS3 PE=1 SV=1	94	104135	7	2	8.1	4.43
117	P08294	Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3 PE=1 SV=2	94	25835	1	1	5.4	6.14
118	P00450	Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1	94	122128	3	1	2	5.44
119	P08473	Neprilysin OS=Homo sapiens GN=MME PE=1 SV=2	93	85460	2	2	3.2	5.54
120	P04745	Alpha-amylase 1 OS=Homo sapiens GN=AMY1A PE=1 SV=2	91	57731	2	2	5.5	6.47
121	P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	91	83212	3	2	4	4.97
122	P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	89	280564	5	3	2.6	5.7
123	Q8NI35	InaD-like protein OS=Homo sapiens GN=INADL PE=1 SV=3	89	196247	8	1	0.3	4.84
124	P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	88	44586	2	1	7.9	8.3
125	P48723	Heat shock 70 kDa protein 13 OS=Homo sapiens GN=HSPA13 PE=1 SV=1	88	51895	3	3	8.1	5.52
126	Q8TEV9_REVERSED	Smith-Magenis syndrome chromosomal region candidate gene 8 protein OS=Homo sapiens	86	104956	10	1	1.2	5.36

HDF								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
		GN=SMCR8 PE=1 SV=2 - REVERSED						
127	P09486	SPARC OS=Homo sapiens GN=SPARC PE=1 SV=1	85	34610	3	2	16.5	4.73
128	P68371	Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1	85	49799	5	3	15.7	4.79
129	P27487	Dipeptidyl peptidase 4 OS=Homo sapiens GN=DPP4 PE=1 SV=2	85	88222	2	1	3	5.67
130	P09238	Stromelysin-2 OS=Homo sapiens GN=MMP10 PE=1 SV=1	84	54117	4	2	6.1	5.49
131	Q8N436	Inactive carboxypeptidase-like protein X2 OS=Homo sapiens GN=CPXM2 PE=2 SV=3	84	85816	2	2	4	6.4
132	O95497	Pantetheinase OS=Homo sapiens GN=VNN1 PE=1 SV=2	81	56975	1	1	3.7	5.32
133	Q06828	Fibromodulin OS=Homo sapiens GN=FMOD PE=1 SV=2	80	43152	1	1	3.5	5.66
134	O00560	Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1	79	32424	4	2	21.1	7.05
135	P23526	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	79	47685	4	3	12	5.92
136	P33908	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA OS=Homo sapiens GN=MAN1A1 PE=1 SV=3	78	72922	3	2	6.4	6.04
137	O14773	Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2	77	61210	1	1	4.8	6.01
138	P01008	Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1	77	52569	5	2	7.3	6.32
139	P16035	Metalloproteinase inhibitor 2 OS=Homo sapiens GN=TIMP2 PE=1 SV=2	77	24383	4	2	12.7	7.45
140	P11717	Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=3	77	274199	4	3	2.2	5.64
141	Q12860	Contactin-1 OS=Homo sapiens GN=CNTN1 PE=1 SV=1	75	113249	3	2	3.4	5.62
142	Q92743	Serine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1	75	51255	1	1	2.9	8.09
143	P05067	Amyloid beta A4 protein OS=Homo sapiens GN=APP PE=1 SV=3	74	86888	2	1	2.6	4.73
144	Q8TAA3	Proteasome subunit alpha type-7-like OS=Homo sapiens GN=PSMA8 PE=1 SV=3	74	28512	1	1	5.5	9.07
145	Q5D862	Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	72	247928	2	2	1	8.45
146	O00300	Tumor necrosis factor receptor superfamily member 11B OS=Homo sapiens GN=TNFRSF11B PE=1 SV=3	71	45996	1	1	4.2	8.66
147	P02790	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	71	51643	4	1	1.9	6.55
148	O15111_REVERSED	Inhibitor of nuclear factor kappa-B kinase subunit alpha OS=Homo sapiens GN=CHUK PE=1 SV=2 - REVERSED	71	84585	6	1	1.6	6.28
149	P28799	Granulins OS=Homo sapiens GN=GRN PE=1 SV=2	69	63500	4	2	6.2	6.43
150	O75508	Claudin-11 OS=Homo sapiens GN=CLDN11 PE=1 SV=2	69	21978	1	1	6.8	8.22
151	P81605	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	68	11277	2	2	20	6.08
152	P55058	Phospholipid transfer protein OS=Homo sapiens GN=PLTP PE=1 SV=1	68	54705	1	1	2.2	6.53
153	P02749	Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3	68	38273	3	1	4.3	8.34
154	P60033	CD81 antigen OS=Homo sapiens GN=CD81 PE=1 SV=1	67	25792	2	1	18.2	5.09
155	Q8WXE9	Stonin-2 OS=Homo sapiens GN=STON2 PE=1 SV=1	67	101102	2	1	1	5.2
156	O95445	Apolipoprotein M OS=Homo sapiens GN=APOM PE=1 SV=2	66	21239	5	1	6.9	5.66

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157	Q7Z304	MAM domain-containing protein 2 OS=Homo sapiens GN=MAMDC2 PE=2 SV=3	66	77506	3	2	3.9	5.05
158	Q12931	Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3	65	80060	3	1	2.8	8.3
159	P19883	Follistatin OS=Homo sapiens GN=FST PE=1 SV=2	65	37981	2	1	7	5.53
160	P61224	Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B PE=1 SV=1	64	20812	2	2	12.5	5.65
161	P20908	Collagen alpha-1(V) chain OS=Homo sapiens GN=COL5A1 PE=1 SV=3	64	183447	1	1	1.2	4.94
162	P10599	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3	64	11730	1	1	12.4	4.82
163	P08133	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3	62	75826	2	2	4.2	5.42
164	Q9NZP8	Complement C1r subcomponent-like protein OS=Homo sapiens GN=C1RL PE=1 SV=2	62	53464	1	1	2.5	6.75
165	Q03692	Collagen alpha-1(X) chain OS=Homo sapiens GN=COL10A1 PE=1 SV=2	61	66117	1	1	1.9	9.68
166	P26447	Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1	61	11721	2	2	16.8	5.85
167	P14550	Alcohol dehydrogenase [NADP+] OS=Homo sapiens GN=AKR1A1 PE=1 SV=3	61	36550	1	1	3.1	6.32
168	P15121	Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3	61	35830	1	1	3.2	6.51
169	P22105	Tenascin-X OS=Homo sapiens GN=TNXB PE=1 SV=3	60	464034	1	1	0.3	5.19
170	Q9BYX7_REVERSED	Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1 - REVERSED	57	41989	9	1	3.5	5.92
171	P05546	Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3	57	57034	2	1	3.8	6.41
172	P02461	Collagen alpha-1(III) chain OS=Homo sapiens GN=COL3A1 PE=1 SV=4	57	138479	3	1	2.9	6.21
173	P07585	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1	57	39722	2	1	9.7	8.75
174	Q03135	Caveolin-1 OS=Homo sapiens GN=CAV1 PE=1 SV=4	56	20458	1	1	7.9	5.65
175	O43264_REVERSED	Centromere/kinetochore protein zw10 homolog OS=Homo sapiens GN=ZW10 PE=1 SV=3 - REVERSED	55	88773	2	1	0.8	5.89
176	P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2	55	18001	2	1	13.9	7.68
177	P07737	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	55	15045	2	2	12.1	8.44
178	P02760	Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1	55	38974	1	1	2	5.95
179	B9A064	Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2	54	23049	1	1	3.7	9.08
180	P18206	Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4	54	123722	2	1	2	5.5
181	P10643	Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2	54	93457	2	2	2	6.09
182	Q9UK55	Protein Z-dependent protease inhibitor OS=Homo sapiens GN=SERPINA10 PE=1 SV=1	53	50674	4	1	4.1	8.28
183	Q8NBM4	Ubiquitin-associated domain-containing protein 2 OS=Homo sapiens GN=UBAC2 PE=2 SV=1	52	38938	5	1	2.3	9.21
184	Q14624	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4	52	103293	6	1	2.5	6.51
185	Q86VH2	Kinesin-like protein KIF27 OS=Homo sapiens GN=KIF27 PE=2 SV=1	51	160184	1	1	0.6	6.9
186	P28300	Protein-lysine 6-oxidase OS=Homo sapiens GN=LOX PE=1 SV=2	51	46915	1	1	3.1	8.36

HDF

prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
187	P05452	Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=3	51	22522	1	1	10.4	5.52
188	Q8NAV2_REVERSED	Uncharacterized protein C8orf58 OS=Homo sapiens GN=C8orf58 PE=2 SV=2 - REVERSED	51	39636	3	1	4.1	8.54
189	P08962	CD63 antigen OS=Homo sapiens GN=CD63 PE=1 SV=2	51	25619	1	1	4.2	8.14
190	P61769	Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1	51	13706	1	1	8.4	6.06
191	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4	50	69370	1	1	1.5	5.94
192	P04439	HLA class I histocompatibility antigen, A-3 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=2	50	40815	3	2	9.3	5.66
193	Q86Y46	Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1	50	58887	8	3	8.5	6.93
194	P26038	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	50	67778	2	1	3.3	6.08
195	O60312	Probable phospholipid-transporting ATPase VA OS=Homo sapiens GN=ATP10A PE=2 SV=2	50	167582	3	1	0.6	8.7
196	Q9HDC9	Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2	50	46451	1	1	1.7	5.82
197	Q16394	Exostosin-1 OS=Homo sapiens GN=EXT1 PE=1 SV=2	49	86200	3	1	8.6	9.16
198	Q15751_REVERSED	Probable E3 ubiquitin-protein ligase HERC1 OS=Homo sapiens GN=HERC1 PE=1 SV=2 - REVERSED	48	531891	1	1	0.2	5.69
199	P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3	47	77014	2	1	1.7	6.81
200	Q13454	Tumor suppressor candidate 3 OS=Homo sapiens GN=TUSC3 PE=2 SV=1	47	39650	1	1	2	9.93
201	P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	47	36665	1	1	3	8.44
202	P60903	Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2	47	11196	1	1	17.5	6.82
203	P29353_REVERSED	SHC-transforming protein 1 OS=Homo sapiens GN=SHC1 PE=1 SV=4 - REVERSED	46	62782	5	1	1.4	6.01
204	P01042	Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2	46	71912	1	1	1.4	6.34
205	Q76LX8	A disintegrin and metalloproteinase with thrombospondin motifs 13 OS=Homo sapiens GN=ADAMTS13 PE=1 SV=1	45	153505	1	1	0.7	6.96
206	Q9UHL4	Dipeptidyl peptidase 2 OS=Homo sapiens GN=DPP7 PE=1 SV=3	45	54307	1	1	2.4	5.91
207	P07225	Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1	45	75074	2	1	2.4	5.48
208	Q99456	Keratin, type I cytoskeletal 12 OS=Homo sapiens GN=KRT12 PE=1 SV=1	45	53478	3	1	3.2	4.7
209	Q96CD0_REVERSED	F-box/LRR-repeat protein 8 OS=Homo sapiens GN=FBXL8 PE=1 SV=1 - REVERSED	44	40490	6	1	1.9	7.03
210	Q6ZU45	Putative C-type lectin domain-containing protein NCRNA00083 OS=Homo sapiens GN=NCRNA00083 PE=5 SV=1	44	25796	1	1	3.4	6.3
211	Q3KQU3	MAP7 domain-containing protein 1 OS=Homo sapiens GN=MAP7D1 PE=1 SV=1	44	92764	1	1	0.7	10.12
212	Q5U5X0	LYR motif-containing protein 7 OS=Homo sapiens GN=LYRM7 PE=1 SV=1	44	11947	1	1	5.8	9.67
213	Q8N7B9_REVERSED	EF-hand calcium-binding domain-containing protein 3 OS=Homo sapiens GN=EFCAB3 PE=1 SV=1 - REVERSED	44	50114	1	1	1.4	9.31

HDF								
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214	Q8NB25_REVERSED	Protein FAM184A OS=Homo sapiens GN=FAM184A PE=2 SV=3 - REVERSED	44	132883	1	1	0.5	5.59
215	P06732	Creatine kinase M-type OS=Homo sapiens GN=CKM PE=1 SV=2	44	43074	1	1	1.6	6.77
216	Q93096_REVERSED	Protein tyrosine phosphatase type IVA 1 OS=Homo sapiens GN=PTP4A1 PE=1 SV=2 - REVERSED	44	19802	1	1	3.5	9.17
217	Q8IWC1	MAP7 domain-containing protein 3 OS=Homo sapiens GN=MAP7D3 PE=1 SV=2	44	98368	1	1	0.7	9.34
218	P11137	Microtubule-associated protein 2 OS=Homo sapiens GN=MAP2 PE=1 SV=4	42	199404	2	1	1.1	4.82
219	Q16348	Solute carrier family 15 member 2 OS=Homo sapiens GN=SLC15A2 PE=2 SV=2	42	81730	3	1	1.5	8.4
220	P15531	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1	42	17138	1	1	11.2	5.83
221	Q14566_REVERSED	DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1 - REVERSED	41	92831	1	1	0.9	5.28
222	O75830	Serpin I2 OS=Homo sapiens GN=SERPINI2 PE=2 SV=1	41	46116	1	1	3.5	5.08
223	O60568	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1	41	84731	1	1	1.9	5.69
224	Q8NHP8	Putative phospholipase B-like 2 OS=Homo sapiens GN=PLBD2 PE=1 SV=2	41	65430	2	1	3.2	6.34
225	Q99466_REVERSED	Neurogenic locus notch homolog protein 4 OS=Homo sapiens GN=NOTCH4 PE=1 SV=2 - REVERSED	41	209480	2	1	0.4	5.43
226	P17936	Insulin-like growth factor-binding protein 3 OS=Homo sapiens GN=IGFBP3 PE=1 SV=2	41	31654	1	1	3.8	9.03
227	Q14789_REVERSED	Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=1 SV=2 - REVERSED	41	375790	1	1	0.3	4.96
228	Q9BXJ4	Complement C1q tumor necrosis factor-related protein 3 OS=Homo sapiens GN=C1QTNF3 PE=2 SV=1	40	26977	1	1	2.8	6.04
229	P25789	Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1	40	29465	2	2	6.5	7.57
230	Q8WZ42	Titin OS=Homo sapiens GN=TTN PE=1 SV=2	40	3813810	5	1	0.1	6.01
231	P02750	Leucine-rich alpha-2-glycoprotein OS=Homo sapiens GN=LRG1 PE=1 SV=2	40	38154	1	1	1.7	6.45
232	Q9GZR7	ATP-dependent RNA helicase DDX24 OS=Homo sapiens GN=DDX24 PE=1 SV=1	40	96271	1	1	0.7	9.14
233	Q92616_REVERSED	Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6 - REVERSED	40	292572	6	1	0.5	7.28
234	Q03923_REVERSED	Zinc finger protein 85 OS=Homo sapiens GN=ZNF85 PE=2 SV=3 - REVERSED	40	68691	1	1	1.5	9.45
235	Q8IVF5_REVERSED	T-lymphoma invasion and metastasis-inducing protein 2 OS=Homo sapiens GN=TIAM2 PE=2 SV=4 - REVERSED	40	189985	2	1	0.4	6.8
236	A2RRP1_REVERSED	Neuroblastoma-amplified sequence OS=Homo sapiens GN=NBAS PE=1 SV=2 - REVERSED	40	268401	1	1	0.3	5.65
237	P55083	Microfibril-associated glycoprotein 4 OS=Homo sapiens GN=MFAP4 PE=1 SV=2	39	28630	1	1	7.1	5.38
238	O14782	Kinesin-like protein KIF3C OS=Homo sapiens GN=KIF3C PE=1 SV=3	39	89371	3	1	1.1	8.28
239	O14556	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Homo sapiens GN=GAPDHS PE=1 SV=2	39	44473	1	1	3.4	8.38

HDF

prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
240	P05156	Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2	39	65707	1	1	1.2	7.72
241	Q6IWH7	Anoctamin-7 OS=Homo sapiens GN=ANO7 PE=1 SV=1	39	105463	1	1	1	8.33
242	Q14C86_REVERSED	GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 SV=2 - REVERSED	39	164876	2	1	1.1	5.09
243	P02792	Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2	38	20007	2	1	19.4	5.51
244	Q15022	Polycomb protein SUZ12 OS=Homo sapiens GN=SUZ12 PE=1 SV=3	38	83003	1	1	0.8	8.98
245	P33981	Dual specificity protein kinase TTK OS=Homo sapiens GN=TTK PE=1 SV=2	38	97011	1	1	0.7	8.41
246	P27105	Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3	38	31711	1	1	4.2	7.71
247	P28066	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	38	26394	1	1	4.1	4.74
248	Q12968_REVERSED	Nuclear factor of activated T-cells, cytoplasmic 3 OS=Homo sapiens GN=NFATC3 PE=1 SV=1 - REVERSED	37	115522	3	1	0.7	5.91
249	O00754	Lysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE=1 SV=3	37	113672	1	1	1.1	6.84
250	P24347	Stromelysin-3 OS=Homo sapiens GN=MMP11 PE=1 SV=3	36	54556	1	1	1.4	6.38
251	A6H8Y1	Transcription factor TFIIIB component B~~ homolog OS=Homo sapiens GN=BDP1 PE=1 SV=3	36	293705	2	1	0.3	5.06
252	O95071_REVERSED	E3 ubiquitin-protein ligase UBR5 OS=Homo sapiens GN=UBR5 PE=1 SV=2 - REVERSED	36	309158	1	1	0.3	5.59
253	Q9UDT6	CAP-Gly domain-containing linker protein 2 OS=Homo sapiens GN=CLIP2 PE=1 SV=1	36	115767	4	1	1.4	6.29
254	Q9C093_REVERSED	Sperm flagellar protein 2 OS=Homo sapiens GN=SPEF2 PE=1 SV=2 - REVERSED	36	209680	2	1	0.4	5.4
255	Q9NW08	DNA-directed RNA polymerase III subunit RPC2 OS=Homo sapiens GN=POLR3B PE=1 SV=2	36	127702	2	1	0.6	8.77
256	Q5VWK0	Neuroblastoma breakpoint family member 6 OS=Homo sapiens GN=NBPF6 PE=2 SV=2	36	72194	1	1	1.9	4.84
257	O15264	Mitogen-activated protein kinase 13 OS=Homo sapiens GN=MAPK13 PE=1 SV=1	36	42063	4	1	1.9	8.48
258	P21580_REVERSED	Tumor necrosis factor alpha-induced protein 3 OS=Homo sapiens GN=TNFAIP3 PE=1 SV=1 - REVERSED	36	89556	1	1	0.9	8.61
259	P10242_REVERSED	Transcriptional activator Myb OS=Homo sapiens GN=MYB PE=1 SV=2 - REVERSED	36	72296	1	1	1.3	6.35
260	Q96IF1	Protein ajuba OS=Homo sapiens GN=JUB PE=1 SV=1	36	56897	2	1	1.5	6.86
261	Q96RD9_REVERSED	Fc receptor-like protein 5 OS=Homo sapiens GN=FCRL5 PE=1 SV=3 - REVERSED	36	106371	1	1	0.9	6.72

MCF 10A

prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
1	P02751	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	3184	262460	89	44	34.2	5.46
2	P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	3099	65999	85	33	58.1	8.15
3	P13645	Keratin, type I cytoskeletal 10	2577	58792	82	31	61.6	5.13

MCF 10A								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
		OS=Homo sapiens GN=KRT10 PE=1 SV=6						
4	P12111	Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=5	2447	343457	101	65	32.7	6.26
5	P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	2240	62027	64	25	59.9	5.14
6	P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	2090	69321	94	11	11.8	5.92
7	P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	1977	65393	59	28	58.5	8.07
8	Q99715	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2	1875	332941	84	55	28.3	5.38
9	P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	1827	163188	60	9	7.7	6.03
10	P07996	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	1802	129300	68	33	38.1	4.71
11	P02765	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	1724	39300	54	5	8.7	5.43
12	P20742	Pregnancy zone protein OS=Homo sapiens GN=PZP PE=1 SV=4	1283	163760	43	6	4.3	5.97
13	P01024	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	756	187030	35	17	15.6	6.02
14	P12109	Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3	726	108462	23	10	18.9	5.26
15	P02533	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	718	51529	32	14	32.8	5.09
16	P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	676	41710	28	10	47.5	5.29
17	P00734	Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2	607	69992	17	6	10.5	5.64
18	P08779	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	585	51236	29	13	32.1	4.99
19	P19823	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2	534	106397	15	7	9.3	6.4
20	P02788	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6	529	78132	20	3	4.8	8.5
21	Q08380	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	520	65289	20	13	30.4	5.13
22	P24821	Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3	429	240700	21	11	13.8	4.79
23	P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	426	60030	21	12	21.3	8.09
24	P02538	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	401	60008	21	12	21.1	8.09
25	P13647	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	387	62340	23	13	23.7	7.59

MCF 10A

prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
26	P0C0L4	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1	356	192650	15	8	5.2	6.65
27	Q15582	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1	344	74634	18	10	25.2	7.62
28	P68032	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	332	41992	16	6	26.8	5.23
29	P13646	Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4	330	49557	16	6	12.9	4.91
30	P06396	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	324	85644	13	5	11.4	5.9
31	P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	324	36030	10	5	28.4	8.57
32	P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	318	50120	14	10	28.8	4.94
33	Q04695	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	309	48076	19	8	22	4.97
34	P02771	Alpha-fetoprotein OS=Homo sapiens GN=AFP PE=1 SV=1	303	68633	10	4	6.7	5.48
35	P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	291	15248	14	4	33.1	8.72
36	P02774	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1	282	52929	11	5	11.6	5.4
37	Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	280	191493	7	6	6.2	5.48
38	P19012	Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3	256	49181	17	6	12.1	4.71
39	P36955	Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=4	254	46283	6	3	9.1	5.97
40	P02452	Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5	243	138857	10	6	9.6	5.6
41	P04114	Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	237	515283	15	9	2.2	6.58
42	P12110	Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4	235	108512	15	7	15.3	5.85
43	P07355	Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	220	38580	7	6	23.9	7.57
44	Q562R1	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	213	41976	10	3	16	5.39
45	P68366	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	208	49892	10	7	19	4.95
46	P04004	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	196	54271	6	1	4.2	5.55
47	P23142	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4	180	77162	7	4	5.7	5.07

MCF 10A								
prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
48	P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	180	49639	8	5	19.6	4.78
49	Q5XKE5	Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2	179	57800	8	4	6.9	6.75
50	P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	173	11360	7	5	50.5	11.36
51	P02042	Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2	171	16045	10	2	12.9	7.85
52	P05787	Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	170	53671	7	4	5.8	5.52
53	Q07954	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2	167	504276	9	4	2.6	5.16
54	P49747	Cartilage oligomeric matrix protein OS=Homo sapiens GN=COMP PE=1 SV=2	165	82808	6	4	5.8	4.36
55	P02647	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	164	30759	4	1	8.2	5.56
56	P19013	Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4	163	57250	8	4	7.3	6.25
57	P08697	Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3	145	54531	2	1	2.2	5.87
58	P01008	Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1	144	52569	11	5	10.3	6.32
59	P68371	Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1	140	49799	7	4	16.2	4.79
60	Q06033	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2	139	99787	6	3	4.2	5.49
61	P12259	Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4	135	251546	8	4	3.2	5.68
62	P23526	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	133	47685	3	2	9	5.92
63	P51884	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	130	38405	6	2	9.8	6.16
64	Q8NI35	InaD-like protein OS=Homo sapiens GN=INADL PE=1 SV=3	129	196247	11	1	0.3	4.84
65	P19827	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3	120	101326	3	2	3.8	6.31
66	Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3	119	193394	11	4	7.6	5.16
67	P12035	Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3	118	64378	6	4	5.6	6.12
68	P15169	Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1	116	52253	2	1	3.3	6.86
69	P02675	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	114	55892	5	3	5.3	8.54

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prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
70	P02748	Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2	113	63133	2	2	3.8	5.43
71	P11717	Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=3	111	274199	4	2	0.8	5.64
72	P00747	Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2	110	90510	6	2	4.3	7.04
73	P81605	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	110	11277	4	3	22.7	6.08
74	P05543	Thyroxine-binding globulin OS=Homo sapiens GN=SERPINA7 PE=1 SV=2	105	46295	4	2	4.8	5.87
75	P0C0S8	Histone H2A type 1 OS=Homo sapiens GN=HIST1H2AG PE=1 SV=2	105	14083	3	2	21.5	10.9
76	Q86YZ3	Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	102	282228	2	2	1.3	10.05
77	P02749	Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3	101	38273	4	1	5.2	8.34
78	Q08431	Lactadherin OS=Homo sapiens GN=MFGE8 PE=1 SV=2	101	43095	2	1	3.9	8.47
79	P01031	Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4	101	188186	6	2	2.6	6.11
80	Q5D862	Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	100	247928	2	2	1	8.45
81	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	99	36615	2	2	6	5.71
82	P01009	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	98	46707	4	1	3.3	5.37
83	P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	96	89266	5	2	8.8	5.14
84	O43854	EGF-like repeat and discoidin I-like domain-containing protein 3 OS=Homo sapiens GN=EDIL3 PE=1 SV=1	93	53730	4	4	7.5	7.08
85	P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	92	83212	3	2	4.1	4.97
86	O14818	Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1	91	27870	3	3	13.7	8.6
87	O15111_REVERSED	Inhibitor of nuclear factor kappa-B kinase subunit alpha OS=Homo sapiens GN=CHUK PE=1 SV=2 - REVERSED	87	84585	7	1	1.6	6.28
88	P08107	Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	82	70009	4	3	8.3	5.48
89	Q86Y46	Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1	81	58887	6	4	6.7	6.93
90	P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4	81	57900	6	3	14.1	7.96
91	P02461	Collagen alpha-1(III) chain OS=Homo sapiens	80	138479	3	2	2.3	6.21

MCF 10A								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
		GN=COL3A1 PE=1 SV=4						
92	P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	80	39395	4	2	10.7	8.3
93	P61204	ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2	79	20588	1	1	8.3	6.84
94	Q14764	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4	77	99266	4	3	5.6	5.34
95	P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3	77	77014	3	2	1.7	6.81
96	Q5QNW6	Histone H2B type 2-F OS=Homo sapiens GN=HIST2H2BF PE=1 SV=3	76	13912	3	2	15.9	10.31
97	P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	76	84607	3	2	4.9	4.94
98	Q8N7M0_REVERSED	Tctex1 domain-containing protein 1 OS=Homo sapiens GN=TCTEX1D1 PE=2 SV=2 - REVERSED	75	20717	13	1	3.9	9.04
99	P04083	Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	74	38690	2	1	8.4	6.57
100	P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	73	70854	4	2	8.7	5.37
101	P04180	Phosphatidylcholine-sterol acyltransferase OS=Homo sapiens GN=LCAT PE=1 SV=1	70	49546	1	1	2.5	5.71
102	P06702	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	70	13234	3	1	24.6	5.71
103	Q9BXJ4	Complement C1q tumor necrosis factor-related protein 3 OS=Homo sapiens GN=C1QTNF3 PE=2 SV=1	68	26977	2	2	8.1	6.04
104	P02753	Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3	66	22995	2	1	16.4	5.76
105	P29353_REVERSED	SHC-transforming protein 1 OS=Homo sapiens GN=SHC1 PE=1 SV=4 - REVERSED	66	62782	11	1	1.4	6.01
106	Q08554	Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	66	99924	1	1	1.7	5.25
107	Q16853	Membrane primary amine oxidase OS=Homo sapiens GN=AOC3 PE=1 SV=3	66	84568	1	1	1.2	6.05
108	P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	66	36665	2	1	6	8.44
109	P00488	Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4	65	83215	1	1	1.2	5.75
110	Q5VTE0	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1	64	50153	3	2	5.2	9.15
111	Q9H4B7	Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1	64	50295	3	1	9.5	5.05
112	P62979	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2	63	17953	1	1	10.3	9.68

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prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
113	P35443	Thrombospondin-4 OS=Homo sapiens GN=THBS4 PE=1 SV=2	62	105802	5	2	3.9	4.44
114	P02760	Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1	61	38974	2	1	2	5.95
115	P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	60	280564	3	2	1.3	5.7
116	P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	59	226392	2	1	1.5	5.5
117	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2	59	93255	3	1	5.9	7.27
118	P02649	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	59	36132	4	2	8.2	5.65
119	Q14624	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4	59	103293	3	1	2.5	6.51
120	P08758	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2	58	35914	4	2	10.6	4.94
121	P02786	Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	58	84818	1	1	1.6	6.18
122	A6NIZ1	Ras-related protein Rap-1b-like protein OS=Homo sapiens PE=2 SV=1	57	20912	1	1	6.5	5.37
123	Q93070	Ecto-ADP-ribosyltransferase 4 OS=Homo sapiens GN=ART4 PE=2 SV=2	57	35854	8	1	2.2	9.31
124	Q9Y240	C-type lectin domain family 11 member A OS=Homo sapiens GN=CLEC11A PE=1 SV=1	57	35672	1	1	5.3	5.06
125	P32119	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	55	21878	1	1	9.1	5.66
126	Q99456	Keratin, type I cytoskeletal 12 OS=Homo sapiens GN=KRT12 PE=1 SV=1	55	53478	4	1	3.2	4.7
127	P01591	Immunoglobulin J chain OS=Homo sapiens GN=IGJ PE=1 SV=4	54	18087	1	1	6.3	5.12
128	Q6ZU45	Putative C-type lectin domain-containing protein NCRNA00083 OS=Homo sapiens GN=NCRNA00083 PE=5 SV=1	53	25796	1	1	3.4	6.3
129	Q86TI0_REVERSED	TBC1 domain family member 1 OS=Homo sapiens GN=TBC1D1 PE=1 SV=2 - REVERSED	53	133000	1	1	0.7	6.52
130	Q99436	Proteasome subunit beta type-7 OS=Homo sapiens GN=PSMB7 PE=1 SV=1	53	29946	1	1	3.6	7.57
131	P15144	Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4	53	109471	3	1	3.8	5.31
132	P28066	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	52	26394	2	1	12	4.74
133	Q07092	Collagen alpha-1(XVI) chain OS=Homo sapiens GN=COL16A1 PE=1 SV=2	52	157653	1	1	0.7	8.14
134	Q9BYX7_REVERSED	Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP	51	41989	3	1	3.5	5.92

MCF 10A								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
		PE=5 SV=1 - REVERSED						
135	P05452	Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=3	51	22522	1	1	5.9	5.52
136	P35125	Ubiquitin carboxyl-terminal hydrolase 6 OS=Homo sapiens GN=USP6 PE=1 SV=2	50	158557	11	1	0.4	7.87
137	O95445	Apolipoprotein M OS=Homo sapiens GN=APOM PE=1 SV=2	50	21239	2	1	6.9	5.66
138	P02790	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	50	51643	4	1	3.2	6.55
139	Q13454	Tumor suppressor candidate 3 OS=Homo sapiens GN=TUSC3 PE=2 SV=1	50	39650	2	1	2.3	9.93
140	Q8NA29_REVERSED	Major facilitator superfamily domain-containing protein 2A OS=Homo sapiens GN=MFSD2A PE=2 SV=1 - REVERSED	50	60131	1	1	1.3	6.55
141	Q9TNN7	HLA class I histocompatibility antigen, Cw-5 alpha chain OS=Homo sapiens GN=HLA-C PE=2 SV=1	49	40886	1	1	3.6	7.11
142	P12036	Neurofilament heavy polypeptide OS=Homo sapiens GN=NEFH PE=1 SV=4	49	112411	2	1	1.6	5.99
143	Q8N1N4	Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=1 SV=2	49	56830	2	1	2.7	5.79
144	Q9Y490	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	49	269599	1	1	0.6	5.77
145	Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1	49	33846	1	1	3.3	6.7
146	P49720	Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2	48	22933	2	1	12.2	6.14
147	P05546	Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3	48	57034	1	1	2.4	6.41
148	P01042	Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2	48	71912	1	1	1.4	6.34
149	Q96Q89_REVERSED	Kinesin-like protein KIF20B OS=Homo sapiens GN=KIF20B PE=1 SV=3 - REVERSED	48	210500	3	1	0.5	5.54
150	P03956	Interstitial collagenase OS=Homo sapiens GN=MMP1 PE=1 SV=3	48	53973	2	1	3	6.47
151	Q8NDM7_REVERSED	WD repeat-containing protein 96 OS=Homo sapiens GN=WDR96 PE=2 SV=3 - REVERSED	47	191861	1	1	0.5	5.71
152	Q71DI3	Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3	46	15379	4	1	14.7	11.27
153	P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	46	95277	1	1	1.2	6.41
154	Q9Y6X9_REVERSED	MORC family CW-type zinc finger protein 2 OS=Homo sapiens GN=MORC2 PE=1 SV=2 - REVERSED	46	117750	1	1	0.7	8.6
155	P28074	Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3	46	28462	1	1	4.6	6.43

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prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
156	Q9ULC6	Protein-arginine deiminase type-1 OS=Homo sapiens GN=PADI1 PE=1 SV=2	46	74618	1	1	1.4	6.07
157	Q8NBM4	Ubiquitin-associated domain-containing protein 2 OS=Homo sapiens GN=UBAC2 PE=2 SV=1	46	38938	3	1	2.3	9.21
158	Q2VWP7	Protogenin OS=Homo sapiens GN=PRTG PE=2 SV=1	46	126996	1	1	0.6	7.37
159	Q9NPY3_REVERSED	Complement component C1q receptor OS=Homo sapiens GN=CD93 PE=1 SV=3 - REVERSED	45	68515	1	1	1.1	5.27
160	Q9NRY4	Glucocorticoid receptor DNA-binding factor 1 OS=Homo sapiens GN=GRLF1 PE=1 SV=2	45	172121	1	1	0.5	6.33
161	Q9NU02_REVERSED	Ankyrin repeat domain-containing protein 5 OS=Homo sapiens GN=ANKRD5 PE=2 SV=2 - REVERSED	45	86610	5	1	1.8	8.51
162	B9A064	Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2	45	23049	1	1	3.7	9.08
163	Q5T764_REVERSED	Interferon-induced protein with tetratricopeptide repeats 1B OS=Homo sapiens GN=IFIT1B PE=2 SV=1 - REVERSED	45	54958	2	1	3.4	7.69
164	P07339	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	45	44524	1	1	1.9	6.1
165	P02794	Ferritin heavy chain OS=Homo sapiens GN=FTH1 PE=1 SV=2	45	21212	2	1	9.3	5.3
166	Q9UKT8_REVERSED	F-box/WD repeat-containing protein 2 OS=Homo sapiens GN=FBXW2 PE=1 SV=2 - REVERSED	45	51479	2	1	3.1	6.11
167	P29803_REVERSED	Pyruvate dehydrogenase E1 component subunit alpha, testis-specific form, mitochondrial OS=Homo sapiens GN=PDHA2 PE=1 SV=1 - REVERSED	44	42906	3	1	4.1	8.76
168	Q9BY43	Charged multivesicular body protein 4a OS=Homo sapiens GN=CHMP4A PE=1 SV=3	44	25083	3	1	6.3	4.65
169	Q00013	55 kDa erythrocyte membrane protein OS=Homo sapiens GN=MPP1 PE=1 SV=2	44	52264	2	1	1.5	6.91
170	Q13477_REVERSED	Mucosal addressin cell adhesion molecule 1 OS=Homo sapiens GN=MADCAM1 PE=1 SV=2 - REVERSED	43	40130	2	1	2.6	5
171	Q8NFM7_REVERSED	Interleukin-17 receptor D OS=Homo sapiens GN=IL17RD PE=1 SV=3 - REVERSED	43	82358	1	1	0.9	6.81
172	Q92609	TBC1 domain family member 5 OS=Homo sapiens GN=TBC1D5 PE=1 SV=1	43	88949	1	1	1	6.1
173	Q96CD0_REVERSED	F-box/LRR-repeat protein 8 OS=Homo sapiens GN=FBXL8 PE=1 SV=1 - REVERSED	43	40490	9	1	1.9	7.03
174	P04745	Alpha-amylase 1 OS=Homo sapiens GN=AMY1A PE=1 SV=2	43	57731	1	1	2.3	6.47
175	Q9NZM4	Glioma tumor suppressor candidate region gene 1	42	158393	2	1	0.5	6.17

MCF 10A								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
		protein OS=Homo sapiens GN=GLTSCR1 PE=1 SV=2						
176	P10643	Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2	42	93457	2	1	1.1	6.09
177	Q6ZUT9_REVERSED	DENN domain-containing protein 5B OS=Homo sapiens GN=DENND5B PE=1 SV=2 - REVERSED	41	144927	2	1	0.5	6.29
178	Q86UQ0_REVERSED	Zinc finger protein 589 OS=Homo sapiens GN=ZNF589 PE=1 SV=1 - REVERSED	41	41163	2	1	1.6	8.62
179	P43652	Afamin OS=Homo sapiens GN=AFM PE=1 SV=1	41	69024	1	1	1.2	5.64
180	Q96RD9_REVERSED	Fc receptor-like protein 5 OS=Homo sapiens GN=FCRL5 PE=1 SV=3 - REVERSED	41	106371	1	1	0.9	6.72
181	Q16563	Synaptophysin-like protein 1 OS=Homo sapiens GN=SYPL1 PE=1 SV=1	41	28547	1	1	4.2	8.69
182	Q58FF6	Putative heat shock protein HSP 90-beta 4 OS=Homo sapiens GN=HSP90AB4P PE=5 SV=1	40	58228	2	1	5	4.65
183	Q9ULT0	Tetratricopeptide repeat protein 7A OS=Homo sapiens GN=TTC7A PE=1 SV=3	40	96123	3	1	1.2	6.03
184	P98160	Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4	39	468532	1	1	0.2	6.06
185	O14782	Kinesin-like protein KIF3C OS=Homo sapiens GN=KIF3C PE=1 SV=3	39	89371	3	1	1.1	8.28
186	Q99816	Tumor susceptibility gene 101 protein OS=Homo sapiens GN=TSG101 PE=1 SV=2	60	43916	3	1	2.4	9.4
187	P11166	Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens GN=SLC2A1 PE=1 SV=2	39	54049	1	1	1.6	8.93
188	Q00535_REVERSED	Cyclin-dependent kinase 5 OS=Homo sapiens GN=CDK5 PE=1 SV=3 - REVERSED	39	33283	2	1	3.1	7.9
189	Q8N3E9	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-3 OS=Homo sapiens GN=PLCD3 PE=1 SV=3	39	89202	5	1	1.9	6.52
190	P43235	Cathepsin K OS=Homo sapiens GN=CTSK PE=1 SV=1	38	36942	1	1	6.1	8.72
191	P22303	Acetylcholinesterase OS=Homo sapiens GN=ACHE PE=1 SV=1	38	67753	1	1	2.1	5.87
192	Q9P2G4_REVERSED	Uncharacterized protein KIAA1383 OS=Homo sapiens GN=KIAA1383 PE=1 SV=2 - REVERSED	38	100283	1	1	0.8	6.77
193	Q9BZP6	Acidic mammalian chitinase OS=Homo sapiens GN=CHIA PE=1 SV=1	38	52237	1	1	1.7	5.54
194	Q9ULI3_REVERSED	Protein HEG homolog 1 OS=Homo sapiens GN=HEG1 PE=1 SV=3 - REVERSED	38	147369	5	1	0.9	5.81

MCF 10A								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
195	O43264_REVERSED	Centromere/kinetochore protein zw10 homolog OS=Homo sapiens GN=ZW10 PE=1 SV=3 - REVERSED	38	88773	1	1	0.8	5.89
196	P48436_REVERSED	Transcription factor SOX-9 OS=Homo sapiens GN=SOX9 PE=1 SV=1 - REVERSED	38	56102	1	1	1.6	6.33
197	Q5TAH2	Sodium/hydrogen exchanger 11 OS=Homo sapiens GN=SLC9A11 PE=2 SV=1	38	128969	1	1	0.6	6.5
198	Q03518	Antigen peptide transporter 1 OS=Homo sapiens GN=TAP1 PE=1 SV=2	37	87163	10	1	1.9	8.24
199	P06746	DNA polymerase beta OS=Homo sapiens GN=POLB PE=1 SV=3	37	38154	1	1	1.8	9.01
200	Q7Z5M8	Abhydrolase domain-containing protein 12B OS=Homo sapiens GN=ABHD12B PE=2 SV=1	37	40750	3	1	1.7	8.57
201	Q15020_REVERSED	Squamous cell carcinoma antigen recognized by T-cells 3 OS=Homo sapiens GN=SART3 PE=1 SV=1 - REVERSED	37	109865	3	1	0.6	5.45
202	Q9NX14	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial OS=Homo sapiens GN=NDUFB11 PE=1 SV=1	37	17306	1	1	5.2	5.17
203	Q9H115_REVERSED	Beta-soluble NSF attachment protein OS=Homo sapiens GN=NAPB PE=1 SV=2 - REVERSED	37	33535	1	1	4	5.32
204	Q14573_REVERSED	Inositol 1,4,5-trisphosphate receptor type 3 OS=Homo sapiens GN=ITPR3 PE=1 SV=2 - REVERSED	37	303912	3	1	0.4	6.05
205	P00742	Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2	37	54697	1	1	1.8	5.68
206	P26006	Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=4	37	118680	1	1	0.9	6.51
207	Q6DHV7_REVERSED	Adenosine deaminase-like protein OS=Homo sapiens GN=ADAL PE=2 SV=2 - REVERSED	37	40239	1	1	3.1	5.89
208	P21462_REVERSED	fMet-Leu-Phe receptor OS=Homo sapiens GN=FPR1 PE=1 SV=3 - REVERSED	37	38420	2	1	2	9.23
209	Q9UGM3	Deleted in malignant brain tumors 1 protein OS=Homo sapiens GN=DMBT1 PE=1 SV=2	36	260569	1	1	0.2	5.18
210	Q14CM0_REVERSED	FERM and PDZ domain-containing protein 4 OS=Homo sapiens GN=FRMPD4 PE=1 SV=1 - REVERSED	36	144289	3	1	0.6	5.12
211	O00754	Lysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE=1 SV=3	36	113672	1	1	1.1	6.84
212	P05109	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	36	10828	1	1	7.5	6.51
213	O75691_REVERSED	Small subunit processome component 20 homolog OS=Homo sapiens GN=UTP20	36	318182	1	1	0.3	7.09

MCF 10A

prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
		PE=1 SV=3 - REVERSED						
214	Q96ED9_REVERSED	Protein Hook homolog 2 OS=Homo sapiens GN=HOOK2 PE=1 SV=3 - REVERSED	36	83155	3	1	1.5	5.36

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prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
1	P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	3363	65999	84	31	57.3	8.15
2	P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	2875	58792	85	31	58.7	5.13
3	P02751	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	2436	262460	88	40	25.6	5.46
4	P02765	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	2048	39300	52	4	7.1	5.43
5	P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	1994	62027	55	23	65.7	5.14
6	P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	1865	65393	55	25	57.9	8.07
7	P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	1781	69321	112	8	11.8	5.92
8	P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	1613	163188	57	6	5.2	6.03
9	P20742	Pregnancy zone protein OS=Homo sapiens GN=PZP PE=1 SV=4	1346	163760	41	4	3.8	5.97
10	P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	906	89266	35	21	37.1	5.14
11	Q5QNW6	Histone H2B type 2-F OS=Homo sapiens GN=HIST2H2BF PE=1 SV=3	881	13912	22	5	35.7	10.31
12	P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	647	41710	25	13	47.5	5.29
13	P00734	Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2	613	69992	15	6	9.5	5.64
14	P07996	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	580	129300	27	13	13.2	4.71
15	P02533	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	575	51529	25	15	32.4	5.09
16	P01024	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	509	187030	23	11	8.8	6.02
17	P19823	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2	468	106397	15	8	9.3	6.4
18	Q6FI13	Histone H2A type 2-A OS=Homo sapiens GN=HIST2H2AA3 PE=1 SV=3	456	14087	14	4	49.2	10.9
19	P13647	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	450	62340	22	13	25.3	7.59
20	P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	441	49639	20	13	45	4.78
21	Q07954	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2	439	504276	15	8	3.6	5.16
22	P98160	Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4	439	468532	20	13	4.7	6.06
23	P08779	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	394	51236	19	10	18	4.99
24	P02788	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6	380	78132	16	3	4.8	8.5
25	P0C0L4	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1	367	192650	15	7	5.6	6.65

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prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
26	P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	363	11360	15	6	51.5	11.36
27	P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	349	60030	15	8	14	8.09
28	P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	346	70854	12	7	16.7	5.37
29	Q86YZ3	Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	344	282228	3	3	2.1	10.05
30	P02538	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	339	60008	15	8	15.6	8.09
31	P68032	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	333	41992	17	9	26.8	5.23
32	P02771	Alpha-fetoprotein OS=Homo sapiens GN=AFP PE=1 SV=1	310	68633	9	3	5.6	5.48
33	Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1	285	49863	18	6	31.8	4.96
34	P02774	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1	277	52929	10	6	11.8	5.4
35	P04004	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	277	54271	6	1	4.2	5.55
36	Q9BVA1	Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1	270	49921	17	10	36.9	4.78
37	Q04695	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	257	48076	16	9	15	4.97
38	P68366	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	256	49892	13	5	22.5	4.95
39	P13646	Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4	254	49557	12	6	9.2	4.91
40	P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	231	15248	8	3	33.1	8.72
41	P04114	Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	227	515283	14	7	1.9	6.58
42	P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	222	36030	5	2	17.6	8.57
43	Q5XKE5	Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2	221	57800	10	4	6.9	6.75
44	P23142	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4	214	77162	11	4	7.3	5.07
45	P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	193	83212	8	4	10.4	4.97
46	Q562R1	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	189	41976	12	4	16	5.39
47	P06396	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	185	85644	6	5	9.5	5.9
48	Q96QV6	Histone H2A type 1-A OS=Homo sapiens GN=HIST1H2AA PE=1 SV=3	183	14225	6	3	29.8	10.86
49	P36955	Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=4	181	46283	6	3	8.6	5.97
50	Q5VTE0	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1	175	50153	8	6	21	9.15
51	Q06033	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2	168	99787	7	3	4	5.49
52	P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	165	84607	9	4	10.7	4.94
53	P08107	Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	162	70009	4	3	6.2	5.48
54	P17066	Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2	162	70984	4	3	6.2	5.81

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prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
55	P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4	157	57900	7	6	16	7.96
56	P19013	Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4	155	57250	8	4	7.3	6.25
57	P05556	Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	155	88357	7	4	9.6	5.27
58	Q9UPY3	Endoribonuclease, Dicer OS=Homo sapiens GN=DICER PE=1 SV=2	154	218682	9	4	6.6	8.38
59	P62979	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2	154	17953	8	5	34	9.68
60	P02042	Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2	150	16045	9	2	12.9	7.85
61	P08697	Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3	148	54531	2	1	2.2	5.87
62	P02647	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	146	30759	3	1	6	5.56
63	Q7Z3Y8	Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=2	142	49792	6	3	7.4	4.98
64	Q9P2B2	Prostaglandin F2 receptor negative regulator OS=Homo sapiens GN=PTGFRN PE=1 SV=2	140	98495	5	5	5.5	6.16
65	P13497	Bone morphogenetic protein 1 OS=Homo sapiens GN=BMP1 PE=1 SV=2	133	111178	3	2	3.1	6.48
66	P02675	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	132	55892	4	3	4.7	8.54
67	Q9Y6L7	Tolloid-like protein 2 OS=Homo sapiens GN=TLL2 PE=1 SV=1	132	113484	2	2	2.2	5.6
68	P00747	Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2	131	90510	6	3	4.4	7.04
69	Q8WUM4	Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1	126	95963	6	3	8.3	6.13
70	Q71DI3	Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3	121	15379	6	4	44.9	11.27
71	P84243	Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2	111	15318	6	4	44.9	11.27
72	Q86Y46	Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1	110	58887	9	4	8	6.93
73	P12259	Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4	109	251546	6	4	2.3	5.68
74	P01008	Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1	108	52569	7	3	10.1	6.32
75	P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	108	47139	3	3	10.8	7.01
76	P19827	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3	106	101326	4	2	2.9	6.31
77	Q8NI35	InaD-like protein OS=Homo sapiens GN=INADL PE=1 SV=3	106	196247	10	1	0.3	4.84
78	Q8TAA3	Proteasome subunit alpha type-7-like OS=Homo sapiens GN=PSMA8 PE=1 SV=3	106	28512	3	2	19.5	9.07
79	P02452	Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5	104	138857	2	2	1.6	5.6
80	P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2	103	15394	6	4	44.9	11.13
81	P07942	Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=2	102	197909	3	2	1.9	4.83
82	P05787	Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	102	53671	5	3	7.2	5.52
83	P51884	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	101	38405	3	2	8.3	6.16
84	Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	97	191493	2	2	2.9	5.48

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prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
85	P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	93	44586	3	2	8.4	8.3
86	P15531	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1	92	17138	1	1	11.2	5.83
87	P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	92	39395	5	2	12.4	8.3
88	P05452	Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=3	91	22522	3	3	21.8	5.52
89	P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3	91	77014	3	2	1.7	6.81
90	A6NIZ1	Ras-related protein Rap-1b-like protein OS=Homo sapiens PE=2 SV=1	89	20912	2	1	6.5	5.37
91	Q9GZM7	Tubulointerstitial nephritis antigen-like OS=Homo sapiens GN=TINAGL1 PE=1 SV=1	88	52353	1	1	2.8	6.54
92	P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	87	72288	3	2	3.1	5.07
93	P16870	Carboxypeptidase E OS=Homo sapiens GN=CPE PE=1 SV=1	87	53117	2	2	4.8	5.03
94	P81605	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	86	11277	2	2	20	6.08
95	P15169	Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1	84	52253	1	1	3.3	6.86
96	P11717	Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=3	83	274199	4	2	1.2	5.64
97	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	81	36615	2	1	7.5	5.71
98	P06702	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	80	13234	2	1	24.6	5.71
99	Q5D862	Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	79	247928	2	1	0.9	8.45
100	P28066	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	78	26394	1	1	7.9	4.74
101	Q92743	Serine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1	78	51255	3	2	6.5	8.09
102	P23526	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	78	47685	2	2	6.3	5.92
103	P02760	Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1	77	38974	2	1	2	5.95
104	P05543	Thyroxine-binding globulin OS=Homo sapiens GN=SERPINA7 PE=1 SV=2	75	46295	3	1	2.4	5.87
105	P43686	26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2	74	47337	2	1	2.9	5.09
106	Q7RTS7	Keratin, type II cytoskeletal 74 OS=Homo sapiens GN=KRT74 PE=1 SV=2	74	57830	4	2	4.2	7.59
108	Q99456	Keratin, type I cytoskeletal 12 OS=Homo sapiens GN=KRT12 PE=1 SV=1	73	53478	7	2	3.6	4.7
109	P60174	Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=2	72	26653	1	1	5.2	6.45
110	P05156	Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2	71	65707	2	2	3.4	7.72
111	Q12931	Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3	71	80060	1	1	2	8.3
112	P08962	CD63 OS=HOMO SAPIENS GN=CD63 PE=4 SV=2	71	25637	3	3	16.4	5.3
113	P02749	Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3	67	38273	3	1	5.2	8.34
114	B9A064	Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2	66	23049	2	1	3.7	9.08

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prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
115	P12109	Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3	66	108462	1	1	0.9	5.26
116	P04745	Alpha-amylase 1 OS=Homo sapiens GN=AMY1A PE=1 SV=2	66	57731	2	1	2.3	6.47
117	P35052	Glypican-1 OS=Homo sapiens GN=GPC1 PE=1 SV=2	66	61641	4	1	10.9	7.07
118	P08133	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3	65	75826	4	2	5.9	5.42
119	P01031	Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4	65	188186	4	2	1.8	6.11
120	P29353_REVERSED	SHC-transforming protein 1 OS=Homo sapiens GN=SHC1 PE=1 SV=4 - REVERSED	65	62782	10	1	1.4	6.01
121	O15111_REVERSED	Inhibitor of nuclear factor kappa-B kinase subunit alpha OS=Homo sapiens GN=CHUK PE=1 SV=2 - REVERSED	65	84585	6	1	1.6	6.28
123	P01009	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	64	46707	3	2	3.3	5.37
124	P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	64	95277	3	2	6.9	6.41
125	A6NMY6	Putative annexin A2-like protein OS=Homo sapiens GN=ANXA2P2 PE=5 SV=2	63	38635	2	1	6.2	6.49
126	Q99816	Tumor susceptibility gene 101 protein OS=Homo sapiens GN=TSG101 PE=1 SV=2	60	43916	1	1	2.6	6.06
127	P02461	Collagen alpha-1(III) chain OS=Homo sapiens GN=COL3A1 PE=1 SV=4	59	138479	2	2	1.5	6.21
128	Q14624	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4	58	103293	5	2	3.3	6.51
129	P02649	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	57	36132	1	1	2.8	5.65
130	P26641	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	56	50087	2	1	5	6.25
131	P35125	Ubiquitin carboxyl-terminal hydrolase 6 OS=Homo sapiens GN=USP6 PE=1 SV=2	55	158557	13	1	0.4	7.87
132	P02790	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	54	51643	6	1	5.4	6.55
133	Q9BYX7_REVERSED	Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1 - REVERSED	54	41989	6	1	3.5	5.92
135	P14923	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	53	81693	1	1	2.7	5.75
136	Q14764	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4	52	99266	1	1	1.9	5.34
138	P01042	Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2	52	71912	1	1	1.4	6.34
139	Q8N139	ATP-binding cassette sub-family A member 6 OS=Homo sapiens GN=ABCA6 PE=1 SV=2	52	184167	2	1	0.4	7.05
141	Q96Q89_REVERSED	Kinesin-like protein KIF20B OS=Homo sapiens GN=KIF20B PE=1 SV=3 - REVERSED	51	210500	2	1	0.5	5.54
142	Q2Q1W2_REVERSED	Tripartite motif-containing protein 71 OS=Homo sapiens GN=TRIM71 PE=2 SV=1 - REVERSED	51	93326	1	1	1.2	7.62
143	Q9BY43	Charged multivesicular body protein 4a OS=Homo sapiens GN=CHMP4A PE=1 SV=3	51	25083	2	1	3.2	4.65
144	Q8NAV2_REVERSED	Uncharacterized protein C8orf58 OS=Homo sapiens GN=C8orf58 PE=2 SV=2 - REVERSED	51	39636	1	1	1.9	8.54
145	P02748	Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2	51	63133	1	1	1.6	5.43
146	O00754	Lysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE=1 SV=3	51	113672	1	1	1.1	6.84
147	O14817	Tetraspanin-4 OS=Homo sapiens GN=TSPAN4 PE=1 SV=1	50	26100	2	1	10.5	6.07

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prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
148	P11047	Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3	50	177489	3	3	1.9	5.01
149	P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	50	280564	2	1	1.6	5.7
150	A8MT19_REVERSED	Putative rhophilin-2-like protein OS=Homo sapiens PE=5 SV=2 - REVERSED	49	65903	1	1	1.2	6.53
151	P12111	Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=5	48	343457	3	1	1.2	6.26
152	Q00013	55 kDa erythrocyte membrane protein OS=Homo sapiens GN=MPP1 PE=1 SV=2	47	52264	2	1	1.5	6.91
153	Q8IW52	SLIT and NTRK-like protein 4 OS=Homo sapiens GN=SLITRK4 PE=2 SV=1	47	94271	1	1	0.8	7.95
154	O95445	Apolipoprotein M OS=Homo sapiens GN=APOM PE=1 SV=2	47	21239	1	1	3.7	5.66
155	Q13162	Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1	46	30521	1	1	4.1	5.86
156	P00488	Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4	46	83215	2	2	4	5.75
157	P08572	Collagen alpha-2(IV) chain OS=Homo sapiens GN=COL4A2 PE=1 SV=4	46	167449	1	1	0.6	8.89
158	O14782	Kinesin-like protein KIF3C OS=Homo sapiens GN=KIF3C PE=1 SV=3	46	89371	4	1	1.1	8.28
159	P35443	Thrombospondin-4 OS=Homo sapiens GN=THBS4 PE=1 SV=2	45	105802	2	1	2.8	4.44
161	P49747	Cartilage oligomeric matrix protein OS=Homo sapiens GN=COMP PE=1 SV=2	44	82808	2	1	2.8	4.36
162	Q14573_REVERSED	Inositol 1,4,5-trisphosphate receptor type 3 OS=Homo sapiens GN=ITPR3 PE=1 SV=2 - REVERSED	44	303912	1	1	0.4	6.05
163	Q8IWC1	MAP7 domain-containing protein 3 OS=Homo sapiens GN=MAP7D3 PE=1 SV=2	44	98368	2	1	2.1	9.34
164	Q3KQU3	MAP7 domain-containing protein 1 OS=Homo sapiens GN=MAP7D1 PE=1 SV=1	44	92764	1	1	0.7	10.12
165	Q5U5X0	LYR motif-containing protein 7 OS=Homo sapiens GN=LYRM7 PE=1 SV=1	44	11947	1	1	5.8	9.67
166	Q8N7B9_REVERSED	EF-hand calcium-binding domain-containing protein 3 OS=Homo sapiens GN=EFCAB3 PE=1 SV=1 - REVERSED	44	50114	1	1	1.4	9.31
167	Q8NB25_REVERSED	Protein FAM184A OS=Homo sapiens GN=FAM184A PE=2 SV=3 - REVERSED	44	132883	1	1	0.5	5.59
168	P06732	Creatine kinase M-type OS=Homo sapiens GN=CKM PE=1 SV=2	44	43074	1	1	1.6	6.77
169	Q93096_REVERSED	Protein tyrosine phosphatase type IVA 1 OS=Homo sapiens GN=PTP4A1 PE=1 SV=2 - REVERSED	44	19802	1	1	3.5	9.17
170	Q6YHK3	CD109 antigen OS=Homo sapiens GN=CD109 PE=1 SV=2	44	161587	1	1	0.6	5.59
171	Q8IYT4	Katanin p60 ATPase-containing subunit A-like 2 OS=Homo sapiens GN=KATNAL2 PE=2 SV=3	43	61214	2	1	2.2	7.22
172	A8MPT4	Glutathione S-transferase theta-4 OS=Homo sapiens GN=GSTT4 PE=3 SV=2	43	27941	1	1	2.5	6.25
173	Q8N6V9_REVERSED	Testis-expressed sequence 9 protein OS=Homo sapiens GN=TEX9 PE=2 SV=1 - REVERSED	43	44798	1	1	1.5	6.2
174	Q9Y2U8_REVERSED	Inner nuclear membrane protein Man1 OS=Homo sapiens GN=LEMD3 PE=1 SV=2 - REVERSED	43	99935	1	1	0.7	7.31
175	P05154	Plasma serine protease inhibitor OS=Homo sapiens GN=SERPINA5 PE=1 SV=3	43	45646	1	1	1.5	9.3

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prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
176	Q92609	TBC1 domain family member 5 OS=Homo sapiens GN=TBC1D5 PE=1 SV=1	42	88949	1	1	1	6.1
177	Q9H2G4	Testis-specific Y-encoded-like protein 2 OS=Homo sapiens GN=TSPYL2 PE=1 SV=1	42	79387	1	1	1	4.45
178	Q00535_REVERSED	Cyclin-dependent kinase 5 OS=Homo sapiens GN=CDK5 PE=1 SV=3 - REVERSED	42	33283	1	1	3.1	7.9
179	P06703	Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1	41	10173	2	1	8.9	5.33
180	Q6ZMU1	Putative protein C3P1 OS=Homo sapiens GN=C3P1 PE=5 SV=3	41	40171	2	1	5.5	6.32
183	Q86UY8_REVERSED	5'-nucleotidase domain-containing protein 3 OS=Homo sapiens GN=NT5DC3 PE=2 SV=1 - REVERSED	41	63379	2	1	1.5	8.47
184	O75460_REVERSED	Serine/threonine-protein kinase/ endoribonuclease IRE1 OS=Homo sapiens GN=ERN1 PE=1 SV=2 - REVERSED	41	109666	1	1	0.6	5.98
186	Q9Y6X9_REVERSED	MORC family CW-type zinc finger protein 2 OS=Homo sapiens GN=MORC2 PE=1 SV=2 - REVERSED	40	117750	1	1	0.7	8.6
187	Q96TA0_REVERSED	Putative protocadherin beta-18 OS=Homo sapiens GN=PCDHB18 PE=5 SV=1 - REVERSED	40	80423	1	1	0.8	4.87
188	P02458	Collagen alpha-1(II) chain OS=Homo sapiens GN=COL2A1 PE=1 SV=3	40	141698	1	1	0.7	6.58
191	Q8NBM4	Ubiquitin-associated domain-containing protein 2 OS=Homo sapiens GN=UBAC2 PE=2 SV=1	40	38938	1	1	2.3	9.21
193	Q7Z5M8	Abhydrolase domain-containing protein 12B OS=Homo sapiens GN=ABHD12B PE=2 SV=1	40	40750	5	1	1.7	8.57
194	Q15020_REVERSED	Squamous cell carcinoma antigen recognized by T-cells 3 OS=Homo sapiens GN=SART3 PE=1 SV=1 - REVERSED	40	109865	5	1	0.6	5.45
196	O60312	Probable phospholipid-transporting ATPase VA OS=Homo sapiens GN=ATP10A PE=2 SV=2	39	167582	2	1	0.6	8.7
197	Q9Y6Q3_REVERSED	Zinc finger protein 37 homolog OS=Homo sapiens GN=ZFP37 PE=2 SV=3 - REVERSED	39	71164	1	1	1.7	9.26
198	Q96RW7	Hemicentin-1 OS=Homo sapiens GN=HMCN1 PE=1 SV=2	39	613001	2	1	0.1	6.07
199	Q13183_REVERSED	Solute carrier family 13 member 2 OS=Homo sapiens GN=SLC13A2 PE=2 SV=1 - REVERSED	38	64368	2	1	1.4	6.61
200	Q9UK41	Vacuolar protein sorting-associated protein 28 homolog OS=Homo sapiens GN=VPS28 PE=1 SV=1	38	25409	2	1	6.8	5.37
201	Q14C86_REVERSED	GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 SV=2 - REVERSED	38	164876	1	1	0.5	5.09
206	P26640	Valyl-tRNA synthetase OS=Homo sapiens GN=VARS PE=1 SV=4	38	140387	1	1	1.2	7.53
207	Q96JB3	Hypermethylated in cancer 2 protein OS=Homo sapiens GN=HIC2 PE=1 SV=2	38	66114	1	1	1.6	5.95
208	O43309	Zinc finger and SCAN domain-containing protein 12 OS=Homo sapiens GN=ZSCAN12 PE=2 SV=1	38	70178	1	1	2	6.28
209	Q96K21	Zinc finger FYVE domain-containing protein 19 OS=Homo sapiens GN=ZFYVE19 PE=1 SV=3	38	51514	2	1	1.7	5.57
210	Q8WZ42_REVERSED	Titin OS=Homo sapiens GN=TTN PE=1 SV=2 - REVERSED	38	3813810	2	1	0.1	6.01
211	O75865_REVERSED	Trafficking protein particle complex subunit 6A OS=Homo sapiens GN=TRAPPC6A PE=1 SV=2 - REVERSED	38	17593	1	1	3.8	5.14
213	P04083	Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	37	38690	1	1	2.3	6.57

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prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
214	P28070	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4	37	29185	1	1	3.8	5.72
216	P02753	Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3	37	22995	2	1	10	5.76
217	Q12923	Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 PE=1 SV=2	37	276733	1	1	0.5	5.99
218	P05109	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	37	10828	1	1	11.8	6.51
220	Q5SYB0	FERM and PDZ domain-containing protein 1 OS=Homo sapiens GN=FRMPD1 PE=1 SV=1	37	173328	1	1	0.4	5.14
221	A6NC57_REVERSED	Ankyrin repeat domain-containing protein 62 OS=Homo sapiens GN=ANKRD62 PE=2 SV=4 - REVERSED	37	106379	1	1	0.7	6.26
222	Q8IWZ5_REVERSED	Tripartite motif-containing protein 42 OS=Homo sapiens GN=TRIM42 PE=2 SV=2 - REVERSED	37	82690	1	1	0.8	8.31
223	Q9UKU7_REVERSED	Isobutyryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACAD8 PE=1 SV=1 - REVERSED	37	45040	1	1	1.4	8.16
224	Q674X7_REVERSED	Kazrin OS=Homo sapiens GN=KAZN PE=1 SV=2 - REVERSED	37	86298	1	1	0.8	6.59
225	Q14534	Squalene monooxygenase OS=Homo sapiens GN=SQLE PE=2 SV=3	37	63882	1	1	1	8.8
226	P20138	Myeloid cell surface antigen CD33 OS=Homo sapiens GN=CD33 PE=1 SV=2	37	39800	1	1	1.9	8.69
227	A2RRP1_REVERSED	Neuroblastoma-amplified sequence OS=Homo sapiens GN=NBAS PE=1 SV=2 - REVERSED	37	268401	1	1	0.3	5.65
231	O95714_REVERSED	E3 ubiquitin-protein ligase HERC2 OS=Homo sapiens GN=HERC2 PE=1 SV=2 - REVERSED	37	526895	6	1	0.4	5.88
232	Q9UGM3	Deleted in malignant brain tumors 1 protein OS=Homo sapiens GN=DMBT1 PE=1 SV=2	36	260569	1	1	0.2	5.18
233	P26378	ELAV-like protein 4 OS=Homo sapiens GN=ELAVL4 PE=1 SV=2	36	41743	2	1	3.7	9.45
234	Q96A37	RING finger protein 166 OS=Homo sapiens GN=RNF166 PE=2 SV=1	36	26105	1	1	4.2	8.42
236	P22352	Glutathione peroxidase 3 OS=Homo sapiens GN=GPX3 PE=1 SV=2	36	25537	1	1	5.3	8.26
237	Q9Y240	C-type lectin domain family 11 member A OS=Homo sapiens GN=CLEC11A PE=1 SV=1	36	35672	1	1	5.3	5.06
240	P25789	Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1	36	29465	1	1	3.4	7.57
241	P10242_REVERSED	Transcriptional activator Myb OS=Homo sapiens GN=MYB PE=1 SV=2 - REVERSED	36	72296	2	1	1.3	6.35
242	P02794	Ferritin heavy chain OS=Homo sapiens GN=FTH1 PE=1 SV=2	35	21226	1	1	2.5	8.2

NIH 3T3

prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
1	P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	2826	65999	70	31	55.3	8.15
2	P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	2816	58792	83	29	57.9	5.13
3	P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	2011	69321	114	8	13.5	5.92
4	P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	1949	163188	70	8	5.7	6.03

NIH 3T3								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
5	P02765	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	1830	39300	50	4	8.7	5.43
6	P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	1822	62027	44	22	68.7	5.14
7	P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	1641	65393	46	24	58.1	8.07
8	P02751	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	1564	262460	50	29	18.1	5.46
9	P20742	Pregnancy zone protein OS=Homo sapiens GN=PZP PE=1 SV=4	1547	163760	48	5	4.3	5.97
10	P01024	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	704	187030	25	11	8.9	6.02
11	P07996	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	622	129300	26	15	19.1	4.71
12	P19823	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2	593	106397	18	7	9.2	6.4
13	P00734	Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2	527	69992	11	6	8	5.64
14	P13647	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	514	62340	23	16	28.8	7.59
15	P0C0L4	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1	467	192650	18	7	5.2	6.65
16	Q07954	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2	415	504276	14	11	3.5	5.16
17	P02788	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6	406	78132	18	3	4.8	8.5
18	P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	394	60030	17	11	23	8.09
19	P02538	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	388	60008	17	12	24.6	8.09
20	P06396	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	360	85644	11	7	12.8	5.9
21	P02533	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	353	51529	17	9	20.3	5.09
22	P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	315	41710	12	8	33.6	5.29
23	P02771	Alpha-fetoprotein OS=Homo sapiens GN=AFP PE=1 SV=1	288	68633	8	3	6.7	5.48
24	P02774	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1	271	52929	12	5	12	5.4
25	P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	252	15248	13	4	33.1	8.72
26	Q7Z794	Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=1 SV=3	248	61864	7	3	4.8	5.73
27	P36955	Pigment epithelium-derived factor OS=Homo	233	46283	10	3	12	5.97

NIH 3T3								
prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
		sapiens GN=SERPINF1 PE=1 SV=4						
28	P04004	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	226	54271	6	1	4.2	5.55
29	P02647	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	226	30759	4	1	6	5.56
30	P62736	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1	220	41982	7	5	18.8	5.23
31	Q04695	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	205	48076	12	6	14.6	4.97
32	Q5XKE5	Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2	200	57800	7	4	6.9	6.75
33	P13646	Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4	198	49557	8	4	6.1	4.91
34	Q06033	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2	196	99787	9	3	6.3	5.49
35	Q86YZ3	Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	193	282228	3	2	2.3	10.05
36	P02042	Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2	189	16045	10	2	12.9	7.85
37	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2	174	93255	7	2	7.4	7.27
38	P23142	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4	172	77162	9	4	7.3	5.07
39	P02100	Hemoglobin subunit epsilon OS=Homo sapiens GN=HBE1 PE=1 SV=2	160	16192	7	1	12.9	8.67
40	P08697	Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3	143	54531	2	1	2.2	5.87
41	P00747	Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2	139	90510	6	3	4.3	7.04
42	P02675	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	136	55892	5	3	6.7	8.54
43	P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	134	36030	3	3	17.6	8.57
44	P05556	Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	131	88357	4	3	6	5.27
45	Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1	130	49863	7	4	14.9	4.96
46	P01008	Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1	130	52569	10	4	14.7	6.32
47	P02452	Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5	124	138857	3	3	2.4	5.6
48	P01031	Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4	122	188186	6	2	2.9	6.11
49	P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	122	70854	3	3	5.3	5.37

NIH 3T3								
prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
50	P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	121	49639	5	4	24.8	4.78
51	P19013	Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4	120	57250	7	3	7.3	6.25
52	P08107	Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	119	70009	2	2	4.2	5.48
53	P17066	Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2	119	70984	2	2	4.2	5.81
54	P12109	Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3	117	108462	2	2	2.4	5.26
55	P02748	Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2	114	63133	3	2	3.8	5.43
56	P19827	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3	113	101326	4	2	2.9	6.31
57	Q8TAA3	Proteasome subunit alpha type-7-like OS=Homo sapiens GN=PSMA8 PE=1 SV=3	113	28512	2	2	10.9	9.07
58	Q7Z3Y8	Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=2	111	49792	6	3	7.4	4.98
59	P06702	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	109	13234	4	2	43	5.71
60	P05787	Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	109	53671	4	3	5.6	5.52
61	P05109	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	109	10828	3	3	31.2	6.51
62	P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3	109	77014	5	2	1.7	6.81
63	Q562R1	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	108	41976	5	3	13.8	5.39
64	P62979	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2	102	17953	7	3	30.1	9.68
65	P12035	Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3	99	64378	5	2	4	6.12
66	Q8NI35	InaD-like protein OS=Homo sapiens GN=INADL PE=1 SV=3	98	196247	10	1	0.3	4.84
67	Q8TEV9_REVERSED	Smith-Magenis syndrome chromosomal region candidate gene 8 protein OS=Homo sapiens GN=SMCR8 PE=1 SV=2 - REVERSED	97	104956	10	1	1.2	5.36
68	Q5D862	Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	96	247928	2	2	1.3	8.45
69	P12111	Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=5	96	343457	3	3	1.1	6.26
70	P49747	Cartilage oligomeric matrix protein OS=Homo sapiens GN=COMP PE=1 SV=2	94	82808	3	2	4.5	4.36

NIH 3T3

prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
71	A6NIZ1	Ras-related protein Rap-1b-like protein OS=Homo sapiens PE=2 SV=1	91	20912	2	1	6.5	5.37
72	P12259	Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4	89	251546	5	2	2	5.68
73	Q14624	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4	87	103293	5	2	3.3	6.51
74	Q6KB66	Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2	86	50494	3	1	5.1	5.58
75	P13497	Bone morphogenetic protein 1 OS=Homo sapiens GN=BMP1 PE=1 SV=2	83	111178	4	3	3.1	6.48
76	Q86Y46	Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1	78	58887	7	3	8	6.93
77	P04114	Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	77	515283	3	3	0.5	6.58
78	P02790	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	76	51643	6	1	3.2	6.55
79	P35443	Thrombospondin-4 OS=Homo sapiens GN=THBS4 PE=1 SV=2	75	105802	2	2	2.5	4.44
80	P08123	Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=7	75	129235	2	2	2.2	9.08
81	P15169	Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1	73	52253	1	1	3.3	6.86
82	Q92743	Serine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1	73	51255	2	2	4.4	8.09
83	Q9Y6L7	Tolloid-like protein 2 OS=Homo sapiens GN=TLL2 PE=1 SV=1	72	113484	3	2	2.2	5.6
84	P05452	Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=3	69	22522	2	2	12.9	5.52
85	Q96Q89_REVERSED	Kinesin-like protein KIF20B OS=Homo sapiens GN=KIF20B PE=1 SV=3 - REVERSED	68	210500	2	1	0.5	5.54
86	P51884	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	68	38405	4	1	6.8	6.16
87	P02749	Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3	67	38273	3	1	5.2	8.34
88	P63104	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	67	27728	1	1	4.9	4.73
89	O15111_REVERSED	Inhibitor of nuclear factor kappa-B kinase subunit alpha OS=Homo sapiens GN=CHUK PE=1 SV=2 - REVERSED	66	84585	7	1	1.6	6.28
90	Q03692	Collagen alpha-1(X) chain OS=Homo sapiens GN=COL10A1 PE=1 SV=2	64	66117	1	1	1.9	9.68
91	B9A064	Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2	63	23049	2	1	3.7	9.08
92	Q7RTS7	Keratin, type II cytoskeletal 74 OS=Homo sapiens GN=KRT74 PE=1 SV=2	62	57830	3	2	4.2	7.59

NIH 3T3								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
93	Q99456	Keratin, type I cytoskeletal 12 OS=Homo sapiens GN=KRT12 PE=1 SV=1	62	53478	5	2	3.6	4.7
94	Q9BYX7_REVERSED	Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1 - REVERSED	61	41989	6	1	3.5	5.92
95	P00450	Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1	59	122128	3	2	2.9	5.44
96	P23526	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	59	47685	2	1	6.3	5.92
97	P20618	Proteasome subunit beta type-1 OS=Homo sapiens GN=PSMB1 PE=1 SV=2	58	26472	1	1	5.8	8.27
98	P98160	Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4	57	468532	2	2	0.6	6.06
99	Q8WUM4	Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1	57	95963	2	1	2.2	6.13
100	P35125	Ubiquitin carboxyl-terminal hydrolase 6 OS=Homo sapiens GN=USP6 PE=1 SV=2	56	158557	12	1	0.4	7.87
101	P02679	Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	56	51479	1	1	2	5.37
102	P29353_REVERSED	SHC-transforming protein 1 OS=Homo sapiens GN=SHC1 PE=1 SV=4 - REVERSED	56	62782	9	1	1.4	6.01
103	P05546	Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3	55	57034	1	1	2.4	6.41
104	P01344	Insulin-like growth factor II OS=Homo sapiens GN=IGF2 PE=1 SV=1	54	20127	1	1	8.9	9.5
105	P02794	Ferritin heavy chain OS=Homo sapiens GN=FTH1 PE=1 SV=2	54	21212	1	1	5.5	5.3
106	P01009	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	52	46707	3	1	3.3	5.37
107	Q16853	Membrane primary amine oxidase OS=Homo sapiens GN=AOC3 PE=1 SV=3	52	84568	1	1	1.2	6.05
108	P20930	Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3	51	434922	1	1	0.3	9.24
109	Q13454	Tumor suppressor candidate 3 OS=Homo sapiens GN=TUSC3 PE=2 SV=1	49	39650	1	1	2	9.93
110	Q9BXJ4	Complement C1q tumor necrosis factor-related protein 3 OS=Homo sapiens GN=C1QTNF3 PE=2 SV=1	48	26977	2	2	6.5	6.04
111	Q9HAV0	Guanine nucleotide-binding protein subunit beta-4 OS=Homo sapiens GN=GNB4 PE=1 SV=3	48	37543	1	1	2.9	5.6
112	Q9NWT1_REVERSED	p21-activated protein kinase-interacting protein 1 OS=Homo sapiens GN=PAK1IP1 PE=1 SV=2 - REVERSED	48	43936	2	1	1.8	9.07
113	Q6ZU45	Putative C-type lectin domain-containing	48	25796	1	1	3.4	6.3

NIH 3T3								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
		protein NCRNA00083 OS=Homo sapiens GN=NCRNA00083 PE=5 SV=1						
114	Q92609	TBC1 domain family member 5 OS=Homo sapiens GN=TBC1D5 PE=1 SV=1	47	88949	2	1	1	6.1
115	O95497	Pantetheinase OS=Homo sapiens GN=VNN1 PE=1 SV=2	47	56975	1	1	3.7	5.32
116	O95714_REVERSED	E3 ubiquitin-protein ligase HERC2 OS=Homo sapiens GN=HERC2 PE=1 SV=2 - REVERSED	47	526895	4	1	0.2	5.88
117	P11717	Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=3	47	274199	2	1	0.8	5.64
118	Q9NPY3_REVERSED	Complement component C1q receptor OS=Homo sapiens GN=CD93 PE=1 SV=3 - REVERSED	46	68515	1	1	1.1	5.27
119	P31151	Protein S100-A7 OS=Homo sapiens GN=S100A7 PE=1 SV=4	46	11464	2	1	31.7	6.28
120	P19961	Alpha-amylase 2B OS=Homo sapiens GN=AMY2B PE=1 SV=1	46	57673	2	1	5.1	6.64
121	P02760	Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1	46	38974	2	1	2	5.95
122	Q9H4M9	EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2	46	60589	2	1	4.9	6.35
123	Q96CD0_REVERSED	F-box/LRR-repeat protein 8 OS=Homo sapiens GN=FBXL8 PE=1 SV=1 - REVERSED	45	40490	11	1	1.9	7.03
124	Q08554	Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	45	99924	1	1	1.7	5.25
125	P49720	Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2	45	22933	2	2	16.6	6.14
126	P05543	Thyroxine-binding globulin OS=Homo sapiens GN=SERPINA7 PE=1 SV=2	44	46295	1	1	2.4	5.87
127	Q9H2G4	Testis-specific Y-encoded-like protein 2 OS=Homo sapiens GN=TSPYL2 PE=1 SV=1	44	79387	1	1	1	4.45
128	P25787	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2	44	25882	2	1	9	6.92
129	P02461	Collagen alpha-1(III) chain OS=Homo sapiens GN=COL3A1 PE=1 SV=4	43	138479	3	2	1.4	6.21
130	P81605	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	43	11277	2	1	10	6.08
131	Q9Y6X9_REVERSED	MORC family CW-type zinc finger protein 2 OS=Homo sapiens GN=MORC2 PE=1 SV=2 - REVERSED	43	117750	2	1	1.6	8.6
132	Q8NBM4	Ubiquitin-associated domain-containing protein 2 OS=Homo sapiens GN=UBAC2 PE=2 SV=1	43	38938	4	1	2.3	9.21
133	P10643	Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2	43	93457	2	1	2	6.09

NIH 3T3								
prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
134	Q12968_REVERSED	Nuclear factor of activated T-cells, cytoplasmic 3 OS=Homo sapiens GN=NFATC3 PE=1 SV=1 - REVERSED	43	115522	3	1	0.7	5.91
135	P32119	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	42	21878	1	1	9.1	5.66
136	Q9UGM3	Deleted in malignant brain tumors 1 protein OS=Homo sapiens GN=DMBT1 PE=1 SV=2	42	260569	1	1	0.2	5.18
137	O75460_REVERSED	Serine/threonine-protein kinase/endoribonuclease IRE1 OS=Homo sapiens GN=ERN1 PE=1 SV=2 - REVERSED	41	109666	1	1	0.6	5.98
138	Q9UKT8_REVERSED	F-box/WD repeat-containing protein 2 OS=Homo sapiens GN=FBXW2 PE=1 SV=2 - REVERSED	41	51479	2	1	3.1	6.11
139	O95445	Apolipoprotein M OS=Homo sapiens GN=APOM PE=1 SV=2	41	21239	2	1	6.9	5.66
140	P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	40	44586	2	1	8.4	8.3
141	O14578_REVERSED	Citron Rho-interacting kinase OS=Homo sapiens GN=CIT PE=1 SV=2 - REVERSED	40	231286	2	1	0.5	6.16
142	Q7Z5M8	Abhydrolase domain-containing protein 12B OS=Homo sapiens GN=ABHD12B PE=2 SV=1	40	40750	3	1	1.7	8.57
143	Q15020_REVERSED	Squamous cell carcinoma antigen recognized by T-cells 3 OS=Homo sapiens GN=SART3 PE=1 SV=1 - REVERSED	40	109865	3	1	0.6	5.45
144	P29803_REVERSED	Pyruvate dehydrogenase E1 component subunit alpha, testis-specific form, mitochondrial OS=Homo sapiens GN=PDHA2 PE=1 SV=1 - REVERSED	40	42906	2	1	1.8	8.76
145	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2	40	35847	1	1	2.1	8.45
146	Q9NQX4	Myosin-Vc OS=Homo sapiens GN=MYO5C PE=1 SV=2	40	202682	1	1	0.4	7.69
147	Q13183_REVERSED	Solute carrier family 13 member 2 OS=Homo sapiens GN=SLC13A2 PE=2 SV=1 - REVERSED	40	64368	2	1	1.4	6.61
148	A8MPT4	Glutathione S-transferase theta-4 OS=Homo sapiens GN=GSTT4 PE=3 SV=2	39	27941	2	1	2.5	6.25
149	Q8N6V9_REVERSED	Testis-expressed sequence 9 protein OS=Homo sapiens GN=TEX9 PE=2 SV=1 - REVERSED	39	44798	2	1	1.5	6.2
150	Q9Y2U8_REVERSED	Inner nuclear membrane protein Man1 OS=Homo sapiens GN=LEMD3 PE=1 SV=2 - REVERSED	39	99935	2	1	0.7	7.31
151	P05154	Plasma serine protease inhibitor OS=Homo sapiens GN=SERPINA5 PE=1 SV=3	39	45646	2	1	1.5	9.3
152	P11137	Microtubule-associated protein 2 OS=Homo sapiens GN=MAP2 PE=1 SV=4	39	199404	4	1	1.4	4.82

NIH 3T3								
prot_hit	prot_acc	prot_desc	prot_score	prot_mass	prot_matches	prot_sequences_sig	prot_cover	prot_pi
153	Q9BY43	Charged multivesicular body protein 4a OS=Homo sapiens GN=CHMP4A PE=1 SV=3	39	25083	1	1	3.2	4.65
154	P22303	Acetylcholinesterase OS=Homo sapiens GN=ACHE PE=1 SV=1	39	67753	1	1	2.1	5.87
155	P07864	L-lactate dehydrogenase C chain OS=Homo sapiens GN=LDHC PE=2 SV=4	38	36288	3	1	6.6	7.08
156	P28066	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	38	26394	2	1	12	4.74
157	Q14C86_REVERSED	GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 SV=2 - REVERSED	38	164876	2	1	0.5	5.09
158	O75808	Calpain-15 OS=Homo sapiens GN=SOLH PE=1 SV=1	38	117239	1	1	0.6	6.27
159	Q15751_REVERSED	Probable E3 ubiquitin-protein ligase HERC1 OS=Homo sapiens GN=HERC1 PE=1 SV=2 - REVERSED	38	531891	1	1	0.2	5.69
160	Q6R2W3_REVERSED	SCAN domain-containing protein 3 OS=Homo sapiens GN=SCAND3 PE=2 SV=1 - REVERSED	38	151570	3	1	0.7	6.3
161	Q6ZNE9_REVERSED	RUN and FYVE domain-containing protein 4 OS=Homo sapiens GN=RUFY4 PE=2 SV=2 - REVERSED	37	64309	1	1	1.4	6.43
162	Q8N7B9	EF-hand calcium-binding domain-containing protein 3 OS=Homo sapiens GN=EFCAB3 PE=1 SV=1	37	50114	3	1	2.1	9.31
163	O60312	Probable phospholipid-transporting ATPase VA OS=Homo sapiens GN=ATP10A PE=2 SV=2	37	167582	1	1	0.6	8.7
164	O15264	Mitogen-activated protein kinase 13 OS=Homo sapiens GN=MAPK13 PE=1 SV=1	37	42063	3	1	1.9	8.48
165	Q9H2K8	Serine/threonine-protein kinase TAO3 OS=Homo sapiens GN=TAOK3 PE=1 SV=2	37	105340	5	1	1.9	6.83
166	P48634	Protein PRRC2A OS=Homo sapiens GN=PRRC2A PE=1 SV=3	37	228724	4	1	0.3	9.48
167	Q8IVF6	Ankyrin repeat domain-containing protein 18A OS=Homo sapiens GN=ANKRD18A PE=1 SV=3	37	115525	4	1	0.7	7.92
168	P35580	Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3	36	228858	1	1	0.6	5.44
169	P10242_REVERSED	Transcriptional activator Myb OS=Homo sapiens GN=MYB PE=1 SV=2 - REVERSED	36	72296	1	1	1.3	6.35
170	Q9BV38	WD repeat-containing protein 18 OS=Homo sapiens GN=WDR18 PE=1 SV=2	36	47375	1	1	2.1	6.21
171	Q99816	Tumor susceptibility gene 101 protein OS=Homo sapiens	60	43916	1	1	6.4	8.21

NIH 3T3								
prot_hit	**prot_acc**	**prot_desc**	**prot_score**	**prot_mass**	**prot_matches**	**prot_sequences_sig**	**prot_cover**	**prot_pi**
		GN=TSG101 PE=1 SV=2						

Extended Data Table 3

Demographics of Patients and Healthy Participants

	DISCOVERY COHORT		**VALIDATION COHORT**			
	No. of participants (n=321)	**% of participants**	**No. of participants (n=82)**	**% of participants**	**No. of participants (n=32)**	**% of participants**
	Pancreatic Cancer		**Pancreatic Cancer**		**Breast cancer**	
Total	190	**59.19%**	**56**	**68.29%**	32	100%
Sex						
Men	104	54.74%	28	50.00%	0	0%
Women	86	45.26%	28	50.00%	32	100%
Median Age (range)	66 (37 – 86)		70 (40 – 85)		57 (30 – 85)	
AJCC stage						
0	n.a.	-	n.a.	-	2	6%
I	2	1.05%	2	3.57%	12	38%
II	n.a	-	n.a	-	17	53%
IIa	19	10.00%	15	26.79%	n.a.	-
IIb	117	61.58%	36	64.29%	n.a.	-
III	11	5.79%	0	0.00%	1	3%
IV	41	21.58%	3	5.36%	n.a.	-
Tumor grade						
1	1	0.53%	1	1.79%	8	25%
2	91	47.89%	35	62.5%	13	41%
3	49	25.79%	19	33.93%	10	31%
4	1	0.53%	0	0.00%	n.a.	-
Unknown	48	25.26%	1	1.79%	1	3%
Tumor resected						
Yes	152	80.00%	54	96.43%	32	100%
No	38	20.00%	2	3.57%	0	0%
Neoadjuvant Radio- /Chemotherapy						
Received	10	5.26%	0	0.00%	0	0%

		DISCOVERY COHORT			**VALIDATION COHORT**			
		No. of participants (n=321)	**% of participants**		**No. of participants (n=82)**	**% of participants**	**No. of participants (n=32)**	**% of participants**
		Pancreatic Cancer			**Pancreatic Cancer**		**Breast cancer**	
Not received		180	94.74%		56	100.00%	32	100%
Benign Pancreatic disease (BPD)								
Total		26	8.15%					
Sex								
Men		18	69.23%		3	50.00%		
Women		8	30.77%		3	50.00%		
Median Age (range)	58.5 (31 – 77)			49 (43 – 56)				
Diagnosis								
Chronic pancreatits		15	57.69%		6	100%		
Autoimmune pancreatitis		3	11.54%		0	0.00%		
Serous cystadenoma		8	30.77%		0	0.00%		
Pancreatic cancer precursor lesion (PCPL)								
Total		5	1.55%		0	0.00%		
Sex								
Men		2	40.00%		0	0.00%		
Women		3	60.00%		0	0.00%		
Median Age (range)	65 (59 – 74)			-	-	-		
Neoplasms								
*IPMN		5	100.0%		0	0.00%		
Healthy donors								
Total		100	31.15%		20	24.39%		

n.a. - non applicable

Abbreviations: American Joint Committee on Cancer (AJCC), Intraductal papillary mucinous neoplasm (IPMN), Pancreatic Intraepithelial Neoplasia (PanIN).

*The group of IPMNs consist of 2 IPMN associated with a carcinoma in situ, 1 IPMN associated with an early adenocarcinoma of the pancreas (pT1), an IPMN with intermediate dysplasia and an IPMN with low-grade dysplasia.

Extended Data Table 4

Histological report of patients with chronic pancreatitis

The histopathological report is listed for the 15 patients with chronic pancreatitis in the discovery cohort.

Patient No.	PanIN described	Histopathological report
1	No	Pancreatic tissue with chronic pancreatitis and extensive fibrosis and focal necrosis lipolytic and triptolytic areas.
0	No	Diffuse periductal lymphoplasmacytic infiltrates; severe periductal fibrosis and duct obstruction/disappearance; severe interlobular and acinar involvement; severe inflammatory storiform fibrosis and diffuse sclerosis; frequent venulitis and occasional arteritis; scattered and occasionally prominent lymphoid follicles
3	No	Chronic pancreatitis with periductal, inter- and intralobular fibrosis
4	No	Chronic pancreatitis and extensive fibrosis
5	No	Chronic recurrent and acute pancreatitis with plurifocal tryptolytic and lipolytic necrosis
6	No	Low-grade chronic pancreatitis with periductal fibrosis, in the present material no evidence of neoplastic events, no evidence of malignancy.
7	No	Chronic recurrent pancreatitis with some more pronounced fibrosis and intraductal calcifications. Chronic pancreatitis extends to the pancreas resection margin.
8	No	Chronic pancreatitis, cholangitis and papillitis with focally histomorphological aspect of an autoimmune, chronic sclerosing pancreatitis.
9	PanIN 1a	Pancreatic parenchyma (head of the pancreas) and peripancreatic fat and connective tissue with chronic recurrent pancreatitis with some areas fibrosis and abscesses. Pancreatic intraepithelial neoplasia (PanIN) Grade 1A.
10	No	Pancreatic parenchyma with perilobular fibrosis as well as dilated pancreatic ducts. In addition, peripancreatic fat and connective tissue with fibrosis. The finding represents a chronic pancreatitis.
11	PanIN 1a	Chronic-recurrent pancreatitis with pronounced fibrosis and dilated pancreatic ducts with focal inflammatory reactive epithelial cells. Older areas of organized necrosis and focal pancreatic intraepithelial neoplasia (PanIN) Grade 1A. Chronic pancreatitis also affects the pancreas resection margin.
12	No	Pancreatitis with focally accentuated, periductal, perilobular and intralobular fibrosis as well as smaller areas of organized fatty necrosis and presence of singel giant cells of foreign body type.
13	No	Chronic recurrent and acute pancreatitis with plurifocal tryptolytic and lipolytic necrosis with extensive destruction of the pancreatic parenchyma. Smaller secretion - and obliteration of pancreatic ducts with periductal fibrosis and localized squamous metaplasia. Peri- and interlobular fibrosis of the pancreatic parenchyma. Pancreatitis reaches the resection margin. At present, no neoplastic tissue, no evidence of malignancy.
14	No	Pancreatic tissue with some scarring chronic inflammation and chronic pancreatits. In the present material, no evidence of malignancy.
15	No	Tumor -free pancreatic tissue (surgical margins) with low periductal and interlobular fibrosis.

Extended Data Table 5

Histopathological findings and scoring in PKT mice in the cross sectional study

The mouse ID, age, genotype and percent bead with GPC1$^+$ crExos of mice in the cross sectional study are listed. A description of the histopathological findings and associated histological score is listed for PKT mice. Score 1: PanIN1a, Score 2: PanIN1 a/b, Score 3: PanIN2, Score 4: PanIN3, Score 5: Ductal adenocarcinoma (DCA). P: present (lesions were detected). 0: no lesion detected.

Mouse ID	Age (days)	Sex	Genotype	GPC1 (%)	Normal (% area)	Involved (% area)	PanIN1a	PanIN1b	PanIN2	PanIN3	DCA	Other (defined)	Pathological score
T187	16	M	Healthy+control	0.6	100	0	0	0	0	0	0		
T188	16	M	Healthy+control	1.1	100	0	0	0	0	0	0		
T157	20	M	Healthy+control	0.2	100	0	0	0	0	0	0		
T158	20	M	Healthy+control	0.2	100	0	0	0	0	0	0		
T163	20	M	Healthy+control	0.2	100	0	0	0	0	0	0		
T164	20	M	Healthy+control	0.4	100	0	0	0	0	0	0		
T183	16	M	PKT	8.4	98.6	1.4	**P**	0	0	0	0		1
T190	16	F	PKT	5.2	100.0	0.0	0	0	0	0	0	reactive+ducts	0
T191	16	F	PKT	6.4	100.0	0.0	0	0	0	0	0	reactive+ducts	0
T156	20	M	PKT	8.3	100.0	0.0	0	0	0	0	0		0
T159	20	F	PKT	10.8	95.1	4.9	**P**	**P**	**P**	0	0		3
T160	20	F	PKT	9.8	99.3	0.7	**P**	**P**	0	0	0		2
T165	20	F	PKT	9.2	96.1	3.9	**P**	**P**	0	0	0		2

P : present

0 : not detected

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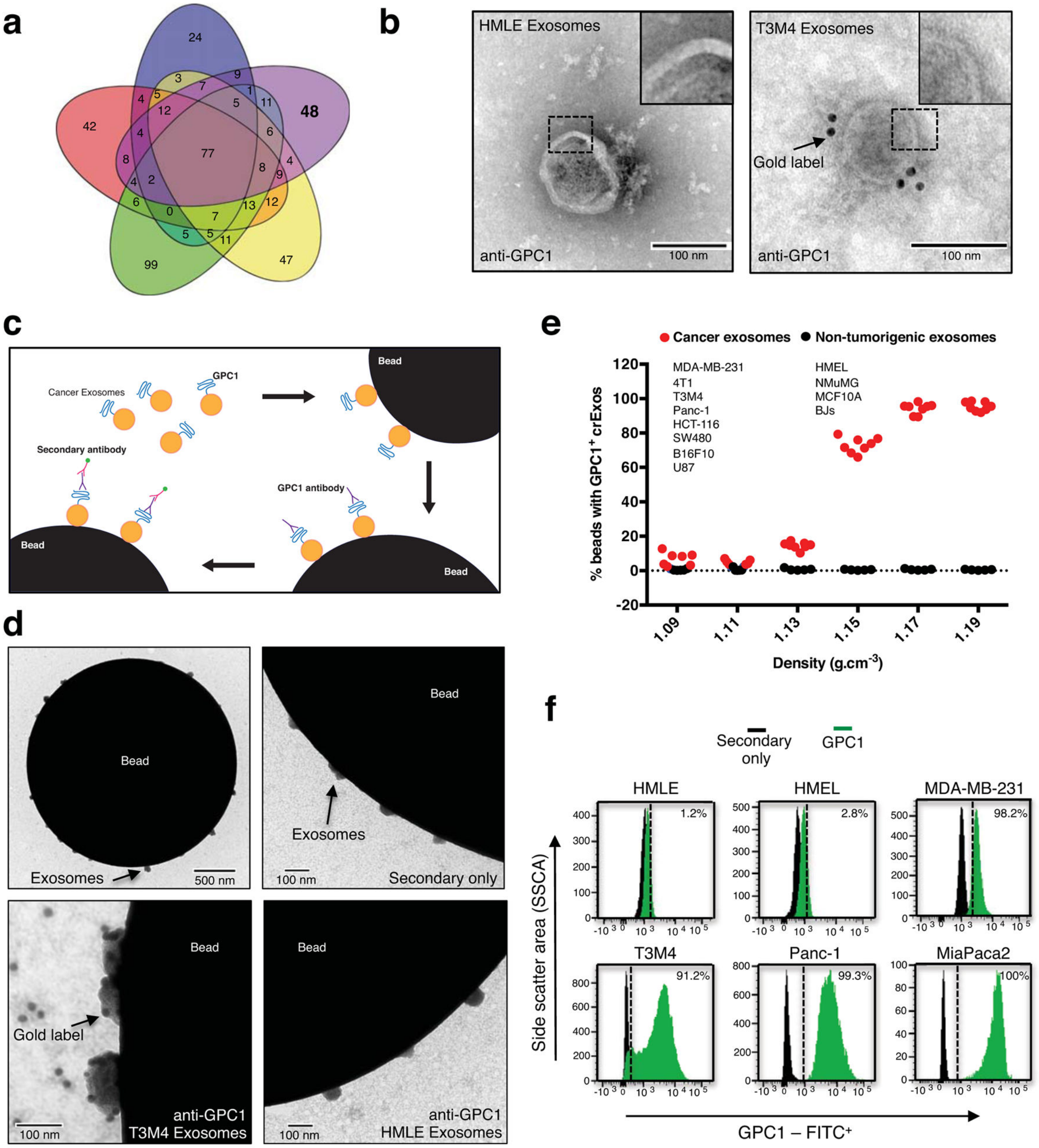

Figure 1. GPC1 is present specifically on cancer exosomes

a, Venn diagram of exosomal proteins from NIH/3T3 (blue), MCF 10A (red), HDF (green), E10 (yellow) and MDA-MB-231 (purple) cells. 48 proteins were exclusively detected in exosomes from MDA-MB-231 cells (n=3 protein samples, technical replicates). **b**, Transmission electron micrographs (TEM; left image) and immunogold TEM (right image) of GPC1. Upper right: digitally zoomed inset (n=2 experiments). **c**, Diagram of flow cytometry experiment to detect GPC1 on the surface of exosomes bound to beads. **d**, TEM of bead-bound exosomes and immunogold labeling of GPC1 (n=2 biological replicates). **e**, Percent beads with GPC1$^+$ exosomes from cancer cells (red) and non-tumorigenic cells (black). **f**, Flow cytometry analyses of percent beads with GPC1$^+$ exosomes from indicated cell lines (n=2 biological replicates). Negative control: secondary antibody only.

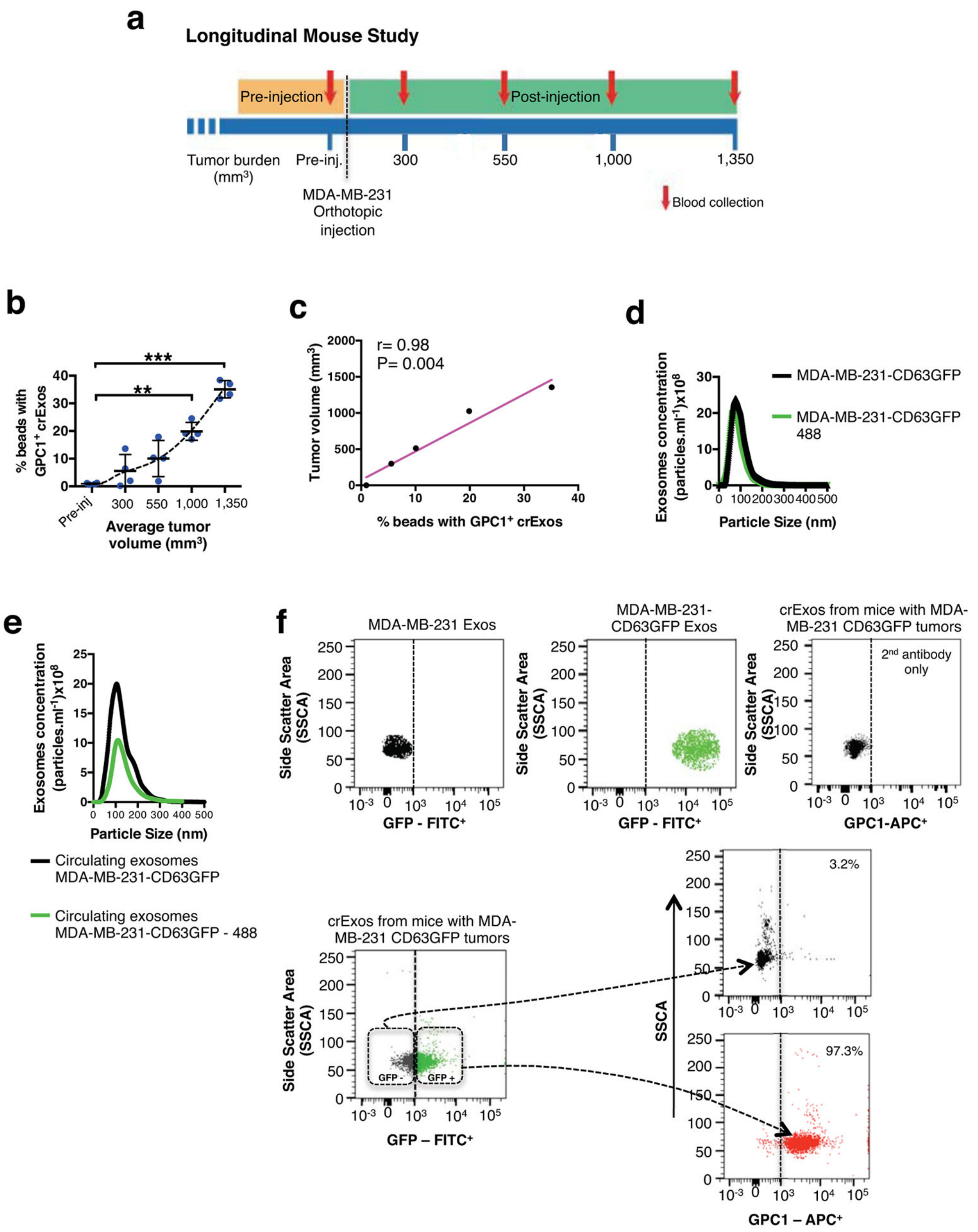

Figure 2. GPC1^{+} crExosomes are derived from cancer cells in tumor-bearing mice

a, Longitudinal blood collection: nude mice with orthotopic MDA-MB-231 tumors (n=4 mice). **b**, Percentage of beads with GPC1^{+} exosomes harvested from systemic circulation (crExos) plotted against average tumor volume (n=4 mice, each sample analyzed in technical triplicates for GPC1). ANOVA, post-hoc Tamhane T_2, ** P<0.01, *** P<0.001. Data is shown as mean ± standard deviation. **c**, Correlation between tumor volume and percent beads with GPC1^{+} crExos (Pearson correlation test). **d**, NanoSight® analyses of exosomes from cultured MDA-MB-231 CD63-GFP cells. Black: all exosomes; green: CD63-GFP^{+} exosomes (n=3 technical replicates). **e**, NanoSight® analyses of crExos from mice with MDA-MB-231 CD63-GFP orthotopic tumor. Black: all exosomes; green: CD63-GFP^{+} exosomes (n=3 technical replicates). **f**, Flow cytometry analyses of beads with exosomes from cultured MDA-MB-231 (upper left) and MDA-MB-231 CD63-GFP (upper middle) cells, and from crExos of mice with MDA-MB-231 CD63-GFP orthotopic tumors (lower left). Staining of CD63-GFP$^+$ (cancer cell derived) and CD63-GFP$^-$ (host derived) crExos for GPC1 (APC$^+$, lower right; n=3 biological replicates and 3 technical replicates). Percent positive beads are listed. Negative control: secondary antibody alone (right upper panel).

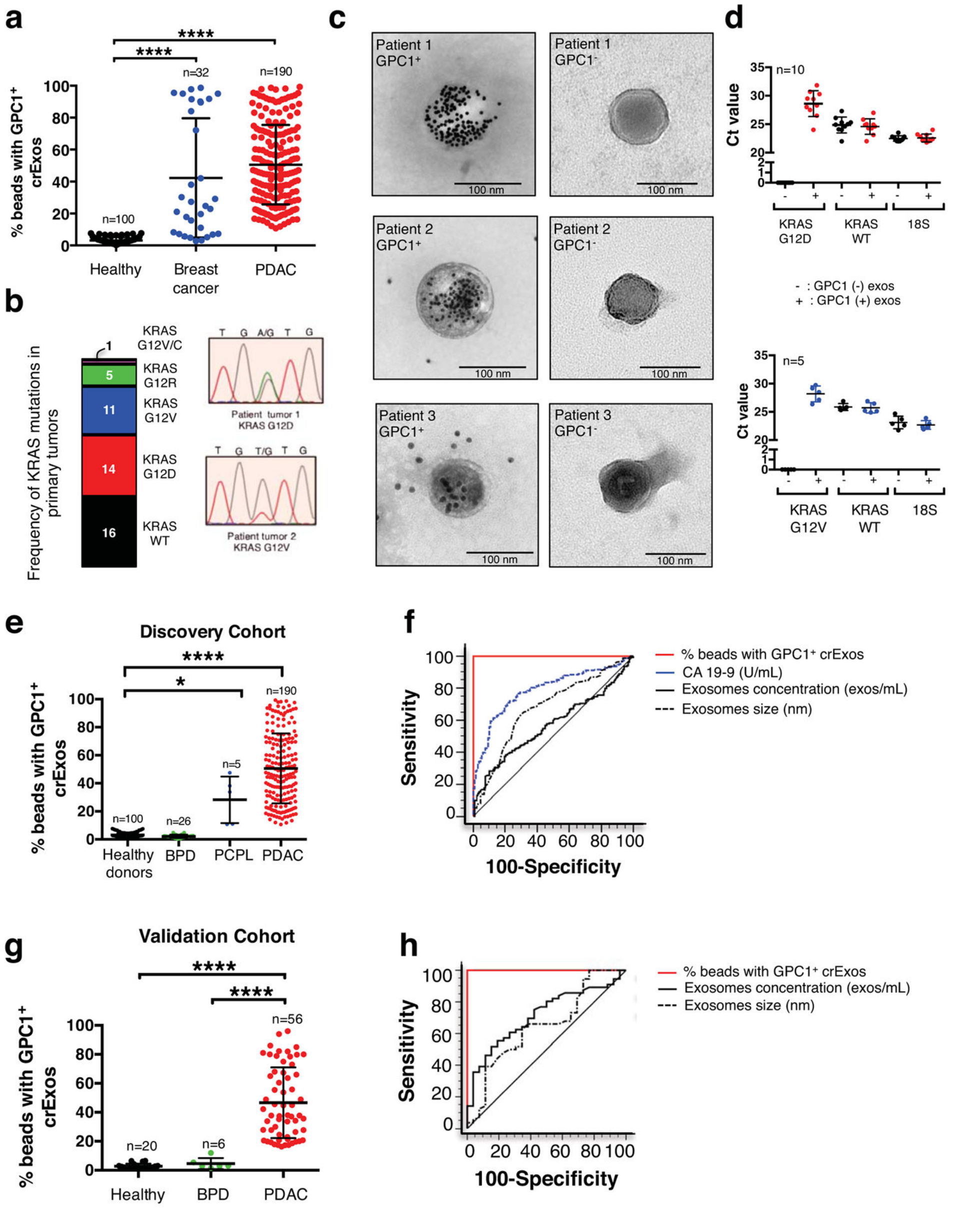

Figure 3. GPC1$^+$ crExos is a non-invasive biomarker for pancreas cancer

a, Percent beads with GPC1$^+$ crExos in healthy donors (n=100), breast cancer patients (n=32) and patients with PDAC (n=190; ANOVA, post-hoc Tamhane T_2, **** P<0.0001). **b**, Frequency of KRAS mutation in 47 tumor specimens and representative DNA sequencing chromatograms. **c**, TEM of GPC1 immunogold of crExos from three PDAC patients following flow cytometry isolation of GPC1$^+$ (left column) and GPC1$^-$ (right column) crExos (n=3, 3 technical replicates). **d**, Ct value for KRAS G12D/G12V, KRAS WT mRNA and 18S rRNA expression in GPC1$^+$ (red and blue) and GPC1$^-$ (black) crExos (after flow cytometry isolation; n=2, 2 biological replicates and 3 technical replicates each) **e**, Percent beads with GPC1$^+$ crExos, discovery cohort (healthy donors, n=100; patients with a benign pancreatic disease (BPD), n=26; pancreatic cancer precursor lesion (PCPL), n=5; and PDAC patients, n=190; ANOVA, post-hoc Tamhane T_2, ** $P<0.01$, **** $P<0.0001$; 3 technical replicates. **f**, ROC curve of discovery cohort. **g**, Percent beads with $GPC1^+$ crExos, validation cohort (healthy donors, n=20; BPD, n=6; PDAC, n=56; ANOVA, post-hoc Tukey-Kramer test, **** $P<0.0001$; 3 technical replicates). **h**, ROC curve of validation cohort. Data is shown as mean ± standard deviation.

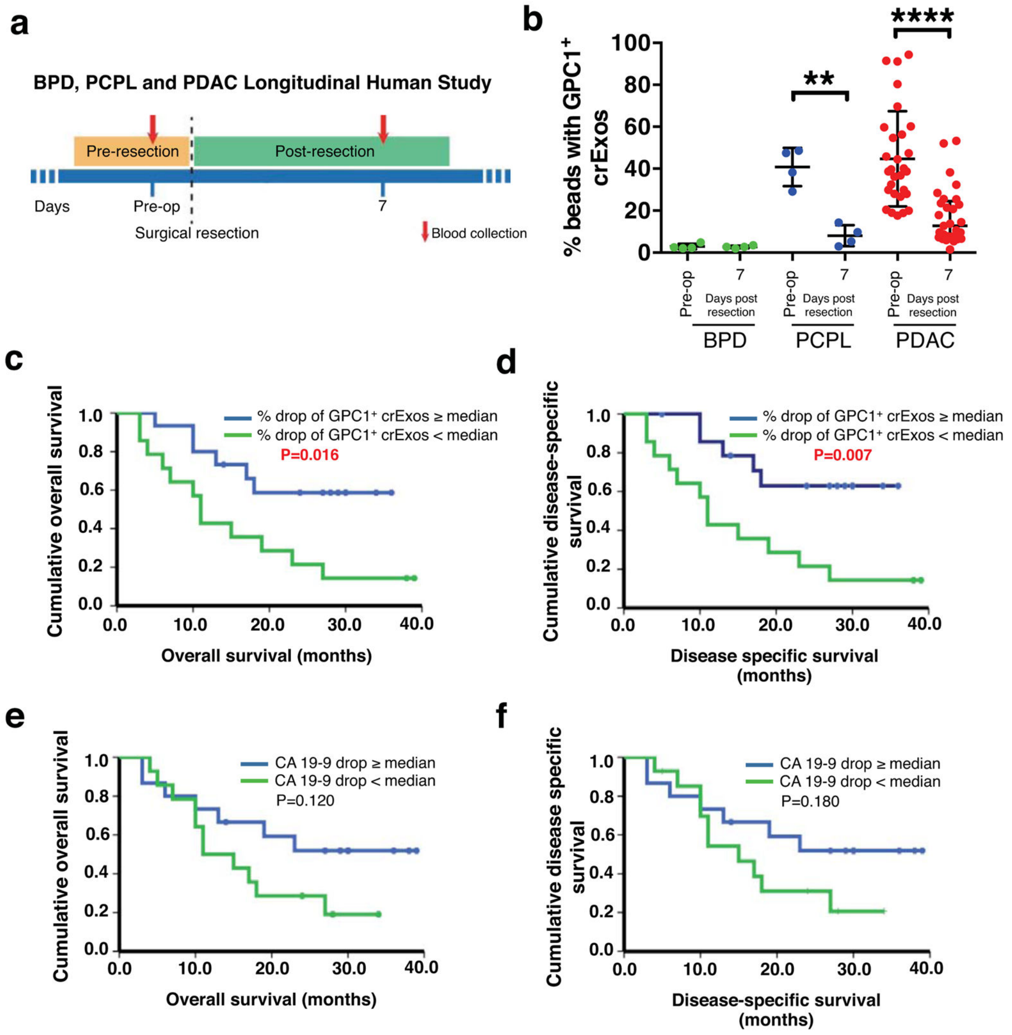

Figure 4. Levels of circulating GPC1$^+$ exosomes inform pancreas cancer resection outcome

a, Longitudinal blood collection pre- (pre-op) and post-operatively (day 7). **b**, Percent beads with GPC1$^+$ crExos from patients with BPD (n=4), PCPL (n=4) or PDAC (n=29) (paired two-tailed Student's *t*-test, ** P<0.01, **** P<0.0001). Data is shown as mean ± standard deviation. **c–d**, Kaplan–Meier curves (log-rank test) displaying overall (c) and disease-specific survival (d) of patients with GPC1$^+$ crExos drop ≥ median (blue) and GPC1$^+$ crExos drop < median (green) drop after resection. **e–f**, Kaplan–Meier curves (log-rank test) displaying overall (e) and disease-specific survival (f) of patients with a CA 19-9 drop ≥ median (blue) and a CA 19-9 drop < median (green) drop after resection.

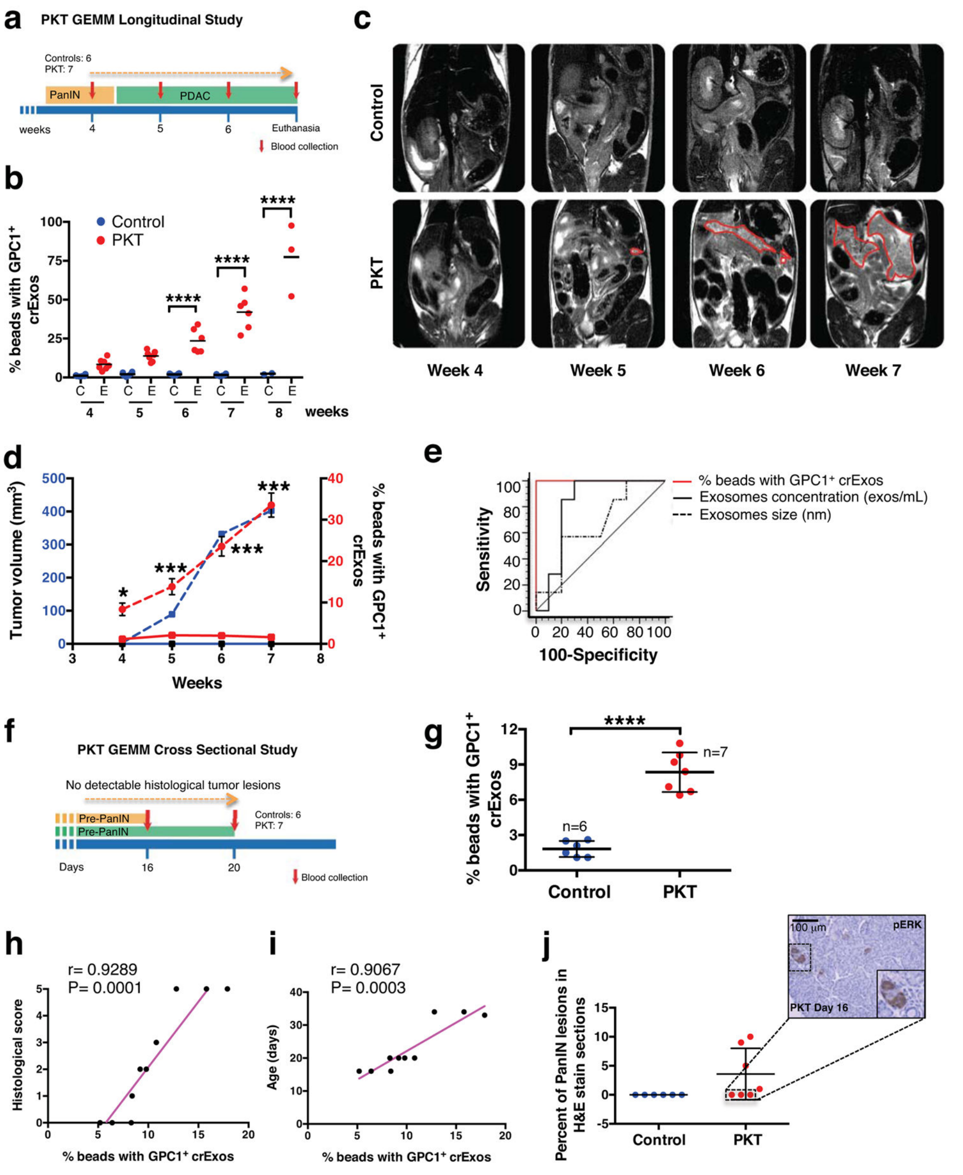

Figure 5. GPC1$^+$ circulating exosomes predict pancreas cancer in GEMM

a, Longitudinal blood collection from control and PKT mice: 4 (n=6 and n=7, respectively), 5 (n=6 and n=7), 6 (n=6 and n=6), 7 (n=6 and n=6) and 8 (n=2 and n=3) weeks of age. **b**, Percent beads with GPC1$^+$ crExos from PKT (red) and control (blue) mice; ANOVA, post-hoc Tukey-Kramer test, **** P<0.0001; 3 technical replicates. **c**, MRI with tumor encircled in red. **d**, Tumor volume and percent GPC1$^+$ crExos in PKT mice at indicated age (ANOVA, post-hoc Tamhane T$_2$), *P<0.05, ** P<0.01, *** P<0.001**** P<0.0001; 3 technical replicates) **e**, ROC curve analysis of 4 weeks-old control mice (n=6) and mice with acute pancreatitis (n=4) vs. 4 weeks-old PKT mice (n=7). **f**, Cross sectional study: blood collected from 16 or 20 days old control (n=6) and PKT (n=7) mice. **g**, Percent beads with GPC1$^+$ crExos from control and PKT (16 – 20 days-old) mice (paired two-tailed Student's *t*-test, P<0.0001; 3 technical replicates). **h–i**, Correlation between histological score (h) or age (i) and percent beads with GPC1$^+$ crExos (Pearson correlation test). **j**, Relative percent PanIN lesions and representative staining for phosphorylated ERK. Data is shown as mean ± standard deviation.