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6 **The human *in vivo* biomolecule corona onto PEGylated**
7 **liposomes: a proof-of-concept clinical study**
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11 Marilena Hadjidemetriou¹, Sarah McAdam², Grace Garner², Chelsey Thackeray³, David Knight⁴, Duncan
12 Smith⁵, Zahraa Al-Ahmady¹, Mariarosa Mazza¹, Jane Rogan², Andrew Clamp³ and Kostas Kostarelos^{1*}
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17 ¹*Nanomedicine Lab, Faculty of Biology, Medicine & Health, AV Hill Building, The University of Manchester, Manchester, United Kingdom;*

18 ²*Manchester Cancer Research Centre Biobank, The Christie NHS Foundation Trust, CRUK Manchester Institute, Manchester, United Kingdom*

19 ³*Institute of Cancer Sciences and The Christie NHS Foundation Trust, Manchester Cancer Research Centre (MCRC),*

20 *University of Manchester, Manchester, United Kingdom*

21 ⁴*Bio-MS Facility, Michael Smith Building, The University of Manchester, Manchester, United Kingdom;*

22 ⁵*CRUK Manchester Institute, The University of Manchester, Manchester, United Kingdom*
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32 * Correspondence should be addressed to: kostas.kostarelos@manchester.ac.uk
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4 **Abstract**
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7 The self-assembled layered adsorption of proteins onto nanoparticle (NP) surfaces, once in contact
8 with biological fluids, has been termed the ‘protein corona’ and it is gradually seen as a determinant
9 factor for the overall biological behavior of NPs. Here, we describe the previously unreported *in vivo*
10 protein corona formed in human systemic circulation. The human-derived protein corona formed
11 onto PEGylated doxorubicin-encapsulated liposomes (Caelyx®) was thoroughly characterized
12 following the recovery of liposomes from the blood circulation of ovarian carcinoma patients. In
13 agreement with our previous investigations in mice, the *in vivo* corona was found to be molecularly
14 richer in comparison to its counterpart *ex vivo* corona. The intravenously infused liposomes were
15 able to scavenge the blood pool and surface-capture low molecular weight, low abundant plasma
16 proteins that could not be detected by conventional plasma proteomic analysis. This study describes
17 the previously elusive or postulated formation of protein corona around nanoparticles *in vivo* in
18 humans and illustrates that it can potentially be used as a novel tool to analyze the blood circulation
19 proteome.
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30 **Keywords:** biomolecule corona, Doxil®, ovarian cancer, nanomedicine
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Introduction

The surface identity of nanoparticles (NPs) is modified once injected in the bloodstream because of their spontaneous interaction with a wide range of surrounding proteins and other biomolecules.^[1] The spontaneous and layered adsorption of proteins onto NPs has been termed the 'protein corona'.^[2] Even though surface modification of NPs with hydrophilic polymers (e.g. PEGylation) results in diminution of protein adsorption onto NPs surfaces, the complete elimination of protein corona formation has not been achieved so far by such functionalization strategies.^[3-7] During the last decade protein corona research has gained popularity with a flurry of attempts made to molecularly characterize corona profiles after the *ex vivo* incubation of NPs with biofluids (mainly plasma) and more recently, *in vivo* (in rodents).^[4-7]

The biological effects arising from the presence of biomolecules onto NPs surfaces can be both unfavorable and advantageous to their biomedical applications.^[1, 8] It is now reasonably established that the protein corona defines the NP surface characteristics and forms the interface between NPs and biological systems, also referred by some to as the 'bio-nano' interface. The presence of the protein corona mediates the interaction of NPs with cells and has been shown to significantly impact on their cytotoxicity, cellular internalization and targeting capability.^[9, 10]

Among a plethora of nanoscale drug delivery systems, liposomes (phospholipid-based vesicles) are considered to be the most clinically-established nanomedicine constructs.^[11] The substantial reduction in the cardiotoxicity of doxorubicin upon encapsulation within PEGylated liposomes led to the approval of the first nanoscale anti-cancer agent (Doxil®, Caelyx®) by the FDA in 1995 for the treatment of for AIDS-related Kaposi Sarcoma and in 1999 for the treatment of recurrent ovarian carcinoma.^[12, 13] This liposomal construct shows superiority to free doxorubicin owing to its prolonged blood circulation time, the stable retention of the drug in the interior of liposomes while in blood circulation, leading to an overall improved toxicity profile and enhanced tumor accumulation.^[12, 14]

Despite the clinical track record of liposomes for more than 20 years, the role that protein corona plays in liposomal pharmacology has been barely studied. To date, only a few studies describe the molecular composition of the protein corona formed around NPs *in vivo*.^[4-6, 15] In the vast majority of investigations, NPs are characterized after their *ex vivo* interaction with plasma proteins (mouse or human), extrapolating on the erroneous assumption that corona fingerprints formed under such a static biological setting can reflect the dynamics and molecular richness of the *in vivo* milieu.^[1]

In our previous studies, we developed a robust protocol to retrieve and purify NPs from blood

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4 to investigate the *in vivo* protein corona formation and its evolution onto clinically-used liposomes
5 after their intravenous administration (tail vein) in rodents. These studies revealed that the molecular
6 composition of the *in vivo* protein corona cannot be sufficiently predicted by the *ex vivo* plasma
7 incubation of NPs.^[4-6] Blood flow dynamics, the interaction with blood circulating cells and immune
8 responses triggered after NPs administration are some of the factors that cannot sufficiently be
9 simulated by *ex vivo* studies and could explain the differences observed between the *ex vivo* and *in*
10 *vivo* formed protein coronas.^[1] Although *in vivo* models shed light on our understanding of the self-
11 assembly mechanism of the protein corona formation under more biologically-relevant settings,
12 extrapolation of data from mice to humans should be made with extreme caution.^[16] Nanoparticle-
13 based systems that work efficiently in rodent disease models often fail to offer similar efficacy in
14 humans.^[17] Yet, the formation of a protein corona around blood-circulating nanoparticles in humans
15 has not been experimentally described at all, let alone studied as a potential factor to explain such
16 discrepancies between preclinical and clinical achievements.
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19 In the present study, we attempted to investigate and characterize the *in vivo* protein corona
20 formation in humans. PEGylated, doxorubicin-encapsulated liposomes (Caelyx®) were infused
21 intravenously in six patients with platinum-resistant recurrent ovarian carcinoma and subsequently
22 recovered from the blood circulation immediately on completion of their first cycle of Caelyx®
23 treatment. Liposomes were isolated from blood components along with their formed protein corona
24 which was quantitatively and qualitatively characterized using a battery of techniques. The data
25 indicated that an *in vivo* human protein corona forming around intravenously-infused liposomal
26 nanoparticles can be reproducibly identified and molecularly described. The human *in vivo* protein
27 corona was rich in multiple low molecular weight and low abundant plasma proteins that could not
28 be detected by conventional plasma proteomic analysis, which revealed the potential utilization of
29 the biomolecule corona as a tool to address the issue of the high dynamic range of plasma
30 proteome.
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Results and Discussion

Physicochemical characterization of liposomes and human *in vivo* corona-coated

liposomes. To characterize the *in vivo* formed, human-derived protein corona, PEGylated doxorubicin-encapsulated liposomes were recovered from the blood circulation of ovarian carcinoma patients (n=6) at the end of their first cycle of intravenous Caelyx[®] infusion (at a dose of 40 mg/m²), for platinum-resistant disease (**Figure 1A**). Patient clinical and basic blood analysis characteristics are summarized in **Table S1**. The physicochemical properties of the commercially available PEGylated doxorubicin-encapsulated liposomes (Caelyx[®]) were investigated by dynamic light scattering (DLS), ζ -potential measurements and negative stain transmission electron microscopy (TEM) before and after their intravenous infusion in patients and are summarized in **Figures 1B and 1C**. Liposomes had a mean hydrodynamic diameter of 82.6 nm, a negative surface charge of -33.8 mV and displayed low polydispersity values (<0.1) representing a narrow size distribution (**Figure 1B**). TEM imaging showed well-dispersed, drug-encapsulated round shaped vesicles, with their size correlating that of DLS measurements (**Figure 1C**).

Immediately after the completion of the intravenous infusion of Caelyx[®] (that lasted for approximately 90 mins), blood (~10ml) was collected and plasma was prepared without delay by centrifugation. A two-step purification protocol (size exclusion chromatography and membrane ultrafiltration) was then employed for the isolation of liposome-corona complexes and the complete elimination of unbound proteins, as we have previously described (**Figure S1**).^[4, 5] **It should be noted that although the protein corona is often described as a multi-layered structure consisting of an inner layer of tightly bound proteins ('hard corona') and an outer dynamically-bound layer of proteins ('soft corona'), current purification protocols might disturb loosely bound biomolecules. Therefore, the existence and the biological relevance of the 'soft corona' remain unclear and we can only refer to the analytically accessible protein corona.**^[18]

Dynamic light scattering measurements of corona-coated liposomes demonstrated that their size distribution broadened (**Figure 1B**). **Formation of the corona is often associated with an increase in the mean nanoparticle diameter since layers of proteins are adhered onto the NP surface. In the case of soft nanomaterials however, adsorption of proteins could also lead to a reduction in their mean diameter due to osmotic "shrinkage". This has been previously reported**^[4, 5, 19] **and also observed here in the case of human *in vivo* and *ex vivo* corona-coated liposomes (Figures 1B and S2).** In addition, our data showed that the mean surface charge of liposomes remained negative after their interaction with plasma proteins (**Figure 1B and S2**) in agreement with previous studies proposing that negatively charged NPs do not exclusively interact with

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4 positively charged proteins, as electrostatic interactions are not the only driving force at the NP–
5 protein interface.^[20]
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8 Moreover, TEM imaging revealed well dispersed and corona-coated liposomes that retained
9 an intact structure after recovery and purification (**Figure 1C**). Although protein corona is usually
10 illustrated as a dense layer covering the entire surface of a nanoparticle, this has not been
11 experimentally confirmed. In agreement with our previously reported observations in rodents,^[4, 5]
12 the human *in vivo* protein corona did not appear to coat entirely the liposome surface. Cryo-EM
13 imaging of the recovered liposomes further confirmed the presence of a protein corona adsorbing
14 around the doxorubicin-encapsulated (Caelyx[®]) liposomes, but without fully covering their surface
15 (**Figure 1C**). Similarly, Kokkinopoulou M *et al.*, have recently described the protein corona formed
16 around polystyrene NPs as an undefined and unfolded network surrounding the NP surface.^[21]
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19 Moreover, small vesicular structures surrounding the liposome surface could be observed by TEM
20 in **Figure 1C**. We hypothesize that these could be either osmotically shrunk liposomes or blood-
21 circulating extracellular vesicles adsorbed onto the surface of liposomes. Based on these
22 observations, further studies will be needed to explore the adherence of other molecules or
23 vesicular structures onto the surface of blood-circulating NPs.
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33 **Characterization of the human *in vivo* protein corona.** Previous anti-opsonisation studies have
34 emphasized that the total amount of protein adhered onto NPs can be used to predict the NPs
35 blood circulation time.^[22-24] Even though the overall protein adsorption is moderated by the PEG
36 chains present onto the NPs surface, it cannot be fully suppressed.^[3-5] In agreement with these
37 previous findings, the present study demonstrated that PEGylated nanoscale surfaces are not
38 entirely inert and interact with plasma proteins upon intravenous administration in humans.
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42 To investigate the total amount of protein adsorbed, we calculated the protein binding ability
43 (Pb), defined as the amount of protein associated with each μ mole of lipid. As shown in **Figure 2A**,
44 the average Pb value observed was 1532 μ g of protein/ μ mole of lipid, that is more than 10 times
45 higher than what was obtained for the same liposome composition (produced in the laboratory)
46 after injection in healthy CD-1 mice.^[5] Whether this is a result of mouse-to-human differences
47 and/or due to the neoplastic disease present at an advanced stage in the patients that participated
48 in this study, is difficult to conclude and will require further investigation. *Ex vivo* incubations of
49 Caelyx[®] liposomes with plasma samples, obtained from the same patients before Caelyx[®] infusion
50 were performed as a control. As shown in **Figure S3**, a significantly lower average Pb value was
51 observed which confirms our previous data suggesting that the *ex vivo* incubation of NPs with
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4 human plasma samples cannot predict the formation of protein corona under realistic *in vivo*
5 conditions.^[4]
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8 The manner in which proteins adsorb and pack onto the NP surface is highly dependent on
9 their physicochemical properties and especially their size, shape and functionalization. However,
10 concrete relationships between the nanomaterial synthetic identity and their ensuing biological
11 identity in physiological environments remain vague and unpredictable.^[1] Distinct proteins could be
12 either enriched or displayed weak affinity for the NP surface depending on the balance between
13 their rates of association (K_{on}) and dissociation (K_{off}).^[25] It has previously been shown by us *in vivo*
14 ^[5] and others *in vitro* ^[26, 27] that the protein corona is a temporally dynamic entity. In complex
15 biofluids, such as blood, proteins present at high concentrations are characterized by high K_{on}
16 values and therefore have high possibility to interact with the surface of NPs. However, these
17 proteins might be replaced by other molecules of lower abundance, but of higher binding energy
18 (characterized by low K_{off} values). Our previous time evolution studies in rodents revealed that a
19 molecularly rich *in vivo* protein corona was formed around PEGylated liposomal doxorubicin
20 (Caelyx®) as early as 10min post-injection. Even though the total amount of protein adsorbed and
21 the identity of the corona proteins did not significantly change, the abundance of each protein
22 fluctuated over time, indicating that competitive exchange processes were taking place.
23 Interestingly, liposomes were coated by a complex mixture of low MW proteins at all different time
24 points of investigation.^[5]
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36 To examine whether our previous observation in rodents applies also under the *in vivo*
37 conditions in humans, we comprehensively identified the protein molecules that self-assembled to
38 form the corona around the intravenously infused liposomes by mass spectrometry. Surface-bound
39 proteins were classified according to their molecular weight. As illustrated in **Figure 2B**, plasma
40 proteins with MW < 80 accounted for almost 80% of the protein coronas formed. It is possible that
41 the low MW proteins identified (**Figure 2B**) have high affinity and interact directly with the surface
42 of PEGylated liposomes and/or they are trapped between other corona-carrier proteins that are
43 adhered to the NPs surface.
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49 To further understand the protein composition of the *in vivo* human corona, the average
50 value (n=6 patients) of relative protein abundance (RPA) for each identified protein was calculated.
51 **Figure 2C** summarizes the 20 most abundant proteins associated onto the surface of recovered
52 Caelyx® liposomes for all patients. The most abundant corona protein was full-length cDNA clone
53 CS0DD006YL02 (with accession number Q86TT1; SwissProt database). **To the best of our**
54 **knowledge, this protein has not been previously reported to associate with the surface of liposomes**
55 **or any other type of nanoparticle after their incubation in full plasma.** It has been only previously
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4 shown to interact with maltose-functionalized PEGylated hybrid magnetic NPs after their incubation
5 with fractionated human plasma sample.^[28] The 20 most abundant proteins identified in each
6 patient and their respective RPA values are also shown in **Table S2** to further illustrate the
7 consistency of the above observation. The fact that the most abundant corona proteins were
8 common between the 6 patients illustrates the consistency of liposome-protein interactions. Out of
9 445 corona proteins identified, 122 were repeatedly detected in all patients (**Figure S4** and **Table**
10 **S5**).

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16 In agreement with our previous investigations of the liposomal protein coronas in mice,^[5]
17 immunoglobulins, lipoproteins and complement proteins were the most abundant classes of
18 proteins, contributing to 28%, 9% and 4% of the total protein content respectively (**Figure 2D** and
19 **Tables S2-S3**). The presence of opsonins (such as immunoglobulins), known to activate the
20 mononuclear phagocytic system (MPS), can favor recognition and clearance of the blood-
21 circulating PEGylated liposomes used in this study. However, the PEG-mediated inhibition of
22 interactions between nanoparticles and circulating blood cells has been proposed to explain their
23 long circulation time.^[29] As the molecular identification of the human corona suggests, lipoproteins
24 were the second most abundant class of proteins, proposed to have dysopsonic activity (i.e. favor
25 long blood circulation), possibly via competitive binding for the liposomal surface with opsonic
26 proteins.^[30] The high affinity and adherence of lipoproteins to the lipid surface of Caelyx[®] NPs
27 observed, was not surprising considering that blood circulating lipoproteins are involved in lipid and
28 cholesterol transport and metabolism.

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38 Intravenously infused, doxorubicin-encapsulated PEGylated liposomes have also been
39 shown to interact with the complement system, in some cases triggering a transient and mostly
40 mild hypersensitive reactions known as C-activation related pseudoallergy (CARPA).^[31, 32] Despite
41 the presence of several key complement cascade proteins in the liposomal corona involved in the
42 classical (complement C1s and C1qb, C4b binding protein) alternative (complement factor h,
43 complement C3) and in lectin (mannan-binding lectin serine protease) pathways of activation
44 (**Figure 2D** and **Table S3**), none of the patients in our study experienced a clinically symptomatic
45 reaction to Caelyx[®] infusion.

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53 **Patient-by-patient blood-circulation proteome analysis.** Blood predominantly contains high
54 abundance, high MW proteins, such as albumin and immunoglobulins, that hamper the detection of
55 the lower MW blood proteomic fractions.^[33] There is an urgent need for tools to facilitate the
56 discovery of new and, more importantly, combinations of protein molecule panels to improve early
57 cancer diagnosis, evaluate disease progression and monitor response to the treatment. Robust
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4 high-throughput proteomic discovery platforms that will enable the identification of blood-buried
5 molecules are of immediate clinical importance.

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7 The fact that albumin ‘masking’ was largely eliminated from in the *in vivo* human-derived
8 corona prompted us to investigate further whether liposomes interacted with plasma proteins that
9 could not be directly detected by plasma proteomic analysis. Proteins associated with liposomes *in*
10 *vivo* were separated by SDS-PAGE and visualized by Imperial Protein stain, as illustrated in **Figure**
11 **3A**. Contrary to plasma control, the distinct bands of corona proteins, even at the low MW region,
12 confirmed the ability of liposomes to surface-capture low abundant proteins minimizing the ‘noise’
13 from highly abundant proteins (**Figure 3A**).

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15 Low molecular weight proteins are easily cleared from blood circulation (mainly through
16 proteolytic plasma clearance), which limits their detection by conventional plasma proteomic
17 analysis.^[34-36] The only way a small molecule can remain in the blood circulation for longer periods
18 is to adhere to a long-circulating high abundance protein, such as albumin. ^[35, 36] The adherence of
19 smaller MW biomolecules onto the surface of NPs once injected in the bloodstream, could
20 significantly increase their blood circulation and allow their successful ‘enrichment’ for detection.
21 Therefore, the characterization of the purified corona proteins can be employed as a ‘fractionation’
22 plasma tool that addresses the signal-to-noise challenge.

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24 The nanoparticle-mediated capture of low MW proteins from biofluids has been so far
25 attempted exclusively *ex vivo*. For instance, Nanotrap® technology developed by Liotta and co-
26 workers, uses core shell hydrogel nanoparticles as protein harvesters. This technology is based on
27 the NP-mediated size and charge dependent fractionation of complex biofluids, such as plasma
28 and urine, prior to proteomic analysis. The porous outer shell of NIPAm (N-isopropylacrylamide)
29 NPs blocks the entry of high MW proteins, while the internal core contains covalently attached
30 chemical affinity baits which capture low MW proteins.^[37, 38]

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32 To compare the human corona proteins with the plasma proteome, we analyzed plasma
33 samples obtained from the same patients before the infusion of Caelyx®. The Venn diagram in
34 **Figure 3B** illustrates the number of common and unique proteins between the liposomal corona
35 and plasma, as identified by mass spectrometry. A significantly higher total number of proteins was
36 detected in the corona samples in comparison to the number of proteins identified when plasma
37 samples were analyzed (**Figure 3B**). In addition, the most abundant plasma proteins were not the
38 predominant corona proteins, as depicted in **Figure 3C** and **Tables S3** and **S4**. Strikingly, the most
39 abundant corona protein (full-length cDNA clone, CS0DD006YL02), which contributed to 8% of the
40 total protein content, was not detected in any of the plasma control samples (**Figure 3C** and **Table**
41 **S4**). Although, full-length cDNA clone CS0DD006YL02 has been previously identified by mass
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4 spectrometry analysis of arachnoid cyst fluid,^[39] peritoneal effluent^[40] and saliva^[41], current
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6 proteomic approaches fail to detect this low abundant protein in complex mixtures like plasma.

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8 The above findings prompted us to further investigate the molecular composition of the *ex*
9 *vivo* protein corona after the incubation of Caelyx[®] liposomes with plasma samples obtained from
10 the same ovarian carcinoma patients before Caelyx[®] infusion. In agreement with our previous data
11 in rodents, a more complex molecular fingerprint was detected for *the in vivo* protein corona in
12 comparison to its counterpart *ex vivo* corona (**Figure S5**). Despite the fact that the cDNA clone
13 CS0DD006YL02 protein was not detected by mass spectrometry in any of the control plasma
14 samples, it was identified as the most abundant protein of both the *in vivo* and *ex vivo* formed
15 protein coronas (**Figure 2A** and **Table S6**). Control investigations of the *ex vivo* corona formed
16 onto Caelyx[®] liposomes upon incubation with plasma samples from healthy volunteers (**Table S6**)
17 were also performed. The cDNA clone CS0DD006YL02 protein was found to be the 5th most
18 abundant protein in the control cohort suggesting that tumorigenesis may affect the dynamics of
19 corona formation. Overall, the above data provide an initial evidence that the liposome protein
20 corona results in an ‘enriched’ sampling of the blood proteome which renders the need for much
21 more work on the biomarker discovery front necessary, but beyond the scope of this study.
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31 Previously unreported experimental evidence that a biomolecule corona self-assembles
32 around nanoparticles in humans while in their blood circulation has been offered in the present
33 study. The successful recovery and purification of corona-coated lipid bilayer vesicles from the
34 blood circulation of ovarian carcinoma patients allowed the proteomic analysis of the human *in vivo*
35 protein corona. We demonstrated that the clinically-used liposomal nanoparticles interact and can
36 be stably coated with a complex mixture of plasma proteins, including low MW and low-abundant
37 molecules otherwise ‘masked’ under the overwhelming signal of highly abundant proteins (such as
38 albumin and immunoglobulins). The corona-based elimination of this ‘masking’ effect, enabled the
39 uncovering of multiple protein molecules that could not be detected by plasma sample analysis
40 performed in comparison. This work is thought to act as the impetus for many future studies needed
41 to improve our further understanding of how the human *in vivo* biomolecule corona can affect the
42 overall clinical performance of NPs, but also provide the technology springboard to allow the clinical
43 exploitation of protein corona fingerprinting as a novel tool to comprehensively analyze the blood
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Experimental

Ethical Approvals. This project was reviewed and approved by the Manchester Cancer Research Centre Biobank Sample Access Committee and all sample collection was conducted under the MCRC Biobank Research Tissue Bank Ethics (ref: 07/H1003/161+5).

Blood sample collection. Caelyx® is indicated for the treatment of advanced ovarian cancer in women who have failed a first-line platinum-based chemotherapy. Patients receive in total 6 cycles of Caelyx with cycle frequency 28 days. Eligible cases for this study included women with recurrent ovarian cancer commencing single agent Caelyx® for the first time, at a dose of 40 mg/m². Caelyx® contains 2mg/ml doxorubicin hydrochloride encapsulated in a PEGylated liposomal formulation (16 mg lipid content). **Based on established pharmacokinetic data for the clinically-used PEGylated liposomes encapsulating doxorubicin, the time of blood collection (after the completion of infusion that lasted for approximately 90 mins), the majority of injected liposomal nanoparticles are still in blood circulation.**^[14, 42]

Paired plasma samples (before and immediately after cycle 1 infusion) were collected into commercially available anticoagulant-treated tubes (K2 EDTA BD Vacutainer®). Plasma was then prepared by inverting 10 times the collection tubes to ensure mixing of blood with EDTA and subsequent centrifugation for 12 minutes at 1300 RCF at 4 °C. Following centrifugation supernatant was immediately collected into labelled Protein LoBind Eppendorf Tubes and samples were maintained on ice while handling.

Separation of corona-coated liposomes from unbound and weakly bound proteins. Corona-coated liposomes were separated from excess plasma proteins by size exclusion chromatography followed by membrane ultrafiltration as we have previously described.^[4, 5]

Ex vivo protein corona formation. To investigate the *ex vivo* protein corona, Caelyx® liposomes were incubated with plasma samples obtained from the same 6 patients prior to Caelyx® infusion and from healthy donors. Considering the impact of the anti-coagulant agent on the formation of protein corona,^[43] the same protocol was followed for the preparation of plasma samples, as described above for the *in vivo* experiment (K2 EDTA BD Vacutainer® tubes, centrifugation for 12 minutes at 1300 RCF at 4 °C). The *ex vivo* protein corona was allowed to form using the same liposome concentration (0.15 mM) as that extracted in 1 mL of plasma from intravenously injected patients. Liposomes were incubated with plasma for 90 min at 37°C in orbital shaker at 250 rpm. The purification of the *ex vivo* corona-coated liposomes was performed as described above for the *in vivo* recovered liposomes.

Size and zeta potential measurements using dynamic light scattering (DLS). Liposome size and surface charge were measured using Zetasizer Nano ZS (Malvern, Instruments, UK).

Transmission Electron Microscopy (TEM). Liposomes were stained by uranyl acetate solution 1% and visualized with transmission electron microscopy (FEI Tecnai 12 BioTwin) before and after their *in vivo* interaction with plasma proteins. Samples were diluted to 0.5 mM lipid concentration and carbon Film Mesh Copper Grids (CF400-Cu, Electron Microscopy Science) were used.

Cryo-electron Microscopy. EM grids of liposomes were prepared in a FEI Vitrobot using 3µL of sample absorbed to freshly glow-discharged R 3.5/1 Quantifoil grids. Grids were blotted for 4-5 s in a 95% humidity chamber before plunge freezing in to liquid ethane. Data were imaged on a Tecnai T20 (FEI) electron microscope operating at 200 keV with a Gatan 626 cryo stage. Images were recorded on a 4K Gatan Ultrascan CCD camera under low-dose conditions between 0.5 and 2.0 µm defocus and at 3.8 Å/pixel and had a maximum electron dose of <25 electrons/Å².

SDS-PAGE electrophoresis. Proteins associated with 0.025 µM of liposomes were loaded onto a 4-20% NOVEX Tris-Glycine Protein Gel (ThermoFisher Scientific). The gel was run until the proteins neared the end of the gel (25-40 minutes at 225V). Staining was performed with Imperial Gel Staining reagent (Sigma Life Science).

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4 **Quantification of adsorbed proteins.** Proteins associated with recovered liposomes were quantified by
5 BCA Protein assay kit according to manufacturer's instructions. To make sure that liposomes in solution do
6 not interfere with the absorbance at 562 nm we measured the absorbance of corona-coated liposomes in
7 HBS buffer and subtract it from the total absorbance, measured when corona-coated liposomes were mixed
8 with the BCA reagent. Lipid concentration was quantified by Stewart assay and Pb values (μg of protein/ μM
9 lipid) were then calculated.

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11 **Mass Spectrometry.** In-gel digestion of corona (40ug) and plasma (5ul) proteins was performed prior to LC-
12 MS/MS analysis, as we have previously described.^[4-6] Digested samples were analysed by LC-MS/MS using
13 an UltiMate® 3000 Rapid Separation LC (RSLC, Dionex Corporation, Sunnyvale, CA) coupled to a Q
14 Exactive™ Hybrid Quadrupole-Orbitrap™ (Thermo Fisher Scientific, Waltham, MA) mass spectrometer. Data
15 produced were searched using Mascot (Matrix Science UK), against the SwissProt_2016_04 database with
16 taxonomy of [human] selected.

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18 The Scaffold software (version 4.3.2, Proteome Software Inc.) was used for relative protein quantification
19 based on spectral counting. Protein identifications were accepted if they could be established at greater than
20 99.0% probability and contained at least 2 identified peptides. Semi quantitative assessment of the protein
21 amounts was conducted using normalized spectral countings as previously described.^[4-6] Heatmaps of
22 Relative Protein Abundance (RPA) values were prepared using Plotly 2.0 software.

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24 **Statistical analysis.** Statistical analysis of the data was performed using GraphPad Prism software. One-
25 way analysis of variance (ANOVA) was used and p values <0.05 were considered significant.

26 27 28 29 **Data availability**

30 The authors declare that all relevant data supporting the findings of this study are available within the paper
31 and its supplementary information files.

32 33 34 **Author contributions**

35 M.H. initiated, designed and performed the experiments, analyzed all data and took responsibility for
36 planning and writing the manuscript. S. McA., G.G and C.T. aided in the collection of blood samples. D.K.
37 performed the Mass Spectrometry experiments. I.J.R. and A.C. contributed to the clinical design, provided
38 oversight of the ethical approval process and were responsible for access and storage of the samples in the
39 MCRC Biobank. Z.A-A and M.M provided intellectual input and experimental guidance at the initial stages of
40 the study. K. K. initiated, designed, directed, provided intellectual input throughout the study and contributed
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FIGURE LEGENDS

Figure 1: The effect of protein corona formation on the physicochemical characteristics and morphology of liposomes. (A) Schematic description of the experimental design. PEGylated, doxorubicin-encapsulated liposomes (Caelyx®) were infused intravenously in patients with recurrent ovarian carcinoma and subsequently recovered from the blood circulation immediately on completion of their first-ever cycle of Caelyx® treatment. Corona coated liposomes were isolated from blood components and protein corona was quantitatively and qualitatively characterized; (B) Table shows the mean diameter (nm), ζ -potential (mV) and polydispersity index (PDI) values of bare and corona-coated liposomes recovered from the blood circulation of 6 adenocarcinoma patients. Representative size and ζ -potential distributions of corona-coated liposomes recovered from Patient 1 are also shown; (C) Negative stain TEM and Cryo-EM imaging of liposomes after their I.V injection and recovery from ovarian carcinoma patients. All scale bars are 100nm.

Figure 2: Characterization of *in vivo* protein corona: (A) The total amount of proteins adsorbed *in vivo* onto liposomes recovered from the blood circulation of ovarian carcinoma patients. Pb values (μg of protein/ μM lipid) represent the mean and standard deviation from 6 patients; (B) Classification of the corona proteins identified according to their molecular mass; (C) Most-abundant proteins (top-20) identified in the protein corona of PEGylated doxorubicin-encapsulated liposomes by LC-MS/MS. Relative protein abundance (RPA) values represent the average and standard deviation from 6 ovarian carcinoma patients; (D) The relative percentage of immunoglobulins, lipoproteins and complement proteins identified in the protein corona. The percentage of relative protein abundance (%RPA) for each protein class represents the average from 6 ovarian carcinoma patients.

Figure 3: Blood-circulation proteome analysis: (A) Imperial stained SDS-PAGE gel of corona proteins associated with liposomes in the blood circulation of 6 ovarian carcinoma patients and plasma control; (B) Venn diagram reports the number of unique and common proteins between corona and plasma proteins and their respective overlaps as identified by LC-MS/MS. Proteins were identified in at least one of the six plasma and/or corona samples; (C) Heatmap of RPA (%) of corona and plasma proteins, as identified by LC-MS/MS. Only proteins with RPA>1% on at least one of the samples are shown. Protein-rows are sorted according to the RPA% values (from highest to lowest) of the first sample (plasma, patient 1). The full list of proteins identified and their respective accession numbers are shown in **Table S3** and **Table S4**.

FIGURE 1

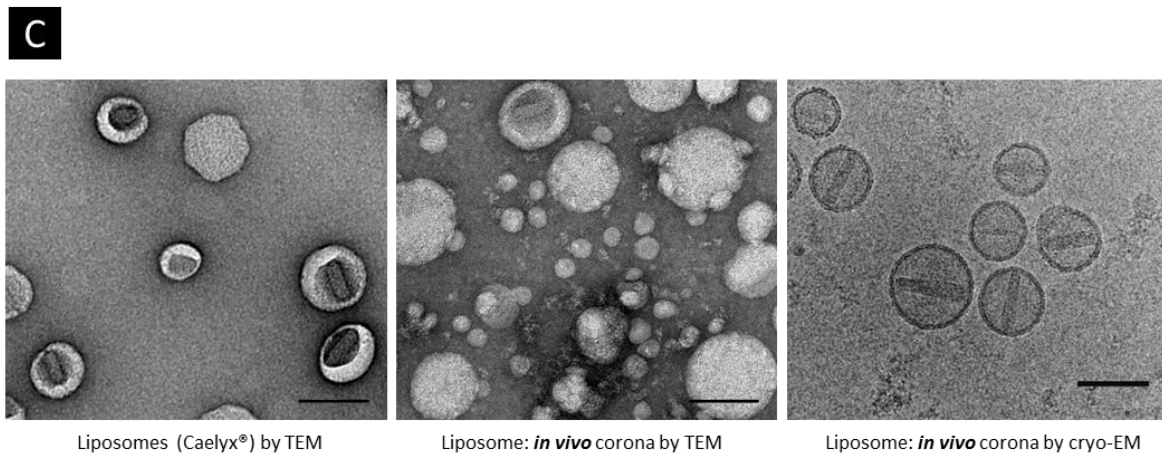
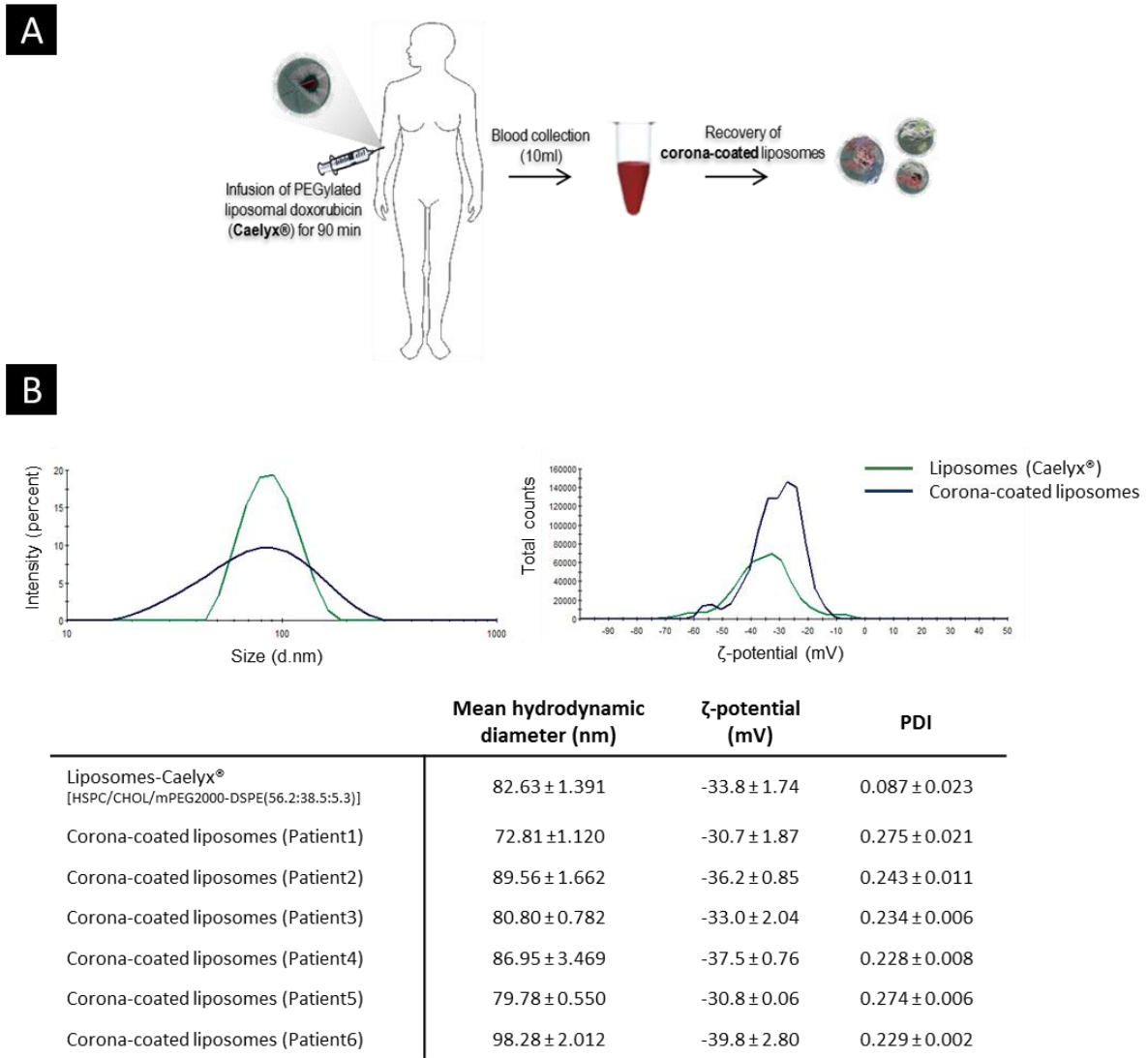
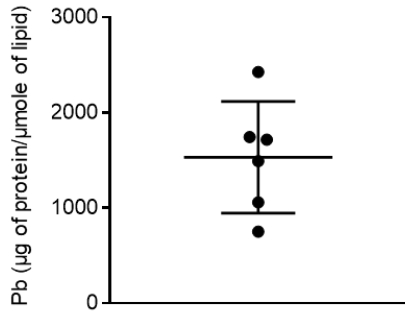
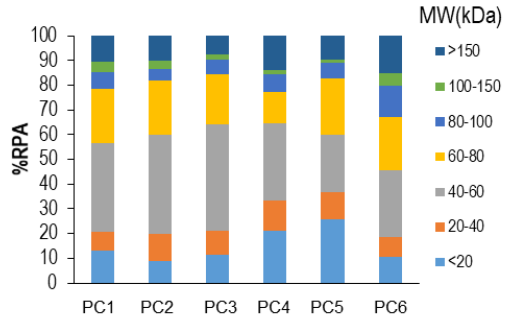


FIGURE 2

A



B



C

TOP 20 IDENTIFIED PROTEINS	RPA%
Full-length cDNA clone CS0DD006YL02 of Homo sapiens (human)	7.99 ± 2.48
Ig mu chain C region (A0A087X2C0)	5.70 ± 1.81
Ig mu chain C region (A0A087WYJ9)	4.56 ± 2.83
Alpha-2-macroglobulin	3.48 ± 1.02
Fibrinogen beta chain	3.45 ± 1.19
Fibrinogen alpha chain	2.98 ± 0.67
Apolipoprotein B (Including Ag(X) antigen)	2.64 ± 1.44
Serum albumin	2.47 ± 2.06
APOB protein	2.22 ± 2.10
Protein IGHV3-72	1.91 ± 0.58
C4b-binding protein alpha chain	1.74 ± 0.59
Fibrinogen gamma chain	1.59 ± 0.53
Haptoglobin (Fragment)	1.35 ± 0.34
Haptoglobin	1.35 ± 0.43
IGH protein	1.14 ± 0.64
Ig gamma-1 chain C region	1.12 ± 0.59
Uncharacterized protein (A8K008)	1.11 ± 0.59
Uncharacterized protein (Q6N089)	1.05 ± 0.60
IgG H chain	1.04 ± 0.64
Actin, cytoplasmic 2	1.04 ± 0.60

D

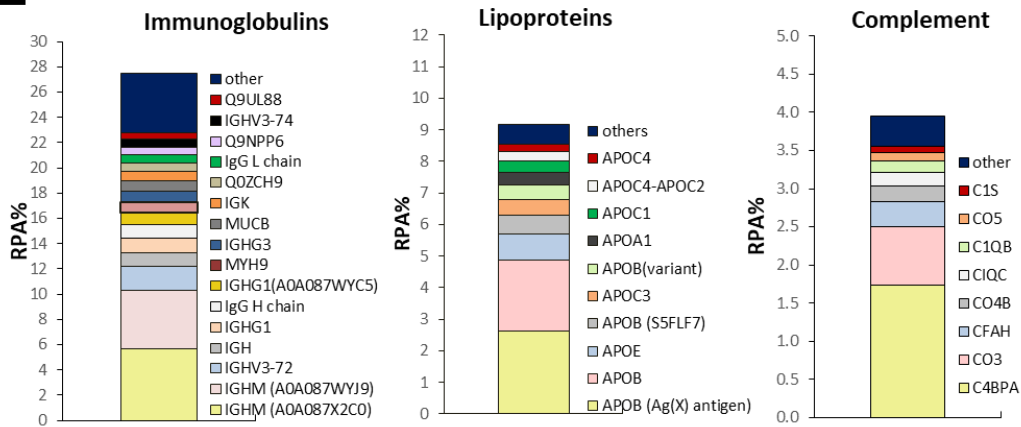
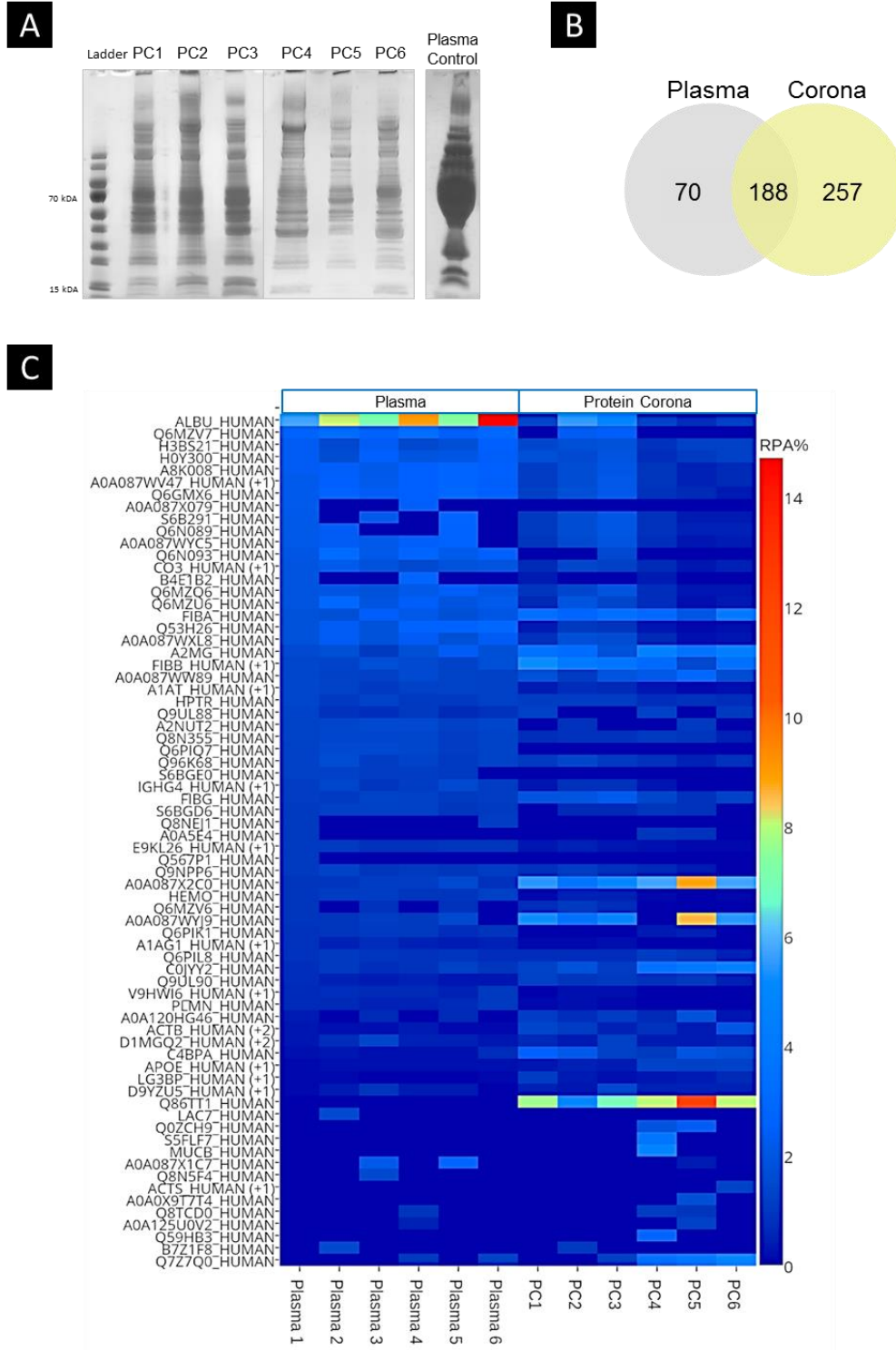


FIGURE 3



SUPPORTING INFORMATION

Supporting Figure 1

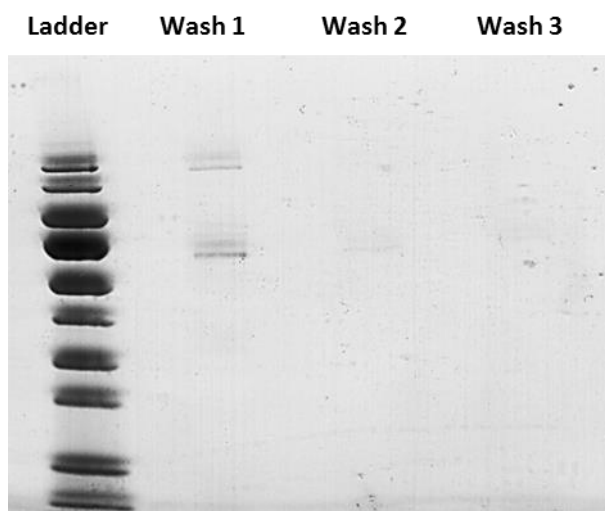


Figure S1: Separation of protein corona coated liposomes from unbound proteins. Corona-coated liposomes were separated from excess plasma proteins by size exclusion chromatography followed by membrane ultrafiltration. Immediately after plasma preparation, plasma samples were loaded onto a Sepharose CL-4B (SIGMA-ALDRICH) column (15x1.5cm) equilibrated with HBS. Fractions containing liposomes (fractions 4,5&6) were then pooled together and concentrated to 500 μ l by centrifugation using Vivaspin 6 column (10000 MWCO, Sartorius, Fisher Scientific) at 3000rpm. Vivaspin 500 centrifugal concentrator (1 000 000 MWCO, Sartorius, Fisher Scientific) was then used at 3000 rpm, to further concentrate the samples to 100 μ l and to ensure separation of protein-coated nanoparticles from the remaining large unbound proteins. This procedure results in the filtration of unbound proteins while corona-coated liposomes because of their higher MW remain at the top of the membrane. Imperial stained SDS-PAGE shows that any remaining proteins in Chromatographic Fractions 4,5 and 6 were removed to the filtrate of Viva Spin (wash1) and no proteins remained at the top of the membrane (column residue). Column residue was washed 2 more time with HBS to ensure complete purification.

Supporting Figure 2

<i>Ex vivo</i>	Mean hydrodynamic diameter (nm)	ζ -potential (mV)	PDI
Corona-coated liposomes (Patient1)	73.80 ± 1.518	-32.1 ± 3.50	0.161 ± 0.005
Corona-coated liposomes (Patient2)	72.28 ± 1.095	-30.2 ± 2.97	0.227 ± 0.006
Corona-coated liposomes (Patient3)	75.05 ± 1.500	-37.2 ± 1.80	0.149 ± 0.005
Corona-coated liposomes (Patient4)	97.88 ± 1.980	-27.8 ± 3.91	0.244 ± 0.015
Corona-coated liposomes (Patient5)	86.61 ± 1.393	-28.7 ± 0.40	0.238 ± 0.006
Corona-coated liposomes (Patient6)	98.03 ± 1.812	-40.9 ± 2.51	0.237 ± 0.007

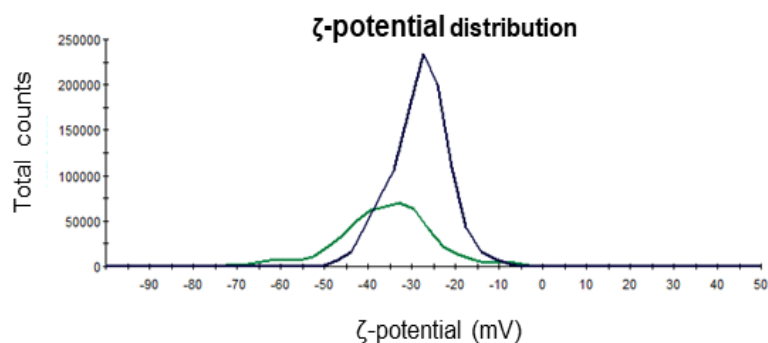
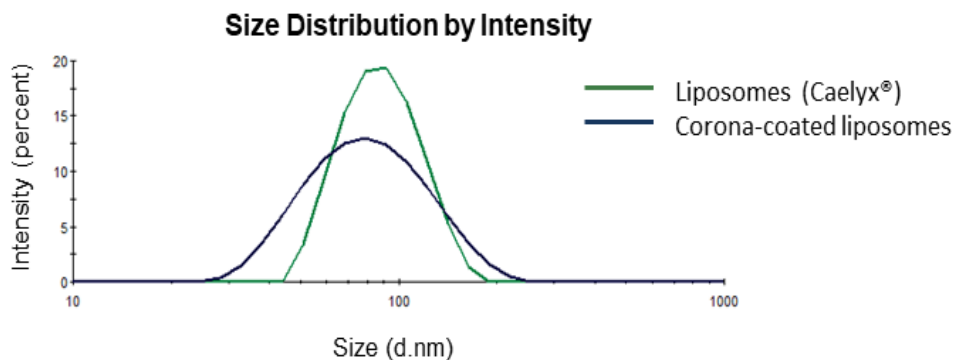


Figure S2: The effect of the *ex vivo* formed protein corona on the physicochemical characteristics of liposomes. Mean diameter (nm), ζ -potential (mV) and polydispersity index (PDI) values and representative size and ζ -potential distributions of bare and corona-coated liposomes incubated *ex vivo* with plasma samples obtained from 6 ovarian adenocarcinoma patient.

Supporting Figure 3

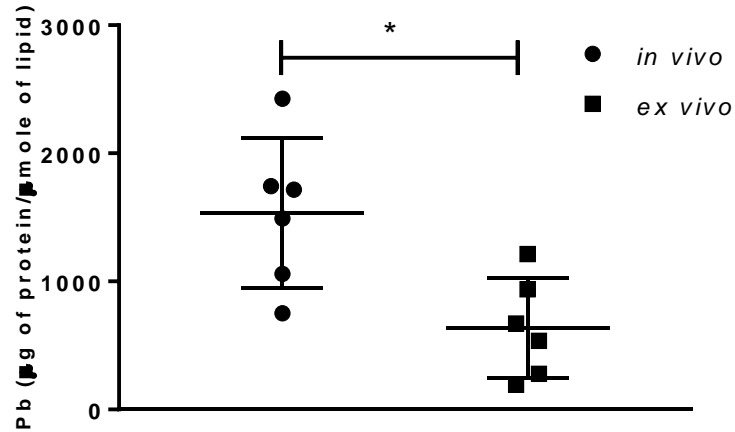


Figure S3: Comparison of *in vivo* vs. *ex vivo* protein coronas. The total amount of proteins adsorbed onto liposomes *in vivo* after recovery from the blood circulation of ovarian carcinoma patients and after their *ex vivo* incubation with plasma samples obtained from the same patients before the infusion of Caelyx®. Pb values (µg of protein/µM lipid) represent the mean and standard deviation from 6 patients; ** indicates $p < 0.01$ ($p = 0.0086$); * indicates $p < 0.05$ ($p = 0.0111$).

Supporting Figure 4

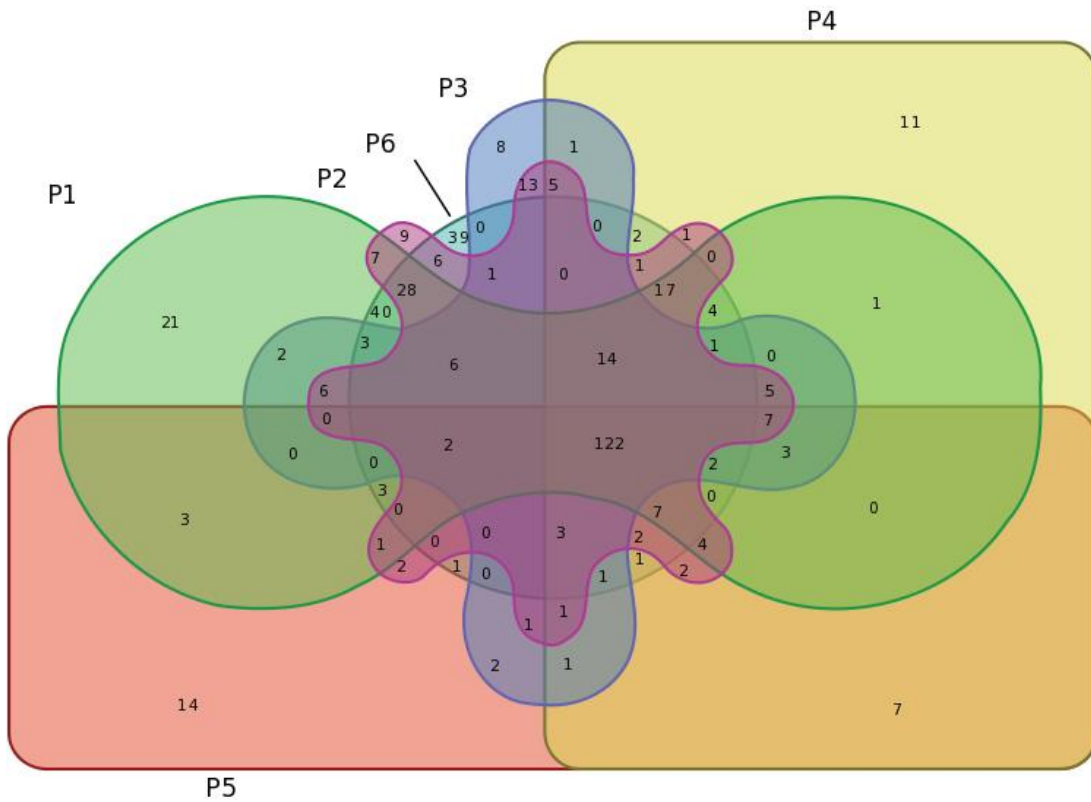


Figure S4: Characterisation of the *in vivo* protein corona: Venn diagram reports the number of unique and common proteins between the liposomal coronas formed in 6 ovarian carcinoma patients and their respective overlaps as identified by LC-MS/MS. The full list of common proteins identified in the liposomal protein corona in all 6 ovarian carcinoma patients are shown in Tables S5.

Supporting Figure 5

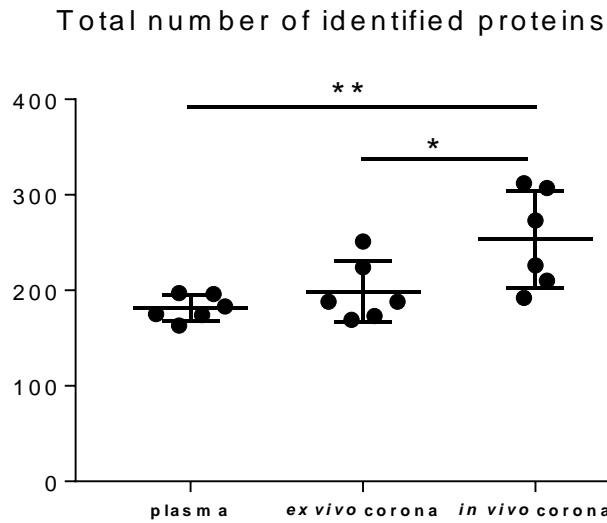


Figure S5: Blood-circulation proteome analysis. Total number of proteins identified by mass spectrometry analysis of plasma samples obtained from ovarian carcinoma patients and corona samples formed *ex vivo* and *in vivo*. Values represent the mean and standard deviation from 6 patients; * indicates $p < 0.05$ ($p = 0.0459$) and ** indicates $p < 0.01$ ($p = 0.0087$).

Supporting Table 1

Table S1: Patient cohort clinical and basic blood characteristics.

Age (yrs)	Median 71 (56-77)
Prior lines of chemotherapy	Median 2 (range 2-3)
Histological subtype	High grade serous carcinoma- 5 Moderately differentiated carcinoma NOS-1
FIGO stage at diagnosis	IIIC-5 IVA-1
Baseline CA125 (at commencement of Caelyx) (U/ml)	Median 665 (103-3081)
Albumin (at commencement of Caelyx) (g/L)	Median 41 (30-44)
Total protein (at commencement of Caelyx) (g/L)	Median 68 (56-72)

Supporting Table 2

Table S2: Most-abundant proteins (top-20) identified by LC-MS/MS in the protein corona of PEGylated liposomal doxorubicin, recovered from 6 different ovarian carcinoma patients.

Patient 1		Patient 2	
Identified Proteins	RPA%	Identified Proteins	RPA%
1 Full-length cDNA clone CS0DD006YL02	7.68	Serum albumin	5.47
2 Ig mu chain C region(A0A087X2C0)	5.42	Full-length cDNA clone CS0DD006YL02	4.90
3 Ig mu chain C region(A0A087WYJ9)	5.17	Fibrinogen beta chain	3.95
4 Fibrinogen beta chain	5.17	Ig mu chain C region(A0A087X2C0)	3.53
5 Alpha-2-macroglobulin	3.49	Ig mu chain C region(A0A087WYJ9)	3.40
6 Fibrinogen alpha chain	3.25	Alpha-2-macroglobulin	3.12
7 C4b-binding protein alpha chain	2.55	Fibrinogen alpha chain	2.70
8 Fibrinogen gamma chain	1.92	Putative uncharacterized protein DKFZp686C11235	2.33
9 Protein IGHV3-72	1.84	C4b-binding protein alpha chain	2.10
10 Haptoglobin	1.65	Fibrinogen gamma chain	1.91
11 Haptoglobin (Fragment)	1.41	Putative uncharacterized protein DKFZp686C15213	1.90
12 Actin, cytoplasmic 2	1.40	Apolipoprotein B (Including Ag(X) antigen)	1.74
13 Serum albumin	1.36	Ig gamma-3 chain C region	1.69
14 Apolipoprotein B (Including Ag(X) antigen)	1.31	IGH protein	1.67
15 Myosin-reactive immunoglobulin heavy chain variable region	1.18	Haptoglobin (Fragment)	1.66
16 IGH protein	1.16	Ig gamma-1 chain C region	1.61
17 Myosin-reactive immunoglobulin heavy chain variable region (Fragment)	1.15	Uncharacterized protein (Q6N089)	1.57
18 GCT-A10 heavy chain variable region (Fragment)	1.14	IgG H chain	1.56
19 Uncharacterized protein (A8K008)	1.13	Uncharacterized protein(A8K008)	1.54
20 Lectin galactoside-binding soluble 3 binding protein isoform 1 (Fragment)	1.11	Haptoglobin	1.49

Patient 3		Patient 4	
Identified Proteins	RPA %	Identified Proteins	RPA %
1 Full-length cDNA clone CS0DD006YL02	6.91	Full-length cDNA clone CS0DD006YL02	7.99
2 Ig mu chain C region(A0A087X2C0)	4.81	Ig mu chain C region(A0A087X2C0)	5.69
3 Serum albumin	4.72	Ig mu heavy chain disease protein	4.68
4 Ig mu chain C region(A0A087WYJ9)	4.66	Alpha-2-macroglobulin	4.55
5 Fibrinogen beta chain	3.60	Lipoprotein B (Fragment)	3.64
6 Fibrinogen alpha chain	3.28	APOB protein	3.42
7 Putative uncharacterized protein DKFZp686C11235	2.38	Apolipoprotein B (Including Ag(X) antigen)	3.37
8 Fibrinogen gamma chain	2.22	Fibrinogen beta chain	3.05
9 IGH protein	2.11	Fibrinogen alpha chain	2.77
10 Ig gamma-1 chain C region	2.03	Apolipoprotein B variant (Fragment)	2.68
11 IgG H chain	2.03	Protein IGHV3-72	2.11
12 Uncharacterized protein (A8K008)	2.02	Immunoglobulin heavy chain variable region (Fragment)	1.86
13 Uncharacterized protein (Q6N089)	1.96	Fibrinogen gamma chain	1.45
14 Haptoglobin	1.92	Apolipoprotein E isoform 1 (Fragment)	1.34
15 Ig gamma-1 chain C region	1.91	Serum albumin	1.32
16 Protein IGHV3-72	1.90	Immunoglobulin light chain (Fragment)	1.23
17 Putative uncharacterized protein DKFZp686G11190	1.84	Myosin-reactive immunoglobulin heavy chain variable region (Fragment)	1.17
18 Haptoglobin (Fragment)	1.77	IGK protein	1.10
19 Alpha-2-macroglobulin	1.76	Lambda-chain (AA -20 to 215)	1.02
20 Ig gamma-3 chain C region	1.59	C4b-binding protein alpha chain	0.98

Patient 5		Patient 6	
Identified Proteins	RPA%	Identified Proteins	RPA%
1 Full-length cDNA clone CS0DD006YL02	12.44	Full-length cDNA clone CS0DD006YL02	8.00
2 Ig mu chain C region(A0A087X2C0)	8.99	Ig mu chain C region(A0A087X2C0)	5.76
3 Ig mu chain C region(A0A087WYJ9)	8.65	Ig mu chain C region(A0A087WYJ9)	5.46
4 Apolipoprotein B (Including Ag(X) antigen)	3.79	APOB protein	4.92
5 APOB protein	3.79	Apolipoprotein B (Including Ag(X) antigen)	4.52
6 Alpha-2-macroglobulin	3.48	Alpha-2-macroglobulin	4.45
7 Protein IGHV3-72	2.85	Fibrinogen alpha chain	3.93
8 Immunoglobulin heavy chain variable region (Fragment)	2.28	Fibrinogen beta chain	3.43
9 Fibrinogen alpha chain	1.96	Actin, cytoplasmic 2	2.00
10 C4b-binding protein alpha chain	1.95	C4b-binding protein alpha chain	1.66
11 GCT-A10 heavy chain variable region (Fragment)	1.80	Protein IGHV3-72	1.60
12 MS-D3 heavy chain variable region (Fragment)	1.74	Actin, alpha skeletal muscle	1.32
13 Fibrinogen beta chain	1.52	Fibrinogen gamma chain	1.31
14 Haptoglobin (Fragment)	1.24	Apolipoprotein E isoform 1 (Fragment)	1.26
15 GCT-A1 heavy chain variable region (Fragment)	1.23	Serum albumin	1.25
16 Apolipoprotein E isoform 1 (Fragment)	1.20	Haptoglobin	1.22
17 Haptoglobin	1.06	Haptoglobin (Fragment)	1.22
18 Immunoglobulin light chain (Fragment)	1.03	Apolipoprotein C-III	1.07
19 Myosin-reactive immunoglobulin heavy chain variable region (Fragment)	0.99	Myosin-reactive immunoglobulin heavy chain variable region (Fragment)	0.97
20 Lambda-chain (AA -20 to 215)	0.97	Vinculin, isoform CRA_c	0.94

Supporting Table 3

Table S3: Characterization of *in vivo* protein corona. Full list of all the proteins identified in the liposomal protein corona recovered from 6 ovarian carcinoma patients (across all samples).

#	Identified Proteins	Accession Number	MW	RPA% (P1)	RPA% (P2)	RPA% (P3)	RPA% (P4)	RPA% (P5)	RPA% (P6)	Average RPA%	STV
1	Full-length cDNA clone CS0DD006YL02 of Homo sapiens (human) OS=Homo sapiens PE=2 SV=1	Q86TT1_HUMAN	41	7.680	4.897	6.908	7.987	12.443	7.997	7.985	2.476
2	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=1	A0A087X2C0_HUMAN	64	5.419	3.529	4.812	5.693	8.994	5.756	5.701	1.813
3	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=1	A0A087WYJ9_HUMAN	66	5.174	3.402	4.659	0.000	8.654	5.457	4.558	2.831
4	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	A2MG_HUMAN	163	3.494	3.119	1.758	4.549	3.482	4.448	3.475	1.018
5	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	FIBB_HUMAN (+1)	56	5.166	3.952	3.604	3.050	1.524	3.431	3.454	1.191
6	Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	FIBA_HUMAN	95	3.253	2.704	3.282	2.766	1.964	3.927	2.983	0.666
7	Apolipoprotein B (Including Ag(X) antigen) OS=Homo sapiens GN=APOB PE=4 SV=1	C0JYY2_HUMAN	516	1.309	1.744	1.096	3.368	3.794	4.518	2.638	1.439
8	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	ALBU_HUMAN	69	1.359	5.469	4.718	1.320	0.692	1.252	2.468	2.062
9	APOB protein OS=Homo sapiens GN=APOB PE=2 SV=1	Q7Z7Q0_HUMAN	92	0.000	0.000	1.205	3.421	3.786	4.924	2.223	2.102
10	Protein IGHV3-72 OS=Homo sapiens GN=IGHV3-72 PE=1 SV=1	A0A087WW89_HUMAN	11	1.840	1.120	1.904	2.112	2.853	1.602	1.905	0.575
11	C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2	C4BPA_HUMAN	67	2.553	2.098	1.179	0.979	1.953	1.657	1.736	0.589
12	Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	FIBG_HUMAN	52	1.916	1.913	2.224	1.445	0.757	1.311	1.594	0.530
13	Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=1 SV=1	H3BS21_HUMAN	25	1.407	1.661	1.771	0.820	1.238	1.222	1.353	0.343
14	Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=4	H0Y300_HUMAN	49	1.653	1.490	1.923	0.734	1.056	1.223	1.347	0.429
15	IGH@ protein OS=Homo sapiens GN=IGH@ PE=1 SV=1	Q6GMX6_HUMAN	51	1.160	1.673	2.109	0.813	0.650	0.438	1.140	0.643
16	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	A0A087WV47_HUMAN (+1)	51	1.055	1.611	2.035	0.893	0.529	0.611	1.122	0.590
17	Uncharacterized protein OS=Homo sapiens PE=1 SV=1	A8K008_HUMAN	52	1.127	1.545	2.023	0.928	0.502	0.565	1.115	0.587
18	Uncharacterized protein OS=Homo sapiens GN=DKFZp686P15220 PE=1 SV=1	Q6N089_HUMAN	52	1.035	1.571	1.959	0.797	0.468	0.497	1.054	0.601
19	IgG H chain OS=Homo sapiens PE=1 SV=1	S6B291_HUMAN	51	1.013	1.557	2.025	0.795	0.451	0.415	1.043	0.638
20	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1	ACTG_HUMAN (+1)	42	1.395	1.141	0.453	0.835	0.421	2.001	1.041	0.605
21	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	A0A087WYC5_HUMAN	52	0.932	1.474	1.913	0.718	0.340	0.373	0.958	0.626
22	GCT-A10 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A120HG46_HUMAN	14	1.142	0.717	1.088	0.651	1.800	0.336	0.956	0.510
23	cDNA FLJ14473 fis, clone MAMMA1001080, highly similar to Homo sapiens SNC73 protein (SNC73) mRNA OS=Homo sapiens PE=2 SV=1	Q96K68_HUMAN	53	1.045	1.412	1.015	0.851	0.551	0.776	0.942	0.292
24	Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=2 SV=2	HPTR_HUMAN	39	1.093	1.135	1.135	0.654	0.816	0.738	0.929	0.217
25	Putative uncharacterized protein DKFZp686G11190 OS=Homo sapiens GN=DKFZp686G11190 PE=2 SV=1	Q6MZQ6_HUMAN	52	0.891	1.404	1.840	0.692	0.323	0.350	0.917	0.602
26	Myosin-reactive immunoglobulin heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	Q9UL90_HUMAN	12	1.154	0.875	0.992	0.759	0.995	0.539	0.885	0.215
27	Putative uncharacterized protein DKFZp686C15213 OS=Homo sapiens GN=DKFZp686C15213 PE=2 SV=1	Q6MZU6_HUMAN	51	0.606	1.897	1.363	0.679	0.251	0.415	0.868	0.631
28	Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=1	A0A087WXL8_HUMAN	57	0.794	1.689	1.587	0.599	0.202	0.289	0.860	0.640
29	Apolipoprotein E isoform 1 (Fragment) OS=Homo sapiens GN=APOE PE=2 SV=1	A0A0S2Z3D5_HUMAN (+1)	36	0.281	0.482	0.410	1.341	1.203	1.257	0.829	0.486
30	Putative uncharacterized protein DKFZp686C11235 OS=Homo sapiens GN=DKFZp686C11235 PE=2 SV=1	Q6MZV7_HUMAN	52	0.000	2.325	2.380	0.000	0.000	0.000	0.784	1.215
31	Ig mu heavy chain disease protein OS=Homo sapiens PE=1 SV=1	MUCB_HUMAN	43	0.000	0.000	0.000	4.682	0.000	0.000	0.780	1.911
32	IGK@ protein OS=Homo sapiens GN=IGK@ PE=1 SV=1	Q6PIL8_HUMAN	26	0.676	0.702	0.677	1.104	0.952	0.520	0.772	0.214
33	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	CO3_HUMAN (+1)	187	0.635	1.376	1.184	0.636	0.260	0.512	0.767	0.425
34	Immunoglobulin heavy chain variable region (Fragment) OS=Homo sapiens PE=4 SV=1	Q0ZCH9_HUMAN	13	0.000	0.000	0.000	1.857	2.278	0.000	0.689	1.076
35	Beta-globin OS=Homo sapiens GN=HBB PE=3 SV=1	D9YZU5_HUMAN (+1)	16	0.499	0.314	1.517	0.541	0.470	0.477	0.636	0.438
36	MS-D4 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A0X9UWK7_HUMAN	14	0.495	0.587	0.612	0.553	0.884	0.630	0.627	0.135

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37	IgG L chain OS=Homo sapiens PE=1 SV=1	S6BGD6_HUMAN	25	0.490	0.621	0.628	0.893	0.760	0.353	0.624	0.191
38	Immunoglobulin heavy chain variant (Fragment) OS=Homo sapiens PE=2 SV=1	Q9NPP6_HUMAN	45	0.781	1.105	0.804	0.617	0.413	0.000	0.620	0.380
39	Anti-FactorVIII scFv (Fragment) OS=Homo sapiens PE=2 SV=1	A2KBC6_HUMAN	25	0.725	0.456	0.666	0.747	0.831	0.235	0.610	0.223
40	Lipoprotein B (Fragment) OS=Homo sapiens GN=APOB PE=4 SV=1	S5FLF7_HUMAN	10	0.000	0.000	0.000	3.644	0.000	0.000	0.607	1.488
41	Lambda-chain (AA -20 to 215) OS=Homo sapiens PE=1 SV=1	A2NUT2_HUMAN	25	0.000	0.803	0.819	1.020	0.973	0.000	0.602	0.474
42	Mutant hemoglobin alpha 2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	A0A0K2BMD8_HUMAN (+2)	15	0.604	0.365	1.174	0.395	0.442	0.548	0.588	0.301
43	Protein IGHV3-74 (Fragment) OS=Homo sapiens GN=IGHV3-74 PE=1 SV=1	A0A0B4J1X5_HUMAN	13	0.656	0.421	0.586	0.596	0.918	0.316	0.582	0.207
44	Protein S isoform 1 (Fragment) OS=Homo sapiens GN=PROS1 PE=2 SV=1	A0A0S2Z4K3_HUMAN (+2)	75	0.838	0.560	0.374	0.425	0.542	0.705	0.574	0.173
45	Myosin-reactive immunoglobulin heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	Q9UL88_HUMAN	14	1.180	0.000	0.000	1.171	0.000	0.965	0.553	0.610
46	Lectin galactoside-binding soluble 3 binding protein isoform 1 (Fragment) OS=Homo sapiens GN=LGALS3BP PE=2 SV=1	A0A0S2Z3Y1_HUMAN (+1)	65	1.115	0.414	0.242	0.343	0.354	0.560	0.505	0.317
47	Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=2 SV=1	A3KPE2_HUMAN (+2)	11	0.145	0.166	0.173	0.828	0.643	1.068	0.504	0.399
48	cDNA FLJ53691, highly similar to Serotransferrin OS=Homo sapiens PE=2 SV=1	B4E1B2_HUMAN	75	0.376	1.028	0.920	0.352	0.088	0.235	0.500	0.383
49	cDNA, FLJ94213, highly similar to Homo sapiens pregnancy-zone protein (PZP), mRNA OS=Homo sapiens PE=2 SV=1	B2R950_HUMAN (+1)	164	0.481	0.545	0.360	0.592	0.466	0.516	0.493	0.079
50	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	TSP1_HUMAN	129	0.785	0.350	0.244	0.300	0.363	0.852	0.482	0.264
51	Protein IGHV5-51 (Fragment) OS=Homo sapiens GN=IGHV5-51 PE=1 SV=1	A0A0C4DH38_HUMAN	13	0.451	0.421	0.439	0.420	0.680	0.407	0.470	0.104
52	Vinculin, isoform CRA_c OS=Homo sapiens GN=VCL PE=4 SV=1	A0A024QZN4_HUMAN (+2)	117	0.610	0.378	0.228	0.358	0.227	0.944	0.458	0.277
53	Fibronectin 1, isoform CRA_n OS=Homo sapiens GN=FN1 PE=4 SV=1	A0A024R462_HUMAN	259	0.485	0.384	0.351	0.378	0.469	0.665	0.455	0.116
54	Apolipoprotein B variant (Fragment) OS=Homo sapiens PE=2 SV=1	Q59HB3_HUMAN	184	0.000	0.000	0.000	2.681	0.000	0.000	0.447	1.094
55	Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1	H6VRF8_HUMAN (+3)	66	0.452	0.512	0.346	0.545	0.342	0.418	0.436	0.084
56	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	FLNA_HUMAN	281	0.595	0.351	0.212	0.311	0.160	0.889	0.420	0.275
57	Putative uncharacterized protein DKFZp686L19235 OS=Homo sapiens GN=DKFZp686L19235 PE=2 SV=1	Q6MZV6_HUMAN	52	0.738	1.000	0.741	0.000	0.000	0.000	0.413	0.463
58	Ig heavy chain V-III region BUT OS=Homo sapiens PE=1 SV=1	HV306_HUMAN	12	0.355	0.266	0.238	0.493	0.774	0.343	0.412	0.198
59	IBM-B2 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A125QYY9_HUMAN	14	0.381	0.554	0.000	0.423	0.726	0.378	0.410	0.241
60	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	A1AT_HUMAN (+1)	47	0.442	0.738	0.638	0.291	0.150	0.200	0.410	0.239
61	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	TLN1_HUMAN	270	0.610	0.370	0.213	0.317	0.170	0.775	0.409	0.236
62	Actinin, alpha 1, isoform CRA_a OS=Homo sapiens GN=ACTN1 PE=4 SV=1	A0A024R694_HUMAN (+1)	103	0.672	0.443	0.194	0.301	0.146	0.673	0.405	0.231
63	Apolipoprotein A-I, isoform CRA_a OS=Homo sapiens GN=APOA1 PE=4 SV=1	A0A024R3E3_HUMAN (+1)	31	0.395	0.442	0.461	0.544	0.242	0.303	0.398	0.110
64	Transferrin variant (Fragment) OS=Homo sapiens PE=2 SV=1	Q53H26_HUMAN	77	0.374	1.037	0.940	0.000	0.000	0.000	0.392	0.485
65	von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4	VWF_HUMAN	309	0.760	0.347	0.421	0.124	0.132	0.546	0.388	0.246
66	Ig gamma-4 chain C region (Fragment) OS=Homo sapiens GN=IGHG4 PE=1 SV=2	A0A0G2JPD4_HUMAN (+1)	36	0.340	0.837	0.820	0.316	0.000	0.000	0.386	0.373
67	von Willebrand factor OS=Homo sapiens GN=VWF PE=4 SV=1	L8E853_HUMAN	298	0.771	0.358	0.441	0.000	0.138	0.592	0.383	0.284
68	Immunoglobulin light chain (Fragment) OS=Homo sapiens PE=1 SV=1	Q0KKI6_HUMAN (+1)	24	0.000	0.000	0.000	1.234	1.032	0.000	0.378	0.588
69	Rheumatoid factor RF-ET9 (Fragment) OS=Homo sapiens PE=2 SV=1	A2J1N6_HUMAN	13	0.000	0.000	0.586	0.876	0.748	0.000	0.368	0.414
70	Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4	F13A_HUMAN	83	0.558	0.341	0.247	0.181	0.117	0.722	0.361	0.234
71	Apolipoprotein C-I, isoform CRA_a OS=Homo sapiens GN=APOC1 PE=4	A0A024R0T8_HUMAN (+2)	9	0.000	0.355	0.000	0.708	0.540	0.522	0.354	0.296

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72	Rheumatoid factor RF-ET6 (Fragment) OS=Homo sapiens PE=2 SV=1	A2J1N5_HUMAN	10	0.479	0.319	0.238	0.410	0.619	0.000	0.344	0.214	
73	Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	CFAH_HUMAN	139	0.383	0.473	0.394	0.295	0.162	0.241	0.325	0.114	
74	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	K1C10_HUMAN	59	0.370	0.325	0.202	0.440	0.187	0.299	0.304	0.097	
75	Protein APOC4-APOC2 OS=Homo sapiens GN=APOC4-APOC2 PE=1 SV=1	K7ER74_HUMAN	20	0.160	0.205	0.119	0.387	0.398	0.529	0.300	0.162	
76	MS-D3 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A0X9T7T4_HUMAN	15	0.000	0.000	0.000	0.000	1.739	0.000	0.290	0.710	
77	Ig heavy chain V-III region WEA OS=Homo sapiens PE=1 SV=1	HV302_HUMAN	12	0.444	0.000	0.238	0.455	0.589	0.000	0.288	0.250	
78	Uncharacterized protein OS=Homo sapiens PE=2 SV=1	A0A5E4_HUMAN	25	0.000	0.000	0.000	0.893	0.831	0.000	0.287	0.446	
79	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	K1C9_HUMAN	62	0.361	0.302	0.200	0.389	0.171	0.227	0.275	0.089	
80	cDNA FLJ75066, highly similar to Homo sapiens complement component 1, r subcomponent (C1R), mRNA OS=Homo sapiens PE=2 SV=1	A8K5J8_HUMAN (+1)	80	0.400	0.285	0.280	0.199	0.177	0.272	0.269	0.078	
81	Epididymis tissue protein Li 173 OS=Homo sapiens GN=SERPING1 PE=2 SV=1	E9KL26_HUMAN (+1)	55	0.281	0.490	0.338	0.248	0.080	0.150	0.264	0.144	
82	Myosin, heavy polypeptide 9, non-muscle, isoform CRA_a OS=Homo sapiens GN=MYH9 PE=4 SV=1	A0A024R1N1_HUMAN (+1)	227	0.439	0.123	0.103	0.209	0.082	0.626	0.264	0.221	
83	Cryocryoglobulin CC1 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	B1N7B6_HUMAN	13	0.410	0.316	0.000	0.315	0.510	0.000	0.259	0.213	
84	Putative uncharacterized protein DKFZp686i04196 (Fragment) OS=Homo sapiens GN=DKFZp686i04196 PE=2 SV=1	Q6N093_HUMAN	46	0.000	0.000	1.469	0.000	0.000	0.000	0.245	0.600	
85	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	HSP7C_HUMAN (+1)	71	0.330	0.296	0.094	0.148	0.062	0.480	0.235	0.161	
86	Apolipoprotein C-IV OS=Homo sapiens GN=APOC4 PE=2 SV=1	A5YAK2_HUMAN	15	0.000	0.091	0.000	0.334	0.472	0.509	0.234	0.233	
87	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	HEMO_HUMAN	52	0.143	0.527	0.449	0.105	0.043	0.079	0.224	0.208	
88	Epididymis secretory protein Li 52 OS=Homo sapiens GN=HEL-S-52 PE=2 SV=1	V9HWG7_HUMAN (+1)	66	0.347	0.228	0.115	0.110	0.067	0.454	0.220	0.153	
89	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1	ACTS_HUMAN (+1)	42	0.000	0.000	0.000	0.000	0.000	1.315	0.219	0.537	
90	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	K22E_HUMAN	65	0.295	0.225	0.154	0.294	0.109	0.217	0.216	0.075	
91	Putative uncharacterized protein DKFZp686M08189 OS=Homo sapiens GN=DKFZp686M08189 PE=2 SV=1	Q6MZX9_HUMAN	52	0.697	0.000	0.000	0.587	0.000	0.000	0.214	0.333	
92	Fermitin family homolog 3 OS=Homo sapiens GN=FERMT3 PE=1 SV=1	URP2_HUMAN	76	0.273	0.150	0.132	0.192	0.064	0.456	0.211	0.139	
93	Complement C4-B OS=Homo sapiens GN=C4B PE=1 SV=2	CO4B_HUMAN	193	0.177	0.331	0.289	0.177	0.103	0.174	0.208	0.085	
94	Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4	KPYM_HUMAN (+1)	58	0.340	0.252	0.148	0.133	0.038	0.334	0.208	0.121	
95	GCT-A1 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A125U0V2_HUMAN	14	0.000	0.000	0.000	0.000	1.231	0.000	0.205	0.503	
96	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	GELS_HUMAN	86	0.304	0.202	0.144	0.148	0.087	0.328	0.202	0.095	
97	cDNA FLJ32131 fis, clone PEBLM2000267, highly similar to Tubulin alpha-ubiquitous chain OS=Homo sapiens PE=2 SV=1	B3KPS3_HUMAN (+2)	46	0.359	0.139	0.197	0.139	0.000	0.307	0.190	0.129	
98	cDNA FLJ56821, highly similar to Inter- alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens PE=2 SV=1	B7Z549_HUMAN (+1)	76	0.154	0.312	0.194	0.204	0.081	0.178	0.187	0.075	
99	CD5 antigen-like OS=Homo sapiens GN=CD5L PE=1 SV=1	CD5L_HUMAN	38	0.210	0.216	0.301	0.156	0.163	0.077	0.187	0.075	
100	Ig heavy chain V-III region GAL OS=Homo sapiens PE=1 SV=1	HV320_HUMAN	13	0.000	0.491	0.000	0.000	0.612	0.000	0.184	0.287	
101	Immunoglobulin heavy chain variable region (Fragment) OS=Homo sapiens PE=4 SV=1	Q0ZCH6_HUMAN	14	0.228	0.163	0.170	0.163	0.253	0.126	0.184	0.047	
102	Complement component 1, q subcomponent, C chain, isoform CRA_a OS=Homo sapiens GN=C1QC PE=4 SV=1	A0A024RAA7_HUMAN (+1)	26	0.164	0.193	0.146	0.193	0.153	0.226	0.179	0.030	
103	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	TBA4A_HUMAN	50	0.341	0.091	0.171	0.109	0.062	0.294	0.178	0.115	

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104	Actinin alpha 4 isoform 1 (Fragment) OS=Homo sapiens GN=ACTN4 PE=2 SV=1	A0A0S2Z3G9_HUMAN (+1)	105	0.416	0.230	0.000	0.108	0.000	0.308	0.177	0.170
105	cDNA FLJ53487, highly similar to Coagulation factor XIII A chain (EC 2.3.2.13) OS=Homo sapiens PE=2 SV=1	B4E2L8_HUMAN	70	0.000	0.274	0.000	0.169	0.000	0.579	0.170	0.230
106	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	PROF1_HUMAN	15	0.213	0.274	0.000	0.121	0.000	0.392	0.167	0.156
107	Immunoglobulin heavy chain variable region (Fragment) OS=Homo sapiens PE=4 SV=1	Q0ZCF6_HUMAN	15	0.213	0.122	0.127	0.243	0.295	0.000	0.167	0.106
108	cDNA FLJ35730 fis, clone TESTI2003131, highly similar to ALPHA-1- ANTICHYMOTRYPSIN OS=Homo sapiens PE=2 SV=1	B3KS79_HUMAN	51	0.146	0.340	0.289	0.089	0.061	0.069	0.166	0.120
109	cDNA FLJ53025, highly similar to Complement C4-B OS=Homo sapiens PE=2 SV=1	B7Z1F8_HUMAN	30	0.000	0.989	0.000	0.000	0.000	0.000	0.165	0.404
110	Immunoglobulin J chain OS=Homo sapiens GN=JCHAIN PE=1 SV=4	IGJ_HUMAN	18	0.178	0.127	0.079	0.202	0.270	0.131	0.164	0.067
111	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	GRP78_HUMAN (+1)	72	0.259	0.165	0.033	0.076	0.031	0.375	0.156	0.139
112	Inter-alpha (Globulin) inhibitor H2 OS=Homo sapiens GN=ITI2H PE=2 SV=1	A2RTY6_HUMAN (+3)	106	0.131	0.241	0.166	0.163	0.079	0.155	0.156	0.053
113	IGL@ protein OS=Homo sapiens GN=IGL@ PE=1 SV=1	Q6PIK1_HUMAN	25	0.000	0.000	0.000	0.437	0.495	0.000	0.155	0.241
114	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	MOES_HUMAN (+1)	68	0.212	0.121	0.077	0.121	0.065	0.337	0.155	0.103
115	cDNA FLJ57038, highly similar to Filamin- A OS=Homo sapiens PE=2 SV=1	B4E2F9_HUMAN	83	0.424	0.000	0.000	0.000	0.000	0.488	0.152	0.236
116	Apolipoprotein M OS=Homo sapiens GN=APOM PE=1 SV=2	APOM_HUMAN	21	0.076	0.152	0.045	0.239	0.168	0.224	0.151	0.078
117	Complement component 1, q subcomponent, B chain, isoform CRA_a OS=Homo sapiens GN=C1QB PE=4 SV=1	A0A024RAB9_HUMAN (+3)	27	0.138	0.152	0.071	0.236	0.098	0.196	0.149	0.061
118	Beta 5-tubulin OS=Homo sapiens GN=TUBB PE=2 SV=1	Q5SU16_HUMAN (+1)	50	0.394	0.082	0.067	0.082	0.018	0.235	0.146	0.142
119	IgG H chain OS=Homo sapiens PE=2 SV=1	S6B2A6_HUMAN	32	0.000	0.000	0.684	0.185	0.000	0.000	0.145	0.274
120	Rheumatoid factor RF-IP12 (Fragment) OS=Homo sapiens PE=2 SV=1	A2J1M8_HUMAN	11	0.242	0.166	0.000	0.166	0.281	0.000	0.143	0.119
121	Protein IGHV3-73 OS=Homo sapiens GN=IGHV3-73 PE=1 SV=1	A0A0G2JN55_HUMAN	9	0.000	0.000	0.000	0.000	0.835	0.000	0.139	0.341
122	Lipoprotein, Lp(A) OS=Homo sapiens GN=LPA PE=1 SV=1	Q1HP67_HUMAN	227	0.005	0.296	0.342	0.014	0.076	0.078	0.135	0.146
123	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	K1C16_HUMAN	51	0.084	0.134	0.065	0.205	0.173	0.127	0.131	0.053
124	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	HS90A_HUMAN (+1)	85	0.176	0.134	0.084	0.070	0.052	0.270	0.131	0.082
125	Putative uncharacterized protein DKFZp686C02220 (Fragment) OS=Homo sapiens GN=DKFZp686C02220 PE=2 SV=1	Q6N091_HUMAN	54	0.000	0.465	0.000	0.287	0.000	0.000	0.125	0.202
126	Platelet factor 4 OS=Homo sapiens GN=PF4 PE=1 SV=2	PLF4_HUMAN	11	0.194	0.124	0.000	0.166	0.000	0.267	0.125	0.108
127	Apolipoprotein D (Fragment) OS=Homo sapiens GN=APOD PE=1 SV=1	C9JF17_HUMAN	24	0.000	0.000	0.000	0.247	0.203	0.294	0.124	0.139
128	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	K1C14_HUMAN	52	0.113	0.123	0.000	0.210	0.136	0.136	0.120	0.068
129	Inter-alpha (Globulin) inhibitor H4 (Plasma Kallikrein-sensitive glycoprotein) OS=Homo sapiens GN=ITI4H PE=2 SV=1	B2RMS9_HUMAN (+1)	103	0.093	0.191	0.254	0.097	0.026	0.051	0.119	0.087
130	Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1	TBB1_HUMAN	50	0.277	0.100	0.076	0.064	0.027	0.165	0.118	0.090
131	Protein SAA2-SAA4 OS=Homo sapiens GN=SAA2-SAA4 PE=4 SV=1	A0A096LPE2_HUMAN	23	0.000	0.139	0.124	0.079	0.135	0.230	0.118	0.076
132	Protein disulfide-isomerase OS=Homo sapiens PE=2 SV=1	B3KQT9_HUMAN (+2)	54	0.266	0.152	0.035	0.042	0.000	0.207	0.117	0.107
133	Band 3 anion transport protein OS=Homo sapiens GN=SLC4A1 PE=1 SV=3	B3AT_HUMAN (+3)	102	0.193	0.018	0.173	0.103	0.104	0.075	0.111	0.064
134	CP protein OS=Homo sapiens GN=CP PE=2 SV=1	A5PL27_HUMAN (+3)	122	0.057	0.269	0.168	0.090	0.022	0.058	0.110	0.092
135	Integrin beta-3 OS=Homo sapiens GN=ITGB3 PE=1 SV=2	ITB3_HUMAN (+1)	87	0.165	0.063	0.044	0.068	0.041	0.277	0.110	0.094
136	Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4	A1BG_HUMAN (+1)	54	0.109	0.279	0.167	0.051	0.016	0.033	0.109	0.100
137	Heparin cofactor 2 OS=Homo sapiens	HEP2_HUMAN	57	0.065	0.200	0.209	0.088	0.039	0.052	0.109	0.076

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	GN=SERPIND1 PE=1 SV=3											
138	Ig heavy chain V-III region CAM OS=Homo sapiens PE=1 SV=1	HV307_HUMAN	14	0.152	0.000	0.136	0.130	0.221	0.000	0.107	0.089	
139	Apolipoprotein L, 1, isoform CRA_b OS=Homo sapiens GN=APOL1 PE=4 SV=1	A0A024R1G8_HUMAN (+11)	46	0.035	0.040	0.052	0.168	0.173	0.166	0.106	0.070	
140	Glycoprotein Ib (Platelet), alpha polypeptide OS=Homo sapiens GN=GP1BA PE=1 SV=1	A0A0C4DGZ8_HUMAN (+2)	69	0.131	0.079	0.021	0.053	0.032	0.298	0.102	0.104	
141	Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4	CO5_HUMAN	188	0.094	0.182	0.180	0.075	0.035	0.044	0.102	0.065	
142	Endoplasmic reticulum chaperone protein OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	ENPL_HUMAN (+2)	92	0.139	0.099	0.047	0.050	0.029	0.243	0.101	0.080	
143	Rheumatoid factor C6 light chain (Fragment) OS=Homo sapiens GN=V<kappa>1 PE=2 SV=1	A0N5G1_HUMAN	13	0.082	0.140	0.000	0.280	0.102	0.000	0.101	0.104	
144	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	CLUS_HUMAN	52	0.113	0.088	0.073	0.105	0.094	0.124	0.099	0.018	
145	Adenylyl cyclase-associated protein OS=Homo sapiens GN=CAP1 PE=3 SV=1	D3DPU2_HUMAN	52	0.246	0.123	0.073	0.044	0.000	0.102	0.098	0.084	
146	Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1	C1S_HUMAN	77	0.090	0.207	0.074	0.059	0.052	0.092	0.096	0.057	
147	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1	A0A0G2JPR0_HUMAN	193	0.000	0.305	0.264	0.000	0.000	0.000	0.095	0.147	
148	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	G3P_HUMAN (+1)	36	0.133	0.165	0.066	0.063	0.037	0.098	0.094	0.048	
149	cDNA FLJ54184, highly similar to Tropomyosin alpha-4 chain OS=Homo sapiens PE=2 SV=1	B4DVY2_HUMAN (+2)	26	0.184	0.088	0.037	0.088	0.000	0.158	0.092	0.070	
150	Heat shock protein 90kDa alpha (Cytosolic), class B member 1, isoform CRA_a OS=Homo sapiens GN=HSP90AB1 PE=3 SV=1	A0A024RD80_HUMAN (+2)	83	0.122	0.088	0.063	0.055	0.048	0.177	0.092	0.050	
151	C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=1 SV=1	C4BPB_HUMAN	28	0.171	0.098	0.051	0.081	0.079	0.063	0.091	0.043	
152	Anti-Influenza A hemagglutinin heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	G1FM90_HUMAN	15	0.213	0.152	0.000	0.000	0.177	0.000	0.090	0.101	
153	Integrin alpha-IIb OS=Homo sapiens GN=ITGA2B PE=1 SV=3	ITA2B_HUMAN	113	0.132	0.040	0.055	0.060	0.047	0.198	0.089	0.063	
154	Vitronectin OS=Homo sapiens GN=VTN PE=4 SV=1	D9ZGG2_HUMAN (+1)	54	0.059	0.127	0.203	0.034	0.025	0.076	0.087	0.067	
155	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	K2C5_HUMAN	62	0.112	0.088	0.069	0.118	0.050	0.085	0.087	0.025	
156	Ig heavy chain V-III region GA OS=Homo sapiens PE=1 SV=1	HV308_HUMAN	13	0.205	0.000	0.000	0.175	0.000	0.136	0.086	0.097	
157	GCT-A2 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A125U0V4_HUMAN	14	0.000	0.098	0.000	0.098	0.316	0.000	0.085	0.123	
158	IgGfC-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=1	A0A087WXI2_HUMAN (+1)	445	0.152	0.084	0.062	0.052	0.062	0.098	0.085	0.037	
159	Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2	PLMN_HUMAN	91	0.076	0.216	0.136	0.030	0.019	0.032	0.085	0.077	
160	Ficolin (Collagen/fibrinogen domain containing) 3 (Hakata antigen), isoform CRA_b OS=Homo sapiens GN=FCN3 PE=2 SV=1	Q6UXM4_HUMAN (+1)	32	0.117	0.057	0.074	0.114	0.055	0.092	0.085	0.027	
161	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1	D6RF35_HUMAN	53	0.030	0.189	0.225	0.026	0.000	0.000	0.078	0.101	
162	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1	CALR_HUMAN (+2)	48	0.144	0.105	0.040	0.028	0.000	0.147	0.077	0.063	
163	cDNA FLJ53075, highly similar to Kininogen-1 OS=Homo sapiens PE=2 SV=1	B4DPP8_HUMAN (+1)	46	0.046	0.149	0.207	0.050	0.000	0.000	0.075	0.084	
164	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	1433Z_HUMAN (+1)	28	0.057	0.098	0.034	0.081	0.032	0.147	0.075	0.044	
165	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	TERA_HUMAN (+1)	89	0.138	0.067	0.016	0.041	0.000	0.185	0.074	0.073	
166	Uncharacterized protein (Fragment) OS=Homo sapiens PE=1 SV=1	A0A0J9YX35_HUMAN	13	0.205	0.000	0.000	0.000	0.238	0.000	0.074	0.115	
167	cDNA FLJ41552 fis, clone COLON2004478, highly similar to Protein Tro alpha1 H, myeloma OS=Homo sapiens PE=2 SV=1	Q6ZW64_HUMAN	53	0.000	0.000	0.000	0.000	0.434	0.000	0.072	0.177	
168	Platelet glycoprotein V OS=Homo sapiens GN=GP5 PE=1 SV=1	GPV_HUMAN	61	0.052	0.120	0.000	0.030	0.029	0.202	0.072	0.075	

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169	Platelet basic protein OS=Homo sapiens GN=PPBP PE=1 SV=3	CXCL7_HUMAN (+1)	14	0.190	0.000	0.000	0.000	0.063	0.168	0.070	0.088
170	Proteoglycan 4, isoform CRA_a OS=Homo sapiens GN=PRG4 PE=4 SV=1	A0A024R930_HUMAN (+2)	151	0.042	0.033	0.035	0.054	0.111	0.132	0.068	0.043
171	Protein IGHV3-13 (Fragment) OS=Homo sapiens GN=IGHV3-13 PE=1 SV=1	A0A0A0MS11_HUMAN	13	0.000	0.000	0.000	0.000	0.408	0.000	0.068	0.167
172	Complement component 9, isoform CRA_a OS=Homo sapiens GN=C9 PE=4 SV=1	A0A024R035_HUMAN (+1)	63	0.059	0.152	0.151	0.022	0.000	0.019	0.067	0.068
173	Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=3 SV=1	A0A024R8S5_HUMAN (+1)	57	0.215	0.064	0.025	0.000	0.000	0.093	0.066	0.082
174	Epididymis luminal protein 180 (Fragment) OS=Homo sapiens GN=HEL180 PE=2 SV=1	B6EDE2_HUMAN	13	0.000	0.000	0.000	0.385	0.000	0.000	0.064	0.157
175	Heat shock 70 kDa protein 1B OS=Homo sapiens GN=HSPA1B PE=1 SV=1	A0A0G2JIW1_HUMAN (+3)	70	0.099	0.085	0.000	0.039	0.000	0.159	0.064	0.063
176	Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1	A1AG1_HUMAN (+1)	24	0.089	0.095	0.159	0.038	0.000	0.000	0.063	0.062
177	Zyxin OS=Homo sapiens GN=ZYG PE=1 SV=1	ZYX_HUMAN	61	0.105	0.015	0.062	0.075	0.036	0.087	0.063	0.033
178	Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	Q96SA9_HUMAN	12	0.000	0.000	0.159	0.000	0.221	0.000	0.063	0.100
179	Catalase OS=Homo sapiens GN=CAT PE=1 SV=3	CATA_HUMAN	60	0.098	0.038	0.095	0.053	0.037	0.059	0.063	0.027
180	Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=1	A0A0A0MTH3_HUMAN (+2)	55	0.126	0.108	0.000	0.025	0.000	0.118	0.063	0.061
181	GCT-A5 light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A0X9UWL5_HUMAN	12	0.000	0.000	0.000	0.228	0.147	0.000	0.063	0.100
182	Myosin-reactive immunoglobulin heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	Q9UL89_HUMAN	13	0.082	0.000	0.293	0.000	0.000	0.000	0.062	0.118
183	cDNA FLJ54622, highly similar to Prothrombin (EC 3.4.21.5) OS=Homo sapiens PE=2 SV=1	B4DDT3_HUMAN (+1)	53	0.060	0.172	0.072	0.034	0.000	0.033	0.062	0.059
184	Prenylcysteine oxidase 1 OS=Homo sapiens GN=PCYOX1 PE=1 SV=3	PCYOX_HUMAN	57	0.019	0.056	0.000	0.096	0.078	0.124	0.062	0.047
185	Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3	CPN2_HUMAN	61	0.070	0.097	0.062	0.067	0.036	0.039	0.062	0.023
186	V2-17 protein (Fragment) OS=Homo sapiens GN=V2-17 PE=1 SV=1	Q5NV90_HUMAN	10	0.000	0.183	0.095	0.000	0.088	0.000	0.061	0.075
187	Multimerin-1 OS=Homo sapiens GN=MMRN1 PE=1 SV=3	MMRN1_HUMAN	138	0.073	0.026	0.045	0.036	0.010	0.166	0.059	0.056
188	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	A0A087X1C7_HUMAN	50	0.000	0.000	0.000	0.000	0.354	0.000	0.059	0.144
189	Tropomyosin 3 isoform 1 (Fragment) OS=Homo sapiens GN=TPM3 PE=2 SV=1	A0A0S2Z4G4_HUMAN (+1)	29	0.129	0.063	0.000	0.000	0.000	0.162	0.059	0.072
190	Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3	A2AP_HUMAN	55	0.058	0.091	0.113	0.033	0.032	0.021	0.058	0.037
191	Calpain 1, (Mu/I) large subunit, isoform CRA_a OS=Homo sapiens GN=CAPN1 PE=4 SV=1	A0A024R580_HUMAN (+2)	82	0.071	0.045	0.012	0.033	0.022	0.165	0.058	0.056
192	Ig heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A068LRW6_HUMAN (+2)	14	0.114	0.000	0.102	0.000	0.000	0.126	0.057	0.063
193	Enolase 1, (Alpha), isoform CRA_a OS=Homo sapiens GN=ENO1 PE=2 SV=1	A0A024R4F1_HUMAN (+1)	47	0.091	0.058	0.051	0.039	0.000	0.100	0.056	0.036
194	Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3	APOA4_HUMAN	45	0.000	0.041	0.042	0.101	0.088	0.065	0.056	0.037
195	MS-D1 light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A0X9TD47_HUMAN	12	0.000	0.000	0.000	0.190	0.147	0.000	0.056	0.088
196	Serpin peptidase inhibitor, clade C (Antithrombin), member 1, isoform CRA_a OS=Homo sapiens GN=SERPINC1 PE=3 SV=1	A0A024R944_HUMAN (+1)	53	0.030	0.129	0.099	0.043	0.000	0.033	0.056	0.048
197	Uncharacterized protein OS=Homo sapiens PE=1 SV=1	B4E1Z4_HUMAN	141	0.038	0.123	0.142	0.023	0.000	0.008	0.056	0.061
198	GCT-A8 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A0X9V9C4_HUMAN	13	0.000	0.000	0.330	0.000	0.000	0.000	0.055	0.135
199	Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1	AMBP_HUMAN	39	0.055	0.140	0.061	0.035	0.023	0.000	0.052	0.048
200	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	ALDOA_HUMAN (+2)	39	0.082	0.047	0.000	0.058	0.000	0.105	0.049	0.043
201	Clathrin heavy chain OS=Homo sapiens GN=CLTC PE=1 SV=1	A0A087VWQ6_HUMAN (+1)	192	0.103	0.031	0.015	0.021	0.012	0.095	0.046	0.041
202	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2	ITIH3_HUMAN	100	0.059	0.100	0.076	0.027	0.013	0.000	0.046	0.039

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203	Pleckstrin OS=Homo sapiens GN=PLEK PE=1 SV=3	PLEK_HUMAN	40	0.080	0.091	0.000	0.000	0.000	0.103	0.046	0.051
204	A30 (Fragment) OS=Homo sapiens PE=4 SV=1	A2MYE1_HUMAN (+1)	10	0.000	0.000	0.000	0.273	0.000	0.000	0.046	0.112
205	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5	PYGB_HUMAN (+1)	97	0.071	0.061	0.015	0.038	0.000	0.085	0.045	0.033
206	Coagulation factor XIII B chain OS=Homo sapiens GN=F13B PE=1 SV=3	F13B_HUMAN	76	0.056	0.054	0.063	0.048	0.017	0.031	0.045	0.017
207	Rheumatoid factor RF-ET10 (Fragment) OS=Homo sapiens PE=2 SV=1	A2J1N7_HUMAN	10	0.000	0.000	0.000	0.000	0.265	0.000	0.044	0.108
208	cDNA FLJ61290, highly similar to Neutral alpha-glucosidase AB OS=Homo sapiens PE=2 SV=1	B4DJ30_HUMAN (+2)	113	0.052	0.044	0.013	0.016	0.008	0.120	0.042	0.042
209	Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1 SV=3	PGM1_HUMAN	61	0.061	0.052	0.000	0.022	0.000	0.116	0.042	0.044
210	Complement component 1, q subcomponent, A chain, isoform CRA_a OS=Homo sapiens GN=C1QA PE=4 SV=1	A0A024RAG6_HUMAN (+2)	26	0.061	0.035	0.000	0.035	0.051	0.068	0.042	0.024
211	HCG2039812, isoform CRA_b (Fragment) OS=Homo sapiens GN=KRT6A PE=2 SV=1	A0A0S2Z428_HUMAN (+3)	60	0.000	0.084	0.000	0.099	0.066	0.000	0.041	0.047
212	Protein IGKV2D-24 (Fragment) OS=Homo sapiens GN=IGKV2D-24 PE=4 SV=1	A0A075B6R9_HUMAN (+1)	13	0.000	0.000	0.000	0.105	0.000	0.136	0.040	0.063
213	Protein IGHV1-46 (Fragment) OS=Homo sapiens GN=IGHV1-46 PE=4 SV=1	A0A0B4J1V4_HUMAN (+1)	13	0.000	0.070	0.000	0.000	0.170	0.000	0.040	0.070
214	Class IVb beta tubulin OS=Homo sapiens PE=2 SV=1	Q8IWP6_HUMAN (+3)	50	0.000	0.000	0.000	0.000	0.000	0.235	0.039	0.096
215	cDNA FLJ78516 OS=Homo sapiens PE=2 SV=1	A8K2W3_HUMAN (+1)	47	0.102	0.000	0.041	0.029	0.000	0.063	0.039	0.039
216	Transketolase (Fragment) OS=Homo sapiens PE=2 SV=1	Q53EM5_HUMAN (+2)	68	0.063	0.040	0.000	0.020	0.000	0.104	0.038	0.040
217	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=1	B7Z6Z4_HUMAN (+6)	27	0.138	0.000	0.000	0.000	0.000	0.087	0.038	0.060
218	Spectrin alpha chain, erythrocytic 1 OS=Homo sapiens GN=SPTA1 PE=1 SV=1	A0A087WZE4_HUMAN (+1)	281	0.072	0.000	0.068	0.039	0.033	0.013	0.037	0.029
219	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	LDHB_HUMAN (+1)	37	0.043	0.037	0.000	0.062	0.000	0.079	0.037	0.032
220	Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3	MASP1_HUMAN	79	0.067	0.040	0.018	0.029	0.028	0.030	0.035	0.017
221	Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3	CO6_HUMAN	105	0.015	0.091	0.073	0.013	0.008	0.011	0.035	0.037
222	GDP dissociation inhibitor 1 isoform 1 (Fragment) OS=Homo sapiens GN=GDI1 PE=2 SV=1	A0A0S2Z3X8_HUMAN (+2)	51	0.104	0.027	0.019	0.000	0.000	0.058	0.035	0.040
223	Ankyrin-1 OS=Homo sapiens GN=ANK1 PE=1 SV=3	ANK1_HUMAN	206	0.067	0.000	0.067	0.031	0.021	0.020	0.034	0.027
224	Ig heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A068LKQ2_HUMAN	13	0.000	0.000	0.000	0.000	0.204	0.000	0.034	0.083
225	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	COF1_HUMAN (+3)	19	0.056	0.048	0.000	0.000	0.000	0.093	0.033	0.039
226	Polymeric immunoglobulin receptor OS=Homo sapiens GN=PIGR PE=1 SV=4	PIGR_HUMAN	83	0.032	0.016	0.017	0.022	0.107	0.000	0.032	0.038
227	Coronin OS=Homo sapiens GN=CORO1A PE=3 SV=1	A0A024R611_HUMAN (+1)	51	0.084	0.027	0.019	0.018	0.000	0.046	0.032	0.029
228	Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	TFR1_HUMAN	85	0.069	0.027	0.028	0.027	0.000	0.041	0.032	0.023
229	Hexokinase (Fragment) OS=Homo sapiens PE=2 SV=1	Q59FD4_HUMAN	106	0.040	0.034	0.000	0.009	0.000	0.105	0.031	0.040
230	Soluble scavenger receptor cysteine-rich domain-containing protein SSC5D OS=Homo sapiens GN=SSC5D PE=1 SV=3	SRCL_HUMAN	166	0.055	0.025	0.029	0.022	0.027	0.032	0.031	0.012
231	cDNA FLJ55606, highly similar to Alpha-2-HS-glycoprotein OS=Homo sapiens PE=2 SV=1	B7Z8Q2_HUMAN (+2)	47	0.000	0.078	0.091	0.019	0.000	0.000	0.031	0.042
232	Ig heavy chain V-III region JON OS=Homo sapiens PE=1 SV=1	HV319_HUMAN	13	0.082	0.000	0.000	0.000	0.102	0.000	0.031	0.048
233	Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens PE=2 SV=1	A8K486_HUMAN (+3)	18	0.000	0.000	0.000	0.051	0.000	0.131	0.030	0.053
234	Spectrin, beta, erythrocytic (Includes spherocytosis, clinical type I) variant (Fragment) OS=Homo sapiens PE=2 SV=1	Q59FP5_HUMAN	268	0.060	0.007	0.052	0.025	0.016	0.018	0.030	0.021
235	RAP1B, member of RAS oncogene family, isoform CRA_a OS=Homo sapiens GN=RAP1B PE=4 SV=1	A0A024RB87_HUMAN (+3)	21	0.000	0.065	0.000	0.000	0.000	0.112	0.030	0.048
236	Coagulation factor V OS=Homo sapiens	A0A0A0MRJ7_HUMAN (+1)	252	0.051	0.025	0.013	0.023	0.021	0.042	0.029	0.014

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	GN=F5 PE=1 SV=1											
237	Ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing), isoform CRA_a OS=Homo sapiens GN=UBE1 PE=3 SV=1	A0A024R1A3_HUMAN (+1)	118	0.050	0.043	0.012	0.000	0.000	0.070	0.029	0.029	
238	cDNA, FLJ93914, highly similar to Homo sapiens histidine-rich glycoprotein (HRG), mRNA OS=Homo sapiens PE=2 SV=1	B2R8I2_HUMAN (+1)	60	0.036	0.061	0.040	0.023	0.015	0.000	0.029	0.021	
239	Protein unc-13 homolog D OS=Homo sapiens GN=UNC13D PE=1 SV=1	UN13D_HUMAN	123	0.052	0.026	0.000	0.000	0.000	0.096	0.029	0.039	
240	Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1	APOA2_HUMAN (+3)	11	0.000	0.000	0.000	0.166	0.000	0.000	0.028	0.068	
241	Nucleosome assembly protein 1-like 1, isoform CRA_a OS=Homo sapiens GN=NAP1L1 PE=3 SV=1	A0A024RBB7_HUMAN (+12)	45	0.059	0.030	0.021	0.000	0.000	0.052	0.027	0.025	
242	Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3	PON1_HUMAN	40	0.000	0.068	0.048	0.046	0.000	0.000	0.027	0.031	
243	Protein IGKV2D-28 OS=Homo sapiens GN=IGKV2D-28 PE=1 SV=1	A0A0A0MTQ6_HUMAN (+2)	11	0.000	0.000	0.000	0.000	0.161	0.000	0.027	0.066	
244	Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3	APOH_HUMAN (+1)	38	0.000	0.060	0.100	0.000	0.000	0.000	0.027	0.043	
245	cDNA FLJ50805, highly similar to Erythrocyte membrane protein band 4.2 OS=Homo sapiens PE=2 SV=1	B7Z4C3_HUMAN (+1)	77	0.055	0.000	0.049	0.035	0.017	0.000	0.026	0.024	
246	Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3	TAGL2_HUMAN (+1)	22	0.048	0.000	0.000	0.000	0.000	0.107	0.026	0.044	
247	Cryocryoglobulin CC1 kappa light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	B1N7B8_HUMAN	12	0.000	0.000	0.000	0.152	0.000	0.000	0.025	0.062	
248	Syntaxin-binding protein 2 OS=Homo sapiens GN=STXBP2 PE=1 SV=2	STXB2_HUMAN	66	0.032	0.035	0.000	0.000	0.000	0.080	0.024	0.032	
249	Phosphoglycerate kinase OS=Homo sapiens PE=2 SV=1	B4E1H9_HUMAN (+2)	35	0.030	0.039	0.000	0.026	0.000	0.050	0.024	0.021	
250	cDNA FLJ77947, highly similar to Human complement protein C8 beta subunit mRNA OS=Homo sapiens PE=2 SV=1	A8K9M5_HUMAN (+6)	67	0.024	0.048	0.071	0.000	0.000	0.000	0.024	0.030	
251	Beta-parvin OS=Homo sapiens GN=PARVB PE=1 SV=1	PARVB_HUMAN	42	0.038	0.033	0.000	0.000	0.000	0.070	0.023	0.029	
252	Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1	PDC6I_HUMAN (+1)	96	0.028	0.019	0.000	0.000	0.000	0.092	0.023	0.036	
253	T-complex protein 1 subunit gamma OS=Homo sapiens PE=2 SV=1	B3KX11_HUMAN (+4)	58	0.064	0.000	0.000	0.000	0.000	0.071	0.023	0.035	
254	Nicotinate phosphoribosyltransferase (Fragment) OS=Homo sapiens GN=NAPRT PE=1 SV=1	H0YDA6_HUMAN	14	0.000	0.000	0.068	0.000	0.063	0.000	0.022	0.034	
255	Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens GN=GPI PE=1 SV=1	A0A0A0M2S2_HUMAN	65	0.066	0.042	0.022	0.000	0.000	0.000	0.022	0.027	
256	Arachidonate 12-lipoxygenase, 12S-type OS=Homo sapiens GN=ALOX12 PE=1 SV=4	LOX12_HUMAN	76	0.056	0.000	0.025	0.000	0.000	0.046	0.021	0.025	
257	ATP-dependent 6-phosphofructokinase, platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2	PFKAP_HUMAN	86	0.037	0.053	0.000	0.000	0.000	0.034	0.021	0.024	
258	IQ motif containing GTPase activating protein 2, isoform CRA_b OS=Homo sapiens GN=IQGAP2 PE=4 SV=1	A0A024RAJ8_HUMAN (+2)	181	0.032	0.023	0.000	0.013	0.000	0.055	0.020	0.021	
259	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4	G6PD_HUMAN	59	0.054	0.031	0.016	0.000	0.000	0.020	0.020	0.021	
260	Nidogen-1 OS=Homo sapiens GN=NID1 PE=1 SV=3	NID1_HUMAN	136	0.051	0.007	0.000	0.013	0.007	0.043	0.020	0.021	
261	cDNA, FLJ95650, highly similar to Homo sapiens karyopherin (importin) beta 1 (KPNB1), mRNA OS=Homo sapiens PE=2 SV=1	B2RBR9_HUMAN (+1)	97	0.044	0.024	0.010	0.000	0.000	0.042	0.020	0.020	
262	cDNA FLJ78207, highly similar to Human complement protein component C7 mRNA OS=Homo sapiens PE=2 SV=1	A8K2T4_HUMAN (+2)	93	0.000	0.074	0.046	0.000	0.000	0.000	0.020	0.032	
263	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4	CLIC1_HUMAN (+2)	27	0.039	0.034	0.000	0.000	0.000	0.044	0.019	0.022	
264	Plasma kallikrein (Fragment) OS=Homo sapiens GN=KLKB1 PE=1 SV=1	H0YAC1_HUMAN (+1)	77	0.014	0.041	0.049	0.012	0.000	0.000	0.019	0.021	
265	Rho-associated protein kinase 2 OS=Homo sapiens GN=ROCK2 PE=1 SV=4	ROCK2_HUMAN	161	0.033	0.014	0.000	0.000	0.000	0.066	0.019	0.026	
266	Tyrosine-protein phosphatase non-receptor type 6 OS=Homo sapiens	PTN6_HUMAN (+2)	68	0.024	0.034	0.000	0.027	0.000	0.026	0.018	0.015	

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	GN=PTPN6 PE=1 SV=1										
267	Triosephosphate isomerase OS=Homo sapiens PE=2 SV=1	B4DUI5_HUMAN (+4)	23	0.069	0.040	0.000	0.000	0.000	0.000	0.018	0.030
268	cDNA FLJ50442, highly similar to T-complex protein 1 subunit epsilon OS=Homo sapiens PE=2 SV=1	B4DDU6_HUMAN (+5)	55	0.048	0.017	0.000	0.000	0.000	0.043	0.018	0.022
269	Ig heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A068LN03_HUMAN	13	0.000	0.000	0.000	0.105	0.000	0.000	0.018	0.043
270	Protein IGKV1-16 (Fragment) OS=Homo sapiens GN=IGKV1-16 PE=1 SV=1	A0A0A0MT74_HUMAN	13	0.000	0.000	0.000	0.105	0.000	0.000	0.018	0.043
271	Chaperonin containing TCP1, subunit 7 (Eta) variant (Fragment) OS=Homo sapiens PE=2 SV=1	Q53HV2_HUMAN (+1)	59	0.036	0.039	0.000	0.000	0.000	0.030	0.017	0.019
272	Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2	CO8A_HUMAN	65	0.025	0.042	0.037	0.000	0.000	0.000	0.017	0.020
273	Coronin OS=Homo sapiens GN=CORO1C PE=3 SV=1	A0A024RBI5_HUMAN (+3)	53	0.080	0.000	0.000	0.000	0.000	0.022	0.017	0.032
274	EH domain-containing protein 3 OS=Homo sapiens GN=EHD3 PE=1 SV=1	A0A0C4DH83_HUMAN (+1)	62	0.026	0.022	0.000	0.015	0.000	0.038	0.017	0.015
275	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2	PSA_HUMAN	103	0.010	0.027	0.000	0.000	0.000	0.063	0.017	0.025
276	Chaperonin containing TCP1, subunit 8 (Theta) variant (Fragment) OS=Homo sapiens PE=2 SV=1	Q53HU0_HUMAN (+2)	60	0.044	0.015	0.000	0.000	0.000	0.039	0.016	0.021
277	Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDI6 PE=1 SV=1	PDI6_HUMAN	48	0.022	0.038	0.000	0.000	0.000	0.037	0.016	0.019
278	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	S10A8_HUMAN	11	0.097	0.000	0.000	0.000	0.000	0.000	0.016	0.040
279	Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1	B1AK87_HUMAN (+3)	29	0.055	0.000	0.000	0.000	0.000	0.041	0.016	0.025
280	Rheumatoid factor RF-IP4 (Fragment) OS=Homo sapiens PE=2 SV=1	A2J1M5_HUMAN	10	0.000	0.000	0.095	0.000	0.000	0.000	0.016	0.039
281	LTPP1 protein OS=Homo sapiens GN=LTPP1 PE=2 SV=1	B7ZLY3_HUMAN (+3)	148	0.029	0.009	0.000	0.012	0.009	0.036	0.016	0.014
282	cDNA FLJ51409, highly similar to Thrombospondin-4 OS=Homo sapiens PE=2 SV=1	B7Z832_HUMAN (+2)	96	0.028	0.010	0.015	0.009	0.014	0.018	0.016	0.007
283	Alpha-1,4 glucan phosphorylase OS=Homo sapiens PE=2 SV=1	B2R825_HUMAN (+1)	97	0.038	0.000	0.000	0.000	0.000	0.055	0.015	0.025
284	Serum amyloid P-component OS=Homo sapiens GN=APCS PE=1 SV=2	SAMP_HUMAN (+1)	25	0.000	0.055	0.038	0.000	0.000	0.000	0.015	0.025
285	Cytoplasmic FMR1 interacting protein 1 isoform A (Fragment) OS=Homo sapiens GN=CYFIP1 PE=2 SV=1	X5D2F4_HUMAN	145	0.029	0.019	0.000	0.006	0.000	0.036	0.015	0.016
286	Protein disulfide-isomerase A4 OS=Homo sapiens GN=ERP70 PE=3 SV=1	A0A090N8Y2_HUMAN (+1)	73	0.029	0.013	0.000	0.000	0.000	0.048	0.015	0.020
287	cDNA FLJ50491, highly similar to Amyloid beta A4 protein (APP) (ABPP)(Alzheimer disease amyloid protein) (Cerebral vascularamyloid peptide) (CVAP) (Protease nexin-II) (PN-II)(APPI) (PreA4) OS=Homo sapiens PE=2 SV=1	B4DGD0_HUMAN	81	0.046	0.000	0.000	0.000	0.000	0.044	0.015	0.023
288	CD36 antigen (Collagen type I receptor, thrombospondin receptor) OS=Homo sapiens GN=CD36 PE=2 SV=1	A4D1B1_HUMAN (+6)	53	0.020	0.000	0.000	0.000	0.000	0.067	0.014	0.027
289	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	LDHA_HUMAN (+1)	37	0.000	0.037	0.000	0.000	0.000	0.048	0.014	0.022
290	Proto-oncogene tyrosine-protein kinase Src OS=Homo sapiens GN=SRC PE=1 SV=3	SRC_HUMAN	60	0.027	0.038	0.000	0.000	0.000	0.020	0.014	0.016
291	V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2	VATA_HUMAN	68	0.024	0.000	0.000	0.000	0.000	0.060	0.014	0.025
292	Heat shock 60kDa protein 1 (Chaperonin), isoform CRA_a OS=Homo sapiens GN=HSPD1 PE=2 SV=1	A0A024R3X4_HUMAN (+2)	61	0.035	0.000	0.000	0.000	0.000	0.048	0.014	0.022
293	cDNA, FLJ93545, highly similar to Homo sapiens 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase (ATIC), mRNA OS=Homo sapiens PE=2 SV=1	B2R7P8_HUMAN (+2)	65	0.041	0.014	0.000	0.000	0.000	0.027	0.014	0.017
294	cDNA, FLJ92620, highly similar to Homo sapiens staphylococcal nuclease domain containing 1 (SND1), mRNA OS=Homo sapiens PE=2 SV=1	B2R5U1_HUMAN (+3)	100	0.027	0.014	0.000	0.000	0.000	0.041	0.014	0.017
295	Ubiquitin-like modifier-activating enzyme 7	UBA7_HUMAN	112	0.010	0.024	0.000	0.000	0.000	0.047	0.014	0.019

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	OS=Homo sapiens GN=UBA7 PE=1 SV=2											
296	Afamin OS=Homo sapiens GN=AFM PE=1 SV=1	AFAM_HUMAN	69	0.000	0.040	0.028	0.013	0.000	0.000	0.013	0.017	
297	Angiotensinogen variant (Fragment) OS=Homo sapiens PE=2 SV=1	Q53GY3_HUMAN (+3)	53	0.000	0.017	0.063	0.000	0.000	0.000	0.013	0.025	
298	Dihydropyrimidinase-like 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1	Q59GB4_HUMAN	68	0.063	0.000	0.000	0.000	0.000	0.017	0.013	0.025	
299	Alpha-1-acid glycoprotein 2 OS=Homo sapiens GN=ORM2 PE=1 SV=2	A1AG2_HUMAN	24	0.000	0.000	0.079	0.000	0.000	0.000	0.013	0.032	
300	Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2	IDHP_HUMAN (+1)	51	0.021	0.000	0.000	0.000	0.000	0.058	0.013	0.023	
301	Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	ITB1_HUMAN	88	0.018	0.000	0.000	0.000	0.000	0.060	0.013	0.024	
302	Bridging integrator 2 OS=Homo sapiens GN=BIN2 PE=1 SV=1	A0A087X188_HUMAN (+4)	65	0.025	0.000	0.000	0.035	0.000	0.018	0.013	0.015	
303	Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=1	A0A0G2JH68_HUMAN (+3)	141	0.019	0.016	0.000	0.000	0.000	0.042	0.013	0.017	
304	Chaperonin containing TCP1, subunit 6A (Zeta 1), isoform CRA_a OS=Homo sapiens GN=CCT6A PE=3 SV=1	A0A024RDL1_HUMAN (+2)	58	0.055	0.000	0.000	0.000	0.000	0.020	0.013	0.022	
305	Lipopolysaccharide-binding protein OS=Homo sapiens GN=LBP PE=1 SV=3	LBP_HUMAN (+1)	53	0.000	0.017	0.036	0.000	0.000	0.022	0.013	0.015	
306	Oncoprotein-induced transcript 3 protein OS=Homo sapiens GN=OIT3 PE=1 SV=2	OIT3_HUMAN	60	0.036	0.000	0.000	0.000	0.000	0.039	0.012	0.019	
307	Calcium-transporting ATPase OS=Homo sapiens PE=2 SV=1	A8K9K1_HUMAN (+1)	109	0.015	0.000	0.000	0.000	0.000	0.059	0.012	0.024	
308	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	LUM_HUMAN (+1)	38	0.000	0.036	0.038	0.000	0.000	0.000	0.012	0.019	
309	cDNA, FLJ94361, highly similar to Homo sapiens serine (or cysteine) proteinase inhibitor, clade A(alpha-1 antiproteinase, antitrypsin), member 6 (SERPINA6), mRNA OS=Homo sapiens PE=2 SV=1	B2R9F2_HUMAN (+1)	45	0.000	0.051	0.021	0.000	0.000	0.000	0.012	0.021	
310	Hydroxysteroid (17-beta) dehydrogenase 4, isoform CRA_b (Fragment) OS=Homo sapiens GN=HSD17B4 PE=2 SV=1	A0A0S2Z4J1_HUMAN (+2)	80	0.020	0.000	0.000	0.000	0.000	0.051	0.012	0.021	
311	Anti-HER3 scFv (Fragment) OS=Homo sapiens PE=2 SV=1	A2J422_HUMAN	26	0.000	0.070	0.000	0.000	0.000	0.000	0.012	0.029	
312	Ig heavy chain V-III region TRO OS=Homo sapiens PE=1 SV=1	HV301_HUMAN	13	0.000	0.000	0.000	0.070	0.000	0.000	0.012	0.029	
313	Beta-arrestin-1 (Fragment) OS=Homo sapiens GN=ARRB1 PE=1 SV=7	E9PM35_HUMAN	29	0.037	0.031	0.000	0.000	0.000	0.000	0.011	0.018	
314	N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2 PE=1 SV=1	PGRP2_HUMAN	62	0.000	0.037	0.031	0.000	0.000	0.000	0.011	0.018	
315	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4	FBLN1_HUMAN	77	0.000	0.041	0.012	0.012	0.000	0.000	0.011	0.016	
316	Selectin P (Granule membrane protein 140kDa, antigen CD62), isoform CRA_b OS=Homo sapiens GN=SELP PE=4 SV=1	A0A024R8Y9_HUMAN (+7)	91	0.018	0.015	0.000	0.000	0.000	0.032	0.011	0.013	
317	LIM and senescent cell antigen-like-containing domain protein 3 OS=Homo sapiens GN=LIMS4 PE=1 SV=1	A0A0J9YXC7_HUMAN (+1)	46	0.035	0.030	0.000	0.000	0.000	0.000	0.011	0.017	
318	T-complex protein 1 subunit delta OS=Homo sapiens PE=2 SV=1	A8K3C3_HUMAN (+1)	58	0.064	0.000	0.000	0.000	0.000	0.000	0.011	0.026	
319	T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	TCPA_HUMAN	60	0.044	0.000	0.000	0.000	0.000	0.020	0.011	0.018	
320	Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR PE=1 SV=2	GSHR_HUMAN (+1)	56	0.048	0.016	0.000	0.000	0.000	0.000	0.011	0.019	
321	Phospholipase A2, group VII (Platelet-activating factor acetylhydrolase, plasma), isoform CRA_a OS=Homo sapiens GN=PLA2G7 PE=4 SV=1	A0A024RD39_HUMAN (+2)	50	0.000	0.000	0.000	0.036	0.027	0.000	0.010	0.017	
322	14-3-3 protein eta OS=Homo sapiens GN=YWHAA PE=1 SV=4	1433F_HUMAN (+1)	28	0.000	0.000	0.000	0.000	0.000	0.063	0.010	0.026	
323	Tripeptidyl-peptidase 2 OS=Homo sapiens GN=PPP2 PE=1 SV=1	Q5VZU9_HUMAN (+1)	140	0.038	0.007	0.000	0.000	0.000	0.017	0.010	0.015	
324	cGMP-dependent protein kinase 1 OS=Homo sapiens GN=PRKG1 PE=1 SV=1	A0A0A0MSB3_HUMAN (+1)	52	0.000	0.026	0.000	0.000	0.000	0.034	0.010	0.016	
325	Alanine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2	SYAC_HUMAN	107	0.010	0.009	0.000	0.009	0.000	0.033	0.010	0.012	
326	Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2	CFAI_HUMAN (+2)	66	0.016	0.014	0.029	0.000	0.000	0.000	0.010	0.012	
327	Reelin OS=Homo sapiens GN=RELN PE=1 SV=1	J3KQ66_HUMAN (+1)	388	0.025	0.011	0.005	0.000	0.000	0.018	0.010	0.010	
328	Dipeptidyl peptidase 3 OS=Homo sapiens	DPP3_HUMAN (+2)	83	0.019	0.000	0.000	0.000	0.000	0.035	0.009	0.015	

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	GN=DPP3 PE=1 SV=2											
329	TNC variant protein (Fragment) OS=Homo sapiens GN=TNC variant protein PE=2 SV=1	Q4LE33_HUMAN	244	0.017	0.006	0.000	0.011	0.020	0.000	0.009	0.009	
330	Phosphodiesterase 5A OS=Homo sapiens PE=2 SV=1	I6NLS4_HUMAN (+1)	100	0.000	0.018	0.000	0.000	0.000	0.035	0.009	0.015	
331	Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1	CBPN_HUMAN	52	0.000	0.035	0.018	0.000	0.000	0.000	0.009	0.015	
332	IgG H chain OS=Homo sapiens PE=2 SV=1	S6AWF0_HUMAN	25	0.000	0.000	0.000	0.000	0.053	0.000	0.009	0.022	
333	NAD-dependent malic enzyme, mitochondrial OS=Homo sapiens GN=ME2 PE=1 SV=1	MAOM_HUMAN	65	0.025	0.000	0.000	0.000	0.000	0.027	0.009	0.013	
334	cDNA FLJ56381, highly similar to Dynamin-1-like protein (EC 3.6.5.5) OS=Homo sapiens PE=2 SV=1	B4DYR6_HUMAN (+5)	85	0.013	0.011	0.000	0.000	0.000	0.028	0.008	0.011	
335	Thyroxine-binding globulin OS=Homo sapiens GN=SERPINA7 PE=1 SV=2	THBG_HUMAN	46	0.000	0.020	0.031	0.000	0.000	0.000	0.008	0.014	
336	Ras-related C3 botulinum toxin substrate 2 (Rho family, small GTP binding protein Rac2), isoform CRA_a OS=Homo sapiens GN=RAC2 PE=3 SV=1	A0A024R1P2_HUMAN (+5)	21	0.051	0.000	0.000	0.000	0.000	0.000	0.008	0.021	
337	Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=1	A0A087X0S5_HUMAN (+1)	108	0.020	0.008	0.000	0.000	0.000	0.022	0.008	0.010	
338	Rho GTPase activating protein OS=Homo sapiens PE=2 SV=1	A9UK01_HUMAN (+1)	75	0.014	0.000	0.000	0.012	0.000	0.024	0.008	0.010	
339	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=3 SV=1	A0A024R1T9_HUMAN (+3)	121	0.018	0.008	0.000	0.000	0.000	0.024	0.008	0.010	
340	Proteoglycan 1, secretory granule, isoform CRA_a OS=Homo sapiens GN=PRG1 PE=4 SV=1	A0A024QZL1_HUMAN (+1)	18	0.000	0.000	0.000	0.000	0.049	0.000	0.008	0.020	
341	Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	COPA_HUMAN	138	0.027	0.000	0.000	0.000	0.000	0.021	0.008	0.013	
342	cDNA FLJ78437, highly similar to Homo sapiens cartilage oligomeric matrix protein (COMP), mRNA OS=Homo sapiens PE=2 SV=1	A8K310_HUMAN (+4)	83	0.026	0.000	0.000	0.000	0.000	0.021	0.008	0.012	
343	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2	GSTP1_HUMAN (+1)	23	0.046	0.000	0.000	0.000	0.000	0.000	0.008	0.019	
344	IgG H chain OS=Homo sapiens PE=2 SV=1	S6B2B6_HUMAN	29	0.000	0.000	0.000	0.000	0.046	0.000	0.008	0.019	
345	Fibulin-1 OS=Homo sapiens PE=2 SV=1	B4DUV1_HUMAN	70	0.000	0.046	0.000	0.000	0.000	0.000	0.008	0.019	
346	Ras suppressor protein 1 variant 5 OS=Homo sapiens GN=RSU1 PE=4 SV=1	B0YJ73_HUMAN (+1)	26	0.000	0.000	0.000	0.000	0.000	0.045	0.008	0.018	
347	Integrin alpha-6 OS=Homo sapiens GN=ITGA6 PE=1 SV=5	ITA6_HUMAN	127	0.017	0.000	0.000	0.000	0.000	0.028	0.007	0.012	
348	PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4	PDL1_HUMAN (+1)	36	0.044	0.000	0.000	0.000	0.000	0.000	0.007	0.018	
349	Vacuolar protein sorting 35 variant (Fragment) OS=Homo sapiens PE=2 SV=1	Q53FR4_HUMAN (+2)	92	0.012	0.010	0.000	0.010	0.000	0.013	0.007	0.006	
350	Vasodilator-stimulated phosphoprotein isoform 1 OS=Homo sapiens GN=VASP PE=2 SV=1	A0A024R0V4_HUMAN (+2)	40	0.000	0.000	0.000	0.000	0.000	0.044	0.007	0.018	
351	Signal transducer and activator of transcription (Fragment) OS=Homo sapiens PE=2 SV=1	Q59H39_HUMAN (+1)	90	0.018	0.000	0.000	0.000	0.000	0.026	0.007	0.012	
352	Septin 6, isoform CRA_b OS=Homo sapiens GN=SEPT6 PE=1 SV=1	B1AMS2_HUMAN (+9)	49	0.043	0.000	0.000	0.000	0.000	0.000	0.007	0.018	
353	Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1	ALS_HUMAN (+2)	66	0.000	0.000	0.043	0.000	0.000	0.000	0.007	0.018	
354	Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=1	A0A0A0MSD0_HUMAN (+1)	390	0.038	0.000	0.002	0.000	0.002	0.000	0.007	0.015	
355	EMILIN-1 OS=Homo sapiens GN=EMILIN1 PE=1 SV=1	A0A0C4DFX3_HUMAN (+1)	107	0.010	0.000	0.000	0.000	0.000	0.033	0.007	0.013	
356	Ras GTPase-activating protein 3 OS=Homo sapiens GN=RASA3 PE=1 SV=3	RASA3_HUMAN	96	0.000	0.000	0.000	0.000	0.000	0.043	0.007	0.017	
357	Glycyl-tRNA synthetase OS=Homo sapiens GN=GARS PE=4 SV=1	A0A090N8G0_HUMAN (+1)	78	0.027	0.000	0.000	0.000	0.000	0.015	0.007	0.012	
358	cDNA FLJ53218, highly similar to Homo sapiens SAC1 suppressor of actin mutations 1-like (SACM1L), mRNA OS=Homo sapiens PE=2 SV=1	B4DVV3_HUMAN (+2)	56	0.000	0.000	0.000	0.000	0.000	0.042	0.007	0.017	
359	Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=5	CO6A3_HUMAN (+1)	344	0.008	0.004	0.000	0.000	0.004	0.026	0.007	0.010	

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360	Platelet endothelial cell adhesion molecule OS=Homo sapiens GN=PECAM1 PE=1 SV=1	A0A075B738_HUMAN (+2)	83	0.013	0.000	0.000	0.000	0.000	0.028	0.007	0.012
361	Solute carrier family 2, facilitated glucose transporter member 14 OS=Homo sapiens GN=SLC2A14 PE=2 SV=1	GTR14_HUMAN (+1)	56	0.019	0.000	0.000	0.000	0.000	0.021	0.007	0.010
362	cDNA, FLJ96812, highly similar to Homo sapiens threonyl-tRNA synthetase (TARS), mRNA OS=Homo sapiens PE=1 SV=1	B2RDX5_HUMAN (+2)	82	0.000	0.011	0.000	0.000	0.000	0.029	0.007	0.012
363	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4	2AAA_HUMAN (+5)	65	0.025	0.014	0.000	0.000	0.000	0.000	0.006	0.011
364	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3	UGGG1_HUMAN	177	0.012	0.000	0.000	0.000	0.000	0.027	0.006	0.011
365	Serpin peptidase inhibitor, clade A (Alpha- 1 antitrypsin), member 4, isoform CRA_a OS=Homo sapiens GN=SERPINA4 PE=3 SV=1	A0A024R6I9_HUMAN (+2)	49	0.000	0.019	0.019	0.000	0.000	0.000	0.006	0.010
366	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3	6PGD_HUMAN (+1)	53	0.020	0.017	0.000	0.000	0.000	0.000	0.006	0.010
367	Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2	DYN2_HUMAN	98	0.011	0.000	0.000	0.000	0.000	0.024	0.006	0.010
368	Myosin light chain kinase, smooth muscle OS=Homo sapiens GN=MYLK PE=1 SV=4	MYLK_HUMAN	211	0.010	0.011	0.000	0.000	0.000	0.014	0.006	0.006
369	Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2	CALX_HUMAN	68	0.000	0.000	0.000	0.000	0.000	0.035	0.006	0.014
370	Lipopolysaccharide-responsive and beige- like anchor protein OS=Homo sapiens GN=LRBA PE=1 SV=1	E9PEM5_HUMAN	287	0.011	0.000	0.000	0.000	0.000	0.023	0.006	0.009
371	Xaa-Pro aminopeptidase 1 OS=Homo sapiens GN=XPNPEP1 PE=1 SV=3	XPP1_HUMAN	70	0.000	0.000	0.000	0.000	0.000	0.034	0.006	0.014
372	CD47 OS=Homo sapiens GN=CD47 PE=2 SV=1	A0A0A1TSG4_HUMAN (+1)	32	0.033	0.000	0.000	0.000	0.000	0.000	0.006	0.014
373	cDNA FLJ59760, highly similar to 1,4- alpha-glucan branching enzyme (EC 2.4.1.18) OS=Homo sapiens PE=2 SV=1	B4DUF1_HUMAN (+3)	76	0.021	0.012	0.000	0.000	0.000	0.000	0.006	0.009
374	Hepatocyte growth factor activator OS=Homo sapiens GN=HGFA PE=1 SV=1	D6RAR4_HUMAN (+1)	71	0.000	0.019	0.013	0.000	0.000	0.000	0.005	0.009
375	cDNA, FLJ94267, highly similar to Homo sapiens glutathione S-transferase omega 1 (GSTO1), mRNA OS=Homo sapiens PE=2 SV=1	B2R983_HUMAN (+4)	28	0.000	0.033	0.000	0.000	0.000	0.000	0.005	0.013
376	Apolipoprotein A-V, isoform CRA_a OS=Homo sapiens GN=APOA5 PE=4 SV=1	A0A0B4RUS7_HUMAN (+3)	41	0.000	0.000	0.000	0.000	0.000	0.032	0.000	0.013
377	Platelet glycoprotein VI OS=Homo sapiens GN=GP6 PE=1 SV=4	GPVI_HUMAN	37	0.000	0.000	0.000	0.000	0.000	0.032	0.005	0.013
378	Aldehyde dehydrogenase family 16 member A1 OS=Homo sapiens GN=ALDH16A1 PE=1 SV=2	A16A1_HUMAN (+3)	85	0.000	0.011	0.000	0.000	0.000	0.021	0.005	0.009
379	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-A PE=3 SV=1	F6IQV5_HUMAN	38	0.000	0.000	0.000	0.000	0.000	0.031	0.005	0.013
380	X-DING-CD4 (Fragment) OS=Homo sapiens PE=2 SV=1	R4H484_HUMAN	30	0.000	0.030	0.000	0.000	0.000	0.000	0.005	0.012
381	cDNA FLJ53963, highly similar to Leukocyte elastase inhibitor OS=Homo sapiens PE=2 SV=1	B4E3A8_HUMAN (+2)	39	0.000	0.000	0.000	0.000	0.000	0.030	0.005	0.012
382	SLAM family member 5 OS=Homo sapiens GN=CD84 PE=1 SV=1	SLAF5_HUMAN	39	0.000	0.000	0.000	0.000	0.000	0.030	0.005	0.012
383	Tyrosine-protein kinase BTK OS=Homo sapiens GN=BTK PE=1 SV=3	BTK_HUMAN	76	0.014	0.000	0.000	0.000	0.000	0.015	0.005	0.008
384	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	ATPA_HUMAN (+1)	60	0.000	0.000	0.000	0.000	0.000	0.029	0.005	0.012
385	Attractin OS=Homo sapiens GN=ATRN PE=1 SV=2	ATRN_HUMAN (+1)	159	0.000	0.017	0.006	0.006	0.000	0.000	0.005	0.007
386	Actin related protein 2/3 complex, subunit 1B, 41kDa OS=Homo sapiens GN=ARPC1B PE=2 SV=1	A4D275_HUMAN (+1)	41	0.000	0.000	0.000	0.000	0.000	0.029	0.005	0.012
387	Coagulation factor VIII OS=Homo sapiens GN=F8 PE=1 SV=1	FA8_HUMAN	267	0.010	0.000	0.007	0.000	0.000	0.011	0.005	0.005
388	ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	ATPB_HUMAN (+3)	57	0.028	0.000	0.000	0.000	0.000	0.000	0.005	0.011

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389	cDNA FLJ45348 fis, clone BRHIP3011269, weakly similar to Prenylcysteine oxidase (EC 1.8.3.5) OS=Homo sapiens PE=2 SV=1	B3KXF9_HUMAN (+2)	42	0.000	0.000	0.000	0.000	0.000	0.028	0.005	0.011
390	HMHA1 protein (Fragment) OS=Homo sapiens GN=HMHA1 PE=2 SV=1	Q8IYN3_HUMAN	124	0.009	0.000	0.000	0.000	0.000	0.019	0.005	0.008
391	Phosphoglucosmutase-2 OS=Homo sapiens GN=PGM2 PE=1 SV=4	PGM2_HUMAN	68	0.000	0.000	0.000	0.000	0.000	0.026	0.004	0.011
392	Protein 4.1 OS=Homo sapiens GN=EPB41 PE=1 SV=4	41_HUMAN (+2)	97	0.011	0.000	0.015	0.000	0.000	0.000	0.004	0.007
393	cDNA FLJ56358, highly similar to Cytosolic nonspecific dipeptidase OS=Homo sapiens PE=2 SV=1	B4DPF1_HUMAN (+2)	42	0.025	0.000	0.000	0.000	0.000	0.000	0.004	0.010
394	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=1	A0A0U1RQF0_HUMAN (+1)	273	0.012	0.000	0.000	0.000	0.000	0.013	0.004	0.006
395	Bromodomain adjacent to zinc finger domain protein 2B OS=Homo sapiens GN=BAZ2B PE=1 SV=3	BAZ2B_HUMAN	240	0.009	0.000	0.000	0.000	0.000	0.015	0.004	0.006
396	Acyl-coenzyme A oxidase OS=Homo sapiens GN=ACOX1 PE=3 SV=1	A0A024R8L7_HUMAN (+2)	75	0.000	0.000	0.000	0.000	0.000	0.024	0.004	0.010
397	ARP3 actin-related protein 3 homolog (Yeast), isoform CRA_a OS=Homo sapiens GN=ACTR3 PE=3 SV=1	A0A024RAI1_HUMAN (+3)	47	0.023	0.000	0.000	0.000	0.000	0.000	0.004	0.009
398	Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1	A0A087X054_HUMAN (+2)	105	0.000	0.000	0.000	0.000	0.000	0.022	0.004	0.009
399	Coatomer subunit beta' OS=Homo sapiens GN=COPB2 PE=1 SV=2	COPB2_HUMAN	102	0.010	0.000	0.000	0.000	0.000	0.012	0.004	0.006
400	Nck-associated protein 1 OS=Homo sapiens GN=NCKAP1 PE=1 SV=1	NCKP1_HUMAN	129	0.008	0.000	0.000	0.000	0.000	0.014	0.004	0.006
401	Carboxypeptidase B2 OS=Homo sapiens GN=CPB2 PE=1 SV=1	A0A087WSY5_HUMAN (+1)	44	0.000	0.000	0.022	0.000	0.000	0.000	0.004	0.009
402	ADAM metalloproteinase domain 10, isoform CRA_b OS=Homo sapiens GN=ADAM10 PE=4 SV=1	A0A024R5U5_HUMAN (+1)	84	0.000	0.000	0.000	0.000	0.000	0.021	0.003	0.009
403	Complement factor properdin isoform 1 (Fragment) OS=Homo sapiens GN=CFP PE=2 SV=1	A0A0S2Z4I5_HUMAN (+1)	51	0.021	0.000	0.000	0.000	0.000	0.000	0.003	0.009
404	Neurobeachin-like protein 2 OS=Homo sapiens GN=NBEAL2 PE=1 SV=2	NBEL2_HUMAN	303	0.005	0.000	0.000	0.000	0.000	0.016	0.003	0.006
405	Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4	CO6A2_HUMAN	109	0.010	0.000	0.000	0.000	0.000	0.011	0.003	0.005
406	cDNA FLJ61564, highly similar to Plexin domain-containing protein 2 OS=Homo sapiens PE=2 SV=1	B4E367_HUMAN (+1)	58	0.000	0.000	0.000	0.000	0.000	0.020	0.003	0.008
407	Kinesin-like protein KIF2A OS=Homo sapiens GN=KIF2A PE=1 SV=3	KIF2A_HUMAN	80	0.020	0.000	0.000	0.000	0.000	0.000	0.003	0.008
408	Protein kinase C substrate 80K-H, isoform CRA_a OS=Homo sapiens GN=PRKCSH PE=4 SV=1	A0A024R7F1_HUMAN (+5)	59	0.000	0.000	0.000	0.000	0.000	0.020	0.003	0.008
409	Coronin OS=Homo sapiens GN=CORO1B PE=3 SV=1	A0A024R5K1_HUMAN (+5)	54	0.020	0.000	0.000	0.000	0.000	0.000	0.003	0.008
410	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=2	F5GWF6_HUMAN (+3)	57	0.019	0.000	0.000	0.000	0.000	0.000	0.003	0.008
411	cDNA FLJ76863, highly similar to Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA OS=Homo sapiens PE=2 SV=1	A8K690_HUMAN (+2)	63	0.000	0.000	0.000	0.000	0.000	0.019	0.003	0.008
412	Laminin, gamma 1 (Formerly LAMB2), isoform CRA_a OS=Homo sapiens GN=LAMC1 PE=4 SV=1	A0A024R972_HUMAN (+1)	174	0.006	0.000	0.000	0.000	0.005	0.007	0.003	0.003
413	Coagulation factor IX OS=Homo sapiens GN=F9 p22 PE=2 SV=1	F2RM37_HUMAN (+1)	52	0.000	0.018	0.000	0.000	0.000	0.000	0.003	0.007
414	Heparanase, isoform CRA_a OS=Homo sapiens GN=HPSE PE=4 SV=1	A0A024RDB8_HUMAN (+2)	61	0.017	0.000	0.000	0.000	0.000	0.000	0.003	0.007
415	cDNA, FLJ95309, highly similar to Homo sapiens adenosine monophosphate deaminase 2 (isoform L)(AMPD2), mRNA OS=Homo sapiens PE=2 SV=1	B2RB47_HUMAN	101	0.000	0.000	0.000	0.000	0.000	0.017	0.003	0.007
416	cDNA FLJ50778, highly similar to Protein flightless-1 homolog OS=Homo sapiens PE=2 SV=1	B4DIX0_HUMAN (+1)	141	0.000	0.000	0.000	0.000	0.000	0.017	0.003	0.007
417	Type 1 tumor necrosis factor receptor shedding aminopeptidase regulator, isoform CRA_a OS=Homo sapiens GN=ARTS-1 PE=4 SV=1	A0A024RAR8_HUMAN (+13)	107	0.000	0.000	0.000	0.000	0.000	0.016	0.003	0.007
418	Phospholipid transfer protein, isoform CRA_c OS=Homo sapiens GN=PLTP PE=2 SV=1	B3KUE5_HUMAN (+2)	57	0.000	0.016	0.000	0.000	0.000	0.000	0.003	0.007

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419	HLA-B associated transcript 5, isoform CRA_b OS=Homo sapiens GN=ABHD16A PE=1 SV=1	A0A0G2JJD3_HUMAN (+2)	68	0.016	0.000	0.000	0.000	0.000	0.000	0.003	0.006
420	Signal transducer and activator of transcription OS=Homo sapiens PE=2 SV=1	B4DNPO_HUMAN (+4)	76	0.000	0.000	0.000	0.000	0.000	0.015	0.003	0.006
421	ATPase Ca++ transporting cardiac muscle slow twitch 2 isoform 1 (Fragment) OS=Homo sapiens GN=ATP2A2 PE=2 SV=1	A0A0S2Z3L2_HUMAN (+2)	115	0.000	0.000	0.000	0.000	0.000	0.015	0.003	0.006
422	Glycerol-3-phosphate dehydrogenase (Fragment) OS=Homo sapiens GN=GPD2 PE=3 SV=1	Q53T76_HUMAN	77	0.000	0.000	0.000	0.000	0.000	0.015	0.003	0.006
423	N-acylaminoacyl-peptide hydrolase, isoform CRA_b OS=Homo sapiens GN=APEH PE=4 SV=1	A0A024R2U9_HUMAN (+2)	81	0.000	0.000	0.000	0.000	0.000	0.015	0.002	0.006
424	Malic enzyme OS=Homo sapiens PE=2 SV=1	A8K168_HUMAN (+1)	64	0.000	0.014	0.000	0.000	0.000	0.000	0.002	0.006
425	Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	ITA2_HUMAN	129	0.000	0.000	0.000	0.000	0.000	0.014	0.002	0.006
426	cDNA FLJ78440, highly similar to Human lactoferrin OS=Homo sapiens PE=2 SV=1	A8K494_HUMAN (+8)	78	0.014	0.000	0.000	0.000	0.000	0.000	0.002	0.006
427	cDNA FLJ55918, highly similar to Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens PE=2 SV=1	B7Z2F5_HUMAN (+2)	87	0.000	0.000	0.000	0.000	0.000	0.014	0.002	0.006
428	NHL repeat-containing protein 2 OS=Homo sapiens GN=NHLRC2 PE=1 SV=1	NHLC2_HUMAN	79	0.013	0.000	0.000	0.000	0.000	0.000	0.002	0.006
429	Coagulation factor XII OS=Homo sapiens GN=F12 PE=4 SV=1	A0A0R7FJH5_HUMAN (+2)	68	0.000	0.013	0.000	0.000	0.000	0.000	0.002	0.005
430	Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=1	A2A274_HUMAN (+7)	88	0.000	0.000	0.000	0.000	0.000	0.013	0.002	0.005
431	Carnitine palmitoyltransferase 1A (Liver), isoform CRA_a OS=Homo sapiens GN=CPT1A PE=3 SV=1	A0A024R5F4_HUMAN (+2)	88	0.000	0.000	0.000	0.000	0.000	0.013	0.002	0.005
432	cDNA FLJ50510, highly similar to Heat shock 70 kDa protein 4 OS=Homo sapiens PE=2 SV=1	B4DH02_HUMAN (+3)	94	0.000	0.000	0.000	0.000	0.000	0.013	0.002	0.005
433	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2	LRP1_HUMAN	505	0.004	0.002	0.000	0.000	0.003	0.003	0.002	0.002
434	Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3	ACOC_HUMAN (+1)	98	0.000	0.000	0.000	0.000	0.000	0.012	0.002	0.005
435	cDNA FLJ77762, highly similar to Homo sapiens cullin-associated and neddylation-dissociated 1 (CAND1), mRNA OS=Homo sapiens PE=2 SV=1	A8K8U1_HUMAN (+1)	136	0.012	0.000	0.000	0.000	0.000	0.000	0.002	0.005
436	Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3	PHLD_HUMAN	92	0.000	0.000	0.010	0.000	0.000	0.000	0.002	0.004
437	cDNA FLJ51067, highly similar to DNA damage-binding protein 1 OS=Homo sapiens PE=2 SV=1	B4DSA8_HUMAN (+3)	112	0.010	0.000	0.000	0.000	0.000	0.000	0.002	0.004
438	Spectrin beta chain, non-erythrocytic 2 OS=Homo sapiens GN=SPTBN2 PE=1 SV=3	SPTN2_HUMAN	271	0.000	0.000	0.009	0.000	0.000	0.000	0.001	0.004
439	Epididymis luminal protein 102 OS=Homo sapiens GN=SPTBN1 PE=2 SV=1	B2ZZ89_HUMAN (+2)	275	0.000	0.000	0.000	0.000	0.000	0.009	0.001	0.003
440	Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=3	DCTN1_HUMAN (+2)	142	0.000	0.000	0.000	0.000	0.000	0.008	0.001	0.003
441	Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=1	G3XAI2_HUMAN (+1)	200	0.000	0.000	0.000	0.000	0.007	0.000	0.001	0.003
442	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	DYHC1_HUMAN	532	0.006	0.000	0.000	0.000	0.000	0.000	0.001	0.002
443	Tenascin-X OS=Homo sapiens GN=TNXB PE=1 SV=1	A0A087X0I0_HUMAN (+2)	213	0.000	0.000	0.000	0.000	0.000	0.006	0.001	0.002
444	Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	HORN_HUMAN	282	0.000	0.000	0.000	0.003	0.000	0.000	0.001	0.001
445	Hemicentin-1 OS=Homo sapiens GN=HMCN1 PE=1 SV=2	HMCN1_HUMAN	613	0.002	0.000	0.000	0.000	0.000	0.000	0.000	0.001

Supporting Table 4

Table S4: Blood-circulation proteome analysis. Full list of proteins identified in plasma samples recovered from 6 ovarian carcinoma patients (across all samples).

#	Identified Proteins	Accession Number	MW	RPA% (P1)	RPA% (P2)	RPA% (P3)	RPA% (P4)	RPA% (P5)	RPA% (P6)	Average RPA%	Standard Deviation
1	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	ALBU_HUMAN	69	5.712	8.072	7.063	9.004	7.367	14.689	8.651	3.154
2	Putative uncharacterized protein DKFZp686C11235 OS=Homo sapiens GN=DKFZp686C11235 PE=1 SV=1	Q6MZV7_HUMAN	52	2.575	3.134	2.616	3.189	2.506	2.863	2.814	0.295
3	IGH@ protein OS=Homo sapiens GN=IGH@ PE=1 SV=1	Q6GMX6_HUMAN	51	2.195	2.551	2.253	2.503	2.837	2.488	2.471	0.230
4	Putative uncharacterized protein DKFZp686I04196 (Fragment) OS=Homo sapiens GN=DKFZp686I04196 PE=1 SV=1	Q6N093_HUMAN	46	2.030	3.134	2.077	2.659	2.218	2.532	2.442	0.421
5	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	A0A087WV47_HUMAN (+1)	51	2.220	2.459	2.184	2.455	2.746	2.424	2.415	0.202
6	cDNA FLJ78387 OS=Homo sapiens PE=1 SV=1	A8K008_HUMAN	52	2.283	2.420	2.142	2.473	2.702	2.451	2.412	0.189
7	Transferrin variant (Fragment) OS=Homo sapiens PE=2 SV=1	Q53H26_HUMAN	77	1.810	2.250	1.807	2.637	2.602	2.911	2.336	0.459
8	Putative uncharacterized protein DKFZp686C15213 OS=Homo sapiens GN=DKFZp686C15213 PE=1 SV=1	Q6MZU6_HUMAN	51	1.855	2.855	1.890	2.408	1.928	2.187	2.187	0.390
9	Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=4	HOY300_HUMAN	49	2.319	1.639	2.471	1.875	2.006	2.433	2.124	0.336
10	Putative uncharacterized protein DKFZp686G11190 OS=Homo sapiens GN=DKFZp686G11190 PE=1 SV=1	Q6MZQ6_HUMAN	52	1.860	2.023	1.820	2.110	2.399	1.976	2.031	0.209
11	Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=4 SV=1	A0A087WXL8_HUMAN	57	1.808	2.290	1.776	2.273	1.676	2.274	2.016	0.291
12	Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=1 SV=1	H3BS21_HUMAN	25	2.332	1.540	2.289	1.508	1.744	2.461	1.979	0.429
13	Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	FIBA_HUMAN	95	1.819	1.720	2.368	2.092	1.694	2.035	1.955	0.260
14	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	A0A087WYC5_HUMAN	52	2.120	2.330	2.083	2.362	2.613	0.000	1.918	0.959
15	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	CO3_HUMAN (+1)	187	1.927	2.207	1.820	1.536	1.835	1.889	1.869	0.216
16	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	A2MG_HUMAN	163	1.514	1.740	1.007	1.667	2.265	1.715	1.651	0.406
17	Fibrinogen beta chain OS=Homo sapiens GN=FBG PE=1 SV=2	FIBB_HUMAN (+1)	56	1.441	1.291	1.667	1.537	1.259	1.707	1.484	0.187
18	Lambda-chain (AA -20 to 215) OS=Homo sapiens PE=1 SV=1	A2NUT2_HUMAN	25	1.284	1.446	1.479	1.489	1.169	1.362	1.372	0.126
19	IGL@ protein OS=Homo sapiens GN=IGL@ PE=2 SV=1	Q6PIQ7_HUMAN	25	1.234	1.465	1.550	1.392	1.113	1.340	1.349	0.158
20	IGL@ protein OS=Homo sapiens GN=IGL@ PE=1 SV=1	Q8N355_HUMAN	25	1.267	1.446	1.444	1.431	1.132	1.340	1.343	0.126
21	Protein IGHV3-72 OS=Homo sapiens GN=IGHV3-72 PE=4 SV=1	A0A087WW89_HUMAN	11	1.421	1.195	1.161	1.538	1.265	1.199	1.296	0.150
22	cDNA FLJ14473 fis, clone MAMMA1001080, highly similar to Homo sapiens SNC73 protein (SNC73) mRNA OS=Homo sapiens PE=2 SV=1	Q96K68_HUMAN	53	1.172	1.630	1.096	1.286	0.980	1.337	1.250	0.226
23	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	A1AT_HUMAN (+1)	47	1.402	1.339	0.965	1.173	1.283	1.169	1.222	0.156
24	Putative uncharacterized protein DKFZp686P15220 OS=Homo sapiens GN=DKFZp686P15220 PE=1 SV=1	Q6N089_HUMAN	52	2.120	2.348	0.000	0.000	2.622	0.000	1.182	1.304
25	Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	IGHG4_HUMAN (+1)	36	1.127	1.370	0.905	1.061	1.494	1.099	1.176	0.216
26	Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=1 SV=2	HPTR_HUMAN	39	1.376	1.048	1.287	0.992	1.035	1.183	1.153	0.155
27	IgG H chain OS=Homo sapiens PE=1 SV=1	S6B291_HUMAN	51	2.137	0.000	2.115	0.000	2.664	0.000	1.153	1.278
28	Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	FIBG_HUMAN	52	1.056	0.984	1.287	1.162	0.972	1.109	1.095	0.119
29	IgG L chain OS=Homo sapiens PE=1 SV=1	S6BGD6_HUMAN	25	1.048	1.165	1.215	1.180	0.890	1.033	1.088	0.122
30	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=1	A0A087X2C0_HUMAN	64	0.937	0.903	1.107	1.065	1.536	0.764	1.052	0.267

31	Immunoglobulin heavy chain variant (Fragment) OS=Homo sapiens PE=2 SV=1	Q9NPP6_HUMAN	45	0.967	1.325	0.910	0.999	0.866	1.086	1.026	0.165
32	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	HEMO_HUMAN	52	0.894	1.102	1.075	0.948	0.865	1.225	1.018	0.139
33	IgG H chain OS=Homo sapiens PE=2 SV=1	S6BGE0_HUMAN	32	1.162	1.247	1.059	1.103	1.043	0.000	0.936	0.464
34	Apolipoprotein B (Including Ag(X) antigen) OS=Homo sapiens GN=APOB PE=4 SV=1	C0JYY2_HUMAN	516	0.736	1.033	0.672	0.840	1.211	0.942	0.906	0.199
35	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=1	A0A087WYJ9_HUMAN	66	0.877	0.904	1.101	1.048	1.497	0.000	0.904	0.496
36	Epididymis tissue protein Li 173 OS=Homo sapiens PE=2 SV=1	E9KL26_HUMAN (+1)	55	1.014	0.990	0.776	0.765	0.902	0.879	0.888	0.104
37	IGL@ protein OS=Homo sapiens GN=IGL@ PE=1 SV=1	Q6PIK1_HUMAN	25	0.828	0.883	1.004	1.025	0.668	0.879	0.881	0.130
38	Myosin-reactive immunoglobulin heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	Q9UL88_HUMAN	14	1.328	0.772	0.692	1.036	0.596	0.824	0.875	0.267
39	IGK@ protein OS=Homo sapiens GN=IGK@ PE=1 SV=1	Q6PIL8_HUMAN	26	0.780	0.993	0.897	0.837	0.910	0.676	0.849	0.111
40	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	A0A087X1C7_HUMAN	50	0.000	0.000	2.148	0.000	2.699	0.000	0.808	1.264
41	cDNA FLJ53691, highly similar to Serotransferrin OS=Homo sapiens PE=2 SV=1	B4E1B2_HUMAN	75	1.870	0.000	0.000	2.746	0.000	0.000	0.769	1.224
42	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	A0A087X079_HUMAN	52	2.161	0.000	0.000	2.399	0.000	0.000	0.760	1.180
43	Epididymis secretory protein Li 51 OS=Homo sapiens GN=HEL-S-51 PE=2 SV=1	V9HWI6_HUMAN (+1)	53	0.630	0.682	0.581	0.648	0.543	0.974	0.676	0.154
44	Kininogen 1, isoform CRA_a OS=Homo sapiens GN=KNG1 PE=4 SV=1	D3DNU8_HUMAN	48	0.493	0.587	0.688	0.584	0.580	0.858	0.632	0.127
45	Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2	PLMN_HUMAN	91	0.613	0.578	0.542	0.473	0.571	1.008	0.631	0.191
46	Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2_HUMAN (+2)	15	0.253	0.657	1.379	0.548	0.495	0.330	0.610	0.404
47	Vitronectin OS=Homo sapiens GN=VTN PE=4 SV=1	D9ZGG2_HUMAN (+1)	54	0.634	0.557	0.660	0.537	0.558	0.692	0.606	0.064
48	Inter-alpha (Globulin) inhibitor H4 (Plasma Kallikrein-sensitive glycoprotein) OS=Homo sapiens GN=ITIH4 PE=2 SV=1	B2RMS9_HUMAN (+1)	103	0.578	0.675	0.603	0.530	0.698	0.533	0.603	0.071
49	Complement C4-B OS=Homo sapiens GN=C4B PE=1 SV=2	CO4B_HUMAN	193	0.560	0.749	0.586	0.441	0.613	0.666	0.603	0.104
50	Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1	A1AG1_HUMAN (+1)	24	0.792	0.528	0.715	0.544	0.406	0.504	0.582	0.144
51	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=1	Q5T985_HUMAN	105	0.539	0.599	0.495	0.529	0.663	0.659	0.581	0.071
52	Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	CFAH_HUMAN	139	0.538	0.530	0.557	0.390	0.574	0.830	0.570	0.143
53	Ig kappa chain V-III region WOL OS=Homo sapiens PE=1 SV=1	KV305_HUMAN	12	0.493	0.626	0.404	0.604	0.541	0.595	0.544	0.084
54	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2	CO4A_HUMAN	193	0.552	0.749	0.591	0.000	0.598	0.646	0.523	0.265
55	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3	ITIH1_HUMAN	101	0.489	0.590	0.466	0.469	0.652	0.451	0.520	0.082
56	CP protein OS=Homo sapiens GN=CP PE=2 SV=1	A5PL27_HUMAN (+1)	122	0.381	0.620	0.476	0.472	0.566	0.572	0.514	0.087
57	cDNA FLJ35730 fis, clone TESTI2003131, highly similar to ALPHA-1- ANTICHYMOTRYPSIN OS=Homo sapiens PE=2 SV=1	B3KS79_HUMAN	51	0.646	0.562	0.518	0.379	0.546	0.399	0.508	0.102
58	IBM-B2 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A125QYY9_HUMAN	14	0.422	0.570	0.472	0.587	0.563	0.392	0.501	0.084
59	Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2	THR_B_HUMAN	70	0.416	0.429	0.296	0.435	0.384	0.738	0.450	0.150
60	Myosin-reactive immunoglobulin heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	Q9UL90_HUMAN	12	0.669	0.509	0.367	0.483	0.309	0.275	0.435	0.147
61	Putative uncharacterized protein DKFZp686L19235 OS=Homo sapiens GN=DKFZp686L19235 PE=2 SV=1	Q6MZV6_HUMAN	52	0.886	0.000	0.838	0.000	0.803	0.000	0.421	0.462
62	Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4	A1BG_HUMAN (+1)	54	0.391	0.487	0.399	0.233	0.421	0.498	0.405	0.095
63	APOB protein OS=Homo sapiens GN=APOB PE=2 SV=1	Q7Z7Q0_HUMAN	92	0.000	0.000	0.000	1.030	0.000	1.290	0.387	0.605
64	Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3	HEP2_HUMAN	57	0.378	0.379	0.332	0.441	0.415	0.357	0.384	0.039
65	cDNA, FLJ93914, highly similar to Homo sapiens histidine-rich glycoprotein (HRG), mRNA OS=Homo sapiens PE=2 SV=1	B2R8I2_HUMAN	60	0.437	0.368	0.367	0.298	0.332	0.449	0.375	0.058

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66	Apolipoprotein A-I, isoform CRA_a OS=Homo sapiens GN=APOA1 PE=4 SV=1	A0A024R3E3_HUMAN (+1)	31	0.313	0.364	0.284	0.421	0.509	0.319	0.368	0.084
67	Myosin-reactive immunoglobulin light chain variable region (Fragment) OS=Homo sapiens PE=1 SV=1	Q9UL83_HUMAN	12	0.317	0.352	0.330	0.524	0.271	0.366	0.360	0.087
68	Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	D9YZU5_HUMAN (+1)	16	0.079	0.411	0.880	0.393	0.377	0.000	0.357	0.311
69	Uncharacterized protein OS=Homo sapiens PE=2 SV=1	B4E1Z4_HUMAN	141	0.333	0.350	0.375	0.309	0.293	0.471	0.355	0.064
70	Uncharacterized protein OS=Homo sapiens PE=2 SV=1	Q8NEJ1_HUMAN	25	1.031	0.000	0.000	0.000	0.000	1.077	0.351	0.544
71	Beta-2-glycoprotein I (Fragment) OS=Homo sapiens PE=2 SV=1	D9IWP9_HUMAN	36	0.293	0.313	0.281	0.215	0.271	0.641	0.336	0.153
72	Anti-FactorVIII scFv (Fragment) OS=Homo sapiens PE=2 SV=1	A2KBC6_HUMAN	25	0.355	0.376	0.370	0.387	0.352	0.132	0.329	0.097
73	Transthyretin OS=Homo sapiens PE=2 SV=1	A6XGL1_HUMAN (+2)	20	0.169	0.188	0.374	0.556	0.348	0.330	0.327	0.141
74	Fibronectin 1, isoform CRA_n OS=Homo sapiens GN=FN1 PE=4 SV=1	A0A024R462_HUMAN	259	0.334	0.181	0.369	0.226	0.398	0.378	0.314	0.089
75	cDNA FLJ56954, highly similar to Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens PE=2 SV=1	B7Z539_HUMAN	72	0.510	0.000	0.520	0.000	0.715	0.000	0.291	0.327
76	C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2	C4BPA_HUMAN	67	0.202	0.294	0.151	0.180	0.201	0.689	0.286	0.203
77	MS-D4 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A0X9UWK7_HUMAN	14	0.332	0.268	0.346	0.242	0.331	0.196	0.286	0.060
78	GCT-A10 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A120HG46_HUMAN	14	0.392	0.000	0.566	0.000	0.629	0.000	0.265	0.300
79	Serpin peptidase inhibitor, clade C (Antithrombin), member 1, isoform CRA_a OS=Homo sapiens GN=SERPINC1 PE=3 SV=1	A0A024R944_HUMAN (+1)	53	0.255	0.239	0.241	0.283	0.280	0.259	0.260	0.019
80	cDNA FLJ53025, highly similar to Complement C4-B OS=Homo sapiens PE=2 SV=1	B7Z1F8_HUMAN	30	0.000	1.534	0.000	0.000	0.000	0.000	0.256	0.626
81	Protein IGHV3-74 (Fragment) OS=Homo sapiens GN=IGHV3-74 PE=1 SV=1	A0A0B4J1X5_HUMAN	13	0.357	0.253	0.339	0.223	0.357	0.000	0.255	0.137
82	Protein SAA2-SAA4 OS=Homo sapiens GN=SAA2-SAA4 PE=4 SV=1	A0A096LPE2_HUMAN	23	0.275	0.286	0.306	0.294	0.101	0.263	0.254	0.077
83	IGL@ protein OS=Homo sapiens GN=IGL@ PE=1 SV=1	Q8N5F4_HUMAN	25	0.000	0.000	1.514	0.000	0.000	0.000	0.252	0.618
84	A30 (Fragment) OS=Homo sapiens PE=4 SV=1	A2MYE1_HUMAN (+1)	10	0.211	0.470	0.220	0.290	0.186	0.110	0.248	0.123
85	Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1	AMBP_HUMAN	39	0.217	0.229	0.271	0.161	0.214	0.394	0.248	0.080
86	Ig lambda-7 chain C region OS=Homo sapiens GN=IGLC7 PE=1 SV=2	LAC7_HUMAN	11	0.000	1.452	0.000	0.000	0.000	0.000	0.242	0.593
87	Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4	CO5_HUMAN	188	0.234	0.270	0.255	0.201	0.234	0.240	0.239	0.023
88	Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1	APOA2_HUMAN (+1)	11	0.269	0.213	0.240	0.308	0.379	0.000	0.235	0.129
89	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	GELS_HUMAN	86	0.182	0.137	0.184	0.292	0.243	0.275	0.219	0.061
90	cDNA FLJ55606, highly similar to Alpha-2-HS-glycoprotein OS=Homo sapiens PE=2 SV=1	B7Z8Q2_HUMAN (+2)	47	0.144	0.220	0.178	0.267	0.178	0.304	0.215	0.061
91	Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1	ALS_HUMAN (+1)	66	0.198	0.178	0.253	0.212	0.232	0.208	0.214	0.026
92	Histidine-rich glycoprotein OS=Homo sapiens GN=HRG PE=1 SV=1	HRG_HUMAN	60	0.000	0.415	0.382	0.000	0.000	0.467	0.211	0.232
93	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	ACTB_HUMAN (+2)	42	0.272	0.179	0.241	0.368	0.077	0.105	0.207	0.109
94	Ig heavy chain V-III region GAL OS=Homo sapiens PE=1 SV=1	HV320_HUMAN	13	0.000	0.433	0.000	0.409	0.392	0.000	0.206	0.226
95	Complement factor H-related protein 1 OS=Homo sapiens GN=CFHR1 PE=1 SV=2	FHR1_HUMAN	38	0.289	0.210	0.324	0.000	0.000	0.405	0.205	0.170
96	Complement component 9, isoform CRA_a OS=Homo sapiens GN=C9 PE=4 SV=1	A0A024R035_HUMAN (+1)	63	0.221	0.268	0.189	0.161	0.118	0.218	0.196	0.052
97	N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2 PE=1 SV=1	PGRP2_HUMAN	62	0.191	0.212	0.149	0.203	0.180	0.230	0.194	0.028
98	cDNA, FLJ94213, highly similar to Homo sapiens pregnancy-zone protein (PZP), mRNA OS=Homo sapiens PE=2 SV=1	B2R950_HUMAN (+1)	164	0.188	0.235	0.156	0.139	0.257	0.184	0.193	0.045
99	GCT-A4 light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A0X9T7V9_HUMAN	12	0.176	0.157	0.147	0.201	0.193	0.229	0.184	0.030
100	Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3	APOA4_HUMAN	45	0.094	0.115	0.205	0.247	0.155	0.244	0.177	0.066
101	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2	ITIH3_HUMAN	100	0.241	0.244	0.176	0.111	0.190	0.093	0.176	0.063

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102	MS-D1 light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A0X9TD47_HUMAN	12	0.000	0.235	0.220	0.322	0.271	0.000	0.175	0.140
103	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	APOE_HUMAN (+1)	36	0.141	0.183	0.159	0.188	0.167	0.198	0.173	0.021
104	Uncharacterized protein OS=Homo sapiens PE=2 SV=1	A0A5E4_HUMAN	25	1.031	0.000	0.000	0.000	0.000	0.000	0.172	0.421
105	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1	APOD_HUMAN	21	0.161	0.112	0.147	0.184	0.177	0.235	0.169	0.041
106	Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=2	ZA2G_HUMAN	34	0.174	0.152	0.207	0.185	0.082	0.210	0.168	0.048
107	IGL@ protein OS=Homo sapiens GN=IGL@ PE=2 SV=1	Q567P1_HUMAN	25	0.997	0.000	0.000	0.000	0.000	0.000	0.166	0.407
108	Immunglobulin heavy chain variable region (Fragment) OS=Homo sapiens PE=4 SV=1	Q0ZCH6_HUMAN	14	0.211	0.134	0.126	0.242	0.166	0.118	0.166	0.050
109	Coagulation factor XII OS=Homo sapiens GN=F12 PE=1 SV=3	FA12_HUMAN (+1)	68	0.155	0.138	0.129	0.142	0.157	0.259	0.163	0.048
110	Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3	A2AP_HUMAN	55	0.154	0.154	0.160	0.149	0.143	0.210	0.162	0.024
111	GCT-A5 light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A0X9UWL5_HUMAN	12	0.317	0.352	0.293	0.000	0.000	0.000	0.160	0.177
112	Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3	CO6_HUMAN	105	0.177	0.165	0.134	0.115	0.168	0.194	0.159	0.029
113	Serum amyloid P-component OS=Homo sapiens GN=APCS PE=1 SV=2	SAMP_HUMAN (+1)	25	0.203	0.188	0.141	0.116	0.130	0.176	0.159	0.035
114	Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3	CO8G_HUMAN	22	0.211	0.171	0.160	0.176	0.042	0.175	0.156	0.058
115	Alpha-1-acid glycoprotein 2 OS=Homo sapiens GN=ORM2 PE=1 SV=2	A1AG2_HUMAN	24	0.141	0.196	0.220	0.101	0.116	0.137	0.152	0.047
116	Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3	PON1_HUMAN	40	0.106	0.141	0.121	0.169	0.139	0.233	0.152	0.045
117	Complement component 1, q subcomponent, B chain, isoform CRA_a OS=Homo sapiens GN=C1QB PE=4 SV=1	A0A024RAB9_HUMAN (+3)	27	0.125	0.157	0.114	0.161	0.120	0.224	0.150	0.041
118	Uncharacterized protein OS=Homo sapiens PE=1 SV=1	Q8TCD0_HUMAN	26	0.000	0.000	0.000	0.874	0.000	0.000	0.146	0.357
119	Retinol binding protein 4, plasma, isoform CRA_b OS=Homo sapiens GN=RBP4 PE=1 SV=2	Q5VY30_HUMAN (+2)	23	0.129	0.061	0.153	0.168	0.121	0.239	0.145	0.059
120	IGL@ protein OS=Homo sapiens GN=IGL@ PE=1 SV=1	Q5FWF9_HUMAN	25	0.000	0.000	0.863	0.000	0.000	0.000	0.144	0.352
121	Complement component 1, q subcomponent, C chain, isoform CRA_a OS=Homo sapiens GN=C1QC PE=4 SV=1	A0A024RAA7_HUMAN (+1)	26	0.114	0.163	0.169	0.112	0.089	0.190	0.139	0.040
122	HCG40889, isoform CRA_b OS=Homo sapiens GN=hCG_40889 PE=4 SV=1	A0A024R962_HUMAN	139	0.000	0.000	0.000	0.000	0.000	0.834	0.139	0.340
123	GCT-A5 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A0X9T0H6_HUMAN	12	0.458	0.000	0.367	0.000	0.000	0.000	0.137	0.215
124	Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2	CO8A_HUMAN	65	0.175	0.152	0.135	0.112	0.121	0.127	0.137	0.023
125	Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1	PROS_HUMAN (+2)	75	0.141	0.175	0.088	0.084	0.179	0.139	0.134	0.041
126	Afamin OS=Homo sapiens GN=AFM PE=1 SV=1	AFAM_HUMAN	69	0.073	0.102	0.057	0.112	0.188	0.271	0.134	0.081
127	Plasma kallikrein heavy chain (Fragment) OS=Homo sapiens GN=KLKB1 PE=3 SV=1	H0YAC1_HUMAN	77	0.082	0.098	0.120	0.113	0.157	0.221	0.132	0.050
128	Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=2 SV=1	B4DPQ0_HUMAN	82	0.113	0.155	0.113	0.112	0.102	0.181	0.129	0.031
129	CD5 antigen-like OS=Homo sapiens GN=CD5L PE=1 SV=1	CD5L_HUMAN	38	0.122	0.111	0.127	0.089	0.122	0.202	0.129	0.038
130	GCT-A8 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A0X9V9C4_HUMAN	13	0.227	0.000	0.237	0.000	0.000	0.296	0.127	0.141
131	Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1	C1S_HUMAN	77	0.104	0.140	0.103	0.107	0.133	0.164	0.125	0.025
132	Complement component 8, beta polypeptide, isoform CRA_b OS=Homo sapiens GN=C8B PE=2 SV=1	B7Z550_HUMAN (+4)	60	0.120	0.110	0.125	0.105	0.100	0.165	0.121	0.023
133	cDNA FLJ78207, highly similar to Human complement protein component C7 mRNA OS=Homo sapiens PE=2 SV=1	A8K2T4_HUMAN (+1)	93	0.141	0.146	0.099	0.068	0.080	0.189	0.121	0.046
134	Ig heavy chain V-III region WEA OS=Homo sapiens PE=1 SV=1	HV302_HUMAN	12	0.211	0.000	0.293	0.201	0.000	0.000	0.118	0.133
135	Carboxypeptidase B2 OS=Homo sapiens GN=CPB2 PE=4 SV=1	A0A087WSY5_HUMAN (+1)	44	0.086	0.128	0.100	0.143	0.116	0.125	0.116	0.020
136	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	LUM_HUMAN (+1)	38	0.100	0.124	0.116	0.127	0.098	0.116	0.113	0.012
137	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1	D6RF35_HUMAN	53	0.000	0.000	0.665	0.000	0.000	0.000	0.111	0.271

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138	Rheumatoid factor G9 light chain (Fragment) OS=Homo sapiens GN=V<lambda>3 PE=2 SV=1	A0N5G3_HUMAN	13	0.000	0.000	0.643	0.000	0.000	0.000	0.107	0.263
139	Protein IGLV8-61 (Fragment) OS=Homo sapiens GN=IGLV8-61 PE=4 SV=2	A0A075B6I0_HUMAN (+1)	13	0.325	0.000	0.169	0.149	0.000	0.000	0.107	0.132
140	Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=2 SV=1	A3KPE2_HUMAN (+2)	11	0.077	0.085	0.120	0.176	0.084	0.100	0.107	0.037
141	Protein IGLV2-11 (Fragment) OS=Homo sapiens GN=IGLV2-11 PE=4 SV=1	A0A075B6K3_HUMAN (+1)	13	0.260	0.000	0.373	0.000	0.000	0.000	0.105	0.167
142	Protein IGHV3-13 (Fragment) OS=Homo sapiens GN=IGHV3-13 PE=4 SV=1	A0A0A0MS11_HUMAN	13	0.227	0.217	0.000	0.186	0.000	0.000	0.105	0.116
143	Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1	H6VRF8_HUMAN (+3)	66	0.141	0.107	0.093	0.059	0.176	0.042	0.103	0.050
144	Cryocryoglobulin CC1 kappa light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	B1N7B8_HUMAN	12	0.141	0.000	0.000	0.282	0.193	0.000	0.103	0.121
145	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	CLUS_HUMAN	52	0.097	0.099	0.110	0.074	0.089	0.116	0.098	0.015
146	Protein IGKV2D-24 (Fragment) OS=Homo sapiens GN=IGKV2D-24 PE=4 SV=1	A0A075B6R9_HUMAN (+1)	13	0.065	0.072	0.000	0.149	0.214	0.085	0.097	0.074
147	Leucine-rich alpha-2-glycoprotein OS=Homo sapiens GN=HMFT1766 PE=2 SV=1	Q68CK4_HUMAN	38	0.111	0.111	0.104	0.115	0.085	0.058	0.097	0.022
148	Ig heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A068LKQ2_HUMAN	13	0.000	0.144	0.135	0.074	0.107	0.085	0.091	0.052
149	Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=4	PEDF_HUMAN	46	0.092	0.061	0.096	0.116	0.060	0.119	0.091	0.025
150	Immunoglobulin J chain OS=Homo sapiens GN=IGJ PE=1 SV=4	IGJ_HUMAN	18	0.047	0.000	0.098	0.161	0.103	0.122	0.089	0.057
151	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	K1C10_HUMAN	59	0.129	0.111	0.082	0.025	0.134	0.047	0.088	0.045
152	Complement C2 OS=Homo sapiens GN=C2 PE=1 SV=2	CO2_HUMAN (+3)	83	0.000	0.000	0.127	0.122	0.123	0.152	0.087	0.069
153	GCT-A1 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A125U0V2_HUMAN	14	0.000	0.000	0.000	0.518	0.000	0.000	0.086	0.211
154	IgG H chain OS=Homo sapiens PE=2 SV=1	S6B2B6_HUMAN	29	0.000	0.000	0.516	0.000	0.000	0.000	0.086	0.211
155	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	K22E_HUMAN	65	0.097	0.116	0.075	0.037	0.143	0.000	0.078	0.052
156	APOL1 protein (Fragment) OS=Homo sapiens GN=APOL1 PE=2 SV=1	A5PL32_HUMAN (+2)	49	0.078	0.077	0.045	0.109	0.114	0.045	0.078	0.030
157	Angiotensinogen variant (Fragment) OS=Homo sapiens PE=2 SV=1	Q53GY3_HUMAN (+3)	53	0.064	0.044	0.042	0.073	0.096	0.104	0.070	0.026
158	Protein IGHV3-73 (Fragment) OS=Homo sapiens GN=IGHV3-73 PE=1 SV=1	A0A0B4J1V6_HUMAN	9	0.000	0.000	0.000	0.000	0.412	0.000	0.069	0.168
159	Rheumatoid factor C6 light chain (Fragment) OS=Homo sapiens GN=V<kappa>1 PE=2 SV=1	A0N5G1_HUMAN	13	0.195	0.108	0.000	0.000	0.107	0.000	0.068	0.081
160	Thyroxine-binding globulin OS=Homo sapiens GN=SERPINA7 PE=1 SV=2	THBG_HUMAN	46	0.073	0.092	0.048	0.084	0.071	0.036	0.067	0.021
161	Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3	CPN2_HUMAN	61	0.062	0.069	0.043	0.048	0.084	0.081	0.065	0.017
162	Ficolin-3 OS=Homo sapiens GN=FCN3 PE=1 SV=2	FCN3_HUMAN	33	0.077	0.057	0.053	0.073	0.056	0.067	0.064	0.010
163	Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2	CFAI_HUMAN (+2)	66	0.032	0.064	0.047	0.029	0.056	0.142	0.062	0.041
164	IgG L chain OS=Homo sapiens PE=2 SV=1	S6AWF4_HUMAN	20	0.000	0.000	0.000	0.363	0.000	0.000	0.060	0.148
165	Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1	CBPN_HUMAN	52	0.049	0.081	0.051	0.074	0.054	0.053	0.060	0.014
166	VH6DJ protein (Fragment) OS=Homo sapiens GN=VH6DJ PE=2 SV=1	A2N0T1_HUMAN	13	0.000	0.217	0.000	0.000	0.143	0.000	0.060	0.096
167	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	K1C9_HUMAN	62	0.055	0.083	0.057	0.031	0.112	0.018	0.059	0.034
168	Coagulation factor V OS=Homo sapiens GN=F5 PE=4 SV=1	A0A0A0MRJ7_HUMAN (+1)	252	0.064	0.071	0.054	0.046	0.070	0.048	0.059	0.011
169	Ig heavy chain V-III region BUT OS=Homo sapiens PE=1 SV=1	HV306_HUMAN	12	0.000	0.000	0.110	0.242	0.000	0.000	0.059	0.100
170	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	LG3BP_HUMAN (+1)	65	0.117	0.072	0.041	0.022	0.036	0.051	0.056	0.034
171	V1-2 protein (Fragment) OS=Homo sapiens GN=V1-2 PE=4 SV=1	A2MYD6_HUMAN	10	0.338	0.000	0.000	0.000	0.000	0.000	0.056	0.138
172	Serpin peptidase inhibitor, clade A (Alpha-1 antitrypsin), member 4, isoform CRA_a OS=Homo sapiens GN=SERPINA4 PE=3 SV=1	A0A024R6I9_HUMAN (+2)	49	0.043	0.067	0.036	0.079	0.076	0.034	0.056	0.021
173	V1-22 protein (Fragment) OS=Homo sapiens GN=V1-22 PE=1 SV=1	Q5NV88_HUMAN	11	0.000	0.000	0.000	0.176	0.000	0.150	0.054	0.084
174	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	TSP1_HUMAN	129	0.039	0.062	0.065	0.075	0.054	0.021	0.053	0.019

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175	MS-F1 light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A0X9V9B3_HUMAN	12	0.000	0.078	0.073	0.081	0.077	0.000	0.052	0.040
176	Coagulation factor XIII B chain OS=Homo sapiens GN=F13B PE=1 SV=3	F13B_HUMAN	76	0.039	0.025	0.064	0.032	0.055	0.094	0.051	0.025
177	V1-13 protein (Fragment) OS=Homo sapiens GN=V1-13 PE=4 SV=1	Q5NV69_HUMAN	10	0.211	0.000	0.000	0.000	0.093	0.000	0.051	0.087
178	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	TLN1_HUMAN	270	0.095	0.031	0.070	0.088	0.005	0.010	0.050	0.040
179	Lipoprotein, Lp(A) OS=Homo sapiens GN=LPA PE=1 SV=1	Q1HP67_HUMAN	227	0.000	0.112	0.138	0.000	0.016	0.012	0.046	0.062
180	Lipopolysaccharide-binding protein OS=Homo sapiens GN=LBP PE=1 SV=3	LBP_HUMAN (+1)	53	0.040	0.062	0.058	0.055	0.026	0.031	0.045	0.015
181	Myosin-reactive immunoglobulin heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	Q9UL89_HUMAN	13	0.000	0.000	0.271	0.000	0.000	0.000	0.045	0.111
182	Complement factor H-related protein 3 OS=Homo sapiens GN=CFHR3 PE=1 SV=2	FHR3_HUMAN	37	0.148	0.000	0.000	0.000	0.000	0.119	0.045	0.070
183	cDNA, FLJ94361, highly similar to Homo sapiens serine (or cysteine) proteinase inhibitor, clade A(alpha-1 antiproteinase, antitrypsin), member 6 (SERPINA6), mRNA OS=Homo sapiens PE=2 SV=1	B2R9F2_HUMAN (+1)	45	0.019	0.083	0.020	0.043	0.052	0.037	0.042	0.024
184	Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2	CAH1_HUMAN (+1)	29	0.000	0.065	0.152	0.033	0.000	0.000	0.042	0.060
185	Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1	HABP2_HUMAN	63	0.034	0.030	0.014	0.023	0.029	0.096	0.038	0.029
186	Protein IGHV5-51 (Fragment) OS=Homo sapiens GN=IGHV5-51 PE=1 SV=1	A0A0C4DH38_HUMAN	13	0.000	0.072	0.000	0.000	0.143	0.000	0.036	0.060
187	Serpin peptidase inhibitor, clade A (Alpha-1 antiproteinase, antitrypsin), member 10, isoform CRA_b OS=Homo sapiens GN=SERPINA10 PE=3 SV=1	A0A024R6I6_HUMAN (+3)	51	0.050	0.064	0.017	0.038	0.045	0.000	0.036	0.023
188	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	G3P_HUMAN (+1)	36	0.035	0.039	0.061	0.067	0.000	0.000	0.034	0.029
189	Anti-HER3 scFv (Fragment) OS=Homo sapiens PE=2 SV=1	A2J422_HUMAN	26	0.000	0.000	0.085	0.112	0.000	0.000	0.033	0.051
190	Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3	PHLD_HUMAN	92	0.018	0.031	0.024	0.021	0.055	0.036	0.031	0.014
191	Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4	F13A_HUMAN	83	0.046	0.000	0.037	0.041	0.022	0.033	0.030	0.017
192	Attractin OS=Homo sapiens GN=ATRN PE=1 SV=2	ATRN_HUMAN	159	0.016	0.050	0.011	0.018	0.044	0.031	0.028	0.016
193	Single-chain Fv (Fragment) OS=Homo sapiens GN=scFv PE=1 SV=1	Q65ZC9_HUMAN	26	0.146	0.000	0.000	0.000	0.000	0.000	0.024	0.060
194	Myosin-reactive immunoglobulin light chain variable region (Fragment) OS=Homo sapiens PE=1 SV=1	Q9UL70_HUMAN	12	0.000	0.000	0.000	0.000	0.000	0.137	0.023	0.056
195	cDNA FLJ60461, highly similar to Peroxiredoxin-2 (EC 1.11.1.15) OS=Homo sapiens PE=2 SV=1	B4DF70_HUMAN (+2)	20	0.000	0.000	0.132	0.000	0.000	0.000	0.022	0.054
196	Serpin peptidase inhibitor, clade A (Alpha-1 antiproteinase, antitrypsin), member 5, isoform CRA_a OS=Homo sapiens GN=SERPINA5 PE=3 SV=1	A0A024R6N9_HUMAN (+1)	46	0.000	0.000	0.019	0.032	0.020	0.048	0.020	0.018
197	Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2	ECM1_HUMAN	61	0.014	0.000	0.022	0.040	0.000	0.036	0.019	0.017
198	Complement C1r subcomponent-like protein OS=Homo sapiens GN=C1RL PE=1 SV=2	C1RL_HUMAN	53	0.024	0.000	0.033	0.027	0.026	0.000	0.018	0.015
199	V2-19 protein (Fragment) OS=Homo sapiens GN=V2-19 PE=4 SV=1	Q5NV91_HUMAN	10	0.000	0.000	0.000	0.000	0.000	0.110	0.018	0.045
200	Myosin, heavy polypeptide 9, non-muscle, isoform CRA_a OS=Homo sapiens GN=MYH9 PE=4 SV=1	A0A024R1N1_HUMAN (+1)	227	0.035	0.008	0.004	0.062	0.000	0.000	0.018	0.025
201	Fibulin-1 OS=Homo sapiens PE=2 SV=1	B4DUV1_HUMAN	70	0.030	0.040	0.019	0.000	0.020	0.000	0.018	0.016
202	Ig heavy chain V-III region GA OS=Homo sapiens PE=1 SV=1	HV308_HUMAN	13	0.000	0.108	0.000	0.000	0.000	0.000	0.018	0.044
203	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	FLNA_HUMAN	281	0.032	0.013	0.022	0.040	0.000	0.000	0.018	0.016
204	Coagulation factor IX OS=Homo sapiens GN=F9 p22 PE=2 SV=1	F2RM37_HUMAN (+1)	52	0.024	0.000	0.000	0.000	0.027	0.053	0.017	0.021
205	Complement component 1, q subcomponent, A chain, isoform CRA_a OS=Homo sapiens GN=C1QA PE=4 SV=1	A0A024RAG6_HUMAN (+2)	26	0.049	0.054	0.000	0.000	0.000	0.000	0.017	0.027
206	Coagulation factor XI OS=Homo sapiens GN=F11 PE=1 SV=1	FA11_HUMAN	70	0.012	0.013	0.025	0.021	0.000	0.031	0.017	0.011
207	Apolipoprotein M OS=Homo sapiens GN=APOM PE=1 SV=2	APOM_HUMAN	21	0.101	0.000	0.000	0.000	0.000	0.000	0.017	0.041

208	Ig heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A068LRW6_HUMAN (+2)	14	0.000	0.000	0.000	0.000	0.099	0.000	0.017	0.041
209	Hepatocyte growth factor activator OS=Homo sapiens GN=HGFA PE=1 SV=1	HGFA_HUMAN	71	0.024	0.020	0.019	0.014	0.000	0.023	0.017	0.009
210	HCG1782423 (Fragment) OS=Homo sapiens GN=IGLV2-18 PE=4 SV=1	A0A075B6J9_HUMAN (+1)	13	0.097	0.000	0.000	0.000	0.000	0.000	0.016	0.040
211	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4	FBLN1_HUMAN	77	0.016	0.024	0.017	0.019	0.012	0.000	0.015	0.008
212	Complement factor H-related protein 2 OS=Homo sapiens GN=CFHR2 PE=1 SV=1	FHR2_HUMAN (+1)	31	0.000	0.000	0.000	0.000	0.000	0.089	0.015	0.036
213	Fetuin-B OS=Homo sapiens GN=FETUB PE=1 SV=2	FETUB_HUMAN	42	0.000	0.022	0.000	0.000	0.022	0.039	0.014	0.016
214	A0A0F7TC28_HUMAN	A0A0F7TC28_HUMAN	11	0.000	0.000	0.080	0.000	0.000	0.000	0.013	0.033
215	Properdin OS=Homo sapiens GN=CFP PE=1 SV=2	PROP_HUMAN (+1)	51	0.000	0.018	0.017	0.000	0.000	0.043	0.013	0.017
216	Ig heavy chain V-III region CAM OS=Homo sapiens PE=1 SV=1	HV307_HUMAN	14	0.000	0.000	0.000	0.000	0.000	0.078	0.013	0.032
217	Ig kappa chain V-1 region DEE OS=Homo sapiens PE=1 SV=1	KV105_HUMAN	12	0.000	0.000	0.000	0.000	0.077	0.000	0.013	0.032
218	Sex hormone-binding globulin OS=Homo sapiens GN=SHBG PE=4 SV=1	I3L145_HUMAN (+1)	37	0.023	0.025	0.000	0.026	0.000	0.000	0.012	0.014
219	Alpha-synuclein OS=Homo sapiens GN=SNCA PE=1 SV=1	E7EPV7_HUMAN (+3)	12	0.000	0.000	0.073	0.000	0.000	0.000	0.012	0.030
220	Sulphydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3	QSOX1_HUMAN	83	0.010	0.017	0.011	0.017	0.017	0.000	0.012	0.007
221	C-reactive protein OS=Homo sapiens GN=CRP PE=1 SV=1	CRP_HUMAN	25	0.034	0.038	0.000	0.000	0.000	0.000	0.012	0.018
222	Peptidase inhibitor 16 OS=Homo sapiens GN=PI16 PE=1 SV=1	PI16_HUMAN	49	0.017	0.000	0.000	0.020	0.000	0.034	0.012	0.014
223	Fermitin family homolog 3 OS=Homo sapiens GN=FERMT3 PE=1 SV=1	URP2_HUMAN	76	0.044	0.012	0.012	0.000	0.000	0.000	0.011	0.017
224	IBM-A3 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A0X9UWM4_HUMAN	14	0.000	0.000	0.000	0.000	0.066	0.000	0.011	0.027
225	Catalase OS=Homo sapiens GN=CAT PE=1 SV=3	CATA_HUMAN	60	0.000	0.000	0.066	0.000	0.000	0.000	0.011	0.027
226	Ficolin-2 OS=Homo sapiens GN=FCN2 PE=1 SV=2	FCN2_HUMAN	34	0.000	0.000	0.000	0.028	0.000	0.032	0.010	0.016
227	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2	CAH2_HUMAN (+2)	29	0.000	0.000	0.061	0.000	0.000	0.000	0.010	0.025
228	Cartilage acidic protein 1 OS=Homo sapiens GN=CRAC1 PE=1 SV=2	CRAC1_HUMAN (+1)	71	0.012	0.013	0.012	0.020	0.000	0.000	0.010	0.008
229	Vinculin, isoform CRA_c OS=Homo sapiens GN=VCL PE=4 SV=1	A0A024QZN4_HUMAN (+2)	117	0.022	0.000	0.011	0.025	0.000	0.000	0.010	0.011
230	cDNA FLJ51023, highly similar to Vitamin K-dependent protein C (EC 3.4.21.69) OS=Homo sapiens PE=2 SV=1	B4DPC8_HUMAN (+4)	31	0.027	0.000	0.000	0.000	0.030	0.000	0.010	0.015
231	von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4	VWF_HUMAN	309	0.019	0.005	0.031	0.000	0.000	0.000	0.009	0.013
232	cDNA FLJ78437, highly similar to Homo sapiens cartilage oligomeric matrix protein (COMP), mRNA OS=Homo sapiens PE=2 SV=1	A8K310_HUMAN (+4)	83	0.015	0.000	0.000	0.000	0.011	0.026	0.009	0.011
233	Conserved oligomeric Golgi complex subunit 3 OS=Homo sapiens GN=COG3 PE=1 SV=3	COG3_HUMAN	94	0.000	0.000	0.037	0.015	0.000	0.000	0.009	0.015
234	Macrophage stimulating 1 (Hepatocyte growth factor-like) variant (Fragment) OS=Homo sapiens PE=2 SV=1	Q53GN8_HUMAN	80	0.021	0.018	0.000	0.000	0.000	0.014	0.009	0.010
235	Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1	ZYX_HUMAN	61	0.028	0.000	0.000	0.016	0.000	0.000	0.007	0.012
236	Proteoglycan 4, isoform CRA_a OS=Homo sapiens GN=PRG4 PE=4 SV=1	A0A024R930_HUMAN (+2)	151	0.000	0.012	0.006	0.000	0.012	0.011	0.007	0.006
237	Butyrylcholinesterase, isoform CRA_b OS=Homo sapiens GN=BCHE PE=3 SV=1	D3DNN4_HUMAN	73	0.000	0.000	0.012	0.013	0.013	0.000	0.006	0.007
238	cDNA FLJ78503, highly similar to Homo sapiens keratin 13 (KRT13), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	A8K2H9_HUMAN	50	0.000	0.038	0.000	0.000	0.000	0.000	0.006	0.015
239	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	K2C5_HUMAN	62	0.000	0.000	0.000	0.000	0.037	0.000	0.006	0.015
240	Extracellular link domain containing 1 OS=Homo sapiens GN=XLKD1 PE=2 SV=1	B2R672_HUMAN (+1)	35	0.000	0.000	0.000	0.000	0.000	0.031	0.005	0.013
241	Stomatin, isoform CRA_a OS=Homo sapiens GN=STOM PE=4 SV=1	A0A024R882_HUMAN (+2)	32	0.000	0.000	0.000	0.030	0.000	0.000	0.005	0.012
242	Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4	KPYM_HUMAN (+1)	58	0.029	0.000	0.000	0.000	0.000	0.000	0.005	0.012
243	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA OS=Homo sapiens GN=MAN1A1 PE=1 SV=3	MA1A1_HUMAN	73	0.012	0.000	0.000	0.000	0.000	0.015	0.004	0.007

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244	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1	BGH3_HUMAN (+1)	75	0.000	0.000	0.000	0.013	0.012	0.000	0.004	0.007
245	Vitamin K-dependent protein Z OS=Homo sapiens GN=PROZ PE=1 SV=2	PROZ_HUMAN	45	0.000	0.000	0.000	0.000	0.000	0.024	0.004	0.010
246	Integrin alpha-IIb OS=Homo sapiens GN=ITGA2B PE=1 SV=3	ITA2B_HUMAN	113	0.007	0.000	0.000	0.013	0.000	0.000	0.003	0.006
247	Actinin, alpha 1, isoform CRA_a OS=Homo sapiens GN=ACTN1 PE=4 SV=1	A0A024R694_HUMAN (+1)	103	0.008	0.000	0.000	0.009	0.000	0.000	0.003	0.005
248	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	MOES_HUMAN (+1)	68	0.000	0.000	0.000	0.014	0.000	0.000	0.002	0.006
249	Biotinidase OS=Homo sapiens GN=BTD PE=1 SV=2	BTD_HUMAN	61	0.014	0.000	0.000	0.000	0.000	0.000	0.002	0.006
250	Band 3 anion transport protein OS=Homo sapiens GN=SLC4A1 PE=1 SV=3	B3AT_HUMAN (+3)	102	0.000	0.000	0.013	0.000	0.000	0.000	0.002	0.005
251	Epididymis secretory protein Li 52 OS=Homo sapiens GN=HEL-S-52 PE=2 SV=1	V9HWG7_HUMAN (+1)	66	0.013	0.000	0.000	0.000	0.000	0.000	0.002	0.005
252	Dopamine beta-hydroxylase OS=Homo sapiens GN=DBH PE=1 SV=3	DOPO_HUMAN	69	0.000	0.000	0.013	0.000	0.000	0.000	0.002	0.005
253	Integrin beta-3 OS=Homo sapiens GN=ITGB3 PE=1 SV=2	ITB3_HUMAN (+1)	87	0.000	0.000	0.000	0.011	0.000	0.000	0.002	0.005
254	IgGfC-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3	FCGBP_HUMAN	572	0.001	0.003	0.002	0.002	0.000	0.003	0.002	0.001
255	Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3	MASP1_HUMAN	79	0.011	0.000	0.000	0.000	0.000	0.000	0.002	0.004
256	Spectrin alpha chain, erythrocytic 1 OS=Homo sapiens GN=SPTA1 PE=1 SV=1	A0A087WZE4_HUMAN (+1)	281	0.000	0.000	0.005	0.000	0.000	0.000	0.001	0.002
257	Ankyrin-1 OS=Homo sapiens GN=ANK1 PE=1 SV=3	ANK1_HUMAN	206	0.000	0.000	0.004	0.000	0.000	0.000	0.001	0.002
258	Spectrin, beta, erythrocytic (Includes spherocytosis, clinical type I) variant (Fragment) OS=Homo sapiens PE=2 SV=1	Q59FP5_HUMAN	268	0.000	0.000	0.003	0.000	0.000	0.000	0.001	0.001

Supporting Table 5

Table S5: Characterization of the *in vivo* protein corona. Full list of common proteins identified in the liposomal protein corona in all 6 ovarian carcinoma patients.

#	Identified protein	Accession Number	Average RPA%	STV
1	Full-length cDNA clone CS0DD006YL02 of Neuroblastoma of Homo sapiens (human) OS=Homo sapiens PE=2 SV=1	Q86TT1_HUMAN	7.98	2.44
2	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=1	A0A087X2C0_HUMAN	5.70	1.78
3	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	A2MG_HUMAN	3.47	1.01
4	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	FIBB_HUMAN (+1)	3.46	1.20
5	Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	FIBA_HUMAN	2.99	0.67
6	Apolipoprotein B (Including Ag(X) antigen) OS=Homo sapiens GN=APOB PE=4 SV=1	C0JYY2_HUMAN	2.64	1.43
7	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	ALBU_HUMAN	2.48	2.08
8	Protein IGHV3-72 OS=Homo sapiens GN=IGHV3-72 PE=4 SV=1	A0A087WW89_HUMAN	1.91	0.57
9	C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2	C4BPA_HUMAN	1.74	0.59
10	Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	FIBG_HUMAN	1.60	0.54
11	Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=1 SV=1	H3BS21_HUMAN	1.36	0.35
12	Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=4	H0Y300_HUMAN	1.35	0.44
13	IGH@ protein OS=Homo sapiens GN=IGH@ PE=1 SV=1	Q6GMX6_HUMAN	1.14	0.65
14	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	A0A087WV47_HUMAN (+1)	1.13	0.60
15	cDNA FLJ78387 OS=Homo sapiens PE=1 SV=1	A8K008_HUMAN	1.12	0.60
16	Putative uncharacterized protein DKFZp686P15220 OS=Homo sapiens GN=DKFZp686P15220 PE=1 SV=1	Q6N089_HUMAN	1.06	0.61
17	IgG H chain OS=Homo sapiens PE=1 SV=1	S6B291_HUMAN	1.05	0.65
18	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	ACTB_HUMAN (+2)	1.04	0.60
19	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	A0A087WYC5_HUMAN	0.96	0.63
20	GCT-A10 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A120HG46_HUMAN	0.96	0.51
21	cDNA FLJ14473 fis, clone MAMMA1001080, highly similar to Homo sapiens SNC73 protein (SNC73) mRNA OS=Homo sapiens PE=2 SV=1	Q96K68_HUMAN	0.94	0.30
22	Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=1 SV=2	HPTR_HUMAN	0.93	0.22
23	Putative uncharacterized protein DKFZp686G11190 OS=Homo sapiens GN=DKFZp686G11190 PE=1 SV=1	Q6MZQ6_HUMAN	0.92	0.61
24	Myosin-reactive immunoglobulin heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	Q9UL90_HUMAN	0.89	0.22
25	Putative uncharacterized protein DKFZp686C15213 OS=Homo sapiens GN=DKFZp686C15213 PE=1 SV=1	Q6MZU6_HUMAN	0.87	0.64
26	Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=4 SV=1	A0A087WXL8_HUMAN	0.86	0.65
27	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	APOE_HUMAN (+1)	0.83	0.48
28	IGL@ protein OS=Homo sapiens GN=IGL@ PE=1 SV=1	Q8N355_HUMAN	0.80	0.18
29	IGK@ protein OS=Homo sapiens GN=IGK@ PE=1 SV=1	Q6PIL8_HUMAN	0.77	0.21
30	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	CO3_HUMAN (+1)	0.77	0.43
31	Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	D9YZU5_HUMAN (+1)	0.64	0.44
32	MS-D4 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	A0A0X9UWK7_HUMAN	0.63	0.13
33	Anti-FactorVIII scFv (Fragment) OS=Homo sapiens PE=2 SV=1	A2KBC6_HUMAN	0.61	0.22
34	Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2_HUMAN (+2)	0.59	0.31
35	Protein IGHV3-74 (Fragment) OS=Homo sapiens GN=IGHV3-74 PE=1 SV=1	A0A0B4J1X5_HUMAN	0.58	0.21
36	Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1	PROS_HUMAN (+2)	0.57	0.17
37	Transferrin variant (Fragment) OS=Homo sapiens PE=2 SV=1	Q53H26_HUMAN	0.51	0.39

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38	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	LG3BP_HUMAN (+1)	0.50	0.32
39	Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=2 SV=1	A3KPE2_HUMAN (+2)	0.50	0.40
40	cDNA, FLJ94213, highly similar to Homo sapiens pregnancy-zone protein (PZP), mRNA OS=Homo sapiens PE=2 SV=1	B2R950_HUMAN (+1)	0.49	0.08
41	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	TSP1_HUMAN	0.48	0.26
42	Protein IGHV5-51 (Fragment) OS=Homo sapiens GN=IGHV5-51 PE=1 SV=1	A0A0C4DH38_HUMAN	0.47	0.10
43	Vinculin, isoform CRA_c OS=Homo sapiens GN=VCL PE=4 SV=1	A0A024QZN4_HUMAN (+2)	0.46	0.28
44	Fibronectin 1, isoform CRA_n OS=Homo sapiens GN=FN1 PE=4 SV=1	A0A024R462_HUMAN	0.46	0.11
45	Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1	H6VRF8_HUMAN (+3)	0.44	0.08
46	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	FLNA_HUMAN	0.42	0.27
47	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	A1AT_HUMAN (+1)	0.41	0.24
48	Ig heavy chain V-III region BUT OS=Homo sapiens PE=1 SV=1	HV306_HUMAN	0.41	0.20
49	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	TLN1_HUMAN	0.41	0.24
50	Actinin, alpha 1, isoform CRA_a OS=Homo sapiens GN=ACTN1 PE=4 SV=1	A0A024R694_HUMAN (+1)	0.41	0.23
51	Apolipoprotein A-I, isoform CRA_a OS=Homo sapiens GN=APOA1 PE=4 SV=1	A0A024R3E3_HUMAN (+1)	0.40	0.11
52	von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4	VWF_HUMAN	0.39	0.25
53	Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4	F13A_HUMAN	0.36	0.23
54	Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	CFAH_HUMAN	0.33	0.12
55	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	K1C10_HUMAN	0.30	0.10
56	Protein APOC4-APOC2 OS=Homo sapiens GN=APOC4-APOC2 PE=4 SV=1	K7ER74_HUMAN	0.30	0.16
57	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	K1C9_HUMAN	0.28	0.09
58	Epididymis tissue protein Li 173 OS=Homo sapiens PE=2 SV=1	E9KL26_HUMAN (+1)	0.27	0.15
59	Myosin, heavy polypeptide 9, non-muscle, isoform CRA_a OS=Homo sapiens GN=MYH9 PE=4 SV=1	A0A024R1N1_HUMAN (+1)	0.26	0.22
60	Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=2 SV=1	B4DPQ0_HUMAN	0.26	0.08
61	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	HSP7C_HUMAN (+1)	0.24	0.16
62	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	HEMO_HUMAN	0.23	0.21
63	Epididymis secretory protein Li 52 OS=Homo sapiens GN=HEL-S-52 PE=2 SV=1	V9HWG7_HUMAN (+1)	0.22	0.15
64	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	K22E_HUMAN	0.22	0.07
65	Fermitin family homolog 3 OS=Homo sapiens GN=FERMT3 PE=1 SV=1	URP2_HUMAN	0.21	0.14
66	Complement C4-B OS=Homo sapiens GN=C4B PE=1 SV=2	CO4B_HUMAN	0.21	0.09
67	Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4	KPYM_HUMAN (+1)	0.21	0.12
68	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	GELS_HUMAN	0.20	0.10
69	CD5 antigen-like OS=Homo sapiens GN=CD5L PE=1 SV=1	CD5L_HUMAN	0.19	0.08
70	Immunoglobulin heavy chain variable region (Fragment) OS=Homo sapiens PE=4 SV=1	Q0ZCH6_HUMAN	0.18	0.05
71	Complement component 1, q subcomponent, C chain, isoform CRA_a OS=Homo sapiens GN=C1QC PE=4 SV=1	A0A024RAA7_HUMAN (+1)	0.18	0.03
72	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	TBA4A_HUMAN	0.18	0.11
73	cDNA FLJ35730 fis, clone TEST12003131, highly similar to ALPHA-1-ANTICHYMOTRYPSIN OS=Homo sapiens PE=2 SV=1	B3KS79_HUMAN	0.17	0.12
74	Immunoglobulin J chain OS=Homo sapiens GN=IGJ PE=1 SV=4	IGJ_HUMAN	0.16	0.07
75	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=1	Q5T985_HUMAN	0.16	0.05
76	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	GRP78_HUMAN (+1)	0.16	0.14
77	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	MOES_HUMAN (+1)	0.16	0.10
78	Apolipoprotein M OS=Homo sapiens GN=APOM PE=1 SV=2	APOM_HUMAN	0.15	0.08
79	Complement component 1, q subcomponent, B chain, isoform CRA_a OS=Homo sapiens GN=C1QB PE=4 SV=1	A0A024RAB9_HUMAN (+3)	0.15	0.06
80	Beta 5-tubulin OS=Homo sapiens GN=TUBB PE=2 SV=1	Q5SU16_HUMAN (+1)	0.15	0.14

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81	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3	ITIH1_HUMAN	0.14	0.06
82	Lipoprotein, Lp(A) OS=Homo sapiens GN=LPA PE=1 SV=1	Q1HP67_HUMAN	0.14	0.15
83	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	K1C16_HUMAN	0.13	0.05
84	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	HS90A_HUMAN (+1)	0.13	0.08
85	Inter-alpha (Globulin) inhibitor H4 (Plasma Kallikrein-sensitive glycoprotein) OS=Homo sapiens GN=ITIH4 PE=2 SV=1	B2RMS9_HUMAN (+1)	0.12	0.09
86	Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1	TBB1_HUMAN	0.12	0.09
87	Band 3 anion transport protein OS=Homo sapiens GN=SLC4A1 PE=1 SV=3	B3AT_HUMAN (+3)	0.11	0.06
88	CP protein OS=Homo sapiens GN=CP PE=2 SV=1	A5PL27_HUMAN (+1)	0.11	0.09
89	Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4	A1BG_HUMAN (+1)	0.11	0.10
90	Integrin beta-3 OS=Homo sapiens GN=ITGB3 PE=1 SV=2	ITB3_HUMAN (+1)	0.11	0.09
91	Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3	HEP2_HUMAN	0.11	0.08
92	APOL1 protein (Fragment) OS=Homo sapiens GN=APOL1 PE=2 SV=1	A5PL32_HUMAN (+2)	0.10	0.06
93	Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4	CO5_HUMAN	0.10	0.07
94	Endoplasmic reticulum chaperone protein OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	ENPL_HUMAN (+2)	0.10	0.08
95	Platelet glycoprotein Ib alpha (Fragment) OS=Homo sapiens GN=GP1BA PE=4 SV=1	A5CKE2_HUMAN (+2)	0.10	0.10
96	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	CLUS_HUMAN	0.10	0.02
97	Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1	C1S_HUMAN	0.10	0.06
98	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	G3P_HUMAN (+1)	0.09	0.05
99	Heat shock protein 90kDa alpha (Cytosolic), class B member 1, isoform CRA_a OS=Homo sapiens GN=HSP90AB1 PE=3 SV=1	A0A024RD80_HUMAN (+2)	0.09	0.05
100	C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=1 SV=1	C4BPB_HUMAN	0.09	0.04
101	Integrin alpha-1Ib OS=Homo sapiens GN=ITGA2B PE=1 SV=3	ITA2B_HUMAN	0.09	0.06
102	Vitronectin OS=Homo sapiens GN=VTN PE=4 SV=1	D9ZGG2_HUMAN (+1)	0.09	0.07
103	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	K2C5_HUMAN	0.09	0.03
104	Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2	PLMN_HUMAN	0.09	0.08
105	Ficolin-3 OS=Homo sapiens GN=FCN3 PE=1 SV=2	FCN3_HUMAN	0.08	0.03
106	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	1433Z_HUMAN (+1)	0.07	0.04
107	Proteoglycan 4, isoform CRA_a OS=Homo sapiens GN=PRG4 PE=4 SV=1	A0A024R930_HUMAN (+2)	0.07	0.04
108	IgGfC-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3	FCGBP_HUMAN	0.07	0.03
109	Catalase OS=Homo sapiens GN=CAT PE=1 SV=3	CATA_HUMAN	0.06	0.03
110	Zyxin OS=Homo sapiens GN=ZYG PE=1 SV=1	ZYX_HUMAN	0.06	0.03
111	Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3	CPN2_HUMAN	0.06	0.02
112	Multimerin-1 OS=Homo sapiens GN=MMRN1 PE=1 SV=3	MMRN1_HUMAN	0.06	0.06
113	Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3	A2AP_HUMAN	0.06	0.04
114	Calpain 1, (Mu/l) large subunit, isoform CRA_a OS=Homo sapiens GN=CAPN1 PE=4 SV=1	A0A024R580_HUMAN (+2)	0.06	0.06
115	Clathrin heavy chain OS=Homo sapiens GN=CLTC PE=1 SV=1	A0A087WVQ6_HUMAN (+1)	0.05	0.04
116	Coagulation factor XIII B chain OS=Homo sapiens GN=F13B PE=1 SV=3	F13B_HUMAN	0.04	0.02
117	cDNA FLJ61290, highly similar to Neutral alpha-glucosidase AB OS=Homo sapiens PE=2 SV=1	B4DJ30_HUMAN (+2)	0.04	0.04
118	Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3	CO6_HUMAN	0.04	0.04
119	Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3	MASP1_HUMAN	0.04	0.02
120	Soluble scavenger receptor cysteine-rich domain-containing protein SSC5D OS=Homo sapiens GN=SSC5D PE=2 SV=3	SRCLR_HUMAN	0.03	0.01
121	Spectrin, beta, erythrocytic (Includes spherocytosis, clinical type I) variant (Fragment) OS=Homo sapiens PE=2 SV=1	Q59FP5_HUMAN	0.03	0.02
122	Coagulation factor V OS=Homo sapiens GN=F5 PE=4 SV=1	A0A0A0MRJ7_HUMAN (+1)	0.03	0.01

Supporting Table 6

Table S6: Most-abundant proteins (top-20) identified by LC-MS/MS in *ex vivo* protein coronas (formed after incubation of PEGylated liposomal doxorubicin with plasma samples) obtained from ovarian carcinoma patients (n=6) and from healthy controls (n=6). RPA% values represent the average and standard deviation from the 6 biological replicates.

<i>Ex vivo</i> corona (Ovarian Carcinoma Patients; n=6)		<i>Ex vivo</i> corona (Healthy Controls; n=6)	
Identified Protein	RPA%	Identified Protein	RPA%
Full-length cDNA clone CS0DD006YL02 of Neuroblastoma of Homo sapiens	4.79 ± 0.92	Apolipoprotein B (Including Ag(X) antigen)	4.60 ± 2.55
Apolipoprotein B (Including Ag(X) antigen)	3.49 ± 1.27	Alpha-2-macroglobulin	4.56 ± 2.11
Ig mu chain C region (A0A087X2C0)	3.44 ± 0.74	Ig mu chain C region (A0A087X2C0)	4.53 ± 0.77
Fibrinogen beta chain	3.11 ± 0.87	Fibrinogen beta chain	3.69 ± 0.60
Haptoglobin	3.10 ± 1.22	Full-length cDNA clone CS0DD006YL02 of Neuroblastoma of Homo sapiens	3.43 ± 3.80
Haptoglobin (Fragment) (H3BS21)	3.05 ± 1.15	Ig mu chain C region (A0A087WYJ9)	3.03 ± 2.41
Ig mu chain C region (A0A087WYJ9)	2.65 ± 1.45	Fibrinogen alpha chain	2.80 ± 1.07
Alpha-2-macroglobulin	2.51 ± 0.84	Protein IGHV3-72	2.78 ± 0.58
Beta-globin (D9YZU5)	2.43 ± 1.29	IGK@ protein (Q6PIL8)	2.15 ± 0.15
Fibrinogen alpha chain	2.42 ± 0.86	cDNA FLJ51597, highly similar to C4b-binding protein alpha chain	2.12 ± 1.17
Haptoglobin-related protein (HPTR)	2.28 ± 0.99	Fibrinogen gamma chain	2.09 ± 0.74
Apolipoprotein E isoform 1 (Fragment)	2.08 ± 0.84	Lipoprotein B (Fragment)	2.09 ± 3.25
Mutant hemoglobin alpha 2 globin chain (A0A0K2BMD8)	2.07 ± 1.47	Haptoglobin	2.06 ± 1.02
Fibrinogen gamma chain	1.98 ± 0.54	Lambda-chain (AA -20 to 215)	1.99 ± 0.16
Lipoprotein B (Fragment)	1.94 ± 4.74	Haptoglobin (Fragment) (H3BS21)	1.99 ± 1.31
Protein IGHV3-72	1.92 ± 0.74	Uncharacterized protein (Q8TCD0)	1.69 ± 0.84
cDNA FLJ51597, highly similar to C4b-binding protein alpha chain	1.78 ± 0.53	Haptoglobin-related protein (HPTR)	1.55 ± 0.73
IGK@ protein (Q6PIL8)	1.63 ± 0.43	Serum albumin	1.33 ± 0.74
Lambda-chain (AA -20 to 215)	1.41 ± 0.20	Apolipoprotein E isoform 1 (Fragment)	1.28 ± 0.46
Serum albumin	1.37 ± 0.32	Ig gamma-1 chain C region (A0A087WV47)	1.18 ± 0.40