Circulation
Cardiovascular Genetics
JOURNAL OF THE AMERICAN HEART ASSOCIATION

American Heart Association
Learn and Live

Proteomics, Metabolomics, and Immunomics on Microparticles Derived From Human Atherosclerotic Plaques

Manuel Mayr, David Grainger, Ursula Mayr, Aurelie S. Leroyer, Guy Leseche, Anissa Sidibe, Olivier Herbin, Xiaoke Yin, Aldrin Gomes, Bassetti Madhu, John R. Griffiths, Qingbo Xu, Alain Tedgui and Chantal M. Boulanger

Circ Cardiovasc Genet 2009;2;379-388; originally published online May 14, 2009;
DOI: 10.1161/CIRCGENETICS.108.842849
Circulation: Cardiovascular Genetics is published by the American Heart Association. 7272 Greenville Avenue, Dallas, TX 72514

Proteomics, Metabolomics, and Immunomics on Microparticles Derived From Human Atherosclerotic Plaques

Manuel Mayr, MD, PhD; David Grainger, PhD; Ursula Mayr, MD; Aurelie S. Leroyer, PhD;
Guy Leseche, MD; Anissa Sidibe, PhD; Olivier Herbin, MSc; Xiaoke Yin, PhD; Aldrin Gomes, PhD;
Bassetti Madhu, PhD; John R. Griffiths, MD; Qingbo Xu, MD, PhD;
Alain Tedgui, PhD; Chantal M. Boulanger, PhD

Background**—**Microparticles (MPs) with procoagulant activity are present in human atherosclerosis, but no detailed information is available on their composition.

Methods and Results**—**To obtain insights into the role of MPs in atherogenesis, MP proteins were identified by tandem mass spectrometry, metabolite profiles were determined by high-resolution nuclear magnetic resonance spectroscopy, and antibody reactivity was assessed against combinatorial antigen libraries. Plaque MPs expressed surface antigens consistent with their leukocyte origin, including major histocompatibility complex classes I and II, and induced a dose-dependent stimulatory effect on T-cell proliferation. Notably, taurine, the most abundant free organic acid in human neutrophils, which scavenges myeloperoxidase-catalyzed free radicals, was highly enriched in plaque MPs. Moreover, fluorescent labeling of proteins on the MP surface suggested immunoglobulins to be trapped inside, which was confirmed by flow cytometry analysis on permeabilized and nonpermeabilized plaque MPs. Colabeling for CD14 and IgG established that more than 90% of the IgG containing MPs were CD14$^+$, indicating a macrophage origin. Screening against an antigen library revealed that the immunologic profiles of antibodies in MPs were similar to those found in plaques but differed profoundly from antibodies in plasma and unexpectedly, showed strong reactions with oligosaccharide antigens, in particular blood group antigen A.

Conclusions**—**This study provides the first evidence that immunoglobulins are present within MPs derived from plaque macrophages, that the portfolio of plaque antibodies is different from circulating antibodies in plasma, and that anticarbohydrate antibodies are retained in human atherosclerotic lesions. **(*Circ Cardiovasc Genet*. 2009;2:379-388.)**

Key Words: antigens ■ atherosclerosis ■ carotid arteries ■ plaque ■ proteins ■ proteomics

Cell activation by agonists, physical, or chemical stresses stimulates bleb formation from the cell membrane, which is triggered by a rise of intracellular calcium and facilitated by modifications of the plasma membrane (ie, externalization of phosphatidylserine). From these blebs, virtually all cell types generate even smaller particles, termed microparticles (MPs). With a size of <1 μm, MPs were merely considered as a marker of cellular activation and damage, including apoptosis.[1,2] However, MPs are also released in the circulation[3] and ever since their potent procoagulatory properties were first recognized in the field of hemostasis,[4–6] the interest in their potential pathophysiological importance has increased.[7,8]

Clinical Perspective on p 388

We have recently characterized MPs present in human atherosclerotic lesions.[9] Notably, plaque MPs are derived from leukocytes (≈50%), erythrocytes, smooth muscle cells, and endothelial cells but not from platelets.[9] They possess high tissue factor activity and expose phosphatidylserine, a major determinant of their procoagulant activity and their clearance by macrophages.[10] However, no detailed information is currently available on the overall molecular composition. The aim of this study was to characterize MPs from human atherosclerotic plaques by using a combination of proteomic, metabolomic, and immunomic techniques.[11] To

---

Received December 9, 2008; accepted May 8, 2009.

From the Cardiovascular Division (M.M., U.M., A.S., X.Y., Q.X.), King's BHF Centre of Research Excellence, King's College London, London, United Kingdom; Department of Medicine (D.G.), Addenbrooke's Hospital, Cambridge, United Kingdom; Paris-Cardiovascular Research Center (A.S.L., G.L., O.H., A.T., C.M.B.), INSERM U970, Hôpital Européen Georges Pompidou, Université Paris-Descartes, Paris, France; Section of Neurobiology (A.G.), Physiology, and Behavior, University of California, Davis, Calif; Cancer Research UK Cambridge Research Institute (B.M., J.R.G.), Robinson way, Cambridge, United Kingdom.

The online-only Data Supplement is available at http://circgenetics.ahajournals.org/cgi/content/full/CIRCGENETICS.108.842849/DC1.

Correspondence to Manuel Mayr, MD, PhD, Cardiovascular Division, King's College London, 125 Coldharbour Lane, London SE5 9NU, United Kingdom. E-mail manuel.mayr@kcl.ac.uk

Circ Cardiovasc Genet **is available at http://circgenetics.ahajournals.org** **DOI: 10.1161/CIRCGENETICS.108.842849**

analyze the protein composition, MP proteins were separated on large-format gradient gels and identified by tandem mass spectrometry (MS/MS). To investigate protein localization, MPs were surface labeled with CyDyes and separated by 2-dimensional gel electrophoresis (2-DE). The fluorescent tag allowed discriminating membrane-associated proteins from proteins within MPs. The proteomic analysis was complemented by high-resolution proton nuclear magnetic resonance spectroscopy to assess MP metabolites. Finally, the immunoglobulin portfolio of plaque MPs was screened against a combinatorial peptide and carbohydrate library to establish where the majority of antibody reactivity was found and then a sublibrary with defined antigens to partially identify the antigen specificity. We provide the first evidence that plaque MPs stimulate T-cell proliferation, that immunoglobulins are trapped within macrophage-derived MPs in human atherosclerosis, and that plaque antibodies show different antigen specificity compared with circulating plasma immunoglobulins and recognize carbohydrate antigens, including blood group antigen A.

Methods

Isolation of MPs From Atherosclerotic Plaques

MPs derived from human carotid atherosclerotic plaques were prepared as described previously.[9] Surgical samples were rapidly rinsed in cold sterile phosphate-buffered saline solution supplemented with 100 U of streptomycin and 100 U/mL of penicillin, and atherosclerotic lesions were separated from the apparently healthy vessel wall. Plaques were then thoroughly minced using fine scissors in a volume of Dulbecco's modified eagle medium (supplemented with 10 μg/mL of polymyxin B, 100 U streptomycin and 100 U/mL of penicillin and filtered on 0.22-μm membranes) corresponding to the respective weight of each lesion. The preparations were centrifuged first at 400*g* (15 minutes) and then at 12 500*g* (5 minutes) to remove cells and cell debris. The resulting supernatant was referred to as "plaque homogenate." Part of the plaque homogenate was further centrifuged at 20 500*g* for 150 minutes at 4°C to pellet MPs.[9] Pellets were gently suspended in fresh Dulbecco's modified eagle medium (1/10 of volume corresponding to the respective weight of each lesion). Human atherosclerotic plaques (mean±SD, 713±70 mg) from 26 patients (72±2 years old, 69% men) undergoing carotid endarterectomy (CE) were included in the study, which was approved by the Hospital ethical committee. All patients gave their informed consent to the study. Indications for the CE were critical asymptomatic stenosis (>75%, n=13), stroke, or transient ischemic attack (n=13). Patients had common cardiovascular risk factors, such as hypertension (65%), diabetes (31%), hypercholesterolemia (62%), and smoking (42%). All patients were treated with antiaggregants. The cellular origin of plaque MPs was evaluated as reported before.[9] One sample was used per subject.

1-DE-Liquid Chromatography-MS/MS

For proteomics, MPs of 3 patients were reconstituted in Laemmli buffer and separated by SDS-PAGE gels. After silver staining, gel bands were excised, subjected to in-gel tryptic digestion, and proteins identified by liquid chromatography (LC)-MS/MS (LCQ Deca XP Plus, Thermo Fisher). The outputs for each lane picked were combined in Scaffold (Proteome Software). The detailed methodology is available online.

Surface Labeling and 2-DE

Proteins on the MP surface were CyDye tagged using a modified protocol by Mayrhofer et al.[12] In brief, CyDyes (GE Healthcare) were reconstituted in dimethylformamide, *N*,*N*-anhydrous, 99.8% (Aldrich) to make up stocks of 1 nmol/μL. These were then diluted in Hanks balanced salt solution (Gibco), pH 8.5, containing 1 mol/L urea to make up a 1 nmol/mL CyDye solution.[13] MPs were labeled using the CyDye/urea solution. After 20 minutes, the reaction was stopped using 1 mL of L-Lysine (10 mmol/L, L8662, Sigma) for 15 minutes. Surface-labeled MPs were lysed in a complete lysis buffer (8 mol/L urea, 4% wt/vol CHAPS, 30 mmol/L TrisCl, pH 8.5). The separation by 2-DE involve adaptations of previously published protocols[14,15] and is described online. Detailed protocols are provided on our website (http://www.vascular-proteomics.com).

Proton Nuclear Magnetic Resonance Spectroscopy

Metabolites were extracted from CE samples (n=4) and plaque MPs (n=4) as published previously[16] and described online.

Flow Cytometry Analysis

Plaque homogenates were used for flow cytometry experiments. Labeling for immunoglobulin, apolipoprotein A1 (apoA1) and B (apoB) were performed before and after MPs permeabilization to determine surface versus intramicroparticle labeling. The detailed methodology is provided online.

Assessment of CD4$^+$ T-Cell Proliferation

Blood mononuclear cells were isolated using Pancoll gradient of blood collected on heparin from patients undergoing endarterectomy. Negative selection of CD4$^+$ cells was performed using an indirect magnetic labeling system for the isolation of CD4$^+$ T cells from human PBMCs (CD4$^+$ T-cell isolation kit II) on autoMACS columns (Miltenyi Biotec). CD4+ cells were pulsed with tritium and incubated with plaque MPs as described online.

Immunomics

For these experiments, MPs (20 500 g pellet), MP-depleted plaque homogenates and platelet-free plasma samples were obtained from 6 patients undergoing the CE. Venous blood was drawn at the time of surgery, and platelet-free plasma was prepared on 0.129 mol/L sodium citrate tubes as described previously.[9] All samples were exposed to a PeptidePanel and GlycoPanel antigen library coated onto tiny aluminum particles with a unique barcode (Ultraplex, Pronostics, Cambridge, United Kingdom). The immunoreactivity of the samples was determined by labeling the bound antibodies with a fluorescent detection reagent in which different antibody subclasses were labeled with different colors. After mixing, the barcode of the particles with positive reactivity was read in a microscope-based reader (UltraPlex Smart Reader, Pronostics, Cambridge, United Kingdom), and the amount of label bound to each bead code was plotted providing an immunomic profile. Further details are provided online.

Statistical Analysis

Statistical analysis was performed using either the paired or unpaired Student *t* test. A *P* value of <0.05 was considered significant.

Results

Proteomics

MP proteins were separated by SDS-PAGE using large format gradient gels (4% to 12%). After silver staining, 64 bands (A1-H8, Figure 1) were excised and analyzed by LC-MS/MS (Figure 2) resulting in the identification of 151 unique proteins with a peptide probability >95.0%, a minimum of 2 peptides, and a protein probability >99.0%. A protein summary is provided in supplemental Table I. The identified peptides are listed in supplemental Table II. A functional classification of the identified proteins based on information from the Gene Ontology database returned the categories "membrane," "extracellular matrix," and "protein complexes" for cellular components (Figure 3A) and "metabolism" for biological processes (Figure 3B).

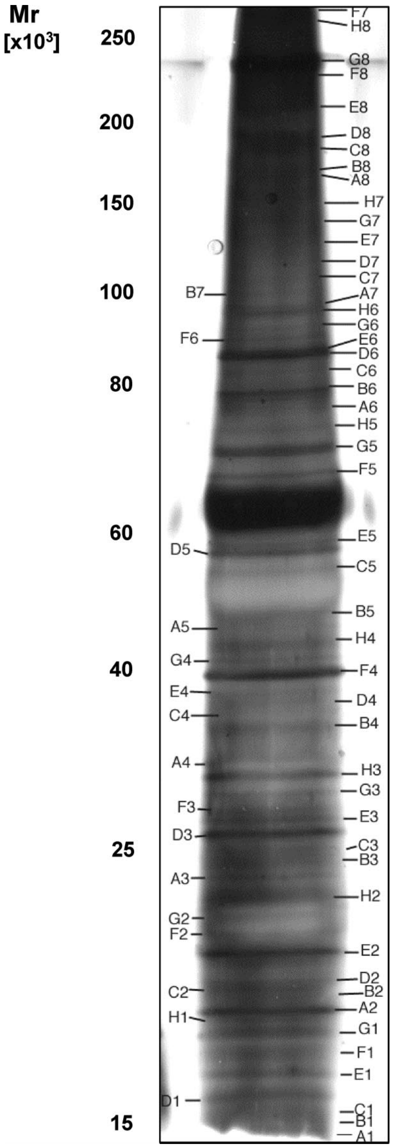

Figure 1. Protein separation by SDS-PAGE. Plaque-derived MPs were separated on large format gradient gels (4% to 12%) and stained with silver. Numbered bands (A1–H8) were excised and identified by LC-MS/MS. A summary of protein identifications is provided in supplemental Table I.

Membrane Proteins Reveal MP Origin

Consistent with their cellular origin,[9] membrane proteins were predominantly derived from leukocytes, including CD14, CD36, CD11c (integrin α-X), CD18 (integrin β2), CD29 (integrin-β1), CD51 (integrin α-V), the B-cell receptor-associated protein 31, H-cadherin, and the vascular adhesion protein 1 (membrane copper amine oxidase). Smooth muscle cell (SM22-α) and erythrocyte markers (CD233) were also identified. In addition, plaque MPs contained the B2 bradykinin receptor and both subunits of the enzyme dolichyl-diphosphooligosaccharide-protein glycosyltransferase, also referred to as advanced glycosylation end-product receptor-1. Notably, human leukocyte antigen class I and class II molecules were among the MP proteins. Validation by flow cytometry (n=12) confirmed that 15±2% of plaque MPs expressed major histocompatibility complex class II on their surface. Our observations, that MPs isolated from human atherosclerotic plaques express major histocompatibility complex class II together with potent costimulatory molecules such as CD40L,[17] suggest that macrophage-derived MPs may contribute to lymphocyte activation within atherosclerotic lesions.[18] A stimulatory effect was subsequently confirmed by incubating CD4$^+$ T-lymphocytes with increasing concentrations of plaque MPs from the same patients (Figure 4, n=4).

Taurine Is the Most Abundant MP Metabolite

"Metabolism" emerged as the top category for biological processes in the Gene Ontology annotation. To obtain insights into the metabolite composition, we used proton nuclear magnetic resonance spectroscopy and compared plaque-derived MPs with CE samples. Quantitative data for water-soluble metabolites not present in the isolation medium are listed in supplemental Table III. Pie charts showing their relative abundance and representative nuclear magnetic resonance profiles are provided in Figure 5. Strikingly, taurine, the most abundant free organic acid in human neutrophils,[19] which is implicated in the feedback inhibition of neutrophil/macrophage respiratory burst by scavenging myeloperoxidase-catalyzed free radicals,[20] was highly enriched in plaque MPs compared with CE samples. MPs also contained high concentrations of lactate, the end product of anaerobic glycolysis, which is consistent with our proteomic findings that almost all glycolytic enzymes were present in plaque MPs, indicating that MPs might be still actively metabolizing subcellular entities. The smallest enrichment was observed for glycerophosphocholine, a degradation product of phosphatidylcholine, which was a major metabolite in the CE samples.

Surface Labeling Unravels Engulfment of Immunoglobulins

To address protein distribution in addition to composition, proteins on the MP surface were labeled with CyDyes before separation by 2-DE. Protein identifications are listed in supplemental Table IV. Only 2 proteins (marked with an asterisk) were found in the 2-DE but not the 1-DE-LC-MS/MS experiment. Strikingly, hemoglobin, apoA1, and vitronectin showed intensive fluorescence (Figure 6A, yellow boxes), but the heavy and light chains of immunoglobulins were not surface labeled despite their prominent silver staining (Figure 6B, red boxes). Although this dual labeling approach is only semiquantitative, it suggested that immunoglobulins might be trapped within plaque-derived MPs. Subsequent flow cytometry analysis confirmed this finding: the signal with fluorescein isothiocyanate conjugated anti-IgG antibodies was substantially stronger on permeabilized than on nonpermeabilized plaque MPs (Figure 7A and 7B). A similar 4-fold increase in the average number of positive events (permablized versus unpermeabilized) was obtained for Igkappa (Figure 7B) whereas the percentage of MPs staining for apoA1 was almost identical before and after permeabilization (Figure 7B), a finding consistent with the preferential surface labeling of apoA1 in our proteomic analysis. Interestingly, more MPs showed surface labeling for apoB than for apoA1 (3.6±1.0% versus 1.4±0.4%, n=10,

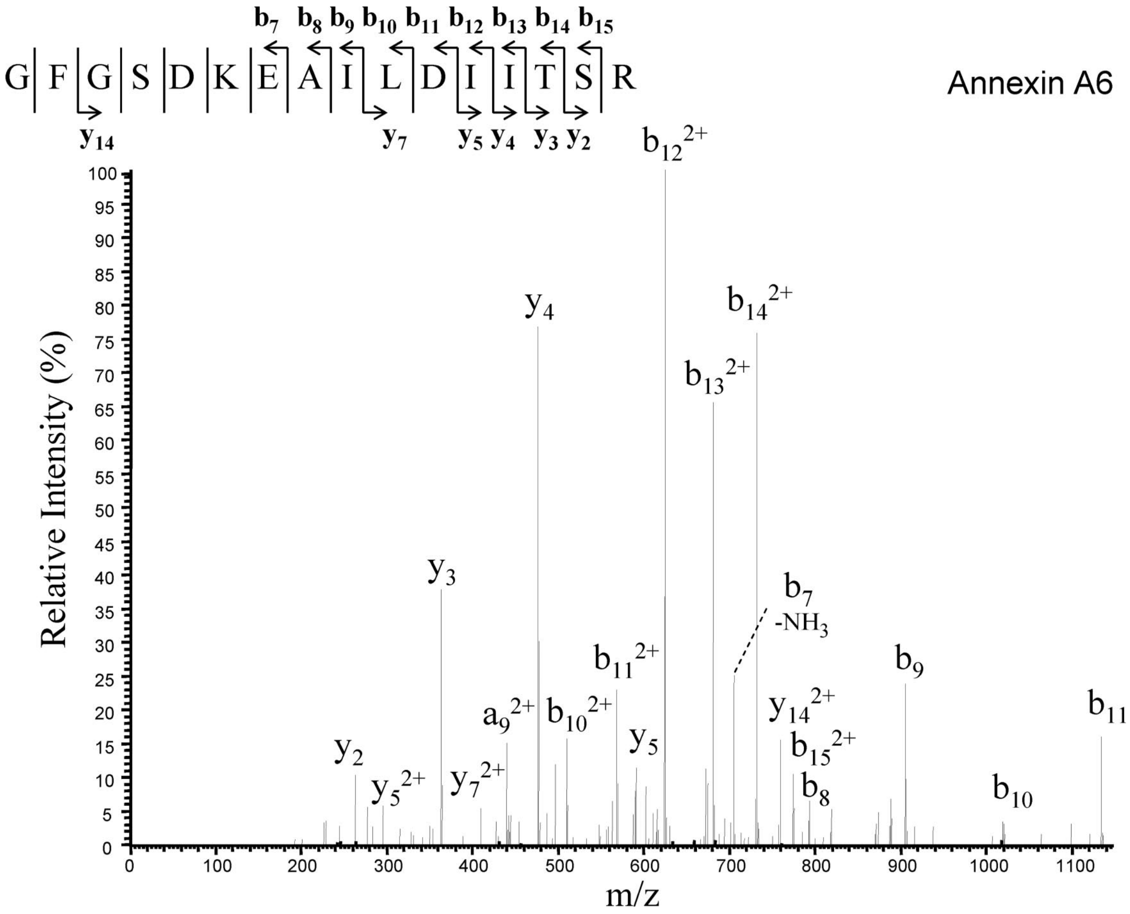

Figure 2. Tandem mass spectrometry (MS/MS). The product ion spectrum of the tryptic peptide GFGSDKEAILDIITSR was identified as annexin A6. All peptide identifications are provided in supplemental Table II.

t test $P=0.039$), although both apolipoproteins are present in similar concentrations in human plasma. Colabeling for CD14 and IgG revealed that almost all IgG containing MPs (93±7%) were $CD14^+$, indicating a macrophage origin. However, only 31±13% of $CD14^+$ MPs were double positive for IgG and surface CD14, whereas 69±13% stained for CD14 but not for IgG. Moreover, immunoglobulins were present in the MP-depleted supernatant even after filtration through a 0.1-μm filter indicating that immunoglobulins exist within macrophage-derived MPs and as free deposits in human atherosclerotic lesions (Figure 7C).

Antigen Specificity of Plaque Immunoglobulins

To examine whether the antibodies trapped within MPs were reactive and whether their specificity differed from immunoglobulins found in plaque and plasma, we used a novel bead-based technology to screen antibodies against a combinatorial antigen library. Surprisingly, most of the antibody reactivity within MPs was with carbohydrate but not peptide antigens. Further analyses were, therefore, directed against a sublibrary containing defined common carbohydrates to determine the antigen specificity of MP antibodies. For comparison, immunologic profiles were also obtained from the MP-depleted supernatant and from plasma samples of the same patients (n=6). Notably, although the immunologic profiles from plaque MPs (blue line) and the MP-depleted plaque homogenate (red line) were similar, plaque antibodies differed profoundly from plasma antibodies, which were profiled with and without an excess of calcium ions (Figure 8, green and black line, respectively). The addition of calcium did not change the antigenic profiles excluding calcium-dependent interactions. The plaque antibodies of all but 1 patient recognized the same antigen: blood group antigen A. IgG_2, IgA, and IgM against the blood group antigen A are represented as peaks 10, 42, and 58 on the x-axis of the immunologic profiles (Figure 8A and 8B). Notably, the patient without reactivity in the plaque was blood group A positive (Figure 8C). Apart from antiblood group A, there were no additional major peaks in the IgG_2, IgA, and IgD regions. The only other immunoglobulins detected were IgMs, some of which were directed against the Gal-α-(1,3)-Gal linkage, the antigen responsible for hyperacute rejection in xenotransplantation.[21]

Discussion

A combination of "-omic" techniques was used to comprehensively analyze the MPs derived from human atherosclerotic lesions. The proteomic arm of the study identified membrane proteins confirming that plaque MPs stem primarily from leukocytes but also originate from smooth muscle cells and erythrocytes. The metabolomic approach revealed taurine as the most prominent metabolite in plaque-derived

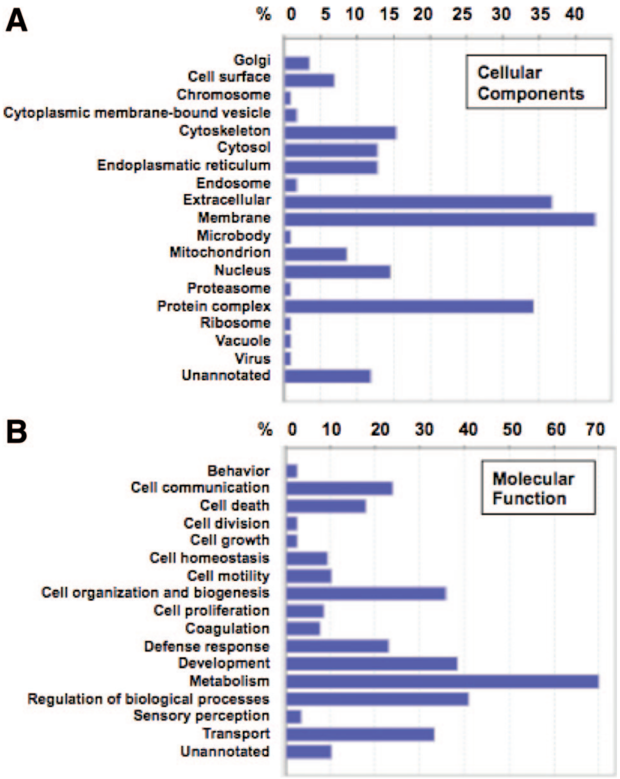

Figure 3. Functional classification according to the Gene Ontology database. The proteins listed in supplemental Table I are shown as percentage of categories "cellular components" (A) and "biological processes" (B).

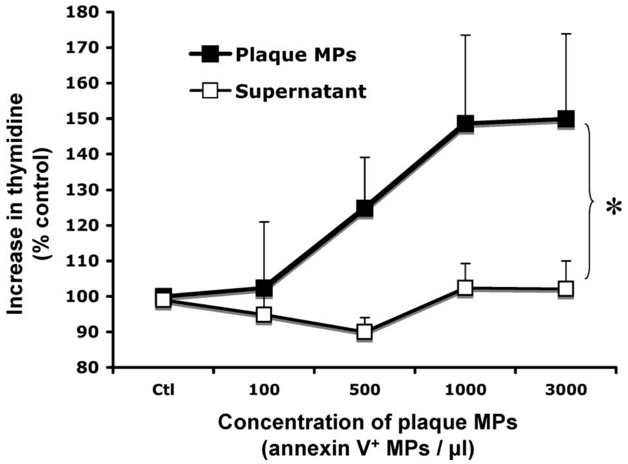

Figure 4. Stimulatory effect of plaque MPs on T-cell proliferation. CD4$^+$ T cells and plaque microparticles were obtained from the same patients. Note the proliferative response of T lymphocytes with increasing concentrations of plaque MPs. *Significant difference from supernatant (n=4), paired *t* test $P<0.05$.

MPs further emphasizing the monocyte/neutrophil-created oxidative microenvironment in atherosclerotic plaques. The successful application of immunomic methods revealed that certain anticarbohydrate-moiety antibodies were enriched in the plaque and that a subpopulation of CD14$^+$ MPs carried an intravesicular antibody load within atherosclerotic lesions. Our study provides the first evidence for an engulfment of immunologlobulins within MPs of plaque macrophages and partially unravels their antigen specificity. Thus, besides being an important determinant of plaque thrombogenicity, MPs might play a previously unrecognized role in modulating tissue inflammation as supported by their proliferative effect on CD4$^+$ T lymphocytes.

Proteomics of MPs to Target Membrane Proteins

Of the different cellular subproteomes, those embedded in the plasma membrane are of substantial interest because they regulate key biological functions, but the physiochemical characteristics and low abundance render analysis by proteomics challenging.[13] Although proteomics has been previously applied to atherosclerosis,[22–24] none of these studies has successfully targeted the membrane subproteome. To overcome the obstacles of membrane proteomics in complex tissues, we used a novel approach by analyzing tissue-derived MPs. So far, proteomic studies have been published on MPs from plasma,[25] platelets[26] and cultivated endothelial cells,[27] and T lymphocytes.[28] However, MP generated in vitro are not necessarily representative for MPs present in vivo because the phenotype of the released MPs is dependent on the agonist used to activate the parent cells. Besides, plaque-derived MPs are a population of membrane blebs originating from the cells constituting the atherosclerotic lesion and reflect their biological complexity and heterogeneous composition.[9] Thus, it is essential to complement the existing in vitro data sets by addressing the composition of in vivo-derived MPs. In this study, we were able to identify more than 150 proteins including membrane receptors of plaque-derived MP, despite the scarcity of the biological material available and the presence of high-abundant plasma proteins.

Immunoglobulins Are Contained Within Plaque MPs

Immunocomplexes resulting from the interaction of IgM natural antibodies with oxidized lipids are known to contribute to the removal of plaque antigens and prevent foam cell formation by blocking the uptake of oxidized lipids by plaque macrophages.[29] However, in vitro studies indicate that other antibodies with different isotypes (eg, IgG) also bind oxidized lipids and contain Fc domains capable of binding to macrophage Fc receptors, which could actually promote the uptake of immune complexes and contribute to the formation of lipid-filled macrophage-derived foam cells.[29] A potential proatherogenic role of IgG Fc receptors is supported by the protective effect of Fcγ deficiency in apoE-knockout mice.[30] Our finding that IgG is trapped inside macrophage-derived MPs isolated from human atherosclerotic lesions provides additional evidence that IgG might be taken up by macrophage Fcγ receptors previously described in human atherosclerotic plaques.[31] Although the presence of antibodies and complement components would support the existence of immune complexes, it is currently unclear to what extent the antibodies within plaque MPs are bound to complement/antigens or present as free immunoglobulins. This warrants further investigation in future studies because overloading plaque resident macrophages with immune complexes, oxi-

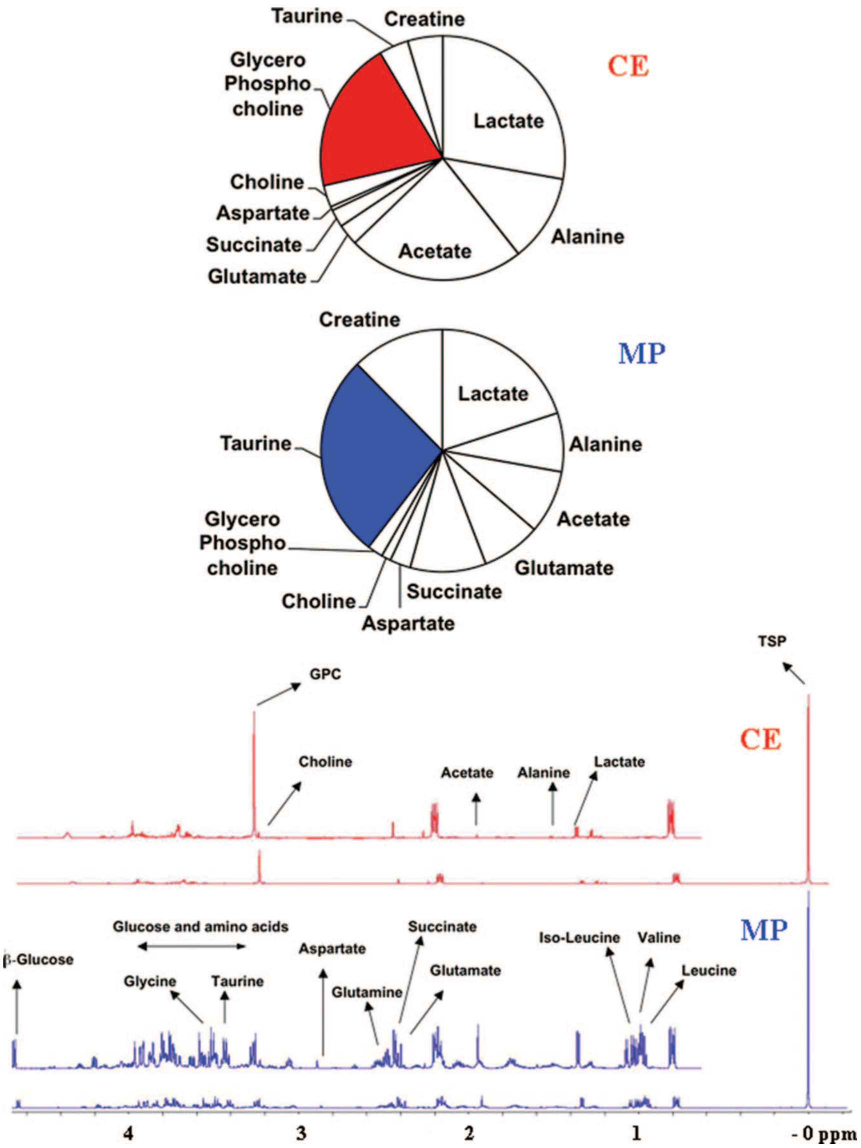

Figure 5. Proton nuclear magnetic resonance spectroscopy. Pie charts display the relative abundance of metabolites. Metabolite concentrations, their margins of error, and levels of statistical significance are given in supplemental Table III. Representative spectra of the CE (red) and MP (blue) samples are shown including a 4-fold enhanced image of the region 0.8 to 4.7 ppm in the upper panel for better visualization of the smaller peaks.

dized lipids, or apoptotic cells could lead to macrophage apoptosis and trigger MP release within the lesion.

It has been shown previously that oxidized plasma lipoproteins (low-density lipoprotein [LDL] or high-density lipoprotein) are incorporated by macrophage scavenger receptors for subsequent lysosomal degradation and relocation of modified apoA1 and apoB to the plasma membrane.[32] Moreover, CD4$^+$ T cells reactive to oxidized LDL have been cloned from human lesions,[33] and IgG and IgM antibodies that recognize epitopes of oxidized lipids are present in large amounts in advanced human atherosclerotic plaques.[34–36] Our data add to these findings by demonstrating that plaque MPs express major histocompatibility complex on their surface and activate CD4$^+$ T lymphocytes, which could contact and stimulate B lymphocytes, although scarce in atherosclerotic plaques, to produce immunoglobulins specific against plaque antigens. Notably, antigens, such as phosphatidylcholine, are found not only in oxidized LDL but also on apoptotic cell membranes,[37] and therefore likely to be present on plaque MPs.

The Portfolio of Plaque Antibodies Differs From Plasma

Our immunomic experiments revealed that plaque antibodies react with other antigens apart from oxidized LDL: First, the antibodies trapped within MPs were still reactive as demonstrated unambiguously by their strong signal in the immunomic profiling experiment. Second, although there is no selective retention of plaque antibodies in MPs, their antigen specificity is clearly distinct from the antibodies circulating in plasma. These findings do not exclude a carryover of plasma antibodies into the MP preparations, but at least the capture of plasma antibodies within atherosclerotic plaques must highly specific. Third, although the plasma profiles varied greatly between patients, antibodies against the blood group antigen A were consistently detected in atherosclerotic plaques and these anti-A antibodies were of 3 heavy chain isotypes (IgG$_2$, IgA, and IgM), providing additional evidence that this result is not an artifact. For unknown reasons, specific immune responses against many carbohydrates are preferentially

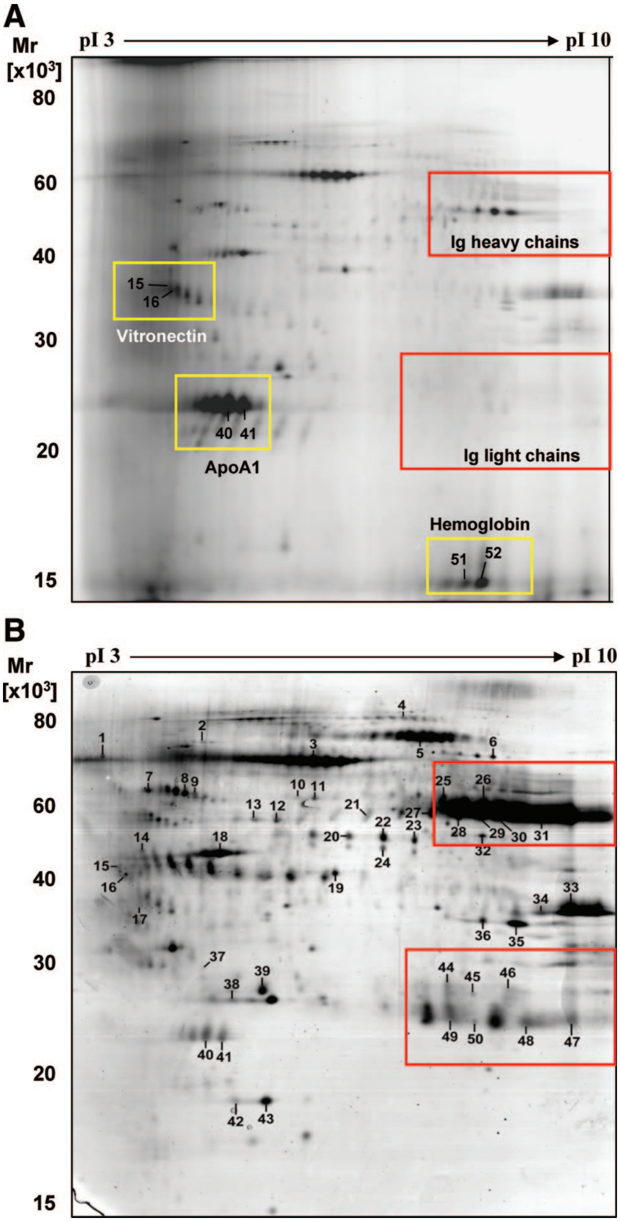

Figure 6. Surface labeling of plaque-derived MPs. Proteins on the MP surface were tagged with fluorescence dyes. After blocking the labeling reaction, MP proteins were separated by 2DE. Images were acquired using a fluorescence scanner (A). For total protein, counterstaining was performed with silver (B). Note that certain proteins are preferentially labeled with fluorescence (yellow boxes), ie, apoA1, whereas others show prominent silver staining, ie, immunoglobulins, but no surface labeling (red boxes). Numbered spots were identified by LC-MS/MS and are listed in supplemental Table IV.

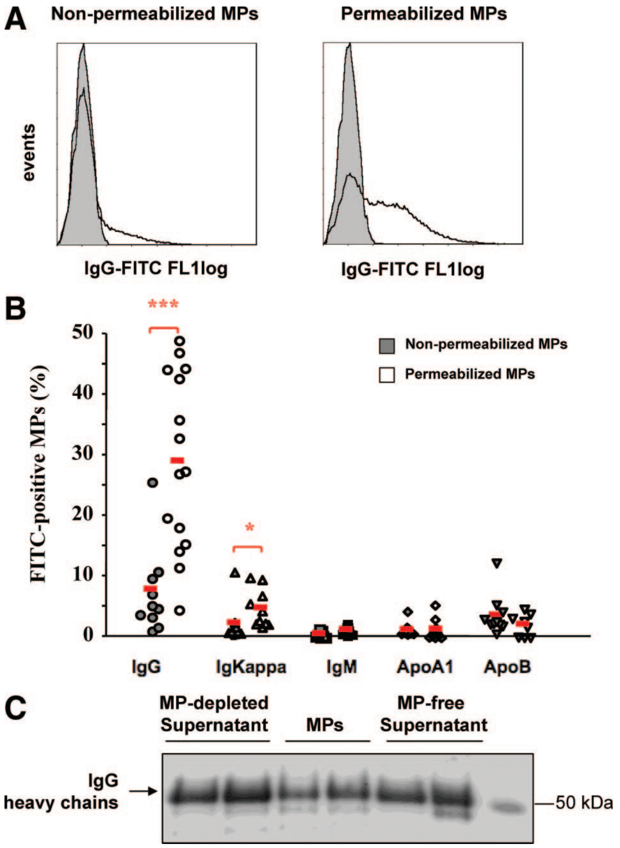

Figure 7. Flow cytometry analysis of plaque-derived MPs. A, Representative graph for IgG labeling on permeabilized and nonpermeabilized plaque-derived plaque MPs. The shadowed peak represents labeling with corresponding isotype-fluorescein isothiocyanate and the white peak, labeling with anti-IgG antibody. B, Percentage of MPs positive for IgG, Igkappa, IgM, apoA1, and apoB. Full symbols represent nonpermeabilized and open symbols permabilized MPs. Note that the flow cytometry data are consistent with the proteomic data presented in Figure 6. C, Western blot analysis for IgG content. MP-depleted supernatants were obtained by centrifugation. MP-free supernatants were subjected to an additional filtration step to remove residual MPs. *Significant difference, *t* test $P<0.05$; ***$P<0.001$.

IgG_2, and the carbohydrate antigens recognized by IgG2 are present not only in several tumor cells but also in endothelial cells. Carbohydrate antigens of the ABO blood group are expressed at high levels on endothelium, probably attached to von Willebrand factor. The ABO blood group influences the rate of proteolysis of von Willebrand factor[38] and increase its adhesive activity.[39] In fact, there is a direct relationship between ABO genotype and the amount of A antigen expressed on circulating von Willebrand factor.[40] The latter has been shown to increase the risk of ischemic stroke.[41] Other antibodies detected in the atherosclerotic plaques were human IgM against Gal-α-(1,3)-Gal. This terminal carbohydrate epitope is the major target for natural antibodies to pig cells in humans and formed by the α-1,3 galactosyl transferase, which places a terminal galactose residue in an α-linkage to another galactose.[42] These results extend our previous observation that the pattern of the anticarbohydrate immune response is different in plasma from patients with advanced atherosclerosis.[43] We now provide the first evidence that besides antibodies to oxidized LDL,[44] anticarbohydrate antibodies are also retained within human atherosclerotic lesions. Their presence, however, does not necessarily imply alterations in the amount or disposition of carbohydrate antigens but may reflect alterations in the immune system affecting the levels of natural antibodies to common environmental antigens.[45–47]

Limitations of the Study

Although proteomics and metabolomics have proven valuable tools to array authentic proteins and metabolites from

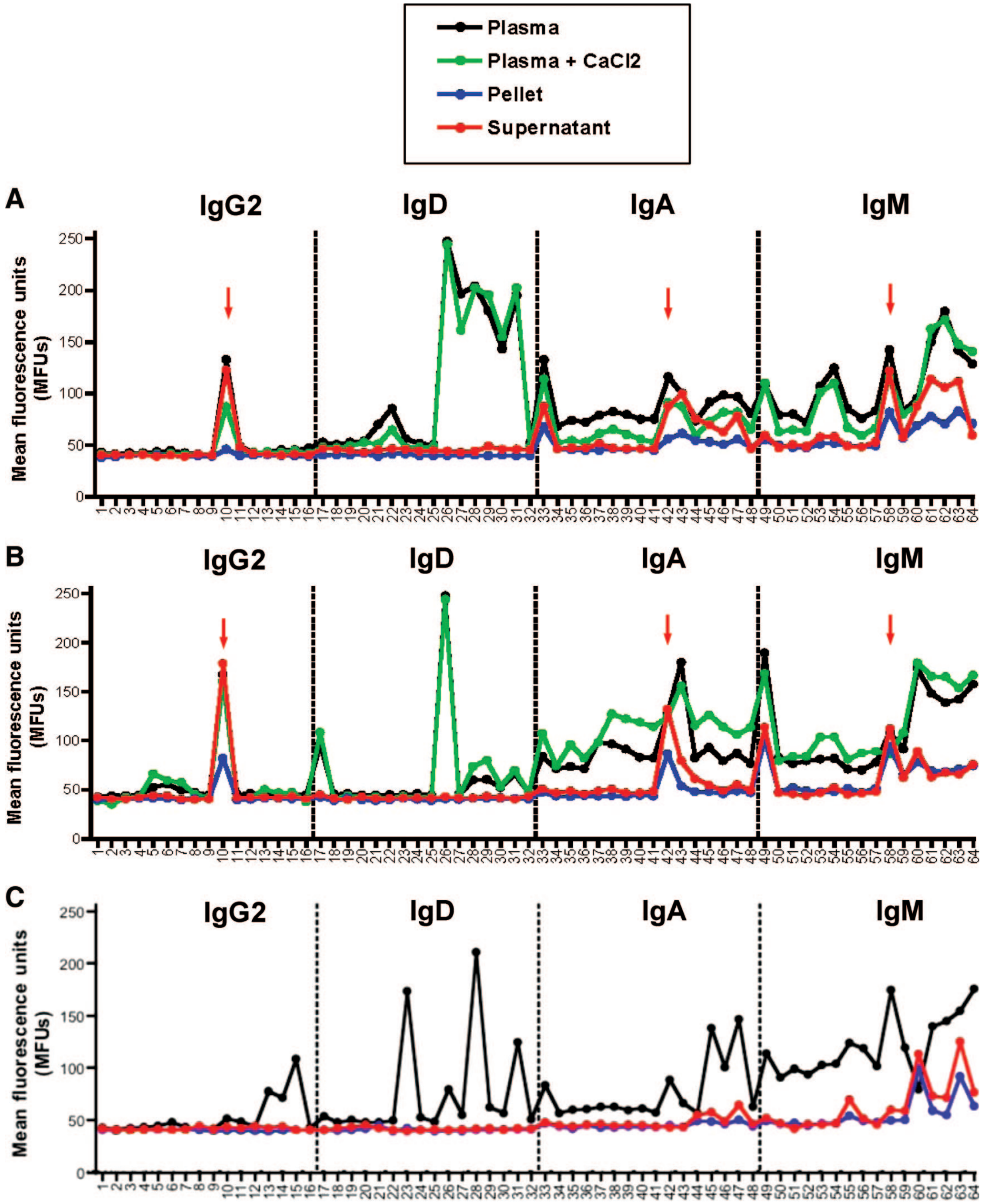

Figure 8. Immunomic profiling of plaque and circulating antibodies. Plaque MPs, MP-depleted supernatant, and plasma were obtained from the same patients (n=6, supplemental Table V) and screened against a sublibrary, containing various carbohydrate antigens (supplemental Table VI). The antibody reactivity (*y*-axis) against antigens (*x*-axis) is plotted. Plasma antibodies were measured twice, once with and without the presence of extra Ca^{2+} (green and black line, respectively). Note that the antibody portfolio of pelleted MPs (blue line) and the MP-depleted supernatant (red line) is similar, but clearly distinct from plasma antibodies. The red arrows depict peaks with strong reactivity against the blood group antigen A. Examples are shown from 3 different patients: blood group O RhD positive (panel A), blood group O RhD negative (panel B), and blood group A RhD positive (panel C). The patient with blood group A had no detectable anti-A antibody signal in the plaque. The level of background fluorescence without antibody is ≈45 MFUs.

human tissues, it is important to acknowledge that additional proteins and metabolites are likely tobe present in plaque MPs.[17] Moreover, although this study identified anticarbohydrate immunoglobulins as a component of the plaque antibodies present, our findings do not exclude other antibody specificities within the portfolio, in particular against peptide antigens, which tend to be recognized as conformational rather than linear epitopes. In addition, lipids, modified lipid reactivities, and peptides with posttranslational modifications were not present in the combinatorial antigen library. Hence, antioxidized LDL antibodies, which are probably a major component of plaque MPs,[48] would remain undetected by our assays.

Conclusion

To the best of our knowledge, this study is the first to investigate not only the protein composition but also the protein distribution, metabolite content, and immunologic profiles of MPs[49] by using 3 state-of-the-art techniques. The comprehensiveness provided by proteomics, metabolomics, and immunomics revealed a novel role of MPs in inflammation, which is a key determinant of plaque stability and progression.

Sources of Funding

This work was funded by the European Vascular Genomics Network (LSHM-CT-2003-503254; Brussels, Belgium) and grants from the British Heart Foundation, Oak Fundation, Agence Nationale de la Recherche (ANR-06-Physio-038), and Leducq Foundation LINK project. Dr Boulanger is supported by a Contrat d'Interface INSERM-APHP and Dr Mayr by a Senior Research Fellowship of the British Heart Foundation.

Disclosures

Dr Grainger was Chief Scientific Officer at Pronostics.

References

1. Mallat Z, Tedgui A. Current perspective on the role of apoptosis in atherothrombotic disease. *Circ Res*. 2001;88:998–1003.
2. Kockx MM. Apoptosis in the atherosclerotic plaque: quantitative and qualitative aspects. *Arterioscler Thromb Vasc Biol*. 1998;18:1519–1522.
3. Boulanger CM, Scoazec A, Ebrahimian T, Henry P, Mathieu E, Tedgui A, Mallat Z. Circulating microparticles from patients with myocardial infarction cause endothelial dysfunction. *Circulation*. 2001;104:2649–2652.
4. Nomura S, Nagata H, Suzuki M, Kondo K, Ohga S, Kawakatsu T, Kido H, Fukuori T, Yamaguchi K, Iwata K, Yanabu M, Soga T, Kokawa T, Yasunaga K. Microparticle generation during in vitro platelet activation by anti-CD9 murine monoclonal antibodies. *Thromb Res*. 1991;62:429–439.
5. Cohen Z, Gonzales RF, Davis-Gorman GF, Copeland JG, McDonagh PF. Thrombin activity and platelet microparticle formation are increased in type 2 diabetic platelets: a potential correlation with caspase activation. *Thromb Res*. 2002;107:217–221.
6. Falati S, Liu Q, Gross P, Merrill-Skoloff G, Chou J, Vandendries E, Celi A, Croce K, Furie BC, Furie B. Accumulation of tissue factor into developing thrombi in vivo is dependent upon microparticle P-selectin glycoprotein ligand 1 and platelet P-selectin. *J Exp Med*. 2003;197:1585–1598.
7. Bonderman D, Teml A, Jakowitsch J, Adlbrecht C, Gyongyosi M, Sperker W, Lass H, Mosgoeller W, Glogar DH, Probst P, Maurer G, Nemerson Y, Lang IM. Coronary no-reflow is caused by shedding of active tissue factor from dissected atherosclerotic plaque. *Blood*. 2002;99:2794–2800.
8. Llorente-Cortes V, Otero-Vinas M, Camino-Lopez S, Llampayas O, Badimon L. Aggregated low-density lipoprotein uptake induces membrane tissue factor procoagulant activity and microparticle release in human vascular smooth muscle cells. *Circulation*. 2004;110:452–459.
9. Leroyer AS, Isobe H, Leseche G, Castier Y, Wassef M, Mallat Z, Binder BR, Tedgui A, Boulanger CM. Cellular origins and thrombogenic activity of microparticles isolated from human atherosclerotic plaques. *J Am Coll Cardiol*. 2007;49:772–777.
10. Mallat Z, Hugel B, Ohan J, Leseche G, Freyssinet JM, Tedgui A. Shed membrane microparticles with procoagulant potential in human atherosclerotic plaques: a role for apoptosis in plaque thrombogenicity. *Circulation*. 1999;99:348–353.
11. Mayr M, Zhang J, Greene AS, Gutterman D, Perloff J, Ping P. Proteomics-based development of biomarkers in cardiovascular disease: mechanistic, clinical, and therapeutic insights. *Mol Cell Proteomics*. 2006;5:1853–1864.
12. Mayrhofer C, Krieger S, Allmaier G, Kerjaschki D. DIGE compatible labelling of surface proteins on vital cells in vitro and in vivo. *Proteomics*. 2006;6:579–585.
13. Sidibe A, Yin X, Tarelli E, Xiao Q, Zampetaki A, Xu Q, Mayr M. Integrated membrane protein analysis of mature and embryonic stem cell-derived smooth muscle cells using a novel combination of CyDye/biotin labeling. *Mol Cell Proteomics*. 2007;6:1788–1797.
14. Mayr M, Zampetaki A, Sidibe A, Mayr U, Yin X, De Souza AI, Chung YL, Madhu B, Quax PH, Hu Y, Griffiths JR, Xu Q. Proteomic and metabolomic analysis of smooth muscle cells derived from the arterial media and adventitial progenitors of apolipoprotein E-deficient mice. *Circ Res*. 2008;102:1046–1056.
15. Mayr M, Siow R, Chung YL, Mayr U, Griffiths JR, Xu Q. Proteomic and metabolomic analysis of vascular smooth muscle cells: role of PKCdelta. *Circ Res*. 2004;94:e87–e96.
16. Mayr M, Yusuf S, Weir G, Chung YL, Mayr U, Yin X, Ladroue C, Madhu B, Roberts N, De Souza A, Fredericks S, Stubbs M, Griffiths JR, Jahangiri M, Xu Q, Camm AJ. Combined metabolomic and proteomic analysis of human atrial fibrillation. *J Am Coll Cardiol*. 2008;51:585–594.
17. Leroyer AS, Rautou PE, Silvestre JS, Castier Y, Leseche G, Devue C, Duriez M, Brandes RP, Lutgens E, Tedgui A, Boulanger CM. CD40 ligand+ microparticles from human atherosclerotic plaques stimulate endothelial proliferation and angiogenesis a potential mechanism for intraplaque neovascularization. *J Am Coll Cardiol*. 2008;52:1302–1311.
18. Hansson GK. Inflammation, atherosclerosis, and coronary artery disease. *N Engl J Med*. 2005;352:1685–1695.
19. Stapleton PP, Redmond HP, Bouchier-Hayes DJ. Myeloperoxidase (MPO) may mediate neutrophil adherence to the endothelium through upregulation of CD11B expression—an effect downregulated by taurine. *Adv Exp Med Biol*. 1998;442:183–192.
20. Hellstrand K, Asea A, Dahlgren C, Hermodsson S. Histaminergic regulation of NK cells. Role of monocyte-derived reactive oxygen metabolites. *J Immunol*. 1994;153:4940–4947.
21. Sandrin MS, McKenzie IF. Gal alpha (1,3)Gal, the major xenoantigen (s) recognised in pigs by human natural antibodies. *Immunol Rev*. 1994;141:169–190.
22. Mayr M, Chung YL, Mayr U, Yin X, Ly L, Troy H, Fredericks S, Hu Y, Griffiths JR, Xu Q. Proteomic and metabolomic analyses of atherosclerotic vessels from apolipoprotein E-deficient mice reveal alterations in inflammation, oxidative stress, and energy metabolism. *Arterioscler Thromb Vasc Biol*. 2005;25:2135–2142.
23. Martin-Ventura JL, Duran MC, Blanco-Colio LM, Meilhac O, Leclercq A, Michel JB, Jensen ON, Hernandez-Merida S, Tunon J, Vivanco F, Egido J. Identification by a differential proteomic approach of heat shock protein 27 as a potential marker of atherosclerosis. *Circulation*. 2004;110:2216–2219.
24. Bagnato C, Thumar J, Mayya V, Hwang SI, Zebroski H, Claffey KP, Haudenschild C, Eng JK, Lundgren DH, Han DK. Proteomics analysis of human coronary atherosclerotic plaque: a feasibility study of direct tissue proteomics by liquid chromatography and tandem mass spectrometry. *Mol Cell Proteomics*. 2007;6:1088–1102.
25. Jin M, Drwal G, Bourgeois T, Saltz J, Wu HM. Distinct proteome features of plasma microparticles. *Proteomics*. 2005;5:1940–1952.
26. Garcia BA, Smalley DM, Cho H, Shabanowitz J, Ley K, Hunt DF. The platelet microparticle proteome. *J Proteome Res*. 2005;4:1516–1521.
27. Banfi C, Brioschi M, Wait R, Begum S, Gianazza E, Pirillo A, Mussoni L, Tremoli E. Proteome of endothelial cell-derived procoagulant microparticles. *Proteomics*. 2005;5:4443–4455.
28. Miguet L, Pacaud K, Felden C, Hugel B, Martinez MC, Freyssinet JM, Herbrecht R, Potier N, van Dorsselaer A, Mauvieux L. Proteomic analysis of malignant lymphocyte membrane microparticles using double ionization coverage optimization. *Proteomics*. 2006;6:153–171.
29. Khoo JC, Miller E, Pio F, Steinberg D, Witztum JL. Monoclonal antibodies against LDL further enhance macrophage uptake of LDL aggregates. *Arterioscler Thromb*. 1992;12:1258–1266.
30. Hernandez-Vargas P, Ortiz-Munoz G, Lopez-Franco O, Suzuki Y, Gallego-Delgado J, Sanjuan G, Lazaro A, Lopez-Parra V, Ortega L, Egido J, Gomez-Guerrero C. Fcgamma receptor deficiency confers protection against atherosclerosis in apolipoprotein E knockout mice. *Circ Res*. 2006;99:1188–1196.
31. Ratcliffe NR, Kennedy SM, Morganelli PM. Immunocytochemical detection of Fcgamma receptors in human atherosclerotic lesions. *Immunol Lett*. 2001;77:169–174.
32. Jonasson L, Holm J, Skalli O, Gabbiani G, Hansson GK. Expression of class II transplantation antigen on vascular smooth muscle cells in human atherosclerosis. *J Clin Invest*. 1985;76:125–131.
33. Stemme S, Faber B, Holm J, Wiklund O, Witztum JL, Hansson GK. T lymphocytes from human atherosclerotic plaques recognize oxidized low density lipoprotein. *Proc Natl Acad Sci USA*. 1995;92:3893–3897.

34. Yla-Herttuala S, Palinski W, Butler SW, Picard S, Steinberg D, Witztum JL. Rabbit and human atherosclerotic lesions contain IgG that recognizes epitopes of oxidized LDL. *Arterioscler Thromb*. 1994;14:32–40.
35. Hollander W, Colombo MA, Kirkpatrick B, Paddock J. Soluble proteins in the human atherosclerotic plaque. With spectral reference to immunoglobulins, C3-complement component, alpha 1-antitrypsin and alpha 2-macroglobulin. *Atherosclerosis*. 1979;34:391–405.
36. Parums D, Mitchinson MJ. Demonstration of immunoglobulin in the neighbourhood of advanced atherosclerotic plaques. *Atherosclerosis*. 1981;38:211–216.
37. Binder CJ, Hartvigsen K, Chang MK, Miller M, Broide D, Palinski W, Curtiss LK, Corr M, Witztum JL. IL-5 links adaptive and natural immunity specific for epitopes of oxidized LDL and protects from atherosclerosis. *J Clin Invest*. 2004;114:427–437.
38. Levy GG, Nichols WC, Lian EC, Foroud T, McClintick JN, McGee BM, Yang AY, Siemieniak DR, Stark KR, Gruppo R, Sarode R, Shurin SB, Chandrasekaran V, Stabler SP, Sabio H, Bouhassira EE, Upshaw JD Jr, Ginsburg D, Tsai HM. Mutations in a member of the ADAMTS gene family cause thrombotic thrombocytopenic purpura. *Nature*. 2001;413:488–494.
39. Sarode R, Goldstein J, Sussman II, Nagel RL, Tsai HM. Role of A and B blood group antigens in the expression of adhesive activity of von Willebrand factor. *Br J Haematol*. 2000;109:857–864.
40. O'Donnell J, Boulton FE, Manning RA, Laffan MA. Amount of H antigen expressed on circulating von Willebrand factor is modified by ABO blood group genotype and is a major determinant of plasma von Willebrand factor antigen levels. *Arterioscler Thromb Vasc Biol*. 2002;22:335–341.
41. Bongers TN, de Maat MP, van Goor ML, Bhagwanbali V, van Vliet HH, Gomez Garcia EB, Dippel DW, Leebeek FW. High von Willebrand factor levels increase the risk of first ischemic stroke: influence of ADAMTS13, inflammation, and genetic variability. *Stroke*. 2006;37:2672–2677.
42. Sandrin MS, Vaughan HA, Dabkowski PL, McKenzie IF. Anti-pig IgM antibodies in human serum react predominantly with Gal(alpha 1–3)Gal epitopes. *Proc Natl Acad Sci USA*. 1993;90:11391–11395.
43. Mosedale DE, Chauhan A, Schofield PM, Grainger DJ. A pattern of anti-carbohydrate antibody responses present in patients with advanced atherosclerosis. *J Immunol Methods*. 2006;309:182–191.
44. Tsimikas S, Shortal BP, Witztum JL, Palinski W. In vivo uptake of radiolabeled MDA2, an oxidation-specific monoclonal antibody, provides an accurate measure of atherosclerotic lesions rich in oxidized LDL and is highly sensitive to their regression. *Arterioscler Thromb Vasc Biol*. 2000;20:689–697.
45. Binder CJ, Shaw PX, Chang MK, Boullier A, Hartvigsen K, Horkko S, Miller YI, Woelkers DA, Corr M, Witztum JL. The role of natural antibodies in atherogenesis. *J Lipid Res*. 2005;46:1353–1363.
46. Mayr M, Kiechl S, Willeit J, Wick G, Xu Q. Infections, immunity, and atherosclerosis: associations of antibodies to *Chlamydia pneumoniae*, *Helicobacter pylori*, and cytomegalovirus with immune reactions to heat-shock protein 60 and carotid or femoral atherosclerosis. *Circulation*. 2000;102:833–839.
47. Mayr M, Kiechl S, Tsimikas S, Miller E, Sheldon J, Willeit J, Witztum JL, Xu Q. Oxidized low-density lipoprotein autoantibodies, chronic infections, and carotid atherosclerosis in a population-based study. *J Am Coll Cardiol*. 2006;47:2436–2443.
48. Shaw PX, Horkko S, Tsimikas S, Chang MK, Palinski W, Silverman GJ, Chen PP, Witztum JL. Human-derived anti-oxidized LDL autoantibody blocks uptake of oxidized LDL by macrophages and localizes to atherosclerotic lesions in vivo. *Arterioscler Thromb Vasc Biol*. 2001;21:1333–1339.
49. Mayr M, Madhu B, Xu Q. Proteomics and metabolomics combined in cardiovascular research. *Trends Cardiovasc Med*. 2007;17:43–48.

CLINICAL PERSPECTIVE

Cell activation stimulates bleb formation from the cell membrane. From these blebs, virtually all cell types generate even smaller particles, which are termed microparticles (MPs). MPs with procoagulant activity are present in human atherosclerosis, but detailed information on their composition is not available. In the present investigation, we used a combination of "-omic" techniques to comprehensively analyze MPs derived from human atherosclerotic lesions. The proteomic arm of the study identified membrane proteins confirming that plaque MPs stem primarily from leukocytes but also originate from smooth muscle cells and erythrocytes. The metabolomic approach revealed taurine as the most prominent metabolite in plaque-derived MPs. Because taurine serves as a negative feedback after oxidative burst, these data further emphasize the presence of a monocyte/neutrophil-created oxidative microenvironment in atherosclerotic plaques. The successful application of immunomic methods revealed that certain anticarbohydrate-moiety antibodies were enriched in the plaque and that a subpopulation of $CD14^+$ MPs carried an intravesicular antibody load within atherosclerotic lesions. Notably, carbohydrate antigens of the ABO blood group are expressed at high levels on endothelium, probably attached to von Willebrand factor. Most of the antibody reactivity with carbohydrate antigens were directed against the blood group antigen A and against the Gal-α-(1,3)-Gal linkage, the antigen responsible for hyperacute rejection in xenotransplantation. Our study provides the first evidence for an engulfment of immunologlobulins within MPs of plaque macrophages and provides clues about their antigen specificity. Thus, besides being an important determinant of plaque thrombogenicity, MPs might play a previously unrecognized role in modulating tissue inflammation as supported by their proliferative effect on $CD4^+$ T lymphocytes.

SUPPLEMENTAL MATERIAL

PROTEOMICS, METABOLOMICS AND IMMUNOMICS ON MICROPARTICLES DERIVED FROM HUMAN ATHEROSCLEROTIC PLAQUES

Manuel Mayr, MD, PhD[1]; David Grainger, PhD[2]; Ursula Mayr, MD[1]; Aurelie S. Leroyer, PhD[3]; Guy Leseche, MD[3]; Anissa Sidibe, MSc[1]; Olivier Herbin, MSc[3]; Xiaoke Yin, PhD[1]; Aldrin Gomes, PhD[4]; Basseti Madhu, PhD[5]; John R. Griffiths, MD[5]; Qingbo Xu, MD, PhD[1]; Alain Tedgui, PhD[3]; Chantal M. Boulanger, PhD[3]

[1]Cardiovascular Division, King's BHF Centre, King's College London, London, UK

[2] Department of Medicine, Addenbrooke's Hospital, Cambridge, UK

[3] Paris-Cardiovascular Research Center, INSERM U970, Hôpital Européen Georges Pompidou, Université Paris-Descartes, Paris, F

[4] Section of Neurobiology, Physiology, and Behavior, University of California, Davis, USA

[5] Cancer Research UK Cambridge Research Institute, Robinson way, Cambridge, UK

Correspondence to:

Dr. Manuel Mayr, Cardiovascular Division, King's College London, 125 Coldharbour Lane, London SE5 9NU, UK, Phone: +44 (0) 20 7848 5238, Fax: +44 (0) 20 7848 5296

Email: manuel.mayr@kcl.ac.uk

ONLINE METHODS

1D gel LC-MS/MS. Large-format gradient gels (4-12%) were cast using the a2DE optimizer (NextGen Sciences, Huntingdon, UK). After the gels were overlaid with water-saturated butanol (2:1) and left to polymerise overnight, the stacking gel containing 4-5% acrylamide weakly buffered at pH 9.0 was cast over the already set resolving gel. Once samples were loaded, a constant 50mV current was applied as proteins migrated down the stacking gel, at the stacking gel/running gel boundary the current was increased and maintained at 75mV until the dye front reached the end of the gel. For tandem mass spectrometry (MS/MS), in-gel digestion with trypsin was performed according to published methods [1, 2] modified for use with an Investigator ProGest (Genomic Solutions) robotic digestion system. 10 uL of sample was injected using an autosampler (Thermo Electron Corporation, CA) and loaded onto a 100 x 0.18 mm reverse-phase liquid chromatography (LC) column (BioBasic-18, particle size 5 μm, Thermo Electron Corporation) at 2 μl/min using an Surveyer MS pump (Thermo Electron Corporation, CA) and eluted with a 90 min gradient (0.1-30% B in 35 min, 30-50% B in 10 min and 50-80% B in 5 min where A =99.9% H2O, 0.1% formic acid and B = 99.9% acetonitrile, 0.1% formic acid). The column was coupled to an electrospray source and spectra were collected from an ion-trap mass analyzer (LCQ Deca XP Plus, Thermo Electron Corporation) using full ion scan mode over the mass-to-charge (m/z) range 300-1800. MS/MS was performed on the top three ions in each MS scan using the data-dependent acquisition mode with dynamic exclusion enabled. MS/MS spectra were matched to database entries (UniProt Knowledgebase Release 7.5, consisting of: UniProtKB/Swiss-Prot Release 49.5 and UniProtKB/TrEMBL Release 32.5 of 18-Apr-2006) using TurboSEQUEST software (Bioworks 3.3, Thermo Finnigan). All peptide sequence assignments were required to result from fully tryptic cleavages of the corresponding proteins. Scaffold (version 1.0, Proteome Software Inc., Portland, OR) was used to validate MS/MS based peptide and protein identifications. Peptide identifications were accepted if they could be established at greater than 95.0% probability as specified by the Peptid Prophet algorithm [3]. Protein identifications were accepted if they could be established at greater than 99.0% probability and contained at least 2 identified peptides. Protein probabilities were assigned by the Protein Prophet algorithm [4]. Proteins that contained similar peptides and could not be differentiated based on MS/MS analysis alone were grouped to satisfy the principles of parsimony.

Two-dimensional gel electrophoresis (2-DE). For 2-DE, samples were mixed with 2x buffer (8M urea, 4% w/v CHAPS, 2% w/v DTT, 2% v/v Pharmalytes 3-10 for IEF), 50μg per sample were diluted in rehydration solution (8M urea, 0.5% w/v CHAPS, 0.2% w/v DTT, and 0.2% v/v Pharmalyte pH 3-10). After centrifugation at 13,000 g for 10 min, the supernatant was harvested and the protein concentration was determined using a modification of the method described by Bradford[5]. After overnight rehydration in IPG strips (18cm, pH 3-10, nonlinear, GE healthcare), proteins were focused at 0.05 mA/IPG strip for 60 kVh at 20°C (Multiphor II, GE healthcare). Once IEF was complete the strips were equilibrated in 6M urea containing 30% v/v glycerol, 2% w/v SDS and 0.01% w/v Bromophenol blue, with addition of 1% w/v DTT for 15 min, followed by the same buffer without DTT, but with the addition of 4.8% w/v iodoacetamide for 15 min. SDS-PAGE was performed using 12% T (total acrylamide concentration), 2.6% C (degree of cross-linking) polyacrylamide gels without a stacking gel, using the Ettan DALT six system (GE healthcare). The second dimension was terminated when the Bromophenol blue dye front had migrated off the lower end to the gels. After electrophoresis, fluorescence images were acquired using the Typhoon variable mode imager 9400 (GE healthcare). Finally, gels were fixed overnight in methanol: acetic acid: water solution (4:1:5 v/v/v). Protein profiles were visualised by silver staining using the Plus one silver staining kit (GE healthcare) with slight modifications[6] to ensure compatibility with subsequent mass spectrometry analysis. For documentation, silver-stained gels were scanned in transmission scan mode using a calibrated scanner (GS-800, Bio-Rad).

Assessment of CD4+ T cell proliferation. CD4+ T-Cells were cultured in RPMI 1640 supplemented with Glutamax, 10% FCS, 0.02 mmol/L 2ß-mercaptoethanol, penicillin and streptomycin (both 100U/mL). *In vitro* proliferation of purified CD4+ T cells was assessed in flat-bottomed 96-well microplates (10^5 cells per well; 200 μL/well) in the presence of pre-coated anti-human CD3 (5 μg/ml; purified NA/LE Mouse anti Human CD3, BD Biosciences, F) and purified soluble CD28-specific antibody (2 μg/mL; purified NA/LE mouse anti-human CD 28, BD Biosciences, F). Cells were exposed to increasing concentrations of plaque MP isolated from the endarterectomized plaque of the same patient or the corresponding volume of MP supernatant, and were cultured at 37°C for 48 hours. Cells were pulsed with 1 μCi of 3[H] thymidine (Amersham Biosciences Inc, Piscataway, NJ) for the last 18 hours of culture and thymidine incorporation was assessed with a TopCount NXT scintillation counter (Perkin Elmer, Waltham, MA).

Proton nuclear magnetic resonance spectroscopy (NMR). Metabolites were extracted from human carotid endarterectomy (CE) samples and plaque MPs in 6% PCA [7]. Neutralised extracts were freeze-dried and reconstituted in D_2O. 0.5ml of the extracts were placed in 5mm NMR tubes. ^{1}H NMR spectra were obtained using a Bruker 600MHz spectrometer. The water resonance was suppressed by using gated irradiation centred on the water frequency. Sodium 3-trimethylsilyl-2,2,3,3-tetradeuteropropionate (TSP) was added to the samples for chemical shift calibration. Immediately before the NMR analysis, the pH was readjusted to 7 with PCA or KOH. Resonances have been assigned as leucine: 0.96 ppm, valine: 0.99 ppm, isoleucine: 1.01 ppm, lactate: 1.33 ppm, alanine: 1.48 ppm, acetate: 1.92 ppm, glutamate: 2.35 ppm, succinate: 2.41 ppm, glutamine: 2.45 ppm, aspartate: 2.81 ppm, choline: 3.20 ppm, glycerophosphocholine (GPC): 3.22 pm, taurine: 3.43 ppm, glycine: 3.56 ppm, creatine: 3.92 ppm, glucose: 5.23 ppm, tyrosine: 6.90 ppm, phenylalanine: 7.32 ppm, and formate: 8.45 ppm. TSP is added for chemical shift calibration and quantitation. Metabolite abundance was adjusted for protein concentration.

FACS analysis. For surface labelling, the plaque pellet (5 μL) was incubated with different fluorochrome-labelled antibodies or their corresponding isotype-matched IgG controls (RT; 30 minutes in the dark). The presence of intracellular IgG or apolipoproteins was assayed after MP fixation (2% paraformaldehyde, 20 min) and permeabilization (0.1% saponin, 10 min). Goat anti-human IgG-FITC (10μL/test), anti-human IgM-FITC (5μL/test), and anti-human kappa light chain-FITC (50μL/test) were obtained from Serotec (Oxford, UK). Goat F(ab')2 FITC/RPE (from Serotec) served as a negative control to adjust for non-specific antibody binding. Anti-human apoA1 (clone 1405, 10μL, dilution 1/28) and anti-human apoB (clone 1607, 10μL, dilution 1/28) were purchased from Biodesign (Saco, ME, US), IgG1 mouse (from Serotec) was used in parallel as negative control. After washing the MPs, an anti-mouse-PC5 (10μL, dilution 1/20) (Dakocytomation, Denmark) was added for 30 min in the dark as anti-apoA1, anti-apoB and their isotype were unconjugated. At the end of the incubation period, samples were diluted in filtered PBS (0.22 μm). MPs were analysed on a Coulter EPICS XL flow cytometer (Beckman Coulter, Villepinte, France). Regions corresponding to MPs were identified in forward light scatter (FCS) and side-angle light scatter (SSC) intensity dot plot representation set at logarithmic gain. The gate for MPs was defined as events with a 0,1-1 μm diameter, in comparison with calibrator beads, and then plotted on a FL/FSC fluorescence dot plot to determinate positively labelled MPs by specific antibodies.

Immunoblotting. MPs and MP-depleted supernatants were obtained from plaque homogenates by centrifugation as mentioned above. MP-free supernatants were obtained by passing the MP-depleted supernatant through a 0.1 μm filter. 10μg of protein extracts from MP-depleted supernatants, MPs and MP-free supernatants was separated on 4-20% gradient gels (Novex, Invitrogen) and transferred to nitrocellulose membranes. Membranes were blocked in 5% PBS milk (overnight, 4 °C), probed with an HRP-conjugated rabbit anti-human IgG antibody (Dako, P0214, 1:2000) diluted in 5% PBS milk. After washing in 0.5% tween/PBS, immunoglobulins were detected on X-ray films using enhanced chemiluminescence (ECL, GE healthcare).

Immunomics. The assay is performed with 16 different antigens (x4 isotype detections for 64-plex read out). In each case, the antigens are in the same order, so sample 1, 17, 33 and 49 are all the same antigen, and there is only a single carbohydrate antigen presented as a conjugate to either bovine or human serum albumin (BSA or HSA). Sample 3/19/35/51 is a no-coat control with no antigen present, 2/18/34/50 is BSA only and 4/20/36/52 is HSA only. The other 13 antigens are all carbohydrates epitopes against which natural antibodies are commonly found. The list (in order) is provided as Supplemental Table VI.

SUPPLEMENTAL TABLES

Supplemental Table I. Summary of MP proteins identified by LC-MS/MS from 1D SDS-PAGE gradient gels. MS/MS data were analyzed using a combination of two search engines (Sequest and X! Tandem). Scaffold was then used to validate MS/MS based peptide and protein identifications. Peptide identifications were accepted if they could be established at greater than 95.0% probability as specified by the Peptide Prophet algorithm[3]. Protein identifications were accepted if they could be established at greater than 99.0% probability and contained at least 2 identified peptides.

Supplemental Table II. Summary of peptide identifications. Scores and amino acid sequences of all peptides identified by MS/MS are provided.

Supplemental Table III. Metabolite concentrations of carotid endarterectomies and plaque MPs. Concentrations of water-soluble metabolites not present in the isolation medium were normalized for protein content and are given in μmol/g protein (mean±SE).

Supplemental Table IV. Summary of MP proteins identified by LC-MS/MS from 2D gels. See legend to Supplemental Table I.

Supplemental Table V. Clinical characteristics. For immunomics, plasma and carotid endarterectomy samples were obtained from 6 patients.

Supplemental Table VI. Carbohydrate antigens coated on the Gycopanel.

Supplemental Table I. Summary of microparticle proteins identified by LC-MS/MS from 1D SDS-PAGE gradient gels.

Protein identity	SWISS PROT Entry name	Molecular Weight	Unique Peptides	Unique Spectra	Total Spectra	Sequence coverage
Plasma membrane						
Monocyte differentiation antigen CD14	CD14_HUMAN	40058.6	3	3	3	13.1%
Leukocyte differentiation antigen CD36	CD36_HUMAN	53036.3	2	3	3	4.2%
Integrin alpha-X, CD11c	ITAX_HUMAN	127812.3	3	3	4	2.7%
Integrin beta-2, CD18	ITB2_HUMAN	84764.0	6	7	9	8.5%
Integrin beta-1, CD29	ITB1_HUMAN	88447.1	2	3	3	2.4%
Integrin alpha-V, CD51	ITAV_HUMAN	116023.0	2	2	2	1.8%
B-cell receptor-associated protein 31	BAP31_HUMAN	27974.6	2	2	3	9.8%
Cadherin-13 (H-cadherin)	CAD13_HUMAN	78269.6	2	4	6	3.7%
Membrane copper amine oxidase (Vascular adhesion protein 1)	AOC3_HUMAN	84604.1	4	4	7	6.0%
Lactadherin	MFGM_HUMAN	43104.9	2	3	4	5.4%
Band 3 anion transport protein, CD233	B3AT_HUMAN	101778.0	5	7	11	6.4%
B2 bradykinin receptor	BKRB2_HUMAN	44443.4	2	2	3	6.4%
MHC complex						
HLA class I histocompatibility antigen B-41 alpha chain	1B41_HUMAN	40520.7	2	2	4	9.1%
HLA class I histocompatibility antigen A-68 alpha chain	1A68_HUMAN	40890.2	4	5	8	17.0%
HLA class II histocompatibility antigen MHC class I antigen DRB3*2	2B32_HUMAN	29970.4	3	3	3	12.8%
HLA class II histocompatibility antigen DP(W2) beta chain	HB2Q_HUMAN	29271.7	2	2	2	8.9%
HLA class II histocompatibility antigen DQ(6) alpha chain	HA26_HUMAN	28015.0	2	2	2	10.2%

Ion pumps						
Sodium/potassium-transporting ATPase alpha-1 chain	AT1A1_HUMAN	112881.5	4	4	4	4.7%
Chloride intracellular channel protein 1	CLIC1_HUMAN	26905.3	3	3	3	16.2%
Voltage-dependent anion-selective channel protein 3	VDAC3_HUMAN	30641.9	2	3	3	5.7%
Extracellular matrix						
Vitronectin	VTNC_HUMAN	54288.1	7	16	34	16.3%
Fibronectin	FINC_HUMAN	262581	8	10	13	4.2%
Lumican	LUM_HUMAN	38413.5	2	2	2	9.5%
Myofilaments and associated proteins						
Vinculin	VINC_HUMAN	123783.3	14	16	21	12.9%
Alpha-actinin-1	ACTN1_HUMAN	103043.1	4	4	6	4.8%
Actin, aortic smooth muscle	ACTA_HUMAN	41992.1	5	9	13	46.7%
Actin, cytoplasmic 1 (Beta-actin)	ACTB_HUMAN	41719.8	22	61	190	59.7%
Actin-like protein 2	ARP2_HUMAN	44743.7	3	3	4	6.9%
Actin-like protein 3	ARP3_HUMAN	47353.8	2	2	2	4.3%
Myosin light polypeptide 6	MYL6_HUMAN	16911.8	5	10	12	41.7%
Myosin-9	MYH9_HUMAN	226519.5	13	14	19	8.0%
Myosin-10	MYH10_HUMAN	228927.2	4	4	4	5.1%
Myosin-11	MYH11_HUMAN	227326.6	24	30	40	12.1%
Filamin-A	FLNA_HUMAN	280711.4	18	22	29	9.3%
Profilin-1	PROF1_HUMAN	15036.3	5	7	12	45.7%
Cofilin-1	COF1_HUMAN	18485.2	2	2	3	15.1%
F-actin capping protein subunit alpha-1	CAZA1_HUMAN	32905.1	2	2	3	8.7%
Macrophage-capping protein	CAPG_HUMAN	38499.9	4	6	10	14.9%
Adenylyl cyclase-associated protein 1 (CAP 1)	CAP1_HUMAN	51837.5	5	6	7	18.3%
Gelsolin	GELS_HUMAN	85679.8	9	12	17	12.9%
Transgelin (Smooth muscle protein 22-alpha)	TAGL_HUMAN	22592.9	2	6	10	11.0%
Transgelin-2 (SM22-alpha homolog)	TAGL2_HUMAN	22373.9	4	6	6	24.1%
Ezrin (p81) (Cytovillin)	EZRI_HUMAN	69396.6	2	2	2	3.1%
Major vault protein (MVP)	MVP_HUMAN	99308.0	4	4	4	4.1%

Intermediate filaments						
Tubulin chain	TBA3_HUMAN TBA6_HUMAN TBAK_HUMAN	49877.4	2	4	5	5.6%
Vimentin	VIME_HUMAN	53634.7	22	44	96	47.4%
Plasma proteins						
Serum albumin	ALBU_HUMAN	69348.9	34	81	435	57.0%
Alpha-2-macroglobulin	A2MG_HUMAN	163258.8	14	36	113	9.9%
Alpha-1B-glycoprotein	A1BG_HUMAN	54254.4	2	2	2	4.7%
Hemoglobin subunit beta	HBB_HUMAN	15980.0	10	38	213	76.9%
Hemoglobin subunit alpha	HBA_HUMAN	15239.6	6	21	123	43.0%
Hemoglobin subunit delta	HBD_HUMAN	16037.1	4	8	10	68.0%
Serotransferrin	TRFE_HUMAN	77032.2	20	29	34	30.5%
Haptoglobin	HPT_HUMAN	45186.9	12	22	51	27.3%
Hemopexin	HEMO_HUMAN	51658.5	6	6	8	14.9%
Ferritin light chain	FRIL_HUMAN	20002.6	8	18	38	43.4%
Ferritin heavy chain	FRIH_HUMAN	21208.2	3	5	5	15.9%
Serum amyloid P-component	SAMP_HUMAN	25369.7	11	19	26	36.8%
Alpha-1-antitrypsin	A1AT_HUMAN	46719.9	20	39	71	53.6%
Transthyretin (Prealbumin)	TTHY_HUMAN	15868.9	2	3	4	9.5%
Inter-alpha-trypsin inhibitor heavy chain H4	ITIH4_HUMAN	103308.4	3	3	6	2.7%
Coagulation						
Fibrinogen alpha chain	FIBA_HUMAN	94955.4	3	3	5	3.4%
Fibrinogen beta chain	FIBB_HUMAN	55910.6	17	24	37	48.1%
Fibrinogen gamma chain	FIBG_HUMAN	51495.3	11	20	39	32.9%
Plasminogen	PLMN_HUMAN	90549.4	2	3	3	2.5%
Antithrombin-III	ANT3_HUMAN	52586.0	3	4	6	7.1%
Prothrombin	THRB_HUMAN	70018.8	2	2	2	5.0%
Apolipoproteins						
Apolipoprotein E	APOE_HUMAN	36135.5	13	26	68	47.0%
Apolipoprotein A-I	APOA1_HUMAN	30760.5	12	18	24	43.5%

Apolipoprotein D	APOD_HUMAN	21258.0	4	6	19	22.2%
Apolipoprotein B-100	APOB_HUMAN	515554.3	30	35	59	7.2%
Beta-2-glycoprotein 1 (Apo-H)	APOH_HUMAN	38280.5	4	9	16	15.9%
Apolipoprotein(a), Lp(a)	APOA_HUMAN	501270.9	3	5	8	0.7%
Immunoglobulins						
Ig gamma-1 chain C region	IGHG1_HUMAN	36087.0	12	36	199	47.0%
Ig gamma-2 chain C region	IGHG2_HUMAN	35865.2	7	12	36	38.3%
Ig gamma-3 chain C region	IGHG3_HUMAN	32312.0	3	4	5	34.8%
Ig kappa chain V-I region AG	KV101_HUMAN	11974.8	2	2	2	31.5%
Ig kappa chain V-II region Cum	KV201_HUMAN, KV204_HUMAN, KV205_HUMAN	12658.6	2	3	3	17.4%
Ig kappa chain V-III region WOL	KV305_HUMAN	11728.5	3	5	10	39.5%
Ig kappa chain V-IV region Len	KV402_HUMAN	12622.4	2	2	4	23.7%
Ig kappa chain C region	KAC_HUMAN	11590.5	5	9	45	67.9%
Ig lambda chain C regions	LAC_HUMAN	11218.1	5	7	15	61.0%
Ig mu chain C region	MUC_HUMAN	49537.9	9	14	22	22.7%
Ig alpha-1 chain C region	IGHA1_HUMAN	37635.8	5	9	21	16.4%
Complement & associated proteins						
Complement C1q subcomponent	C1QB_HUMAN	26442.4	2	3	6	6.4%
Complement C1q subcomponent subunit C	C1QC_HUMAN	25756.0	3	4	7	15.9%
Complement C3	CO3_HUMAN	187131.1	41	55	77	27.5%
Complement C4-A	CO4A_HUMAN	192776.8	9	13	15	6.0%
Complement component C9	CO9_HUMAN	63156.8	5	7	11	8.1%
C4b-binding protein alpha chain	C4BP_HUMAN	67015.0	4	4	5	7.2%
Clusterin precursor (Apo-J)	CLUS_HUMAN	52477.0	4	4	9	12.5%
Complement factor H	CFAH_HUMAN	139052.1	4	5	6	3.9%
Plasma protease C1 inhibitor	IC1_HUMAN	55137.5	3	3	4	6.2%
Glucose metabolism						
Glucose-6-phosphate isomerase	G6PI_HUMAN	63130.5	2	4	7	5.7%
Fructose-bisphosphate aldolase A	ALDOA_HUMAN	39402.6	7	8	10	17.0%

Triosephosphate isomerase	TPIS_HUMAN	26651.1	8	10	13	45.4%
Glyceraldehyde-3-phosphate dehydrogenase	G3P_HUMAN	36035.3	10	19	43	32.2%
Phosphoglycerate kinase 1	PGK1_HUMAN	44597.3	8	10	13	26.9%
Alpha-enolase	ENOA_HUMAN	47152.2	15	19	23	38.5%
Pyruvate kinase isozymes M1/M2	KPYM_HUMAN	57919.5	22	31	46	47.8%
L-lactate dehydrogenase A chain	LDHA_HUMAN	36671.2	6	9	17	16.3%
L-lactate dehydrogenase B chain	LDHB_HUMAN	36620.6	2	2	2	12.3%
Other enzymes						
Alcohol dehydrogenase 1B	ADH1B_HUMAN	39836.3	3	5	6	7.5%
Malate dehydrogenase, mitochondrial	MDHM_HUMAN	35513.7	2	2	2	7.1%
Cytochrome c oxidase subunit 2	COX2_HUMAN	25548.4	2	2	2	10.1%
Antioxidants						
Peroxiredoxin-1	PRDX1_HUMAN	22092.9	3	4	9	19.6%
Peroxiredoxin-2	PRDX2_HUMAN	21874.4	6	7	11	28.3%
Catalase	CATA_HUMAN	59738.5	5	6	8	15.4%
Superoxide dismutase, Mn	SODM_HUMAN	24704.6	2	5	6	10.4%
Glutathione S-transferase P	GSTP1_HUMAN	23338.7	3	3	3	21.9%
Protein degradation						
Leukocyte elastase inhibitor	ILEU_HUMAN	42725.8	2	3	3	6.3%
Lysozyme C	LYSC_HUMAN	16518.9	2	3	3	12.8%
Cathepsin D	CATD_HUMAN	44535	5	7	13	13.6%
Lysosome-associated membrane glycoprotein 1	LAMP1_HUMAN	44755.5	4	5	10	11.8%
Epoxide hydrolase 1	HYEP_HUMAN	52933.1	3	4	4	5.3%
Secreted proteins						
Adipocyte-derived leucine aminopeptidase	ARTS1_HUMAN	105832.1	2	2	2	2.5%
Galectin-3 (Mac-2 BP)	LG3BP_HUMAN	65314.1	2	2	3	5.1%
Annexins						
Annexin A1	ANXA1_HUMAN	38697.9	19	32	62	51.7%
Annexin A2	ANXA2_HUMAN	38588.1	33	71	159	74.0%

Annexin A4	ANXA4_HUMAN	35866.3	12	15	21	44.2%
Annexin A5	ANXA5_HUMAN	35920.6	20	37	53	64.4%
Annexin A6	ANXA6_HUMAN	75859.5	24	32	43	40.7%
Annexin A7	ANXA7_HUMAN	52722.5	2	2	2	6.2%
Annexin A11	ANX11_HUMAN	54373.7	3	3	4	6.7%
ER proteins						
Endoplasmin (GRP94)	ENPL_HUMAN	92453.7	14	20	25	16.2%
78 kDa glucose-regulated protein (GRP 78)	GRP78_HUMAN	72316.7	5	5	6	11.6%
Transitional endoplasmic reticulum ATPase (Valosin-containing protein)	TERA_HUMAN	89306.8	3	4	4	4.3%
Endoplasmic reticulum protein ERp29	ERP29_HUMAN	28976.9	3	3	3	14.2%
Thioredoxin domain-containing protein 5	TXND5_HUMAN	47611.1	2	3	3	4.2%
Peptidyl-prolyl cis-trans isomerase	PPIA_HUMAN	17994.9	3	3	4	24.9%
Peptidyl-prolyl cis-trans isomerase B	PPIB_HUMAN	22724.9	3	5	8	16.8%
Protein disulfide-isomerase	PDIA1_HUMAN	57100.1	14	19	25	29.1%
Protein disulfide-isomerase A3	PDIA3_HUMAN	56766.6	11	16	20	27.5%
Protein disulfide-isomerase A6	PDIA6_HUMAN	48104.3	6	7	9	15.5%
Calnexin (Major histocompatibility complex class I antigen-binding protein p88)	CALX_HUMAN	67552.2	5	7	7	7.8%
Erlin 2 (SPFH domain-containing protein 2)	ERLN2_HUMAN	37822.4	3	3	3	5.9%
Dolichyl-diphosphooligosaccharide-protein glycosyltransferase 48 kDa subunit	OST48_HUMAN	48793.0	4	4	4	7.3%
Dolichyl-diphosphooligosaccharide-protein glycosyltransferase 67 kDa subunit	RIB1_HUMAN	68553.0	2	3	3	4.5%
Chaperones						
60 kDa heat shock protein,	CH60_HUMAN	61037.7	9	11	13	23.7%
Heat shock cognate 71 kDa	HSP7C_HUMAN	70881.8	11	16	19	20.3%
Heat-shock protein beta-1 (HSP 27)	HSPB1_HUMAN	22764.6	2	2	2	16.1%
pH regulation						
Carbonic anhydrase 1	CAH1_HUMAN	28852.4	2	2	3	9.6%
Vacuolar ATP synthase catalytic subunit A (Vacuolar	VATA_HUMAN	68287.4	5	5	6	11.0%

proton pump subunit alpha)						
Vacuolar ATP synthase subunit d 1	VA0D1_HUMAN	40312.8	2	2	2	6.6%
Signaling						
Guanine nucleotide-binding protein G(i), alpha-2 subunit	GNAI2_HUMAN	40434.0	5	8	11	14.1%
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1	GBB1_HUMAN	37359.5	2	3	4	6.5%
Ras-related protein Rab-1A	RAB1A_HUMAN	22660.5	3	4	7	18.5%
14-3-3 protein epsilon (14-3-3E)	1433E_HUMAN	29157.0	2	2	2	7.5%
Others						
Elongation factor 2 (EF-2)	EF2_HUMAN	95322.1	4	5	6	4.3%
Elongation factor 1-alpha 1	EF1A1_HUMAN	50123.2	3	4	4	6.9%
Clathrin heavy chain 1	CLH1_HUMAN	191600.9	7	8	11	4.3%

Assignments were accepted for peptide probabilities >95%, a minimum of two unique peptides and protein probability >99%.

SUPPLEMENTAL TABLE II

Experiment: Mayr_Microparticle

Database Name: a subset of the uniprot_sprot_humancow database
Taxonomy: All Entries
Number of Proteins: 3378
Database Name: the uniprot_sprot_human.fasta.hdr database
Taxonomy: All Entries
Number of Proteins: 29597
Search Engine: Sequest
Version: 27, rev. 12
Samples: All Samples
Fragment Tolerance: 1.00 Da (Monoisotopic)
Parent Tolerance: 1.5 Da (Monoisotopic)
Fixed Modifications: +57 on C (Carbamidomethyl)
Variable Modifications: +16 on M (Oxidation)
Database: the uniprot_sprot_human.fasta.hdr database (unknown version, 29597 entries)
Digestion Enzyme: Trypsin
Max Missed Cleavages: 2
Search Engine: X! Tandem
Version: 2007.01.01.2
Samples: All Samples
Fragment Tolerance: 1.00 Da (Monoisotopic)
Parent Tolerance: 1.5 Da (Monoisotopic)
Fixed Modifications: +57 on C (Carbamidomethyl)
Variable Modifications: +16 on M (Oxidation)
Database: a subset of the uniprot_sprot_humancow database
Digestion Enzyme: Trypsin
Max Missed Cleavages: 2
Peptide Thresholds: 95.0% minimum
Protein Thresholds: 99.0% minimum and 2 peptides minimum

Search Engine Set: 2 Search Engines

Protein name	**Accession numbers**	**MW (Da)**	**Protein ID probability**	**Peptide sequence**	**XCorr score**	**DCn score**	**X! Tandem -**
1433E_HUMAN							
14-3-3 protein epsilon (14-3-3E) - Homo sapiens (Human)	1433E_HUMAN	29157	99.80%	EAAENSLVAYK	2.35	0.454	0.959
14-3-3 protein epsilon (14-3-3E) - Homo sapiens (Human)	1433E_HUMAN	29157	99.80%	NLLSVAYK	2.13	0.194	0.276
1A68_HUMAN							
HLA class I histocompatibility antigen, A-68 alpha chain precursor	1A68_HUMAN	40890.2	100.00%	DGEDQTQDTELVETRPAGDGTFQK	2.06	0.318	0.237
HLA class I histocompatibility antigen, A-68 alpha chain precursor	1A68_HUMAN	40890.2	100.00%	FIAVGYVDDTQFVR	3.61	0.504	5.6
HLA class I histocompatibility antigen, A-68 alpha chain precursor	1A68_HUMAN	40890.2	100.00%	WVAVVVPSGQEQR	2.83	0.407	1.57
HLA class I histocompatibility antigen, A-68 alpha chain precursor	1A68_HUMAN	40890.2	100.00%	YLENGKETLQR	2.28	0.404	0.456
1B41_HUMAN							
HLA class I histocompatibility antigen, B-41 alpha chain precursor	1B41_HUMAN	40520.7	99.90%	DGEDQTQDTELVETRPAGDR	2.27	0.343	-1.77
HLA class I histocompatibility antigen, B-41 alpha chain precursor	1B41_HUMAN	40520.7	99.90%	WAAVVVPSGEEQR	2.91	0.295	2
2B32_HUMAN							
HLA class II histocompatibility antigen, DRB3-2 beta chain precur	2B32_HUMAN	29970.4	100.00%	FDSDVGEYR	2.62	0.367	2
HLA class II histocompatibility antigen, DRB3-2 beta chain precur	2B32_HUMAN	29970.4	100.00%	GHSGLQPTGFLS	1.43	0.325	0.194
HLA class II histocompatibility antigen, DRB3-2 beta chain precur	2B32_HUMAN	29970.4	100.00%	HNYGVGESFTVQR	2.46	0.367	0
A1AT_HUMAN							
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	AVLTIDEK	2.33	0.245	0.602
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	DTEEEDFHVDQVTTVK	3.11	0.312	-0.959
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	FNKPFVFLMIEQNTK	4.44	0.233	1.15

Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	GTEAAGAMFLEAIPMSIPPEVK	2.88	0.482	3.64
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	ITPNLAEFAFSLYR	2.14	0.625	4.19
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	IVDLVK	1.99	0.126	0
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	KLSSWVLLMK	3.15	0.135	0.796
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	LGMFNIQHCK	1.7	0.221	-0.23
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	LSITGTYDLK	2.63	0.249	1
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	LSSWVLLMK	2.06	0.43	0.824
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	LVDKFLEDVKK	2.78	0.318	-0.447
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	LYHSEAFTVNFGDTEEAKK	3.31	0.52	1.33
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	QINDYVEK	1.81	0.203	-0.0792
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	QINDYVEKGTQGK	2.3	0.332	0.854
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	SASLHLPK	2.49	0.217	0.523
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	SPLFMGK	1.45	0.067	0.658
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	SVLGQLGITK	1.9	0.352	0.187
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	TLNQPDSQLQLTTGNGLFLSEGLK	0	0	3.8
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	VFSNGADLSGVTEEAPLK	4.8	0.594	3.8
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-	A1AT_HUMAN	46719.9	100.00%	VFSNGADLSGVTEEAPLKLSK	2.72	0.519	1.24
A1BG_HUMAN							
Alpha-1B-glycoprotein precursor (Alpha-1-B glycoprotein) - Homo	A1BG_HUMAN	54254.4	99.90%	LELHVDGPPPRPQLR	1.23	0.412	0
Alpha-1B-glycoprotein precursor (Alpha-1-B glycoprotein) - Homo	A1BG_HUMAN	54254.4	99.90%	LLELTGPK	2.1	0.0716	-0.447
A2MG_HUMAN							
Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Hu	A2MG_HUMAN	163258.8	100.00%	AIGYLNTGYQR	1.4	0.207	0.0506
Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Hu	A2MG_HUMAN	163258.8	100.00%	ATVLNYLPK	1.89	0.38	1.47
Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Hu	A2MG_HUMAN	163258.8	100.00%	FEVQVTVPK	3.01	0.375	0.42
Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Hu	A2MG_HUMAN	163258.8	100.00%	GEAFTLK	1.35	0.228	0.0177
Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Hu	A2MG_HUMAN	163258.8	100.00%	LPPNVVEESAR	2.01	0.241	1.8
Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Hu	A2MG_HUMAN	163258.8	100.00%	NEDSLVFVQTDK	3.17	0.616	2.51
Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Hu	A2MG_HUMAN	163258.8	100.00%	QGIPFFGQVR	1.93	0.14	2.04
Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Hu	A2MG_HUMAN	163258.8	100.00%	QTVSWAVTPK	2.42	0.357	-0.0792
Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Hu	A2MG_HUMAN	163258.8	100.00%	SASNMAIVDVK	2.19	0.222	1.66
Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Hu	A2MG_HUMAN	163258.8	100.00%	SSGSLLNNAIK	2.82	0.267	0.0655
Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Hu	A2MG_HUMAN	163258.8	100.00%	TEHPFTVEEFVLPK	3.59	0.276	1.64
Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Hu	A2MG_HUMAN	163258.8	100.00%	VGFYESDVMGR	2.89	0.459	3.92
Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Hu	A2MG_HUMAN	163258.8	100.00%	VTAAPQSVCALR	2.29	0.52	3.42
Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Hu	A2MG_HUMAN	163258.8	100.00%	YGAATFTR	2.18	0.461	1.18
ACTA_HUMAN							
Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibitin	ACTA_HUMAN	41992.1	100.00%	AGFAGDDAPR	1.71	0.412	1.28
Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibitin	ACTA_HUMAN	41992.1	100.00%	AVFPSIVGR	1.4	0.227	0
Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibitin	ACTA_HUMAN	41992.1	100.00%	AVFPSIVGRPR	1.87	0.409	0
Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibitin	ACTA_HUMAN	41992.1	100.00%	DLTDYLMK	2.08	0.298	-0.826
Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibitin	ACTA_HUMAN	41992.1	100.00%	DLYANNVLSGGTTMYPGIADR	4.37	0.674	5.46
Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibitin	ACTA_HUMAN	41992.1	100.00%	DSYVGDEAQSK	3.27	0.52	2.1
Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibitin	ACTA_HUMAN	41992.1	100.00%	DSYVGDEAQSKR	1.72	0.439	2.35
Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibitin	ACTA_HUMAN	41992.1	100.00%	EITALAPSTMK	2.38	0.363	1.24
Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibitin	ACTA_HUMAN	41992.1	100.00%	GYSFVTTAER	3.05	0.522	1.96
Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibitin	ACTA_HUMAN	41992.1	100.00%	HQGVMVGMGQK	3.08	0.407	3.1
Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibitin	ACTA_HUMAN	41992.1	100.00%	IIAPPERK	1.74	0.194	0.0177
Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibitin	ACTA_HUMAN	41992.1	100.00%	IKIIAPPER	2.2	0.25	-0.477
Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibitin	ACTA_HUMAN	41992.1	100.00%	LDLAGRDLTDYLMK	2.08	0.125	0.824
Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibitin	ACTA_HUMAN	41992.1	100.00%	MQKEITALAPSTMK	2.39	0.0532	1.11
Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibitin	ACTA_HUMAN	41992.1	100.00%	QEYDEAGPSIVHR	2.61	0.467	-0.204
Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibitin	ACTA_HUMAN	41992.1	100.00%	SYELPDGQVITIGNER	2.07	0.522	3.42
Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibitin	ACTA_HUMAN	41992.1	100.00%	VAPEEHPTLLTEAPLNPK	3.35	0.607	2.3
Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibitin	ACTA_HUMAN	41992.1	100.00%	YPIEHGIITNWDDMEK	3.51	0.301	0.824
ACTB_HUMAN							
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	AGFAGDDAPR	1.71	0.412	1.28
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	AVFPSIVGR	1.4	0.227	0

Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	AVFPSIVGRPR	1.87	0.409	0
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	CDVDIRK	2.28	0.138	0
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	DLTDYLMK	2.08	0.298	-0.826
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	DLYANTVLSGGTTMYPGIADR	4.16	0.58	4.03
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	DSYVGDEAQSK	3.27	0.52	2.1
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	DSYVGDEAQSKR	1.72	0.439	2.35
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	EITALAPSTMK	2.38	0.363	1.24
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	GYSFTTTAER	1.41	0.393	1.24
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	GYSFTTTAEREIVR	1.56	0.278	0
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	HQGVMVGMGQK	3.08	0.407	3.1
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	IIAPPERK	1.74	0.194	0.0177
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	IKIIAPPER	2.2	0.25	-0.477
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	KDLYANTVLSGGTTMYPGIADR	4.07	0.531	2.37
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	LCYVALDFEQEMATAASSSSLEK	4.83	0.566	5.59
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	LDLAGRDLTDYLMK	2.08	0.125	0.824
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	MQKEITALAPSTMK	2.39	0.0532	1.11
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	QEYDESGPSIVHR	2.67	0.546	3.3
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	SYELPDGQVITIGNER	2.07	0.522	3.42
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	4.94	0.568	2.26
Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)	ACTB_HUMAN	41719.8	100.00%	VAPEEHPVLLTEAPLNPK	3.58	0.375	2.5
ACTN1_HUMAN							
Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (Non-muscle	ACTN1_HUMAN	103043.1	100.00%	ALDFIASK	1.64	0.236	0.276
Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (Non-muscle	ACTN1_HUMAN	103043.1	100.00%	EGLLLWCQR	1.94	0.238	0.149
Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (Non-muscle	ACTN1_HUMAN	103043.1	100.00%	FAIQDISVEETSAK	3.74	0.422	3.96
Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (Non-muscle	ACTN1_HUMAN	103043.1	100.00%	LAILGIHNEVSK	1.96	0.43	2.5
ADH1B_HUMAN							
Alcohol dehydrogenase 1B (EC 1.1.1.1) (Alcohol dehydrogenase b	ADH1B_HUMAN	39836.3	100.00%	IDAASPLEK	2.16	0.384	0.854
Alcohol dehydrogenase 1B (EC 1.1.1.1) (Alcohol dehydrogenase b	ADH1B_HUMAN	39836.3	100.00%	MVAVGICR	1.95	0.332	-0.146
Alcohol dehydrogenase 1B (EC 1.1.1.1) (Alcohol dehydrogenase b	ADH1B_HUMAN	39836.3	100.00%	VIPLFTPQCGK	1.7	0.42	0.268
ALBU_HUMAN							
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	AACLLPK	1.81	0.197	-0.204
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	AAFTECCQAADK	2.19	0.261	1.54
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	AAFTECCQAADKAACLLPK	2.17	0.228	-0.623
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	ADDKETCFAEEGKK	2.55	0.322	0.357
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	AEFAEVSK	1.52	0.182	-0.362
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	AEFAEVSKLVTDLTK	1.55	0.428	1
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	ALVLIAFAQYLQQCPFEDHVK	2.22	0.317	2
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	AVMDDFAAFVEK	3.77	0.58	2.7
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	CCAAADPHECYAK	0	0	4.36
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	CCTESLVNR	2.58	0.463	1.3
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	DDNPNLPR	1.99	0.334	1.46
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	DVFLGMFLYEYAR	3.34	0.578	3.32
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	FKDLGEENFK	2.19	0.292	0.699
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	FQNALLVR	1.73	0.141	0.0458
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	KQTALVELVK	2.88	0.252	-0.0414
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	KVPQVSTPTLVEVSR	2.33	0.457	1.29
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	LCTVATLR	1.8	0.225	0
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	LDELRDEGK	1.48	0.354	0.114
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	LKECCEKPLLEK	4.26	0.267	1.62
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	LVAASQAALGL	1.4	0.398	-0.672
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	LVNEVTEFAK	2.18	0.175	-0.505
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	LVTDLTK	1.91	0.237	-0.462
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	QNCELFEQLGEYK	1.57	0.419	2.51
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	QTALVELVK	1.36	0.237	-0.0414
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	RHPDYSVVLLLR	3.01	0.341	-0.0414
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	RPCFSALEVDETYVPK	2.31	0.399	0.658
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	SHCIAEVENDEMPADLPSLAADFVESK	2.25	0.124	-0.114

Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	SLHTLFGDK	1.8	0.246	0.0315
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	TPVSDRVTK	1.59	0.144	0.0177
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	TYETTLEK	1.62	0.172	0.041
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	VFDEFKPLVEEPQNLIK	3.48	0.523	3.8
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	VPQVSTPTLVEVSR	2.67	0.416	2.57
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	YICENQDSISSK	2.94	0.54	3.68
Serum albumin precursor - Homo sapiens (Human)	ALBU_HUMAN	69348.9	100.00%	YLYEIAR	1.71	0.19	0
ALDOA_HUMAN							
Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldc	ALDOA_HUMAN	39402.6	100.00%	ADDGRPFPQVIK	2.23	0.299	0
Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldc	ALDOA_HUMAN	39402.6	100.00%	ALANSLACQGK	2.16	0.419	0.444
Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldc	ALDOA_HUMAN	39402.6	100.00%	ALQASALK	1.76	0.0749	-0.0414
Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldc	ALDOA_HUMAN	39402.6	100.00%	GILAADESTGSIAK	3.44	0.633	2.92
Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldc	ALDOA_HUMAN	39402.6	100.00%	GILAADESTGSIAKR	1.81	0.147	0.585
Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldc	ALDOA_HUMAN	39402.6	100.00%	QLLLTADDR	1.72	0.327	0.432
Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldc	ALDOA_HUMAN	39402.6	100.00%	VLAAVYK	1.9	0.138	0.553
ANT3_HUMAN							
Antithrombin-III precursor (ATIII) - Homo sapiens (Human)	ANT3_HUMAN	52586	100.00%	ANRPFLVFIR	2.3	0.295	-0.869
Antithrombin-III precursor (ATIII) - Homo sapiens (Human)	ANT3_HUMAN	52586	100.00%	EVPLNTIIFMGR	3.26	0.511	2.92
Antithrombin-III precursor (ATIII) - Homo sapiens (Human)	ANT3_HUMAN	52586	100.00%	TSDQIHFFFAK	1.38	0.377	0
ANX11_HUMAN							
Annexin A11 (Annexin XI) (Calcyclin-associated annexin 50) (CAP	ANX11_HUMAN	54373.7	100.00%	GVGTDEACLIEILASR	3.45	0.237	0
Annexin A11 (Annexin XI) (Calcyclin-associated annexin 50) (CAP	ANX11_HUMAN	54373.7	100.00%	TILALMK	2	0.283	0.0915
Annexin A11 (Annexin XI) (Calcyclin-associated annexin 50) (CAP	ANX11_HUMAN	54373.7	100.00%	TPVLFDIYEIK	2.77	0.422	2.85
ANXA1_HUMAN							
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	ALYEAGER	2.48	0.393	0.959
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	CATSKPAFFAEK	2.35	0.318	0.31
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	CLTAIVK	2.4	0.15	0.42
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	DITSDTSGDFR	3.14	0.472	2.7
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	DITSDTSGDFRNALLSLAK	0.8	0.0296	1.57
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	DLAKDITSDTSGDFR	2.62	0.46	-0.591
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	GDRSEDFGVNEDLADSDAR	3.6	0.5	3.09
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	GGPGSAVSPYPTFNPSSDVAALHK	2.29	0.345	1.64
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	GLGTDEDTLIEILASR	3.36	0.26	2.46
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	GTDVNVFNTILTTR	4.97	0.493	3.54
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	GVDEATIIDILTK	3.56	0.414	2.43
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	GVDEATIIDILTKR	3.65	0.497	1.08
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	ILVALCGGN	1.97	0.473	1.04
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	KGTDVNVFNTILTTR	2.38	0.442	1.18
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	NALLSLAK	1.72	0.251	0.319
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	SEDFGVNEDLADSDAR	2.33	0.458	2.04
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	SEIDMNDIK	2.84	0.41	0.824
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	TPAQFDADELR	3.53	0.403	3.34
Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	ANXA1_HUMAN	38697.9	100.00%	VLDLELKGDIEK	1.95	0.279	-0.708
ANXA2_HUMAN							
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	AEDGSVIDYELIDQDAR	4.46	0.516	2.85
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	ALLYLCGGDD	2.12	0.618	-0.0414
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	ASMKGLGTDEDSLIEIICSR	2.65	0.214	0
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	AYTNFDAER	1.88	0.196	1.55
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	AYTNFDAERDALNIETAIK	3.65	0.474	1.19
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	DALNIETAIK	3.12	0.174	0.796
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	DKVLIR	1.83	0.0801	-0.544
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	DLYDAGVK	1.88	0.315	-0.69
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	DLYDAGVKR	1.86	0.354	0
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	ELASALK	1.78	0.222	-0.342
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	GLGTDEDSLIEIICSR	3.17	0.533	2.28
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	GTDVPKWISIMTER	3.96	0.473	1.19
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	GVDEVTIVNILTNR	3.54	0.348	1.59

Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	LMVALAK	2.41	0.136	-0.462
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	LSLEGDHSTPPSAYGSVK	2.93	0.425	0.658
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	QDIAFAYQR	3.03	0.299	1.27
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	RAEDGSVIDYELIDQDAR	3.2	0.204	1.14
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	RAEDGSVIDYELIDQDARDLYDAGVK	4.28	0.406	4.06
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	SALSGHLETVILGLLK	4.1	0.438	0.658
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	SEVDMLK	2.15	0.316	0.0655
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	SLYYYIQQDTK	2.22	0.408	3.29
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	SLYYYIQQDTKGDYQK	5.36	0.597	6.19
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	SNAQRQDIAFAYQR	4.01	0.268	2.8
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	SYSPYDMLESIR	3	0.543	1.55
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	SYSPYDMLESIRK	1.83	0.397	-0.724
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	TDLEKDIISDTSGDFR	2.31	0.288	-0.342
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	TDLEKDIISDTSGDFRK	4.71	0.555	2.24
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	TKGVDEVTIVNILTNR	3.8	0.451	3.48
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	TNQELQEINR	3.76	0.333	1.13
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	TNQELQEINRVYK	2.19	0.323	-0.279
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	TPAQYDASELK	4.13	0.574	3
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	TPAQYDASELKASMK	3.13	0.237	0.292
Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	ANXA2_HUMAN	38588.1	100.00%	WISIMTER	2.55	0.344	1.04
ANXA4_HUMAN							
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobi	ANXA4_HUMAN	35866.3	100.00%	AASGFNAMEDAQTLR	3.21	0.514	2.24
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobi	ANXA4_HUMAN	35866.3	100.00%	AEIDMLDIR	3.28	0.337	0.678
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobi	ANXA4_HUMAN	35866.3	100.00%	FLTVLCSR	2.55	0.374	0.0132
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobi	ANXA4_HUMAN	35866.3	100.00%	GAGTDEGCLIEILASR	4.64	0.582	4.04
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobi	ANXA4_HUMAN	35866.3	100.00%	GLGTDDNTLIR	1.56	0.322	0.456
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobi	ANXA4_HUMAN	35866.3	100.00%	GLGTDEDAIISVLAYR	3.67	0.61	5.02
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobi	ANXA4_HUMAN	35866.3	100.00%	ISQTYQQQYGR	2.65	0.433	2.38
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobi	ANXA4_HUMAN	35866.3	100.00%	SAYFAEK	1.67	0.34	1.17
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobi	ANXA4_HUMAN	35866.3	100.00%	SDTSFMFQR	2.18	0.215	1.12
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobi	ANXA4_HUMAN	35866.3	100.00%	SETSGSFEDALLAIVK	3.47	0.612	4.03
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobi	ANXA4_HUMAN	35866.3	100.00%	SLEDDIR	1.77	0.214	-1
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobi	ANXA4_HUMAN	35866.3	100.00%	TPEEIR	1.79	0.139	-0.491
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobi	ANXA4_HUMAN	35866.3	100.00%	VLLVLCGGDD	2.23	0.642	1.7
ANXA5_HUMAN							
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	ALLLLCGEDD	2.12	0.477	1.42
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	DLLDDLKSELTGK	3.13	0.483	2.16
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	ETSGNLEQLLLAVVK	3.39	0.58	1.46
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	FITIFGTR	1.86	0.204	-0.0792
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	GAGTDDHTLIR	2.2	0.304	0.678
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	GLGTDEESILTLLTSR	3.63	0.507	3.3
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	GTVTDFPGFDER	2.56	0.423	1.42
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	GTVTDFPGFDERADAETLR	2.57	0.384	0.387
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	LIVALMKPSR	1.79	0.205	-0.954
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	LYDAYELK	1.84	0.176	0
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	NFATSLYSMIK	3.4	0.368	1.92
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	QEISAAFK	1.51	0.113	0.495
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	QVYEEEYGSSLEDDVVGDTSGYYQR	3.28	0.553	1.96
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	SEIDLFNIR	3.6	0.246	0
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	SEIDLFNIRK	2.94	0.314	0.854
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	SIPAYLAETLYYAMK	1.69	0.484	0.959
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	SNAQRQEISAAFK	2.51	0.422	0
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	TPEELR	1.79	0.139	-0.491
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	VLTEIIASR	2.23	0.404	0.398
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	ANXA5_HUMAN	35920.6	100.00%	WGTDEEKFITIFGTR	2.84	0.492	1.47
ANXA6_HUMAN							
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	ALIEILATR	2.27	0.377	0.0177

Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	ALLALCGGED	1.94	0.535	1.1
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	DAFVAIVQSVK	3.72	0.43	2.82
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	DLEADIIGDTSGHFQK	2.96	0.193	0.367
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	DLMTDLKSEISGDLAR	0	0	2.85
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	EDAQVAAEILEIADTPSGDK	3.84	0.611	2.96
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	EMSGDVRDAFVAIVQSVK	2.64	0.427	0.921
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	FMTILCTR	2.51	0.354	-0.279
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	GELSGDFEK	2.23	0.409	2.23
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	GFGSDKEAILDIITSR	2.66	0.331	1.11
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	GLGTDEDTIIDIITHR	4.29	0.592	3.72
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	GSIHDFPGFDPNQDAEALYTAMK	3.81	0.538	3.15
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	GTVRPANDFNPDADAK	2.21	0.0475	1.8
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	LMLAVVK	1.82	0.222	-0.23
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	LVFDEYLK	2.07	0.189	0.796
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	NKPLFFADK	2.51	0.292	0.602
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	SEIDLLNIR	2.99	0.34	0.854
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	SEIDLLNIRR	1.42	0.228	-0.0792
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	SELDMLDIR	2.61	0.354	1.4
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	SLHQAIEGDTSGDFLK	0	0	2.5
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	SLYSMIK	1.8	0.0965	0.131
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	STPEYFAER	1.62	0.334	0.569
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	VFQEFIK	1.79	0.0708	0.0269
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)	ANXA6_HUMAN	75859.5	100.00%	WGTDEAQFIYILGNR	3.69	0.473	3.51
ANXA7_HUMAN							
Annexin A7 (Annexin VII) (Synexin) - Homo sapiens (Human)	ANXA7_HUMAN	52722.5	99.80%	DIRSDTSGHFERLLVSMCQGNR	2.43	0.076	1.11
Annexin A7 (Annexin VII) (Synexin) - Homo sapiens (Human)	ANXA7_HUMAN	52722.5	99.80%	DLLSSVSR	2.07	0.108	-0.176
AOC3_HUMAN							
Membrane copper amine oxidase (EC 1.4.3.6) (Semicarbazide-sei	AOC3_HUMAN	84604.1	100.00%	DAFCVFEQNQGLPLRR	1.99	0.288	0.921
Membrane copper amine oxidase (EC 1.4.3.6) (Semicarbazide-sei	AOC3_HUMAN	84604.1	100.00%	EALAIVFFGR	3.58	0.424	2.96
Membrane copper amine oxidase (EC 1.4.3.6) (Semicarbazide-sei	AOC3_HUMAN	84604.1	100.00%	LGPGLVDAAQAR	3.14	0.44	0
Membrane copper amine oxidase (EC 1.4.3.6) (Semicarbazide-sei	AOC3_HUMAN	84604.1	100.00%	YQLAVTQR	2.46	0.273	0.721
APOA_HUMAN							
Apolipoprotein(a) precursor (EC 3.4.21.-) (Apo(a)) (Lp(a)) - Hom	APOA_HUMAN	501270.9	100.00%	GTFSTTVTGR	1.75	0.302	1.24
Apolipoprotein(a) precursor (EC 3.4.21.-) (Apo(a)) (Lp(a)) - Hom	APOA_HUMAN	501270.9	100.00%	GTYSTTVTGR	2.55	0.441	2.5
Apolipoprotein(a) precursor (EC 3.4.21.-) (Apo(a)) (Lp(a)) - Hom	APOA_HUMAN	501270.9	100.00%	NPDAVAAPYCYTR	1.81	0.315	2.92
APOA1_HUMAN							
Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) [Contains: Apolipc	APOA1_HUMAN	30760.5	100.00%	AKPALEDLR	1.94	0.157	0.143
Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) [Contains: Apolipc	APOA1_HUMAN	30760.5	100.00%	ATEHLSTLSEK	2.58	0.504	1.92
Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) [Contains: Apolipc	APOA1_HUMAN	30760.5	100.00%	DSGRDYVSQFEGSALGK	4.53	0.43	1.08
Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) [Contains: Apolipc	APOA1_HUMAN	30760.5	100.00%	DYVSQFEGSALGK	3.99	0.639	5.05
Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) [Contains: Apolipc	APOA1_HUMAN	30760.5	100.00%	LEALKENGGAR	2.79	0.227	0.347
Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) [Contains: Apolipc	APOA1_HUMAN	30760.5	100.00%	LLDNWDSVTSTFSK	3.22	0.597	2.51
Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) [Contains: Apolipc	APOA1_HUMAN	30760.5	100.00%	QGLLPVLESFK	3.09	0.342	3.6
Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) [Contains: Apolipc	APOA1_HUMAN	30760.5	100.00%	THLAPYSDELR	2.6	0.278	0
Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) [Contains: Apolipc	APOA1_HUMAN	30760.5	100.00%	VQPYLDDFQK	2.41	0.428	1.92
Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) [Contains: Apolipc	APOA1_HUMAN	30760.5	100.00%	VQPYLDDFQKK	2.32	0.267	1.33
Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) [Contains: Apolipc	APOA1_HUMAN	30760.5	100.00%	VSFLSALEEYTK	4.03	0.499	2.77
Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) [Contains: Apolipc	APOA1_HUMAN	30760.5	100.00%	WQEEMELYR	2.66	0.433	1.75
APOB_HUMAN							
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	AAIQALR	1.51	0.221	-0.0414
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	ALVEQGFTVPEIK	3.05	0.433	3.6
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	ALYWVNGQVPDGVSK	2.21	0.35	1.05
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	ANLFNK	1.82	0.188	-0.708
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	ATGVLYDYVNK	2.75	0.459	1.01
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	AVSMPSFSILGSDVR	3.32	0.478	4.68
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	DLKVEDIPLAR	2.04	0.136	0.237
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	EFQVPTFTIPK	1.85	0.248	0.0757

Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	EIFNMAR	1.52	0.258	-0.613
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	FPEVDVLTK	1.78	0.325	-0.556
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	IAELSATAQEIIK	3.03	0.462	2.02
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	IEIPLPFGGK	1.27	0.339	0
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	INNQLTLDSNTK	2.22	0.167	0.252
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	INPLALK	1.64	0.229	-0.301
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	KLTISEQNIQR	2.54	0.306	0
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	LNGEIQALELPQK	2.43	0.432	1.6
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	LPQQANDYLNSFNWER	2.03	0.389	0.796
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	LSNVLQQVK	2.5	0.248	0.0269
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	NIILPVYDK	2.34	0.218	-0.0792
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	NNALDFVTK	2.36	0.405	-0.477
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	QGFFPDSVNK	2.1	0.238	0.699
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	QSFDLSVK	1.72	0.233	-0.415
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	SEYQADYESLR	0	0	3.64
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	SPAFTDLHLR	1.55	0.332	1.52
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	SVSLPSLDPASAK	2.77	0.434	1.01
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	TEVIPPLIENR	2.23	0.348	1.6
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	TGISPLALIK	2.22	0.107	0.921
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	VIGNMGQTMEQLTPELK	2.13	0.249	2.22
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	VSALLTPAEQTGTWK	1.99	0.187	1.75
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipopr	APOB_HUMAN	515554.3	100.00%	VSTAFVYTK	1.78	0.346	0.174
APOD_HUMAN							
Apolipoprotein D precursor (Apo-D) (ApoD) - Homo sapiens (Hum	APOD_HUMAN	21258	100.00%	MTVTDQVNCPK	0	0	2.57
Apolipoprotein D precursor (Apo-D) (ApoD) - Homo sapiens (Hum	APOD_HUMAN	21258	100.00%	NILTSNNIDVK	1.92	0.172	1.28
Apolipoprotein D precursor (Apo-D) (ApoD) - Homo sapiens (Hum	APOD_HUMAN	21258	100.00%	NPNLPPETVDSLK	1.67	0.141	0.244
Apolipoprotein D precursor (Apo-D) (ApoD) - Homo sapiens (Hum	APOD_HUMAN	21258	100.00%	VLNQELR	1.93	0.0663	-0.568
APOE_HUMAN							
Apolipoprotein E precursor (Apo-E) - Homo sapiens (Human)	APOE_HUMAN	36135.5	100.00%	AATVGSLAGQPLQER	4.07	0.587	2.23
Apolipoprotein E precursor (Apo-E) - Homo sapiens (Human)	APOE_HUMAN	36135.5	100.00%	AKLEEQAQQIR	3.65	0.486	1.85
Apolipoprotein E precursor (Apo-E) - Homo sapiens (Human)	APOE_HUMAN	36135.5	100.00%	AYKSELEEQLTPVAEETR	2.3	0.331	0.041
Apolipoprotein E precursor (Apo-E) - Homo sapiens (Human)	APOE_HUMAN	36135.5	100.00%	DRLDEVKEQVAEVR	2.31	0.364	-0.415
Apolipoprotein E precursor (Apo-E) - Homo sapiens (Human)	APOE_HUMAN	36135.5	100.00%	GEVQAMLGQSTEELR	3.15	0.478	2.8
Apolipoprotein E precursor (Apo-E) - Homo sapiens (Human)	APOE_HUMAN	36135.5	100.00%	GEVQAMLGQSTEELRVR	2.1	0.318	-0.0414
Apolipoprotein E precursor (Apo-E) - Homo sapiens (Human)	APOE_HUMAN	36135.5	100.00%	LAVYQAGAR	1.36	0.362	1.03
Apolipoprotein E precursor (Apo-E) - Homo sapiens (Human)	APOE_HUMAN	36135.5	100.00%	LGADMEDVCGR	3.47	0.47	2.09
Apolipoprotein E precursor (Apo-E) - Homo sapiens (Human)	APOE_HUMAN	36135.5	100.00%	LGPLVEQGR	1.29	0.214	0.041
Apolipoprotein E precursor (Apo-E) - Homo sapiens (Human)	APOE_HUMAN	36135.5	100.00%	LQAEAFQAR	3.18	0.407	0.959
Apolipoprotein E precursor (Apo-E) - Homo sapiens (Human)	APOE_HUMAN	36135.5	100.00%	LSKELQAAQAR	1.68	0.234	0
Apolipoprotein E precursor (Apo-E) - Homo sapiens (Human)	APOE_HUMAN	36135.5	100.00%	QWAGLVEK	1.45	0.22	-0.602
Apolipoprotein E precursor (Apo-E) - Homo sapiens (Human)	APOE_HUMAN	36135.5	100.00%	VQAAVGTSAAPVPSDNH	3.03	0.44	4.15
APOH_HUMAN							
Beta-2-glycoprotein 1 precursor (Beta-2-glycoprotein I) (Apolipop	APOH_HUMAN	38280.5	100.00%	ATVVYQGER	2.61	0.41	1
Beta-2-glycoprotein 1 precursor (Beta-2-glycoprotein I) (Apolipop	APOH_HUMAN	38280.5	100.00%	FICPLTGLWPINTLK	1.13	0.127	1.38
Beta-2-glycoprotein 1 precursor (Beta-2-glycoprotein I) (Apolipop	APOH_HUMAN	38280.5	100.00%	TCPKPDDLPFSTVVPLK	3.08	0.342	1.21
Beta-2-glycoprotein 1 precursor (Beta-2-glycoprotein I) (Apolipop	APOH_HUMAN	38280.5	100.00%	VCPFAGILENGAVR	3.06	0.174	0
ARP2_HUMAN							
Actin-like protein 2 (Actin-related protein 2) - Homo sapiens (Hun	ARP2_HUMAN	44743.7	100.00%	ILLTEPPMNPTK	2.88	0.311	0.886
Actin-like protein 2 (Actin-related protein 2) - Homo sapiens (Hun	ARP2_HUMAN	44743.7	100.00%	IRIEDPPR	2.43	0.226	0.959
Actin-like protein 2 (Actin-related protein 2) - Homo sapiens (Hun	ARP2_HUMAN	44743.7	100.00%	VGNIEIK	1.95	0.14	-0.38
ARP3_HUMAN							
Actin-like protein 3 (Actin-related protein 3) - Homo sapiens (Hun	ARP3_HUMAN	47353.8	99.80%	EFSIDVGYER	1.77	0.207	0.553
Actin-like protein 3 (Actin-related protein 3) - Homo sapiens (Hun	ARP3_HUMAN	47353.8	99.80%	FMEQVIFK	2.11	0.196	0.125
ARTS1_HUMAN							
Adipocyte-derived leucine aminopeptidase precursor (EC 3.4.11.-)	ARTS1_HUMAN	105832.1	99.80%	ESALLFDAEK	2.06	0.21	1.29
Adipocyte-derived leucine aminopeptidase precursor (EC 3.4.11.-)	ARTS1_HUMAN	105832.1	99.80%	ILASTQFEPTAAR	2.84	0.497	1.85
AT1A1_HUMAN							

Sodium/potassium-transporting ATPase alpha-1 chain precursor (	AT1A1_HUMAN	112881.5	100.00%	GIVVYTGDR	2.2	0.427	2.08
Sodium/potassium-transporting ATPase alpha-1 chain precursor (	AT1A1_HUMAN	112881.5	100.00%	IVEIPFNSTNK	2.5	0.233	1.64
Sodium/potassium-transporting ATPase alpha-1 chain precursor (	AT1A1_HUMAN	112881.5	100.00%	SPDFTNENPLETR	3.29	0.421	1.6
Sodium/potassium-transporting ATPase alpha-1 chain precursor (	AT1A1_HUMAN	112881.5	100.00%	VDNSSLTGESEPQTR	1.86	0.232	2.72
B3AT_HUMAN							
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)	B3AT_HUMAN	101778	100.00%	AAATLMSER	2.41	0.464	2.51
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)	B3AT_HUMAN	101778	100.00%	ADFLEQPVLGFVR	3.11	0.446	2.21
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)	B3AT_HUMAN	101778	100.00%	ASTPGAAAQIQEVK	2.6	0.432	2.11
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)	B3AT_HUMAN	101778	100.00%	IPPDSEATLVLVGR	1.13	0.35	1.89
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)	B3AT_HUMAN	101778	100.00%	VLLPLIFR	1.19	0.238	0.523
BAP31_HUMAN							
B-cell receptor-associated protein 31 (BCR-associated protein Bap	BAP31_HUMAN	27974.6	99.80%	AENQVLAMR	3.32	0.304	1.54
B-cell receptor-associated protein 31 (BCR-associated protein Bap	BAP31_HUMAN	27974.6	99.80%	LDVGNAEVKLEEENR	3.42	0.455	1
BKRB2_HUMAN							
B2 bradykinin receptor (BK-2 receptor) (B2R) - Homo sapiens (Hu	BKRB2_HUMAN	44443.4	99.80%	SEPIQMENSMGTLR	1.52	0.3	-0.924
B2 bradykinin receptor (BK-2 receptor) (B2R) - Homo sapiens (Hu	BKRB2_HUMAN	44443.4	99.80%	TMSMGRMRGVR	1.49	0.252	0.222
C1QB_HUMAN							
Complement C1q subcomponent subunit B precursor - Homo sapi	C1QB_HUMAN	26442.4	99.80%	GNLCVNLMR	2.67	0.372	1.31
Complement C1q subcomponent subunit B precursor - Homo sapi	C1QB_HUMAN	26442.4	99.80%	IAFSATR	1.71	0.21	0.886
C1QC_HUMAN							
Complement C1q subcomponent subunit C precursor - Homo sapi	C1QC_HUMAN	25756	100.00%	FNAVLTNPQGDYDTSTGK	2.8	0.436	3.85
Complement C1q subcomponent subunit C precursor - Homo sapi	C1QC_HUMAN	25756	100.00%	FQSVFTVTR	1.92	0.0917	0.921
Complement C1q subcomponent subunit C precursor - Homo sapi	C1QC_HUMAN	25756	100.00%	TNQVNSGGVLLR	2.36	0.334	1.8
C4BP_HUMAN							
C4b-binding protein alpha chain precursor (C4bp) (Proline-rich pr	C4BP_HUMAN	67015	100.00%	FSAICQGDGTWSPR	3.69	0.494	3.8
C4b-binding protein alpha chain precursor (C4bp) (Proline-rich pr	C4BP_HUMAN	67015	100.00%	LMQCLPNPEDVK	3.16	0.315	1.64
C4b-binding protein alpha chain precursor (C4bp) (Proline-rich pr	C4BP_HUMAN	67015	100.00%	QSTLDKEL	1.77	0.228	0
C4b-binding protein alpha chain precursor (C4bp) (Proline-rich pr	C4BP_HUMAN	67015	100.00%	YTCLPGYVR	2.46	0.325	1.96
CAD13_HUMAN							
Cadherin-13 precursor (Truncated-cadherin) (T-cadherin) (T-cad)	CAD13_HUMAN	78269.6	99.80%	INENTGSVSVTR	3.38	0.587	3.43
Cadherin-13 precursor (Truncated-cadherin) (T-cadherin) (T-cad)	CAD13_HUMAN	78269.6	99.80%	SIVVSPILIPENQR	3.46	0.354	3.07
CAH1_HUMAN							
Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonic anhydrase I) (Carbo	CAH1_HUMAN	28852.4	100.00%	LYPIANGNNQSPVDIK	1.65	0.203	2.34
Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonic anhydrase I) (Carbo	CAH1_HUMAN	28852.4	100.00%	VLDALQAIK	3.11	0.359	1.48
CALX_HUMAN							
Calnexin precursor (Major histocompatibility complex class I antig	CALX_HUMAN	67552.2	100.00%	GLVLMSR	1.9	0.191	0.252
Calnexin precursor (Major histocompatibility complex class I antig	CALX_HUMAN	67552.2	100.00%	GTLSGWILSK	3.29	0.411	1.31
Calnexin precursor (Major histocompatibility complex class I antig	CALX_HUMAN	67552.2	100.00%	IPNPDFFEDLEPFR	2.25	0.405	3.23
Calnexin precursor (Major histocompatibility complex class I antig	CALX_HUMAN	67552.2	100.00%	IVDDWANDGWGLKK	1.88	0.259	-0.398
Calnexin precursor (Major histocompatibility complex class I antig	CALX_HUMAN	67552.2	100.00%	KIPNPDFFEDLEPFR	3.32	0.49	3.47
CAP1_HUMAN							
Adenylyl cyclase-associated protein 1 (CAP 1) - Homo sapiens (Hu	CAP1_HUMAN	51837.5	100.00%	AGAAPYVQAFDSLLAGPVAEYLK	1.65	0.23	3.01
Adenylyl cyclase-associated protein 1 (CAP 1) - Homo sapiens (Hu	CAP1_HUMAN	51837.5	100.00%	LSDLLAPISEQIK	2.65	0.211	1.32
Adenylyl cyclase-associated protein 1 (CAP 1) - Homo sapiens (Hu	CAP1_HUMAN	51837.5	100.00%	SSEMNVLIPTEGGDFNEFPVPEQFK	1.5	0.38	1.12
Adenylyl cyclase-associated protein 1 (CAP 1) - Homo sapiens (Hu	CAP1_HUMAN	51837.5	100.00%	VENQENVSNLVIEDTELK	2.88	0.532	1.89
Adenylyl cyclase-associated protein 1 (CAP 1) - Homo sapiens (Hu	CAP1_HUMAN	51837.5	100.00%	VPTISINK	1.5	0.164	-0.255
CAPG_HUMAN							
Macrophage-capping protein (Actin-regulatory protein CAP-G) - H	CAPG_HUMAN	38499.9	100.00%	DLALAIRDSER	1.62	0.21	0
Macrophage-capping protein (Actin-regulatory protein CAP-G) - H	CAPG_HUMAN	38499.9	100.00%	EVQGNESDLFMSYFPR	4.09	0.589	2.06
Macrophage-capping protein (Actin-regulatory protein CAP-G) - H	CAPG_HUMAN	38499.9	100.00%	QAALQVAEGFISR	3.17	0.555	3.4
Macrophage-capping protein (Actin-regulatory protein CAP-G) - H	CAPG_HUMAN	38499.9	100.00%	VSDATGQMNLTK	2.44	0.413	3.35
CATA_HUMAN							
Catalase (EC 1.11.1.6) - Homo sapiens (Human)	CATA_HUMAN	59738.5	100.00%	AFYVNVLNEEQR	3.66	0.422	2.7
Catalase (EC 1.11.1.6) - Homo sapiens (Human)	CATA_HUMAN	59738.5	100.00%	FNTANDDNVTQVR	2.65	0.448	1.72
Catalase (EC 1.11.1.6) - Homo sapiens (Human)	CATA_HUMAN	59738.5	100.00%	FSTVAGESGSADTVRDPR	2.12	0.116	0.796
Catalase (EC 1.11.1.6) - Homo sapiens (Human)	CATA_HUMAN	59738.5	100.00%	NLSVEDAAR	2.49	0.404	1.01
Catalase (EC 1.11.1.6) - Homo sapiens (Human)	CATA_HUMAN	59738.5	100.00%	NPVNYFAEVEQIAFDPSNMPPGIEASPDK	1.96	0.515	4.08

CATD_HUMAN							
Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathepsin D light	CATD_HUMAN	44535	100.00%	FDGILGMAYPR	2.12	0.431	1.5
Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathepsin D light	CATD_HUMAN	44535	100.00%	ISVNNVLPVFDNLMQQK	2.28	0.282	1.13
Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathepsin D light	CATD_HUMAN	44535	100.00%	QPGITFIAAK	1.67	0.314	0
Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathepsin D light	CATD_HUMAN	44535	100.00%	VGFAEAAR	1.86	0.125	0.796
Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathepsin D light	CATD_HUMAN	44535	100.00%	VSTLPAITLK	2.07	0.33	3
CAZA1_HUMAN							
F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sa	CAZA1_HUMAN	32905.1	99.80%	FTITPPTAQVVGVLK	1.76	0.26	2.25
F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sa	CAZA1_HUMAN	32905.1	99.80%	LLLNNDNLLR	2.55	0.215	0.77
CD14_HUMAN							
Monocyte differentiation antigen CD14 precursor (Myeloid cell-spe	CD14_HUMAN	40058.6	100.00%	AFPALTSLDLSDNPGLGER	2.39	0.315	1.46
Monocyte differentiation antigen CD14 precursor (Myeloid cell-spe	CD14_HUMAN	40058.6	100.00%	ATVNPSAPR	1.15	0.132	1.36
Monocyte differentiation antigen CD14 precursor (Myeloid cell-spe	CD14_HUMAN	40058.6	100.00%	ITGTMPPLPLEATGLALSSLR	1.52	0.197	1.22
CD36_HUMAN							
Platelet glycoprotein 4 (Platelet glycoprotein IV) (GPIV) (Glycopro	CD36_HUMAN	53036.3	99.80%	QVVLEEGTIAFK	1.83	0.408	1.23
Platelet glycoprotein 4 (Platelet glycoprotein IV) (GPIV) (Glycopro	CD36_HUMAN	53036.3	99.80%	VAIIDTYK	1.84	0.344	0.796
CFAH_HUMAN							
Complement factor H precursor (H factor 1) - Homo sapiens (Hun	CFAH_HUMAN	139052.1	100.00%	CFEGFGIDGPAIAK	2.3	0.548	2.33
Complement factor H precursor (H factor 1) - Homo sapiens (Hun	CFAH_HUMAN	139052.1	100.00%	CLPVTAPENGK	1.62	0.136	0.854
Complement factor H precursor (H factor 1) - Homo sapiens (Hun	CFAH_HUMAN	139052.1	100.00%	SPDVINGSPISQK	2.92	0.449	1.01
Complement factor H precursor (H factor 1) - Homo sapiens (Hun	CFAH_HUMAN	139052.1	100.00%	TGESVEFVCK	3.79	0.371	3.07
CH60_HUMAN							
60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 k	CH60_HUMAN	61037.7	100.00%	ALMLQGVDLLADAVAVTMGPK	0	0	4.7
60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 k	CH60_HUMAN	61037.7	100.00%	DPGMGAMGGMGGGMGGGMF	1.63	0.215	1.01
60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 k	CH60_HUMAN	61037.7	100.00%	GANPVEIR	1.99	0.225	0.0269
60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 k	CH60_HUMAN	61037.7	100.00%	GYISPYFINTSK	2.98	0.447	2.89
60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 k	CH60_HUMAN	61037.7	100.00%	ISSIQSIVPALEIANAHR	3.18	0.484	1.68
60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 k	CH60_HUMAN	61037.7	100.00%	LSDGVAVLK	3.07	0.382	0.921
60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 k	CH60_HUMAN	61037.7	100.00%	LVQDVANNTNEEAGDGTTTATVLAR	0	0	4.82
60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 k	CH60_HUMAN	61037.7	100.00%	VGEVIVTKDDAMLLK	2.87	0.277	1.42
60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 k	CH60_HUMAN	61037.7	100.00%	VTDALNATR	1.82	0.305	1.2
CLH1_HUMAN							
Clathrin heavy chain 1 (CLH-17) - Homo sapiens (Human)	CLH1_HUMAN	191600.9	100.00%	CNEPAVWSQLAK	2.53	0.259	0.174
Clathrin heavy chain 1 (CLH-17) - Homo sapiens (Human)	CLH1_HUMAN	191600.9	100.00%	IAAYLFK	1.69	0.306	-0.176
Clathrin heavy chain 1 (CLH-17) - Homo sapiens (Human)	CLH1_HUMAN	191600.9	100.00%	IYIDSNNNPER	3.25	0.409	2.41
Clathrin heavy chain 1 (CLH-17) - Homo sapiens (Human)	CLH1_HUMAN	191600.9	100.00%	LLYNNVSNFGR	3.13	0.552	1.7
Clathrin heavy chain 1 (CLH-17) - Homo sapiens (Human)	CLH1_HUMAN	191600.9	100.00%	NNLAGAEELFAR	3.8	0.463	3.15
Clathrin heavy chain 1 (CLH-17) - Homo sapiens (Human)	CLH1_HUMAN	191600.9	100.00%	TLQIFNIEMK	3.71	0.254	1.92
Clathrin heavy chain 1 (CLH-17) - Homo sapiens (Human)	CLH1_HUMAN	191600.9	100.00%	VANVELYYR	3.53	0.359	1.25
CLIC1_HUMAN							
Chloride intracellular channel protein 1 (Nuclear chloride ion chan	CLIC1_HUMAN	26905.3	100.00%	IGNCPFSQR	1.54	0.324	0.796
Chloride intracellular channel protein 1 (Nuclear chloride ion chan	CLIC1_HUMAN	26905.3	100.00%	LAALNPESNTAGLDIFAK	4.19	0.587	4.85
Chloride intracellular channel protein 1 (Nuclear chloride ion chan	CLIC1_HUMAN	26905.3	100.00%	NSNPALNDNLEK	1.47	0.286	0.921
CLUS_HUMAN							
Clusterin precursor (Complement-associated protein SP-40,40) (C	CLUS_HUMAN	52477	100.00%	ASSIIDELFQDR	2.03	0.195	0.699
Clusterin precursor (Complement-associated protein SP-40,40) (C	CLUS_HUMAN	52477	100.00%	ELDESLQVAER	2.06	0.278	-0.279
Clusterin precursor (Complement-associated protein SP-40,40) (C	CLUS_HUMAN	52477	100.00%	TLLSNLEEAK	2.24	0.243	0.658
Clusterin precursor (Complement-associated protein SP-40,40) (C	CLUS_HUMAN	52477	100.00%	VTTVASHTSDSDVPSGVTEVVVK	2.79	0.194	1.26
CO3_HUMAN							
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	AAVYHHFISDGVR	2.73	0.445	0.699
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	AEDLVGK	1.64	0.133	0.319
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	AGDFLEANYMNLQR	2.36	0.469	1.82
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	AVLYNYR	1.62	0.309	-0.322
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	AYYENSPQQVFSTEFEVK	3.01	0.471	1.26
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	DFDFVPPVVR	1.84	0.442	2.82
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	DICEEQVNSLPGSITK	3.3	0.5	3.46
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	DSCVGSLVVK	2.02	0.335	-0.362

Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	EGVQKEDIPPADLSDQVPDTESETR	1.39	0.216	0.252
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	FISLGEACK	1.97	0.122	0.796
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	FYYIYNEK	2.29	0.414	0.456
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	GYTQQLAFR	2.72	0.146	1.85
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	IHWESASLLR	2.63	0.301	0
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	ILLQGTPVAQMTEDAVDAER	4.13	0.55	4
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	IPIEDGSGEVVLSR	4.04	0.528	4.66
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	ISLPESLK	1.79	0.0759	0.292
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	IWDVVEK	2.12	0.209	-0.146
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	KGYTQQLAFR	2.5	0.228	0
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	KQELSEAEQATR	2.9	0.205	0.347
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	KVLLDGVQNPR	2.46	0.247	0
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	LMNIFLK	2.46	0.0336	-0.505
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	LVAYYTLIGASGQR	3.41	0.452	3.85
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	NEQVEIR	2.09	0.149	-0.591
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	NTMILEICTR	2.65	0.433	1.17
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	QPSSAFAAFVK	0	0	2.75
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	RIPIEDGSGEVVLSR	3.43	0.4	1.52
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	SDDKVTLEER	1.33	0.152	0.658
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	SEETKENEGFTVTAEGK	3.73	0.503	1.55
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	SGIPIVTSPYQIHFTK	1.98	0.47	2.52
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	SGQSEDRQPVPGQQMTLK	3.06	0.38	1.82
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	SGSDEVQVGQQR	3.17	0.462	2.17
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	SSLSVPYVIVPLK	2.86	0.504	3.72
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	TFISPIK	1.47	0.177	-0.23
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	TGLQEVEVK	3.58	0.345	1.3
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	TIYTPGSTVLYR	2.69	0.478	1.85
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	TKKQELSEAEQATR	2.78	0.287	0
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	VELLHNPAFCSLATTK	3.56	0.453	4
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	VLLDGVQNPR	3.32	0.446	0.796
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	VPVAVQGEDTVQSLTQGDGVAK	5.4	0.615	6.75
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	VVLVAVDKGVFVLNKK	3.02	0.489	2.09
Complement C3 precursor [Contains: Complement C3 beta chain;	CO3_HUMAN	187131.1	100.00%	YYTYLIMNK	2.75	0.474	0.959
CO4A_HUMAN							
Complement C4-A precursor (Acidic complement C4) [Contains:	CO4A_HUMAN,CO4B_HUMA	192776.8	100.00%	CSVFYGAPSK	2.72	0.449	0.319
Complement C4-A precursor (Acidic complement C4) [Contains:	CO4A_HUMAN,CO4B_HUMA	192776.8	100.00%	GLQDEDGYR	1.12	0.361	0.553
Complement C4-A precursor (Acidic complement C4) [Contains:	CO4A_HUMAN,CO4B_HUMA	192776.8	100.00%	GSFEFPVGDAVSK	1.45	0.196	1.25
Complement C4-A precursor (Acidic complement C4) [Contains:	CO4A_HUMAN,CO4B_HUMA	192776.8	100.00%	ITQVLHFTK	2.33	0.292	0.553
Complement C4-A precursor (Acidic complement C4) [Contains:	CO4A_HUMAN,CO4B_HUMA	192776.8	100.00%	LLATLCSAEVCQCAEGK	3.86	0.569	2.16
Complement C4-A precursor (Acidic complement C4) [Contains:	CO4A_HUMAN,CO4B_HUMA	192776.8	100.00%	TTNIQGINLLFSSR	3.65	0.526	2.41
Complement C4-A precursor (Acidic complement C4) [Contains:	CO4A_HUMAN,CO4B_HUMA	192776.8	100.00%	VEYGFQVK	2.17	0.267	0.31
Complement C4-A precursor (Acidic complement C4) [Contains:	CO4A_HUMAN,CO4B_HUMA	192776.8	100.00%	VGDTLNLNLR	3.2	0.355	1.24
Complement C4-A precursor (Acidic complement C4) [Contains:	CO4A_HUMAN,CO4B_HUMA	192776.8	100.00%	YIYGKPVQGVAYVR	1.75	0.274	-0.362
CO9_HUMAN							
Complement component C9 precursor [Contains: Complement co	CO9_HUMAN	63156.8	100.00%	AIEDYINEFSVR	4.03	0.568	3.92
Complement component C9 precursor [Contains: Complement co	CO9_HUMAN	63156.8	100.00%	DRVVEESELAR	2.87	0.509	1.24
Complement component C9 precursor [Contains: Complement co	CO9_HUMAN	63156.8	100.00%	LSPIYNLVPVK	2.62	0.464	3.92
Complement component C9 precursor [Contains: Complement co	CO9_HUMAN	63156.8	100.00%	TSNFNAAISLK	2.32	0.441	1.41
Complement component C9 precursor [Contains: Complement co	CO9_HUMAN	63156.8	100.00%	VVEESELAR	2.16	0.284	0.0177
COF1_HUMAN							
Cofilin-1 (Cofilin, non-muscle isoform) (18 kDa phosphoprotein) (	COF1_HUMAN	18485.2	99.80%	LGGSAVISLEGKPL	2.5	0.282	1.85
Cofilin-1 (Cofilin, non-muscle isoform) (18 kDa phosphoprotein) (	COF1_HUMAN	18485.2	99.80%	YALYDATYETK	3.33	0.567	4.77
COX2_HUMAN							
Cytochrome c oxidase subunit 2 (EC 1.9.3.1) (Cytochrome c oxida	COX2_HUMAN	25548.4	99.80%	ILYMTDEVNDPSLTIK	2.66	0.494	2.24
Cytochrome c oxidase subunit 2 (EC 1.9.3.1) (Cytochrome c oxida	COX2_HUMAN	25548.4	99.80%	LLDVDNR	1.84	0.12	-0.644
EF1A1_HUMAN							
Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor 1 A-	EF1A1_HUMAN	50123.2	100.00%	IGGIGTVPVGR	1.9	0.367	0.678

Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor 1 A-	EF1A1_HUMAN	50123.2	100.00%	MDSTEPPYSQKR	1.11	0.304	-0.591
Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor 1 A-	EF1A1_HUMAN	50123.2	100.00%	QTVAVGVIK	1.59	0.288	0.187
EF2_HUMAN							
Elongation factor 2 (EF-2) - Homo sapiens (Human)	EF2_HUMAN	95322.1	100.00%	FSVSPVVR	2.49	0.296	0.658
Elongation factor 2 (EF-2) - Homo sapiens (Human)	EF2_HUMAN	95322.1	100.00%	SDPVVSYR	1.33	0.248	1.5
Elongation factor 2 (EF-2) - Homo sapiens (Human)	EF2_HUMAN	95322.1	100.00%	STLTDSLVCK	2.59	0.422	0.0555
Elongation factor 2 (EF-2) - Homo sapiens (Human)	EF2_HUMAN	95322.1	100.00%	VFSGLVSTGLK	2.44	0.248	2.13
ENOA_HUMAN							
Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase	ENOA_HUMAN	47152.2	100.00%	DATNVGDEGGFAPNILENK	3.5	0.507	5
Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase	ENOA_HUMAN	47152.2	100.00%	DATNVGDEGGFAPNILENKEGLELLK	3.47	0.0553	2.21
Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase	ENOA_HUMAN	47152.2	100.00%	GNPTVEVDLFTSK	3.51	0.245	4.26
Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase	ENOA_HUMAN	47152.2	100.00%	IGAEVYHNLK	2.95	0.287	0.959
Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase	ENOA_HUMAN	47152.2	100.00%	LAMQEFMILPVGAANFR	2.5	0.422	2.47
Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase	ENOA_HUMAN	47152.2	100.00%	LAQANGWGVMVSHR	2.75	0.409	0.959
Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase	ENOA_HUMAN	47152.2	100.00%	LMIEMDGTENK	3.06	0.281	-0.322
Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase	ENOA_HUMAN	47152.2	100.00%	SCNCLLLK	2.35	0.165	0
Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase	ENOA_HUMAN	47152.2	100.00%	SGKYDLDFK	2.69	0.285	0
Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase	ENOA_HUMAN	47152.2	100.00%	TIAPALVSK	1.35	0.308	0.796
Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase	ENOA_HUMAN	47152.2	100.00%	VNQIGSVTESLQACK	3.49	0.55	3.62
Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase	ENOA_HUMAN	47152.2	100.00%	VVIGMDVAASEFFR	4.28	0.606	3.38
Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase	ENOA_HUMAN	47152.2	100.00%	YGKDATNVGDEGGFAPNILENK	2.67	0.328	-0.699
Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase	ENOA_HUMAN	47152.2	100.00%	YISPDQLADLYK	2.87	0.44	2.62
Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase	ENOA_HUMAN	47152.2	100.00%	YNQLLR	1.88	0.187	0
ENPL_HUMAN							
Endoplasmin precursor (Heat shock protein 90 kDa beta member	ENPL_HUMAN	92453.7	100.00%	DISTNYYASQK	3.29	0.498	2.89
Endoplasmin precursor (Heat shock protein 90 kDa beta member	ENPL_HUMAN	92453.7	100.00%	EAESSPFVER	1.56	0.198	-0.0414
Endoplasmin precursor (Heat shock protein 90 kDa beta member	ENPL_HUMAN	92453.7	100.00%	ELISNASDALDK	3.25	0.521	2.07
Endoplasmin precursor (Heat shock protein 90 kDa beta member	ENPL_HUMAN	92453.7	100.00%	ELISNASDALDKIR	2.59	0.414	1.32
Endoplasmin precursor (Heat shock protein 90 kDa beta member	ENPL_HUMAN	92453.7	100.00%	FAFQAEVNR	3.39	0.453	1.1
Endoplasmin precursor (Heat shock protein 90 kDa beta member	ENPL_HUMAN	92453.7	100.00%	GLFDEYGSK	2.6	0.513	1.6
Endoplasmin precursor (Heat shock protein 90 kDa beta member	ENPL_HUMAN	92453.7	100.00%	GVVDSDDLPLNVSR	3.95	0.308	2.82
Endoplasmin precursor (Heat shock protein 90 kDa beta member	ENPL_HUMAN	92453.7	100.00%	IYFMAGSSR	2.13	0.455	1.27
Endoplasmin precursor (Heat shock protein 90 kDa beta member	ENPL_HUMAN	92453.7	100.00%	LGVIEDHSNR	2.57	0.401	1.11
Endoplasmin precursor (Heat shock protein 90 kDa beta member	ENPL_HUMAN	92453.7	100.00%	LIINSLYK	2.28	0.271	-0.0414
Endoplasmin precursor (Heat shock protein 90 kDa beta member	ENPL_HUMAN	92453.7	100.00%	SGTSEFLNK	2.36	0.418	1.08
Endoplasmin precursor (Heat shock protein 90 kDa beta member	ENPL_HUMAN	92453.7	100.00%	SGYLLPDTK	3.32	0.367	1.08
Endoplasmin precursor (Heat shock protein 90 kDa beta member	ENPL_HUMAN	92453.7	100.00%	SILFVPTSAPR	3.33	0.382	2.68
Endoplasmin precursor (Heat shock protein 90 kDa beta member	ENPL_HUMAN	92453.7	100.00%	TFEINPR	1.63	0.346	0.509
ERLN2_HUMAN							
Erlin 2, SSPFH domain-containing protein 2 precursor - Homo sap	SPFH2_HUMAN	37822.4	100.00%	ISEIEDAAFLAR	3.14	0.393	1.82
Erlin 2, SPFH domain-containing protein 2 precursor - Homo sapie	SPFH2_HUMAN	37822.4	100.00%	KISEIEDAAFLAR	1.39	0.244	1.82
Erlin 2, SSPFH domain-containing protein 2 precursor - Homo sap	SPFH2_HUMAN	37822.4	100.00%	LLIAAQK	1.79	0.172	-0.532
ERP29_HUMAN							
Endoplasmic reticulum protein ERp29 precursor (ERp31) (ERp28)	ERP29_HUMAN	28976.9	100.00%	DGDFENPVPYTGAVK	2.76	0.438	1.41
Endoplasmic reticulum protein ERp29 precursor (ERp31) (ERp28)	ERP29_HUMAN	28976.9	100.00%	GALPLDTVTFYK	1.65	0.273	0.854
Endoplasmic reticulum protein ERp29 precursor (ERp31) (ERp28)	ERP29_HUMAN	28976.9	100.00%	SLNILTAFQK	3.3	0.406	1.64
EZRI_HUMAN							
Ezrin (p81) (Cytovillin) (Villin-2) - Homo sapiens (Human)	EZRI_HUMAN	69396.6	99.80%	ALQLEEER	2.33	0.191	0
Ezrin (p81) (Cytovillin) (Villin-2) - Homo sapiens (Human)	EZRI_HUMAN	69396.6	99.80%	APDFVFYAPR	2.14	0.443	1
FIBA_HUMAN							
Fibrinogen alpha chain precursor [Contains: Fibrinopeptide A] - H	FIBA_HUMAN	94955.4	100.00%	GLIDEVNQDFTNR	1.98	0.434	1.96
Fibrinogen alpha chain precursor [Contains: Fibrinopeptide A] - H	FIBA_HUMAN	94955.4	100.00%	NSLFEYQK	2.23	0.257	0
Fibrinogen alpha chain precursor [Contains: Fibrinopeptide A] - H	FIBA_HUMAN	94955.4	100.00%	QLEQVIAK	2.11	0.149	0.301
FIBB_HUMAN							
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B] - Ho	FIBB_HUMAN	55910.6	100.00%	AHYGGFTVQNEANK	1.6	0.334	1.85
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B] - Ho	FIBB_HUMAN	55910.6	100.00%	DNENVVNEYSSELEK	3.36	0.506	4.07
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B] - Ho	FIBB_HUMAN	55910.6	100.00%	EDGGGWWYNR	1.26	0.404	0

Fibrinogen beta chain precursor [Contains: Fibrinopeptide B] - Ho	FIBB_HUMAN	55910.6	100.00%	EEAPSLRPAPPPISGGGYR	2.75	0.324	1.38
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B] - Ho	FIBB_HUMAN	55910.6	100.00%	GGETSEMYLIQPDSSVKPYR	2.93	0.443	2.12
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B] - Ho	FIBB_HUMAN	55910.6	100.00%	HGTDDGVVWMNWK	3.46	0.414	0.796
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B] - Ho	FIBB_HUMAN	55910.6	100.00%	IRPFFPQQ	1.48	0.233	-0.23
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B] - Ho	FIBB_HUMAN	55910.6	100.00%	ISQLTR	2.05	0.141	0
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B] - Ho	FIBB_HUMAN	55910.6	100.00%	LESDVSAQMEYCR	4.09	0.318	1.44
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B] - Ho	FIBB_HUMAN	55910.6	100.00%	NSVDELNNNVEAVSQTSSSSFQYMYLLK	0	0	4.32
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B] - Ho	FIBB_HUMAN	55910.6	100.00%	NYCGLPGEYWLGNDK	1.14	0.154	1.36
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B] - Ho	FIBB_HUMAN	55910.6	100.00%	QDGSVDFGR	1.84	0.323	1.39
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B] - Ho	FIBB_HUMAN	55910.6	100.00%	QGFGNVATNTDGK	2.38	0.421	2.28
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B] - Ho	FIBB_HUMAN	55910.6	100.00%	TPCTVSCNIPVVSGK	3.43	0.6	2.89
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B] - Ho	FIBB_HUMAN	55910.6	100.00%	VYCDMNTENGGWTVIQNR	3.13	0.528	3.02
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B] - Ho	FIBB_HUMAN	55910.6	100.00%	YQISVNK	1.9	0.0199	0.347
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B] - Ho	FIBB_HUMAN	55910.6	100.00%	YYWGGQYTWDMAK	4.32	0.607	4.48
FIBG_HUMAN							
Fibrinogen gamma chain precursor - Homo sapiens (Human)	FIBG_HUMAN	51495.3	100.00%	AIQLTYNPDESSKPNMIDAATLK	2.3	0.426	0.181
Fibrinogen gamma chain precursor - Homo sapiens (Human)	FIBG_HUMAN	51495.3	100.00%	ASTPNGYDNGIIWATWK	1.89	0.345	2.55
Fibrinogen gamma chain precursor - Homo sapiens (Human)	FIBG_HUMAN	51495.3	100.00%	DNCCILDER	2.38	0.338	0.444
Fibrinogen gamma chain precursor - Homo sapiens (Human)	FIBG_HUMAN	51495.3	100.00%	EGFGHLSPTGTTEFWLGNEK	3.44	0.304	2.21
Fibrinogen gamma chain precursor - Homo sapiens (Human)	FIBG_HUMAN	51495.3	100.00%	IHLISTQSAIPYALR	2.44	0.225	1.68
Fibrinogen gamma chain precursor - Homo sapiens (Human)	FIBG_HUMAN	51495.3	100.00%	QSGLYFIKPLK	2.72	0.396	1.09
Fibrinogen gamma chain precursor - Homo sapiens (Human)	FIBG_HUMAN	51495.3	100.00%	RLDGSVDFKK	2.41	0.273	0
Fibrinogen gamma chain precursor - Homo sapiens (Human)	FIBG_HUMAN	51495.3	100.00%	TSTADYAMFK	2.07	0.386	1.85
Fibrinogen gamma chain precursor - Homo sapiens (Human)	FIBG_HUMAN	51495.3	100.00%	VELEDWNGR	2.16	0.195	0.62
Fibrinogen gamma chain precursor - Homo sapiens (Human)	FIBG_HUMAN	51495.3	100.00%	YEASILTHDSSIR	2.66	0.559	1.55
Fibrinogen gamma chain precursor - Homo sapiens (Human)	FIBG_HUMAN	51495.3	100.00%	YLQEIYNSNNQK	3.79	0.494	3.28
FINC_HUMAN							
Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG) - Homo	FINC_HUMAN	262581	100.00%	GNLLQCICTGNGR	3.55	0.412	2.96
Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG) - Homo	FINC_HUMAN	262581	100.00%	IYLYTLNDNAR	3.31	0.394	1.2
Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG) - Homo	FINC_HUMAN	262581	100.00%	LTVGLTR	1.8	0.201	0
Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG) - Homo	FINC_HUMAN	262581	100.00%	SSPVVIDASTAIDAPSNLR	2.43	0.432	1.4
Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG) - Homo	FINC_HUMAN	262581	100.00%	STTPDITGYR	1.46	0.32	0.77
Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG) - Homo	FINC_HUMAN	262581	100.00%	SYTITGLQPGTDYK	3.37	0.592	3.21
Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG) - Homo	FINC_HUMAN	262581	100.00%	TFYSCTTEGR	1.63	0.459	2.36
Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG) - Homo	FINC_HUMAN	262581	100.00%	VPGTSTSATLTGLTR	3.1	0.582	3.23
FLNA_HUMAN							
Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding pr	FLNA_HUMAN	280711.4	100.00%	AFGPGLQGGSAGSPAR	3.66	0.239	4.41
Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding pr	FLNA_HUMAN	280711.4	100.00%	AGVAPLQVK	1.86	0.197	1.38
Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding pr	FLNA_HUMAN	280711.4	100.00%	ANLPQSFQVDTSK	3.53	0.425	5
Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding pr	FLNA_HUMAN	280711.4	100.00%	AWGPGLEGGVVGK	3.31	0.599	2.57
Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding pr	FLNA_HUMAN	280711.4	100.00%	DAGEGLLAVQITDPEGKPK	1.64	0.244	-0.38
Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding pr	FLNA_HUMAN	280711.4	100.00%	EATTEFSVDAR	2.73	0.362	2
Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding pr	FLNA_HUMAN	280711.4	100.00%	FTIDTK	1.65	0.152	-0.519
Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding pr	FLNA_HUMAN	280711.4	100.00%	GAGTGGLGLAVEGPSEAK	3.19	0.365	2.43
Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding pr	FLNA_HUMAN	280711.4	100.00%	GLVEPVDVVDNADGTQTVNYVPSR	2.29	0.505	2.38
Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding pr	FLNA_HUMAN	280711.4	100.00%	GTVEPQLEAR	2.77	0.275	2.1
Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding pr	FLNA_HUMAN	280711.4	100.00%	IANLQTDLSDGLR	3.88	0.588	5.24
Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding pr	FLNA_HUMAN	280711.4	100.00%	LLGWIQNK	1.99	0.175	-0.613
Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding pr	FLNA_HUMAN	280711.4	100.00%	SPFSVAVSPSLDLSK	2.85	0.379	0.959
Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding pr	FLNA_HUMAN	280711.4	100.00%	TGVAVNKPAEFTVDAK	1.69	0.219	0.409
Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding pr	FLNA_HUMAN	280711.4	100.00%	VANPSGNLTETYVQDR	3.04	0.508	2.31
Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding pr	FLNA_HUMAN	280711.4	100.00%	VDVGKDQEFTVK	1.66	0.216	0.268
Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding pr	FLNA_HUMAN	280711.4	100.00%	VEPSHDASK	1.47	0.258	0
Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding pr	FLNA_HUMAN	280711.4	100.00%	VTAQGPGLEPSGNIANK	3.48	0.577	3.5
FRIH_HUMAN							
Ferritin heavy chain (EC 1.16.3.1) (Ferritin H subunit) (Proliferatic	FRIH_HUMAN	21208.2	100.00%	ELGDHVTNLRK	2.1	0.248	-0.431
Ferritin heavy chain (EC 1.16.3.1) (Ferritin H subunit) (Proliferatic	FRIH_HUMAN	21208.2	100.00%	IFLQDIK	2.66	0.134	0

Ferritin heavy chain (EC 1.16.3.1) (Ferritin H subunit) (Proliferatic	FRIH_HUMAN	21208.2	100.00%	NVNQSLLELHK	3.18	0.4	-0.23
FRIL_HUMAN							
Ferritin light chain (Ferritin L subunit) - Homo sapiens (Human)	FRIL_HUMAN	20002.6	100.00%	AAMALEK	1.81	0.129	-0.176
Ferritin light chain (Ferritin L subunit) - Homo sapiens (Human)	FRIL_HUMAN	20002.6	100.00%	ALFQDIK	2.39	0.099	-0.568
Ferritin light chain (Ferritin L subunit) - Homo sapiens (Human)	FRIL_HUMAN	20002.6	100.00%	KLNQALLDLHALGSAR	3.62	0.451	1.34
Ferritin light chain (Ferritin L subunit) - Homo sapiens (Human)	FRIL_HUMAN	20002.6	100.00%	KPAEDEWGKTPDAMK	2.3	0.173	-0.255
Ferritin light chain (Ferritin L subunit) - Homo sapiens (Human)	FRIL_HUMAN	20002.6	100.00%	LGGPEAGLGEYLFER	3.18	0.435	3.1
Ferritin light chain (Ferritin L subunit) - Homo sapiens (Human)	FRIL_HUMAN	20002.6	100.00%	LNQALLDLHALGSAR	3.84	0.439	3.41
Ferritin light chain (Ferritin L subunit) - Homo sapiens (Human)	FRIL_HUMAN	20002.6	100.00%	LTLKHD	1.35	0.244	-0.176
Ferritin light chain (Ferritin L subunit) - Homo sapiens (Human)	FRIL_HUMAN	20002.6	100.00%	MGDHLTNLHR	2.01	0.114	0.77
G3P_HUMAN							
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPD	G3P_HUMAN	36035.3	100.00%	DGRGALQNIIPASTGAAK	1.97	0.0255	1.14
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPD	G3P_HUMAN	36035.3	100.00%	GALQNIIPASTGAAK	3.02	0.185	1.89
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPD	G3P_HUMAN	36035.3	100.00%	IISNASCTTNCLAPLAK	3.11	0.475	3.41
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPD	G3P_HUMAN	36035.3	100.00%	LISWYDNEFGYSNR	2.92	0.543	1.85
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPD	G3P_HUMAN	36035.3	100.00%	LTGMAFR	1.46	0.263	0
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPD	G3P_HUMAN	36035.3	100.00%	LVINGNPITIFQER	1.22	0.366	0.77
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPD	G3P_HUMAN	36035.3	100.00%	LVINGNPITIFQERDPSK	2.46	0.256	-0.0414
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPD	G3P_HUMAN	36035.3	100.00%	VGVNGFGR	2.25	0.328	0.569
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPD	G3P_HUMAN	36035.3	100.00%	VPTANVSVVDLTCR	1.49	0.129	1.4
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPD	G3P_HUMAN	36035.3	100.00%	VVDLMAHMASKE	3.85	0.565	3.38
G6PI_HUMAN							
Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphogluc	G6PI_HUMAN	63130.5	99.80%	ILLANFLAQTEALMR	3.03	0.522	3.28
Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphogluc	G6PI_HUMAN	63130.5	99.80%	TLAQLNPESSLFIIASK	3.68	0.564	3.02
GBB1_HUMAN							
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1	GBB1_HUMAN	37359.5	99.80%	LFVSGACDASAK	3.31	0.429	3.12
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1	GBB1_HUMAN	37359.5	99.80%	LLVSASQDGK	2.53	0.46	2.09
GELS_HUMAN							
Gelsolin precursor (Actin-depolymerizing factor) (ADF) (Brevin) (A	GELS_HUMAN	85679.8	100.00%	AGALNSNDAFVLK	3.52	0.462	2.2
Gelsolin precursor (Actin-depolymerizing factor) (ADF) (Brevin) (A	GELS_HUMAN	85679.8	100.00%	AQPVQVAEGSEPDGFWEALGGK	2.75	0.503	3.38
Gelsolin precursor (Actin-depolymerizing factor) (ADF) (Brevin) (A	GELS_HUMAN	85679.8	100.00%	AVEVLPK	2.47	0.302	0.0223
Gelsolin precursor (Actin-depolymerizing factor) (ADF) (Brevin) (A	GELS_HUMAN	85679.8	100.00%	GGVASGFK	2.29	0	1
Gelsolin precursor (Actin-depolymerizing factor) (ADF) (Brevin) (A	GELS_HUMAN	85679.8	100.00%	HVVPNEVVVQR	1.45	0.142	1.75
Gelsolin precursor (Actin-depolymerizing factor) (ADF) (Brevin) (A	GELS_HUMAN	85679.8	100.00%	QTQVSVLPEGGETPLFK	3.02	0.488	3.18
Gelsolin precursor (Actin-depolymerizing factor) (ADF) (Brevin) (A	GELS_HUMAN	85679.8	100.00%	TASDFITK	2.67	0.433	2.15
Gelsolin precursor (Actin-depolymerizing factor) (ADF) (Brevin) (A	GELS_HUMAN	85679.8	100.00%	TGAQELLR	1.75	0.132	1.16
Gelsolin precursor (Actin-depolymerizing factor) (ADF) (Brevin) (A	GELS_HUMAN	85679.8	100.00%	TPITVVK	2.1	0.161	0.658
GNAI2_HUMAN							
Guanine nucleotide-binding protein G(i), alpha-2 subunit (Adenyla	GNAI2_HUMAN	40434	100.00%	IAQSDYIPTQQDVLR	3.61	0.425	2.6
Guanine nucleotide-binding protein G(i), alpha-2 subunit (Adenyla	GNAI2_HUMAN	40434	100.00%	LLLLGAGESGK	1.97	0.432	1.59
Guanine nucleotide-binding protein G(i), alpha-2 subunit (Adenyla	GNAI2_HUMAN	40434	100.00%	LLLLGAGESGKSTIVK	1.58	0.166	1.15
Guanine nucleotide-binding protein G(i), alpha-2 subunit (Adenyla	GNAI2_HUMAN	40434	100.00%	MFDVGGQR	2.25	0.304	0.77
Guanine nucleotide-binding protein G(i), alpha-2 subunit (Adenyla	GNAI2_HUMAN	40434	100.00%	YDEAASYIQSK	2.68	0.438	2.47
GRP78_HUMAN							
78 kDa glucose-regulated protein precursor (GRP 78) (Heat shock	GRP78_HUMAN	72316.7	100.00%	AKFEELNMDLFR	3.78	0.309	2.19
78 kDa glucose-regulated protein precursor (GRP 78) (Heat shock	GRP78_HUMAN	72316.7	100.00%	IINEPTAAAIAYGLDKR	2.16	0.278	-0.176
78 kDa glucose-regulated protein precursor (GRP 78) (Heat shock	GRP78_HUMAN	72316.7	100.00%	NQLTSNPENTVFDAKR	2.04	0.291	-0.322
78 kDa glucose-regulated protein precursor (GRP 78) (Heat shock	GRP78_HUMAN	72316.7	100.00%	SQIFSTASDNQPTVTIK	2.78	0.481	2.6
78 kDa glucose-regulated protein precursor (GRP 78) (Heat shock	GRP78_HUMAN	72316.7	100.00%	TFAPEEISAMVLTK	2.67	0.588	4.08
GSTP1_HUMAN							
Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-	GSTP1_HUMAN	23338.7	100.00%	AFLASPEYVNLPINGNGKQ	3.05	0.491	1.6
Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-	GSTP1_HUMAN	23338.7	100.00%	FQDGDLTLYQSNTILR	4.1	0.604	4.2
Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-	GSTP1_HUMAN	23338.7	100.00%	HLGRTLGLYGK	1.43	0.355	0
HA26_HUMAN							
HLA class II histocompatibility antigen, DQ(6) alpha chain precurs	HA26_HUMAN	28015	99.80%	NMAVGKHTLEFMMR	2.31	0.23	0
HLA class II histocompatibility antigen, DQ(6) alpha chain precurs	HA26_HUMAN	28015	99.80%	VEHWGLDEPLLK	2.5	0.336	0
HB2Q_HUMAN							

HLA class II histocompatibility antigen, DP(W2) beta chain precur	HB2Q_HUMAN	29271.7	99.80%	FDSDVGEFR	1.69	0.302	0.886
HLA class II histocompatibility antigen, DP(W2) beta chain precur	HB2Q_HUMAN	29271.7	99.80%	HNYELGGPMTLQRR	2.13	0.257	0
HBA_HUMAN							
Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globi	HBA_HUMAN	15239.6	100.00%	FLASVSTVLTSK	1.81	0.218	0.824
Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globi	HBA_HUMAN	15239.6	100.00%	LRVDPVNFK	1.7	0.167	1.36
Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globi	HBA_HUMAN	15239.6	100.00%	MFLSFPTTK	1.53	0.306	0
Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globi	HBA_HUMAN	15239.6	100.00%	TYFPHFDLSHGSAQVK	2.77	0.459	1.41
Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globi	HBA_HUMAN	15239.6	100.00%	VDPVNFK	1.37	0.17	0.602
Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globi	HBA_HUMAN	15239.6	100.00%	VGAHAGEYGAEALER	4.05	0.523	3.62
HBB_HUMAN							
Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) -	HBB_HUMAN	15980	100.00%	EFTPPVQAAYQK	1.91	0.271	2
Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) -	HBB_HUMAN	15980	100.00%	FFESFGDLSTPDAVMGNPK	2.87	0.584	1.7
Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) -	HBB_HUMAN	15980	100.00%	GTFATLSELHCDK	1.6	0.146	0.456
Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) -	HBB_HUMAN	15980	100.00%	LHVDPENFR	1.68	0.242	0.638
Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) -	HBB_HUMAN	15980	100.00%	LLVVYPWTQR	2.29	0.446	1.35
Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) -	HBB_HUMAN	15980	100.00%	SAVTALWGK	1.81	0.262	0
Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) -	HBB_HUMAN	15980	100.00%	SAVTALWGKVNVDEVGGEALGR	2.31	0.411	2.08
Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) -	HBB_HUMAN	15980	100.00%	VLGAFSDGLAHLDNLK	3.14	0.549	3.38
Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) -	HBB_HUMAN	15980	100.00%	VNVDEVGGEALGR	1.92	0.312	0.678
Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) -	HBB_HUMAN	15980	100.00%	VVAGVANALAHK	2.73	0.428	3.48
HBD_HUMAN							
Hemoglobin subunit delta (Hemoglobin delta chain) (Delta-globin	HBD_HUMAN	16037.1	100.00%	EFTPQMQAAYQK	1.67	0.356	1.07
Hemoglobin subunit delta (Hemoglobin delta chain) (Delta-globin	HBD_HUMAN	16037.1	100.00%	FFESFGDLSSPDAVMGNPK	2.35	0.417	4.15
Hemoglobin subunit delta (Hemoglobin delta chain) (Delta-globin	HBD_HUMAN	16037.1	100.00%	LHVDPENFR	1.68	0.242	0.638
Hemoglobin subunit delta (Hemoglobin delta chain) (Delta-globin	HBD_HUMAN	16037.1	100.00%	LLVVYPWTQR	2.29	0.446	1.35
Hemoglobin subunit delta (Hemoglobin delta chain) (Delta-globin	HBD_HUMAN	16037.1	100.00%	TAVNALWGK	2.5	0.231	1.75
Hemoglobin subunit delta (Hemoglobin delta chain) (Delta-globin	HBD_HUMAN	16037.1	100.00%	VLGAFSDGLAHLDNLK	3.14	0.549	3.38
Hemoglobin subunit delta (Hemoglobin delta chain) (Delta-globin	HBD_HUMAN	16037.1	100.00%	VNVDAVGGEALGR	4.72	0.564	7.11
Hemoglobin subunit delta (Hemoglobin delta chain) (Delta-globin	HBD_HUMAN	16037.1	100.00%	VVAGVANALAHK	2.73	0.428	3.48
HEMO_HUMAN							
Hemopexin precursor (Beta-1B-glycoprotein) - Homo sapiens (Hu	HEMO_HUMAN	51658.5	100.00%	GEFVWK	1.74	0.0195	0.721
Hemopexin precursor (Beta-1B-glycoprotein) - Homo sapiens (Hu	HEMO_HUMAN	51658.5	100.00%	GGYTLVSGYPK	3.78	0.32	1.82
Hemopexin precursor (Beta-1B-glycoprotein) - Homo sapiens (Hu	HEMO_HUMAN	51658.5	100.00%	LLQDEFPGIPSPLDAAVECHR	1.68	0.161	1.02
Hemopexin precursor (Beta-1B-glycoprotein) - Homo sapiens (Hu	HEMO_HUMAN	51658.5	100.00%	NFPSPVDAAFR	2.23	0.324	2.89
Hemopexin precursor (Beta-1B-glycoprotein) - Homo sapiens (Hu	HEMO_HUMAN	51658.5	100.00%	VDGALCMEK	2.15	0.322	0.495
Hemopexin precursor (Beta-1B-glycoprotein) - Homo sapiens (Hu	HEMO_HUMAN	51658.5	100.00%	YYCFQGNQFLR	2.77	0.253	0.482
HPT_HUMAN							
Haptoglobin precursor [Contains: Haptoglobin alpha chain; Hapto	HPT_HUMAN	45186.9	100.00%	DIAPTLTLYVGKK	3.31	0.48	2.46
Haptoglobin precursor [Contains: Haptoglobin alpha chain; Hapto	HPT_HUMAN	45186.9	100.00%	DYAEVGR	1.22	0.144	0.959
Haptoglobin precursor [Contains: Haptoglobin alpha chain; Hapto	HPT_HUMAN	45186.9	100.00%	GSFPWQAK	1.6	0.141	1.15
Haptoglobin precursor [Contains: Haptoglobin alpha chain; Hapto	HPT_HUMAN	45186.9	100.00%	ILGGHLDAK	2.22	0.184	-0.0792
Haptoglobin precursor [Contains: Haptoglobin alpha chain; Hapto	HPT_HUMAN	45186.9	100.00%	QLVEIEK	1.92	0.0613	-0.0792
Haptoglobin precursor [Contains: Haptoglobin alpha chain; Hapto	HPT_HUMAN	45186.9	100.00%	SCAVAEYGVYVK	3.78	0.548	3.68
Haptoglobin precursor [Contains: Haptoglobin alpha chain; Hapto	HPT_HUMAN	45186.9	100.00%	TEGDGVYTLNDKK	1.93	0.307	0.284
Haptoglobin precursor [Contains: Haptoglobin alpha chain; Hapto	HPT_HUMAN	45186.9	100.00%	VGYVSGWGR	3.14	0.445	2.09
Haptoglobin precursor [Contains: Haptoglobin alpha chain; Hapto	HPT_HUMAN	45186.9	100.00%	VMPICLPSK	1.48	0.22	-0.23
Haptoglobin precursor [Contains: Haptoglobin alpha chain; Hapto	HPT_HUMAN	45186.9	100.00%	VMPICLPSKDYAEVGR	1.76	0.168	-0.146
Haptoglobin precursor [Contains: Haptoglobin alpha chain; Hapto	HPT_HUMAN	45186.9	100.00%	VTSIQDWVQK	3.44	0.414	2.19
Haptoglobin precursor [Contains: Haptoglobin alpha chain; Hapto	HPT_HUMAN	45186.9	100.00%	YVMLPVADQDQCIR	2.37	0.401	2.23
HSP7C_HUMAN							
Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8	HSP7C_HUMAN	70881.8	100.00%	ARFEELNADLFR	3.21	0.344	0.602
Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8	HSP7C_HUMAN	70881.8	100.00%	DAGTIAGLNVLR	4.11	0.13	1.05
Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8	HSP7C_HUMAN	70881.8	100.00%	GTLDPVEK	2	0.129	0.959
Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8	HSP7C_HUMAN	70881.8	100.00%	IINEPTAAAIAYGLDKK	2.46	0.299	0.31
Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8	HSP7C_HUMAN	70881.8	100.00%	MKEIAEAYLGK	2.96	0.27	0.0809
Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8	HSP7C_HUMAN	70881.8	100.00%	NQVAMNPTNTVFDAK	3.77	0.542	4.14
Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8	HSP7C_HUMAN	70881.8	100.00%	NQVAMNPTNTVFDAKR	2.31	0.444	1.01

Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8)	HSP7C_HUMAN	70881.8	100.00%	SFYPEEVSSMVLTK	0	0	2.51
Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8)	HSP7C_HUMAN	70881.8	100.00%	TTPSYVAFTDTER	2.91	0.516	1.62
Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8)	HSP7C_HUMAN	70881.8	100.00%	TVTNAVVTVPAYFNDSQR	3.11	0.376	2.57
Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8)	HSP7C_HUMAN	70881.8	100.00%	VQVEYKGETK	2.18	0.327	2.01
HSPB1_HUMAN							
Heat-shock protein beta-1 (HspB1) (Heat shock 27 kDa protein) (	HSPB1_HUMAN	22764.6	99.80%	LATQSNEITIPVTFESR	2.48	0.469	0.292
Heat-shock protein beta-1 (HspB1) (Heat shock 27 kDa protein) (	HSPB1_HUMAN	22764.6	99.80%	VSLDVNHFAPDELTVK	2.46	0.348	0.161
HYEP_HUMAN							
Epoxide hydrolase 1 (EC 3.3.2.9) (Microsomal epoxide hydrolase)	HYEP_HUMAN	52933.1	100.00%	FLSVLERQ	2.43	0.263	0.469
Epoxide hydrolase 1 (EC 3.3.2.9) (Microsomal epoxide hydrolase)	HYEP_HUMAN	52933.1	100.00%	IIPLLTDPK	1.65	0.272	0.796
Epoxide hydrolase 1 (EC 3.3.2.9) (Microsomal epoxide hydrolase)	HYEP_HUMAN	52933.1	100.00%	VFYSLMR	1.31	0.426	-0.38
IC1_HUMAN							
Plasma protease C1 inhibitor precursor (C1 Inh) (C1Inh) (C1 este	IC1_HUMAN	55137.5	100.00%	FQPTLLTLPR	2.24	0.328	1.85
Plasma protease C1 inhibitor precursor (C1 Inh) (C1Inh) (C1 este	IC1_HUMAN	55137.5	100.00%	LLDSLPSDTR	2.36	0.297	0.569
Plasma protease C1 inhibitor precursor (C1 Inh) (C1Inh) (C1 este	IC1_HUMAN	55137.5	100.00%	TNLESILSYPK	2.6	0.538	3.25
IGHA1_HUMAN							
Ig alpha-1 chain C region - Homo sapiens (Human)	IGHA1_HUMAN	37635.8	100.00%	DASGVTFTWTPSSGK	3.67	0.454	2.51
Ig alpha-1 chain C region - Homo sapiens (Human)	IGHA1_HUMAN	37635.8	100.00%	QEPSQGTTTFAVTSILR	1.79	0.452	0.77
Ig alpha-1 chain C region - Homo sapiens (Human)	IGHA1_HUMAN	37635.8	100.00%	TPLTATLSK	2.05	0.298	1.22
Ig alpha-1 chain C region - Homo sapiens (Human)	IGHA1_HUMAN	37635.8	100.00%	WLQGSQELPR	2.54	0.371	0.796
Ig alpha-1 chain C region - Homo sapiens (Human)	IGHA1_HUMAN	37635.8	100.00%	YLTWASR	1.53	0.339	-0.342
IGHG1_HUMAN							
Ig gamma-1 chain C region - Homo sapiens (Human)	IGHG1_HUMAN	36087	100.00%	ALPAPIEK	1.35	0.239	1.18
Ig gamma-1 chain C region - Homo sapiens (Human)	IGHG1_HUMAN	36087	100.00%	DTLMISR	1.58	0.211	-0.929
Ig gamma-1 chain C region - Homo sapiens (Human)	IGHG1_HUMAN	36087	100.00%	EPQVYTLPPSR	1.68	0.282	-0.114
Ig gamma-1 chain C region - Homo sapiens (Human)	IGHG1_HUMAN	36087	100.00%	EPQVYTLPPSRDELTK	2.25	0.353	1.52
Ig gamma-1 chain C region - Homo sapiens (Human)	IGHG1_HUMAN	36087	100.00%	FNWYVDGVEVHNAK	3.8	0.564	3.06
Ig gamma-1 chain C region - Homo sapiens (Human)	IGHG1_HUMAN	36087	100.00%	GFYPSDIAVEWESNGQPENNYK	3.73	0.508	3.33
Ig gamma-1 chain C region - Homo sapiens (Human)	IGHG1_HUMAN	36087	100.00%	GPSVFPLAPSSK	1.15	0.206	0.886
Ig gamma-1 chain C region - Homo sapiens (Human)	IGHG1_HUMAN	36087	100.00%	NQVSLTCLVK	2.04	0.266	0
Ig gamma-1 chain C region - Homo sapiens (Human)	IGHG1_HUMAN	36087	100.00%	STSGGTAALGCLVK	4	0.535	4
Ig gamma-1 chain C region - Homo sapiens (Human)	IGHG1_HUMAN	36087	100.00%	TPEVTCVVVDVSHEDPEVK	2.63	0.277	0.678
Ig gamma-1 chain C region - Homo sapiens (Human)	IGHG1_HUMAN	36087	100.00%	TTPPVLDSDGSFFLYSK	1.11	0.299	0.268
Ig gamma-1 chain C region - Homo sapiens (Human)	IGHG1_HUMAN	36087	100.00%	VVSVLTVLHQDWLNGK	3.69	0.622	2.42
IGHG2_HUMAN							
Ig gamma-2 chain C region - Homo sapiens (Human)	IGHG2_HUMAN	35865.2	100.00%	DTLMISR	1.58	0.211	-0.929
Ig gamma-2 chain C region - Homo sapiens (Human)	IGHG2_HUMAN	35865.2	100.00%	EPQVYTLPPSR	1.68	0.282	-0.114
Ig gamma-2 chain C region - Homo sapiens (Human)	IGHG2_HUMAN	35865.2	100.00%	EPQVYTLPPSREEMTK	1.82	0.276	0.678
Ig gamma-2 chain C region - Homo sapiens (Human)	IGHG2_HUMAN	35865.2	100.00%	GFYPSDIAVEWESNGQPENNYK	3.73	0.508	3.33
Ig gamma-2 chain C region - Homo sapiens (Human)	IGHG2_HUMAN	35865.2	100.00%	GLPAPIEK	1.21	0.372	1.24
Ig gamma-2 chain C region - Homo sapiens (Human)	IGHG2_HUMAN	35865.2	100.00%	GPSVFPLAPCSR	2.33	0.471	1.89
Ig gamma-2 chain C region - Homo sapiens (Human)	IGHG2_HUMAN	35865.2	100.00%	NQVSLTCLVK	2.04	0.266	0
Ig gamma-2 chain C region - Homo sapiens (Human)	IGHG2_HUMAN	35865.2	100.00%	STSESTAALGCLVK	4.09	0.396	3.96
Ig gamma-2 chain C region - Homo sapiens (Human)	IGHG2_HUMAN	35865.2	100.00%	TTPPMLDSDGSFFLYSK	2.05	0.327	3.04
Ig gamma-2 chain C region - Homo sapiens (Human)	IGHG2_HUMAN	35865.2	100.00%	VVSVLTVVHQDWLNGK	3.05	0.426	1.89
Ig gamma-2 chain C region - Homo sapiens (Human)	IGHG2_HUMAN	35865.2	100.00%	VVSVLTVVHQDWLNGKEYK	2	0.272	0
IGHG3_HUMAN							
Ig gamma-3 chain C region (Heavy chain disease protein) (HDC)	IGHG3_HUMAN	32312	100.00%	ALPAPIEK	1.35	0.239	1.18
Ig gamma-3 chain C region (Heavy chain disease protein) (HDC)	IGHG3_HUMAN	32312	100.00%	CPAPELLGGPSVFLFPPKPK	0	0	5.24
Ig gamma-3 chain C region (Heavy chain disease protein) (HDC)	IGHG3_HUMAN	32312	100.00%	DTLMISR	1.58	0.211	-0.929
Ig gamma-3 chain C region (Heavy chain disease protein) (HDC)	IGHG3_HUMAN	32312	100.00%	EPQVYTLPPSR	1.68	0.282	-0.114
Ig gamma-3 chain C region (Heavy chain disease protein) (HDC)	IGHG3_HUMAN	32312	100.00%	EPQVYTLPPSREEMTK	1.82	0.276	0.678
Ig gamma-3 chain C region (Heavy chain disease protein) (HDC)	IGHG3_HUMAN	32312	100.00%	NQVSLTCLVK	2.04	0.266	0
Ig gamma-3 chain C region (Heavy chain disease protein) (HDC)	IGHG3_HUMAN	32312	100.00%	TPLGDTTHTCPR	1.23	0.216	-0.38
Ig gamma-3 chain C region (Heavy chain disease protein) (HDC)	IGHG3_HUMAN	32312	100.00%	VVSVLTVLHQNWLDGK	3.72	0.5	3.8
Ig gamma-3 chain C region (Heavy chain disease protein) (HDC)	IGHG3_HUMAN	32312	100.00%	WYVDGVQVHNAK	1.82	0.151	1.66
ILEU_HUMAN							

Leukocyte elastase inhibitor (LEI) (Serpin B1) (Monocyte/neutrop	ILEU_HUMAN	42725.8	99.80%	LVLVNAIYFK	2.73	0.487	1.52
Leukocyte elastase inhibitor (LEI) (Serpin B1) (Monocyte/neutrop	ILEU_HUMAN	42725.8	99.80%	TYNFLPEFLVSTQK	2.66	0.384	2.82
ITAV_HUMAN							
Integrin alpha-V precursor (Vitronectin receptor subunit alpha) (C	ITAV_HUMAN	116023	100.00%	AGTQLLAGLR	1.36	0.223	0.222
Integrin alpha-V precursor (Vitronectin receptor subunit alpha) (C	ITAV_HUMAN	116023	100.00%	MFLLVGAPK	1.85	0.246	1.89
ITAX_HUMAN							
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p15	ITAX_HUMAN	127812.3	100.00%	GGQVSVCPLPR	2.03	0.196	1.46
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p15	ITAX_HUMAN	127812.3	100.00%	GVQSLVLGAPR	3.21	0.259	1.64
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p15	ITAX_HUMAN	127812.3	100.00%	YQVNNLGQR	1.67	0.189	0.482
ITB1_HUMAN							
Integrin beta-1 precursor (Fibronectin receptor subunit beta) (Int	ITB1_HUMAN	88447.1	99.80%	IGFGSFVEK	2.06	0.375	3.16
Integrin beta-1 precursor (Fibronectin receptor subunit beta) (Int	ITB1_HUMAN	88447.1	99.80%	SAVTTVVNPK	2.05	0.394	1.6
ITB2_HUMAN							
Integrin beta-2 precursor (Cell surface adhesion glycoproteins LF	ITB2_HUMAN	84764	100.00%	ALNEITESGR	3.3	0.472	1.19
Integrin beta-2 precursor (Cell surface adhesion glycoproteins LF	ITB2_HUMAN	84764	100.00%	GFLECGICR	1.58	0.189	1.38
Integrin beta-2 precursor (Cell surface adhesion glycoproteins LF	ITB2_HUMAN	84764	100.00%	IGFGSFVDK	1.9	0.295	1.66
Integrin beta-2 precursor (Cell surface adhesion glycoproteins LF	ITB2_HUMAN	84764	100.00%	LAENNIQPIFAVTSR	4.89	0.601	5.41
Integrin beta-2 precursor (Cell surface adhesion glycoproteins LF	ITB2_HUMAN	84764	100.00%	VFLDHNALPDTLK	2.39	0.206	1.46
Integrin beta-2 precursor (Cell surface adhesion glycoproteins LF	ITB2_HUMAN	84764	100.00%	YLIYVDESR	1.45	0.321	1.24
ITIH4_HUMAN							
Inter-alpha-trypsin inhibitor heavy chain H4 precursor (ITI heavy	ITIH4_HUMAN	103308.4	100.00%	ILDDLSPR	1.62	0.168	-0.505
Inter-alpha-trypsin inhibitor heavy chain H4 precursor (ITI heavy	ITIH4_HUMAN	103308.4	100.00%	LGVYELLLK	1.42	0.35	0.796
Inter-alpha-trypsin inhibitor heavy chain H4 precursor (ITI heavy	ITIH4_HUMAN	103308.4	100.00%	NVVFVIDK	2.12	0.166	-0.415
KAC_HUMAN							
Ig kappa chain C region - Homo sapiens (Human)	KAC_HUMAN	11590.5	100.00%	DSTYSLSSTLTLSK	3.54	0.382	3.59
Ig kappa chain C region - Homo sapiens (Human)	KAC_HUMAN	11590.5	100.00%	SGTASVVCLLNNFYPR	3.21	0.555	1.11
Ig kappa chain C region - Homo sapiens (Human)	KAC_HUMAN	11590.5	100.00%	TVAAPSVFIFPPSDEQLK	2.61	0.603	1.77
Ig kappa chain C region - Homo sapiens (Human)	KAC_HUMAN	11590.5	100.00%	VDNALQSGNSQESVTEQDSK	3.3	0.625	3.48
Ig kappa chain C region - Homo sapiens (Human)	KAC_HUMAN	11590.5	100.00%	VQWKVDNALQSGNSQESVTEQDSK	3.47	0.41	1.82
KPYM_HUMAN							
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	AGKPVICATQMLESMIK	3.61	0.425	0
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	APIIAVTR	2.63	0.236	1.75
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	CCSGAIIVLTK	2.54	0.437	1.48
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	FGVEQDVDMVFASFIR	3.72	0.638	6.33
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	GADFLVTEVENGGSLGSK	5.29	0.548	3.35
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	GDLGIEIPAEK	2.79	0.328	1.36
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	GDYPLEAVR	2.09	0.384	0.745
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	GSGTAEVELK	2.3	0.276	0.319
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	GSGTAEVELKK	2.66	0.344	-0.301
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	GVNLPGAAVDLPAVSEKDIQDLK	2.81	0.458	2.41
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	ITLDNAYMEK	3	0.378	2.32
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	IYVDDGLISLQVK	4.31	0.577	2.55
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	KGVNLPGAAVDLPAVSEK	3.83	0.4	1.32
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	KGVNLPGAAVDLPAVSEKDIQDLK	0	0	3.6
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	LAPITSDPTEATAVGAVEASFK	4.73	0.461	6.48
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	LDIDSPPITAR	1.34	0.261	0.208
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	NTGIICTIGPASR	4.01	0.552	1.28
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	QKGADFLVTEVENGGSLGSK	3.01	0.288	-0.23
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	RFDEILEASDGIMVAR	3.75	0.47	1.75
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	SVETLKEMIK	1.78	0.0976	0.201
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	TATESFASDPILYRPVAVALDTK	2.2	0.409	2.54
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase	KPYM_HUMAN	57919.5	100.00%	VNFAMNVGK	2.21	0.387	1.05
KV101_HUMAN							
Ig kappa chain V-I region AG - Homo sapiens (Human)	KV101_HUMAN	11974.8	99.80%	DIQMTQSPSSLSASVGDR	0	0	3.43
Ig kappa chain V-I region AG - Homo sapiens (Human)	KV101_HUMAN	11974.8	99.80%	ILIYDASNLETGVPSR	1.78	0.109	3.25
KV201_HUMAN, KV204_HUMAN, KV205_HUMAN							
Ig kappa chain V-II region Cum - Homo sapiens (Human)	MAN,KV204_HUMAN,KV2	12658.6	99.80%	ASGVPDRFSGSGSGTDFTLK	1.9	0.389	0
Ig kappa chain V-II region Cum - Homo sapiens (Human)	MAN,KV204_HUMAN,KV2	12658.6	99.80%	FSGSGSGTDFTLK	2.61	0.118	1.68

KV305_HUMAN							
Ig kappa chain V-III region WOL - Homo sapiens (Human)	KV305_HUMAN	11728.5	100.00%	EIVLTQSPGTLSLSPGER	4.09	0.0585	3.92
Ig kappa chain V-III region WOL - Homo sapiens (Human)	KV305_HUMAN	11728.5	100.00%	FSGSGSGTDFTLTISR	2.32	0.467	1.39
Ig kappa chain V-III region WOL - Homo sapiens (Human)	KV305_HUMAN	11728.5	100.00%	LLIYGASSR	2.39	0.39	1.31
KV402_HUMAN							
Ig kappa chain V-IV region Len - Homo sapiens (Human)	KV402_HUMAN	12622.4	99.80%	DIVMTQSPDSLAVSLGER	3.33	0.509	4.8
Ig kappa chain V-IV region Len - Homo sapiens (Human)	KV402_HUMAN	12622.4	99.80%	LLIYWASTR	3.12	0.249	1.64
LAC_HUMAN							
Ig lambda chain C regions - Homo sapiens (Human)	LAC_HUMAN	11218.1	100.00%	AAPSVTLFPPSSEELQANK	3.05	0.498	3.04
Ig lambda chain C regions - Homo sapiens (Human)	LAC_HUMAN	11218.1	100.00%	AGVETTTPSK	3.1	0.455	1.38
Ig lambda chain C regions - Homo sapiens (Human)	LAC_HUMAN	11218.1	100.00%	QSNNKYAASSYLSLTPEQWK	2.43	0.369	0
Ig lambda chain C regions - Homo sapiens (Human)	LAC_HUMAN	11218.1	100.00%	SYSCQVTHEGSTVEK	1.74	0.26	0.824
Ig lambda chain C regions - Homo sapiens (Human)	LAC_HUMAN	11218.1	100.00%	YAASSYLSLTPEQWK	2.93	0.531	2.72
LAMP1_HUMAN							
Lysosome-associated membrane glycoprotein 1 precursor (LAMP-	LAMP1_HUMAN	44755.5	100.00%	AFSVNIFK	1.85	0.182	1.25
Lysosome-associated membrane glycoprotein 1 precursor (LAMP-	LAMP1_HUMAN	44755.5	100.00%	ALQATVGNSYK	2.69	0.465	1.05
Lysosome-associated membrane glycoprotein 1 precursor (LAMP-	LAMP1_HUMAN	44755.5	100.00%	FFLQGIQLNTILPDARDPAFK	2.76	0.366	2.35
Lysosome-associated membrane glycoprotein 1 precursor (LAMP-	LAMP1_HUMAN	44755.5	100.00%	TVESITDIR	2.91	0.275	0.444
LDHA_HUMAN							
L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A) (LDH mu	LDHA_HUMAN	36671.2	100.00%	LNLVQR	2.41	0.0933	0
L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A) (LDH mu	LDHA_HUMAN	36671.2	100.00%	LVIITAGAR	2.61	0.399	1.48
L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A) (LDH mu	LDHA_HUMAN	36671.2	100.00%	NVNIFK	1.61	0.192	-0.532
L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A) (LDH mu	LDHA_HUMAN	36671.2	100.00%	QVVESAYEVIK	2.88	0.528	1.85
L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A) (LDH mu	LDHA_HUMAN	36671.2	100.00%	VIGSGCNLDSAR	2.8	0.512	2.92
L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A) (LDH mu	LDHA_HUMAN	36671.2	100.00%	VTLTSEEEAR	2.75	0.453	1.68
LDHB_HUMAN							
L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B) (LDH hea	LDHB_HUMAN	36620.6	99.80%	IVADKDYSVTANSK	1.41	0.207	-0.0414
L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B) (LDH hea	LDHB_HUMAN	36620.6	99.80%	IVVVTAGVR	3.04	0.401	2.33
L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B) (LDH hea	LDHB_HUMAN	36620.6	99.80%	LNLVQR	2.41	0.0933	0
L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B) (LDH hea	LDHB_HUMAN	36620.6	99.80%	VIGSGCNLDSAR	2.8	0.512	2.92
LG3BP_HUMAN							
Galectin-3-binding protein precursor (Lectin galactoside-binding s	LG3BP_HUMAN	65314.1	99.80%	SDLAVPSELALLK	2.16	0.344	0.585
Galectin-3-binding protein precursor (Lectin galactoside-binding s	LG3BP_HUMAN	65314.1	99.80%	TLQALEFHTVPFQLLAR	2.93	0.441	0.42
LUM_HUMAN							
Lumican precursor (Keratan sulfate proteoglycan lumican) (KSPG	LUM_HUMAN	38413.5	100.00%	LKEDAVSAAFK	1.77	0.254	0.678
Lumican precursor (Keratan sulfate proteoglycan lumican) (KSPG	LUM_HUMAN	38413.5	100.00%	NIPTVNENLENYYLEVNQLEK	2.68	0.274	1.57
LYSC_HUMAN							
Lysozyme C precursor (EC 3.2.1.17) (1,4-beta-N-acetylmuramida	LYSC_HUMAN	16518.9	99.80%	LGMDGYR	1.69	0.222	0
Lysozyme C precursor (EC 3.2.1.17) (1,4-beta-N-acetylmuramida	LYSC_HUMAN	16518.9	99.80%	STDYGIFQINSR	2.8	0.377	2.22
MDHM_HUMAN							
Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37) - H	MDHM_HUMAN	35513.7	99.80%	MISDAIPELK	1.67	0.192	0.367
Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37) - H	MDHM_HUMAN	35513.7	99.80%	VDFPQDQLTALTGR	2.52	0.309	1.85
MFGM_HUMAN							
Lactadherin precursor (Milk fat globule-EGF factor 8) (MFG-E8) (	MFGM_HUMAN	43104.9	99.80%	EVTGIITQGAR	2.97	0.34	3.41
Lactadherin precursor (Milk fat globule-EGF factor 8) (MFG-E8) (	MFGM_HUMAN	43104.9	99.80%	NLFETPILAR	2.76	0.325	1.17
MUC_HUMAN							
Ig mu chain C region - Homo sapiens (Human)	MUC_HUMAN	49537.9	100.00%	EGKQVGSGVTTDQVQAEAK	3.75	0.343	0.854
Ig mu chain C region - Homo sapiens (Human)	MUC_HUMAN	49537.9	100.00%	FTCTVTHTDLPSPLK	2.78	0.435	0
Ig mu chain C region - Homo sapiens (Human)	MUC_HUMAN	49537.9	100.00%	GFPSVLR	1.56	0.184	-0.322
Ig mu chain C region - Homo sapiens (Human)	MUC_HUMAN	49537.9	100.00%	LICQATGFSPR	3.27	0.272	2.8
Ig mu chain C region - Homo sapiens (Human)	MUC_HUMAN	49537.9	100.00%	NVPLPVIAELPPK	1.47	0.422	1.11
Ig mu chain C region - Homo sapiens (Human)	MUC_HUMAN	49537.9	100.00%	QVGSGVTTDQVQAEAK	2.87	0.545	1.85
Ig mu chain C region - Homo sapiens (Human)	MUC_HUMAN	49537.9	100.00%	VFAIPPSFASIFLTK	1.87	0.424	2.57
Ig mu chain C region - Homo sapiens (Human)	MUC_HUMAN	49537.9	100.00%	VSVFVPPR	2.39	0.37	-0.146
Ig mu chain C region - Homo sapiens (Human)	MUC_HUMAN	49537.9	100.00%	YVTSAPMPEPQAPGR	2.87	0.459	1.89
MVP_HUMAN							
Major vault protein (MVP) (Lung resistance-related protein) - Hor	MVP_HUMAN	99308	100.00%	GPLEYVPSAK	2.46	0.524	1.25

Major vault protein (MVP) (Lung resistance-related protein) - Hom	MVP_HUMAN	99308	100.00%	IEGEGSVLQAK	2.36	0.209	0.0605
Major vault protein (MVP) (Lung resistance-related protein) - Hom	MVP_HUMAN	99308	100.00%	LLQSLGLK	1.96	0.188	-0.431
Major vault protein (MVP) (Lung resistance-related protein) - Hom	MVP_HUMAN	99308	100.00%	SLQPLAPR	1.16	0.141	0.886
MYH10_HUMAN							
Myosin-10 (Myosin heavy chain 10) (Myosin heavy chain, nonmus	MYH10_HUMAN	228927.2	100.00%	ALELDPNLYR	3.04	0.428	2.77
Myosin-10 (Myosin heavy chain 10) (Myosin heavy chain, nonmus	MYH10_HUMAN	228927.2	100.00%	AVIYNPATQADWTAK	3.04	0.528	2.8
Myosin-10 (Myosin heavy chain 10) (Myosin heavy chain, nonmus	MYH10_HUMAN	228927.2	100.00%	CNGVLEGIR	2.38	0.359	0.602
Myosin-10 (Myosin heavy chain 10) (Myosin heavy chain, nonmus	MYH10_HUMAN	228927.2	100.00%	ELDDATEANEGLSR	2.82	0.515	1.64
Myosin-10 (Myosin heavy chain 10) (Myosin heavy chain, nonmus	MYH10_HUMAN	228927.2	100.00%	EQADFAVEALAK	2.13	0.488	0.553
Myosin-10 (Myosin heavy chain 10) (Myosin heavy chain, nonmus	MYH10_HUMAN	228927.2	100.00%	FDQLLAEEK	1.36	0.339	1.19
Myosin-10 (Myosin heavy chain 10) (Myosin heavy chain, nonmus	MYH10_HUMAN	228927.2	100.00%	IVFQEFR	2.09	0.306	0.42
Myosin-10 (Myosin heavy chain 10) (Myosin heavy chain, nonmus	MYH10_HUMAN	228927.2	100.00%	KFDQLLAEEK	2.32	0.228	0.796
Myosin-10 (Myosin heavy chain 10) (Myosin heavy chain, nonmus	MYH10_HUMAN	228927.2	100.00%	QVLALQSQLADTK	1.62	0.363	0.77
Myosin-10 (Myosin heavy chain 10) (Myosin heavy chain, nonmus	MYH10_HUMAN	228927.2	100.00%	YEILTPNAIPK	1.74	0.402	1.15
MYH11_HUMAN							
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	AENELKELEQK	1.88	0.238	0
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	ALEEALEAKEELER	2	0.309	-0.38
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	ALELDPNLYR	3.04	0.428	2.77
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	ASRDEIFATAK	2.53	0.286	0
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	CNGVLEGIR	2.38	0.359	0.602
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	EQADFAVEALAK	2.13	0.488	0.553
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	FDQLLAEEK	1.36	0.339	1.19
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	FKSTIAALEAK	2.22	0.169	0
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	IAQLEEQVEQEAR	3.18	0.403	4.04
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	ISDLTTNLAEEEEKAK	2.51	0.383	0.538
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	IVFQEFR	2.09	0.306	0.42
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	KFDQLLAEEK	2.32	0.228	0.796
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	KLEAQVQELQSK	3.7	0.34	1.07
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	LEAQVQELQSK	3.57	0.477	2.29
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	LEEEEDRGQQLQAER	2.28	0.0932	-0.322
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	LEVNMQALK	2.51	0.267	0.00437
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	LVWVPSEK	1.76	0.278	0
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	MTESSLPSASK	2.66	0.445	3.59
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	NTTPNFVR	1.57	0.331	0.854
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	QACILMIK	1.59	0.261	-0.0414
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	QLVSNLEK	1.85	0.122	-0.146
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	TVGQLYKEQLGK	1.7	0.255	0.469
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	VIQYLAVVASSHK	2.46	0.368	-0.0792
Myosin-11 (Myosin heavy chain 11) (Myosin heavy chain, smooth	MYH11_HUMAN	227326.6	100.00%	YEILAANAIPK	3.27	0.476	0.921
MYH9_HUMAN							
Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle	MYH9_HUMAN	226519.5	100.00%	ALELDSNLYR	3.79	0.345	2.16
Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle	MYH9_HUMAN	226519.5	100.00%	ASITALEAK	3.37	0.267	0.854
Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle	MYH9_HUMAN	226519.5	100.00%	CNGVLEGIR	2.38	0.359	0.602
Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle	MYH9_HUMAN	226519.5	100.00%	FDQLLAEEK	1.36	0.339	1.19
Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle	MYH9_HUMAN	226519.5	100.00%	IAQLEEQLDNETKER	2.1	0.221	-0.204
Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle	MYH9_HUMAN	226519.5	100.00%	KFDQLLAEEK	2.32	0.228	0.796
Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle	MYH9_HUMAN	226519.5	100.00%	KVEAQLQELQVK	1.65	0.17	0.276
Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle	MYH9_HUMAN	226519.5	100.00%	QAQQERDELADEIANSSGK	3.39	0.462	1.25
Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle	MYH9_HUMAN	226519.5	100.00%	QRYEILTPNSIPK	2.46	0.202	-0.623
Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle	MYH9_HUMAN	226519.5	100.00%	RGDLPFVVPR	1.7	0.277	0.301
Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle	MYH9_HUMAN	226519.5	100.00%	SVHELEK	1.48	0.212	0
Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle	MYH9_HUMAN	226519.5	100.00%	TDLLLEPYNK	1.95	0.0024	0.602
Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle	MYH9_HUMAN	226519.5	100.00%	TVGQLYKEQLAK	1.68	0.376	0.824
Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle	MYH9_HUMAN	226519.5	100.00%	VIQYLAYVASSHK	2.26	0.255	-0.431
Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle	MYH9_HUMAN	226519.5	100.00%	VVFQEFR	2.05	0.345	0.509
Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle	MYH9_HUMAN	226519.5	100.00%	YEILTPNSIPK	2.7	0.253	-0.342
MYL6_HUMAN							

Myosin light polypeptide 6 (Smooth muscle and nonmuscle myosi	MYL6_HUMAN	16911.8	100.00%	ALGQNPTNAEVLK	2.29	0.401	1
Myosin light polypeptide 6 (Smooth muscle and nonmuscle myosi	MYL6_HUMAN	16911.8	100.00%	EAFQLFDR	2.3	0.079	0.921
Myosin light polypeptide 6 (Smooth muscle and nonmuscle myosi	MYL6_HUMAN	16911.8	100.00%	ILYSQCGDVMR	3.37	0.515	3.1
Myosin light polypeptide 6 (Smooth muscle and nonmuscle myosi	MYL6_HUMAN	16911.8	100.00%	NKDQGTYEDYVEGLR	4.21	0.41	2.16
Myosin light polypeptide 6 (Smooth muscle and nonmuscle myosi	MYL6_HUMAN	16911.8	100.00%	VFDKEGNGTVMGAEIR	2.93	0.252	3.26
OST48_HUMAN							
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48	OST48_HUMAN	48793	100.00%	IDPFVR	1.71	0.152	0.347
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48	OST48_HUMAN	48793	100.00%	NTLLIAGLQAR	3.87	0.432	2.6
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48	OST48_HUMAN	48793	100.00%	SSLNPILFR	2.89	0.0847	1.96
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48	OST48_HUMAN	48793	100.00%	YSVQFK	1.64	0.287	0
PDIA1_HUMAN							
Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-	PDIA1_HUMAN	57100.1	100.00%	EADDIVNWLK	2.23	0.311	0.921
Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-	PDIA1_HUMAN	57100.1	100.00%	ENLLDFIK	2.09	0.121	-0.255
Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-	PDIA1_HUMAN	57100.1	100.00%	HNQLPLVIEFTEQTAPK	2.05	0.334	-0.146
Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-	PDIA1_HUMAN	57100.1	100.00%	ILEFFGLK	2.17	0.104	0.337
Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-	PDIA1_HUMAN	57100.1	100.00%	LGETYKDHENIVIAK	3.09	0.464	1.3
Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-	PDIA1_HUMAN	57100.1	100.00%	LITLEEEMTK	2.5	0.43	1.72
Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-	PDIA1_HUMAN	57100.1	100.00%	MDSTANEVEAVK	2.95	0.463	3.43
Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-	PDIA1_HUMAN	57100.1	100.00%	NFEDVAFDEK	2.05	0.27	0.495
Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-	PDIA1_HUMAN	57100.1	100.00%	NFEDVAFDEKK	3.25	0.373	1.42
Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-	PDIA1_HUMAN	57100.1	100.00%	QLAPIWDK	1.6	0.188	0.137
Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-	PDIA1_HUMAN	57100.1	100.00%	TVIDYNGER	1.7	0.42	0.495
Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-	PDIA1_HUMAN	57100.1	100.00%	VDATEESDLAQQYGVR	0	0	3.05
Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-	PDIA1_HUMAN	57100.1	100.00%	YKPESEELTAER	1.6	0.51	0.886
Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-	PDIA1_HUMAN	57100.1	100.00%	YQLDKDGVVLFK	1.78	0.161	0.77
PDIA3_HUMAN							
Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide is	PDIA3_HUMAN	56766.6	100.00%	ELSDFISYLQR	2.85	0.491	1.08
Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide is	PDIA3_HUMAN	56766.6	100.00%	FVMQEEFSR	2.4	0.508	0.921
Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide is	PDIA3_HUMAN	56766.6	100.00%	GFPTIYFSPANK	2.86	0.417	1.41
Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide is	PDIA3_HUMAN	56766.6	100.00%	IFRDGEEAGAYDGPR	4.37	0.328	1.07
Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide is	PDIA3_HUMAN	56766.6	100.00%	LAPEYEAAATR	1.38	0.184	-0.176
Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide is	PDIA3_HUMAN	56766.6	100.00%	LNFAVASR	2.81	0.403	-0.114
Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide is	PDIA3_HUMAN	56766.6	100.00%	LSKDPNIVIAK	3.09	0.463	1.4
Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide is	PDIA3_HUMAN	56766.6	100.00%	MDATANDVPSPYEVR	2.96	0.416	2.32
Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide is	PDIA3_HUMAN	56766.6	100.00%	SEPIPESNDGPVK	2.06	0.413	2.15
Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide is	PDIA3_HUMAN	56766.6	100.00%	TFSHELSDFGLESTAGEIPVVAIR	2.29	0.234	0.959
Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide is	PDIA3_HUMAN	56766.6	100.00%	YGVSGYPTLK	2.76	0.459	2.59
PDIA6_HUMAN							
Protein disulfide-isomerase A6 precursor (EC 5.3.4.1) (Protein dis	PDIA6_HUMAN	48104.3	100.00%	AATALKDVVK	2.48	0.396	0.959
Protein disulfide-isomerase A6 precursor (EC 5.3.4.1) (Protein dis	PDIA6_HUMAN	48104.3	100.00%	GSFSEQGINEFLR	3.61	0.456	2.72
Protein disulfide-isomerase A6 precursor (EC 5.3.4.1) (Protein dis	PDIA6_HUMAN	48104.3	100.00%	LAAVDATVNQVLASR	4.97	0.569	4.19
Protein disulfide-isomerase A6 precursor (EC 5.3.4.1) (Protein dis	PDIA6_HUMAN	48104.3	100.00%	NLEPEWAAAASEVK	2.85	0.496	2
Protein disulfide-isomerase A6 precursor (EC 5.3.4.1) (Protein dis	PDIA6_HUMAN	48104.3	100.00%	TGEAIVDAALSALR	4.49	0.469	3.82
Protein disulfide-isomerase A6 precursor (EC 5.3.4.1) (Protein dis	PDIA6_HUMAN	48104.3	100.00%	VKLAAVDATVNQVLASR	2.93	0.469	0.602
PGK1_HUMAN							
Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protei	PGK1_HUMAN	44597.3	100.00%	ACANPAAGSVILLENLR	3.84	0.559	3.75
Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protei	PGK1_HUMAN	44597.3	100.00%	ALESPERPFLAILGGAK	2.64	0.425	3.14
Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protei	PGK1_HUMAN	44597.3	100.00%	ALMDEVVK	2.09	0.19	0.658
Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protei	PGK1_HUMAN	44597.3	100.00%	ITLPVDFVTADKFDENAK	1.83	0.085	2.39
Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protei	PGK1_HUMAN	44597.3	100.00%	LGDVYVNDAFGTAHR	2.57	0.349	1.75
Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protei	PGK1_HUMAN	44597.3	100.00%	VDFNVPMK	2.18	0.263	-0.342
Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protei	PGK1_HUMAN	44597.3	100.00%	VLNNMEIGTSLFDEEGAK	3.49	0.57	2.72
Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protei	PGK1_HUMAN	44597.3	100.00%	VLPGVDALSNI	1.47	0.327	0.658
PLMN_HUMAN							
Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy ch	PLMN_HUMAN	90549.4	99.80%	EAQLPVIENK	1.7	0.276	1.22
Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy ch	PLMN_HUMAN	90549.4	99.80%	LSSPAVITDK	1.69	0.26	-0.204
PPIA_HUMAN							

Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase A) (Rot	PPIA_HUMAN	17994.9	100.00%	IIPGFMCQGGDFTR	2.48	0.528	2.19
Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase A) (Rot	PPIA_HUMAN	17994.9	100.00%	SIYGEKFEDENFILK	1.66	0.154	0.469
Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase A) (Rot	PPIA_HUMAN	17994.9	100.00%	VSFELFADKVPK	3.07	0.391	0.523
PPIB_HUMAN							
Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIa	PPIB_HUMAN	22724.9	100.00%	DTNGSQFFITTVK	3.91	0.512	1.85
Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIa	PPIB_HUMAN	22724.9	100.00%	TVDNFVALATGEK	1.49	0.26	0.0362
Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIa	PPIB_HUMAN	22724.9	100.00%	VLEGMEVVR	3.2	0.441	0.921
PRDX1_HUMAN							
Peroxiredoxin-1 (EC 1.11.1.15) (Thioredoxin peroxidase 2) (Thior	PRDX1_HUMAN	22092.9	100.00%	ADEGISFR	2.12	0.156	-0.813
Peroxiredoxin-1 (EC 1.11.1.15) (Thioredoxin peroxidase 2) (Thior	PRDX1_HUMAN	22092.9	100.00%	LVQAFQFTDK	1.51	0.382	2.06
Peroxiredoxin-1 (EC 1.11.1.15) (Thioredoxin peroxidase 2) (Thior	PRDX1_HUMAN	22092.9	100.00%	QITVNDLPVGR	2.25	0.268	0.569
Peroxiredoxin-1 (EC 1.11.1.15) (Thioredoxin peroxidase 2) (Thior	PRDX1_HUMAN	22092.9	100.00%	TIAQDYGVLK	1.93	0.197	1.05
PRDX2_HUMAN							
Peroxiredoxin-2 (EC 1.11.1.15) (Thioredoxin peroxidase 1) (Thior	PRDX2_HUMAN	21874.4	100.00%	ATAVVDGAFK	2.29	0.309	1.24
Peroxiredoxin-2 (EC 1.11.1.15) (Thioredoxin peroxidase 1) (Thior	PRDX2_HUMAN	21874.4	100.00%	ATAVVDGAFKEVK	1.84	0.214	0.409
Peroxiredoxin-2 (EC 1.11.1.15) (Thioredoxin peroxidase 1) (Thior	PRDX2_HUMAN	21874.4	100.00%	GLFIIDGK	1.84	0.189	-0.58
Peroxiredoxin-2 (EC 1.11.1.15) (Thioredoxin peroxidase 1) (Thior	PRDX2_HUMAN	21874.4	100.00%	LSEDYGVLKTDEGIAYR	3.44	0.464	1.33
Peroxiredoxin-2 (EC 1.11.1.15) (Thioredoxin peroxidase 1) (Thior	PRDX2_HUMAN	21874.4	100.00%	QITVNDLPVGR	2.25	0.268	0.569
Peroxiredoxin-2 (EC 1.11.1.15) (Thioredoxin peroxidase 1) (Thior	PRDX2_HUMAN	21874.4	100.00%	SVDEALR	1.91	0.0567	0.387
PROF1_HUMAN							
Profilin-1 (Profilin I) - Homo sapiens (Human)	PROF1_HUMAN	15036.3	100.00%	DSLLQDGEFSMDLR	2.88	0.427	2.05
Profilin-1 (Profilin I) - Homo sapiens (Human)	PROF1_HUMAN	15036.3	100.00%	DSPSVWAAVPGK	2.52	0.46	3.14
Profilin-1 (Profilin I) - Homo sapiens (Human)	PROF1_HUMAN	15036.3	100.00%	SSFYVNGLTLGGQK	3.86	0.565	2.72
Profilin-1 (Profilin I) - Homo sapiens (Human)	PROF1_HUMAN	15036.3	100.00%	TFVNITPAEVGVLVGK	2.67	0.447	3.26
Profilin-1 (Profilin I) - Homo sapiens (Human)	PROF1_HUMAN	15036.3	100.00%	TLVLLMGK	1.95	0.126	0.0969
RAB1A_HUMAN							
Ras-related protein Rab-1A (YPT1-related protein) - Homo sapien	RAB1A_HUMAN	22660.5	100.00%	EFADSLGIPFLETSAK	2.18	0.288	1.7
Ras-related protein Rab-1A (YPT1-related protein) - Homo sapien	RAB1A_HUMAN	22660.5	100.00%	LLLIGDSGVGK	2.25	0.198	0.854
Ras-related protein Rab-1A (YPT1-related protein) - Homo sapien	RAB1A_HUMAN	22660.5	100.00%	LQIWDTAGQER	2.89	0.272	1.27
RIB1_HUMAN							
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67	RIB1_HUMAN	68553	100.00%	LPVALDPGAK	2.03	0.131	0.301
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67	RIB1_HUMAN	68553	100.00%	VTAEVVLAHLGGGSTSR	1.95	0.259	-0.38
SAMP_HUMAN							
Serum amyloid P-component precursor (SAP) (9.5S alpha-1-glyc	SAMP_HUMAN	25369.7	100.00%	AYSDLSR	1.37	0.22	0.181
Serum amyloid P-component precursor (SAP) (9.5S alpha-1-glyc	SAMP_HUMAN	25369.7	100.00%	AYSLFSYNTQGR	3.55	0.544	2.48
Serum amyloid P-component precursor (SAP) (9.5S alpha-1-glyc	SAMP_HUMAN	25369.7	100.00%	AYSLFSYNTQGRDNELLVYK	2.35	0.066	0.569
Serum amyloid P-component precursor (SAP) (9.5S alpha-1-glyc	SAMP_HUMAN	25369.7	100.00%	DNELLVYK	2.19	0.199	0
Serum amyloid P-component precursor (SAP) (9.5S alpha-1-glyc	SAMP_HUMAN	25369.7	100.00%	DNELLVYKER	3.18	0.328	0.194
Serum amyloid P-component precursor (SAP) (9.5S alpha-1-glyc	SAMP_HUMAN	25369.7	100.00%	GYVIIKPLVWV	3.35	0.465	1.64
Serum amyloid P-component precursor (SAP) (9.5S alpha-1-glyc	SAMP_HUMAN	25369.7	100.00%	IVLGQEQDSYGGK	3.02	0.442	3.1
Serum amyloid P-component precursor (SAP) (9.5S alpha-1-glyc	SAMP_HUMAN	25369.7	100.00%	IVLGQEQDSYGGKFDR	3.03	0.49	0.721
Serum amyloid P-component precursor (SAP) (9.5S alpha-1-glyc	SAMP_HUMAN	25369.7	100.00%	QGYFVEAQPK	1.67	0.31	-0.301
Serum amyloid P-component precursor (SAP) (9.5S alpha-1-glyc	SAMP_HUMAN	25369.7	100.00%	VFVFPR	1.45	0.228	0.328
Serum amyloid P-component precursor (SAP) (9.5S alpha-1-glyc	SAMP_HUMAN	25369.7	100.00%	VGEYSLYIGR	3.68	0.4	1.75
SODM_HUMAN							
Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1	SODM_HUMAN	24704.6	99.80%	GDVTAQIALQPALK	2.66	0.281	0.921
Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1	SODM_HUMAN	24704.6	99.80%	GELLEAIKR	1.73	0.066	0.208
TAGL_HUMAN							
Transgelin (Smooth muscle protein 22-alpha) (SM22-alpha) (WS3	TAGL_HUMAN	22592.9	99.80%	QMEQVAQFLK	1.89	0.0699	0.658
Transgelin (Smooth muscle protein 22-alpha) (SM22-alpha) (WS3	TAGL_HUMAN	22592.9	99.80%	TLMALGSLAVTK	3.51	0.481	3.27
TAGL2_HUMAN							
Transgelin-2 (SM22-alpha homolog) - Homo sapiens (Human)	TAGL2_HUMAN	22373.9	100.00%	NFSDNQLQEGK	2.32	0.286	0.161
Transgelin-2 (SM22-alpha homolog) - Homo sapiens (Human)	TAGL2_HUMAN	22373.9	100.00%	NVIGLQMGTNR	2.39	0.508	1.72
Transgelin-2 (SM22-alpha homolog) - Homo sapiens (Human)	TAGL2_HUMAN	22373.9	100.00%	QMEQISQFLQAAER	2.17	0.412	0.658
Transgelin-2 (SM22-alpha homolog) - Homo sapiens (Human)	TAGL2_HUMAN	22373.9	100.00%	TLMNLGGLAVAR	3.47	0.386	0.886
TBA3_HUMAN, TBA6_HUMAN, TBAK_HUMAN							
Tubulin alpha-3 chain (Alpha-tubulin 3) (Tubulin B-alpha-1) - Hom	JMAN,TBA6_HUMAN,TBAK	49877.4	99.80%	AVFVDLEPTVIDEVR	2.43	0.174	1.1

Tubulin alpha-3 chain (Alpha-tubulin 3) (Tubulin B-alpha-1) - Hom	JMAN,TBA6_HUMAN,TBAK	49877.4	99.80%	DVNAAIATIK	2.33	0.37	0.398
TERA_HUMAN							
Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg	TERA_HUMAN	89306.8	100.00%	LDQLIYIPLPDEK	3.5	0.37	0.959
Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg	TERA_HUMAN	89306.8	100.00%	LGDVISIQPCPDVK	2.6	0.376	1
Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg	TERA_HUMAN	89306.8	100.00%	MDELQLFR	2.49	0.327	0.569
THRB_HUMAN							
Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II) [Cont	THRB_HUMAN	70018.8	99.80%	ETAASLLQAGYK	2.31	0.543	2.37
Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II) [Cont	THRB_HUMAN	70018.8	99.80%	LAVTTHGLPCLAWASAQAK	3.31	0.307	-0.0792
TPIS_HUMAN							
Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate	TPIS_HUMAN	26651.1	100.00%	HVFGESDELIGQK	1.89	0.405	1.85
Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate	TPIS_HUMAN	26651.1	100.00%	IAVAAQNCYK	3.51	0.484	2.25
Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate	TPIS_HUMAN	26651.1	100.00%	IIYGGSVTGATCK	3.33	0.514	3.77
Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate	TPIS_HUMAN	26651.1	100.00%	QSLGELIGTLNAAK	3.15	0.545	4.7
Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate	TPIS_HUMAN	26651.1	100.00%	SNVSDAVAQSTR	2.92	0.575	4.02
Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate	TPIS_HUMAN	26651.1	100.00%	VPADTEVVCAPPTAYIDFAR	2.4	0.518	4.17
Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate	TPIS_HUMAN	26651.1	100.00%	VTNGAFTGEISPGMIK	2.78	0.38	1.8
Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate	TPIS_HUMAN	26651.1	100.00%	VVLAYEPVWAIGTGK	2.81	0.506	4.85
TRFE_HUMAN							
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	CLKDGAGDVAFVK	2.96	0.36	0.77
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	CSTSSLLEACTFR	4	0.609	1.7
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	DGAGDVAFVK	3.49	0.52	2.7
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	DSGFQMNQLR	3.35	0.394	1.21
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	EDPQTFYYAVAVVK	2.48	0.502	4.44
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	EFQLFSSPHGK	2.38	0.386	1.08
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	EGYYGYTGAFR	2.43	0.45	1.85
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	FDEFFSEGCAPGSK	0	0	3.04
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	FDEFFSEGCAPGSKK	2.21	0.287	-0.279
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	GDVAFVK	1.94	0.118	0.208
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	IMNGEADAMSLDGGFVYIAGK	3.09	0.587	4.17
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	KASYLDCIR	2.17	0.171	0.244
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	MYLGYEYVTAIR	3.02	0.505	2.92
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	NPDPWAK	1.78	0.233	0.0969
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	SAGWNIPIGLLYCDLPEPR	2.94	0.427	4.06
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	SASDLTWDNLK	2.53	0.317	0.585
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	SVIPSDGPSVACVK	2.49	0.509	2.96
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	TAGWNIPMGLLYNK	3.52	0.326	3.22
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	WCAVSEHEATK	2.77	0.283	0.444
Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-met	TRFE_HUMAN	77032.2	100.00%	YLGEEYVK	2.15	0.326	1.06
TTHY_HUMAN							
Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR) - Hom	TTHY_HUMAN	15868.9	99.80%	AADDTWEPFASGK	3.94	0.543	4.08
Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR) - Hom	TTHY_HUMAN	15868.9	99.80%	KAADDTWEPFASGK	3.09	0.23	-0.322
TXND5_HUMAN							
Thioredoxin domain-containing protein 5 precursor (Thioredoxin-li	TXND5_HUMAN	47611.1	99.80%	GYPTLLLFR	2.35	0.273	1.62
Thioredoxin domain-containing protein 5 precursor (Thioredoxin-li	TXND5_HUMAN	47611.1	99.80%	GYPTLLWFR	2.55	0.499	2.62
VA0D1_HUMAN							
Vacuolar ATP synthase subunit d 1 (EC 3.6.3.14) (V-ATPase subur	VA0D1_HUMAN	40312.8	99.80%	LLFEGAGSNPGDK	2.33	0.286	1.16
Vacuolar ATP synthase subunit d 1 (EC 3.6.3.14) (V-ATPase subur	VA0D1_HUMAN	40312.8	99.80%	NVADYYPEYK	1.73	0.391	1.32
VATA_HUMAN							
Vacuolar ATP synthase catalytic subunit A (EC 3.6.3.14) (V-ATPas	VATA_HUMAN	68287.4	100.00%	GVNVSALSR	3.21	0.465	1.4
Vacuolar ATP synthase catalytic subunit A (EC 3.6.3.14) (V-ATPas	VATA_HUMAN	68287.4	100.00%	LAEMPADSGYPAYLGAR	2.35	0.475	2.46
Vacuolar ATP synthase catalytic subunit A (EC 3.6.3.14) (V-ATPas	VATA_HUMAN	68287.4	100.00%	LPANHPLLTGQR	2.53	0.354	-0.255
Vacuolar ATP synthase catalytic subunit A (EC 3.6.3.14) (V-ATPas	VATA_HUMAN	68287.4	100.00%	TVISQSLSK	2.06	0.0839	0.367
Vacuolar ATP synthase catalytic subunit A (EC 3.6.3.14) (V-ATPas	VATA_HUMAN	68287.4	100.00%	VGSHITGGDIYGIVSENSLIK	2.46	0.41	0
VDAC3_HUMAN							
Voltage-dependent anion-selective channel protein 3 (VDAC-3) (h	VDAC3_HUMAN	30641.9	99.80%	FGIAAK	1.99	0.212	-0.176
Voltage-dependent anion-selective channel protein 3 (VDAC-3) (h	VDAC3_HUMAN	30641.9	99.80%	LTLSALIDGK	2.62	0.374	1.24
VIME_HUMAN							

Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	DGQVINETSQHHDDLE	1.84	0.414	2.06
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	EEAENTLQSFR	1.92	0.307	-0.342
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	EEAENTLQSFRQDVDNASLAR	2.91	0.276	0
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	EMEENFAVEAANYQDTIGR	2.91	0.402	2.24
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	ETNLDSLPLVDTHSKR	2.04	0.199	0
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	EYQDLLNVK	2.07	0.166	0.174
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	FADLSEAANR	1.09	0.301	0.0969
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	FADLSEAANRNNDALR	3.24	0.378	1.96
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	FANYIDK	1.94	0.111	-0.255
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	FANYIDKVR	2.17	0.142	0
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	HLREYQDLLNVK	2.49	0.22	0.432
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	ILLAELEQLK	2.48	0.337	1.31
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	ILLAELEQLKGQGK	3.13	0.406	0.886
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	ISLPLPNFSSLNLR	1.49	0.223	1.35
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	KVESLQEEIAFLK	2.87	0.339	0.854
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	KVESLQEEIAFLKK	2.76	0.286	0.959
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	LGDLYEEEMR	1.63	0.391	0.886
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	NLQEAEEWYK	3.88	0.418	1.57
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	QVQSLTCEVDALKGTNESLER	2.4	0.317	0.42
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	SRLGDLYEEEMR	2.37	0.184	-0.431
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	TNEKVELQELNDR	3.44	0.286	-0.255
Vimentin - Homo sapiens (Human)	VIME_HUMAN	53634.7	100.00%	VEVERDNLAEDIMR	1.93	0.313	0
VINC_HUMAN							
Vinculin (Metavinculin) - Homo sapiens (Human)	VINC_HUMAN	123783.3	100.00%	ALASQLQDSLK	2.22	0.502	0.678
Vinculin (Metavinculin) - Homo sapiens (Human)	VINC_HUMAN	123783.3	100.00%	AVAGNISDPGLQK	3.01	0.192	1.42
Vinculin (Metavinculin) - Homo sapiens (Human)	VINC_HUMAN	123783.3	100.00%	DYLIDGSR	1.94	0.296	0.42
Vinculin (Metavinculin) - Homo sapiens (Human)	VINC_HUMAN	123783.3	100.00%	ELTPQVVSAAR	2.73	0.439	2.6
Vinculin (Metavinculin) - Homo sapiens (Human)	VINC_HUMAN	123783.3	100.00%	GNDIIAAAK	1.99	0.191	-0.362
Vinculin (Metavinculin) - Homo sapiens (Human)	VINC_HUMAN	123783.3	100.00%	IPTISTQLK	2.26	0.327	0.276
Vinculin (Metavinculin) - Homo sapiens (Human)	VINC_HUMAN	123783.3	100.00%	QVATALQNLQTK	2.96	0.423	3.02
Vinculin (Metavinculin) - Homo sapiens (Human)	VINC_HUMAN	123783.3	100.00%	SFLDSGYR	2.06	0.35	0.201
Vinculin (Metavinculin) - Homo sapiens (Human)	VINC_HUMAN	123783.3	100.00%	SLGEISALTSK	3.06	0.42	2.82
Vinculin (Metavinculin) - Homo sapiens (Human)	VINC_HUMAN	123783.3	100.00%	SLLDASEEAIKK	2.19	0.302	1.22
Vinculin (Metavinculin) - Homo sapiens (Human)	VINC_HUMAN	123783.3	100.00%	STVEGIQASVK	2.99	0.475	1.92
Vinculin (Metavinculin) - Homo sapiens (Human)	VINC_HUMAN	123783.3	100.00%	TNLLQVCER	2.98	0.189	0.229
Vinculin (Metavinculin) - Homo sapiens (Human)	VINC_HUMAN	123783.3	100.00%	VMLVNSMNTVK	1.72	0.209	0.456
Vinculin (Metavinculin) - Homo sapiens (Human)	VINC_HUMAN	123783.3	100.00%	VMLVNSMNTVKELLPVLISAMK	1.79	0.386	0.284
VTNC_HUMAN							
Vitronectin precursor (Serum-spreading factor) (S-protein) (V75)	VTNC_HUMAN	54288.1	100.00%	DVWGIEGPIDAAFTR	2.23	0.476	3.92
Vitronectin precursor (Serum-spreading factor) (S-protein) (V75)	VTNC_HUMAN	54288.1	100.00%	DWHGVPGQVDAAMAGR	3.29	0.355	3.57
Vitronectin precursor (Serum-spreading factor) (S-protein) (V75)	VTNC_HUMAN	54288.1	100.00%	FEDGVLDPDYPR	1.55	0.306	0.102
Vitronectin precursor (Serum-spreading factor) (S-protein) (V75)	VTNC_HUMAN	54288.1	100.00%	GQYCYELDEK	1.72	0.387	0.638
Vitronectin precursor (Serum-spreading factor) (S-protein) (V75)	VTNC_HUMAN	54288.1	100.00%	IYISGMAPR	2.5	0.251	0
Vitronectin precursor (Serum-spreading factor) (S-protein) (V75)	VTNC_HUMAN	54288.1	100.00%	RVDTVDPPYPR	2.76	0.12	0.215
Vitronectin precursor (Serum-spreading factor) (S-protein) (V75)	VTNC_HUMAN	54288.1	100.00%	TYLFK	1.56	0.302	-0.431

Supplemental Table III. Metabolite concentrations of carotid endarterectomies (CE) and plaque microparticles (MP).

	CE (n=4)	**MP** (n=4)	**P**
Lactate	0.103 (±0.039)	1.398 (±0.409)	0.018
Alanine	0.043 (±0.037)	0.549 (±0.281)	0.124
Acetate	0.087 (±0.072)	0.592 (±0.064)	0.002
Glutamate	0.010 (±0.007)	0.555 (±0.149)	0.011
Succinate	0.009 (±0.006)	0.708 (±0.161)	0.005
Aspartate	0.002 (±0.001)	0.195 (±0.064)	0.024
Choline	0.011 (±0.005)	0.088 (±0.021)	0.011
Glycerophosphocholine	0.074 (±0.031)	0.145 (±0.032)	0.165
Taurine	0.014 (±0.009)	1.907 (±0.569)	0.016
Creatine	0.017 (±0.007)	0.866 (±0.217)	0.008

Data presented are given in μmol/g protein (mean±SE)
P-values for differences between all groups were derived from unpaired Student t-tests
Relative metabolite abundance is displayed in the pie charts of Figure 5

Supplemental Table IV. Summary of microparticle proteins identified by LC-MS/MS from 2D gels.

No.	Protein identification	SWISS_PROT Entry name	SWISS_PROT Accession no.	Theoretical Mr/pI	Observed Mr/pI	Peptides (n)	Sequence Coverage (%)
	Extracellular matrix						
15	Vitronectin (Serum spreading factor)	VTNC_HUMAN	P04004	54.3/5.55	40/4.5	3	6.1
16	Vitronectin (Serum spreading factor)	VTNC_HUMAN	P04004	54.3/5.55	39/4.6	1	2.1
	Myofilaments and associated proteins						
17	Tropomyosin 1 beta chain *	TPM2_HUMAN	P07951	32.8/4.66	36/4.7	1	3.9
18	Actin, cytoplasmic 1 (Beta-actin)	ACTB_HUMAN	P60709	41.7/5.29	42/5.3	10	25.6
	Actin, alpha cardiac (Alpha-cardiac actin)	ACTC_HUMAN	P68032	42.1/5.23	42/5.3	3	10.9
19	Actin, Cytoplasmic 1 (Beta-actin)	ACTB_HUMAN	P60709	41.7/5.29	39/6.2	2	6.9
	Actin (Alpha-cardiac)	ACTC_HUMAN	P68032	42.0/5.23	39/6.2	2	6.1
	Intermediate filaments						
9	Vimentin	VIME_HUMAN	P08670	53.6/5.06	56/5.3	3	9.7
14	Vimentin	VIME_HUMAN	P08670	53.6/5.06	43/4.7	3	6.7
	Plasma proteins						
2	Alpha-1B-glycoprotein	A1BG_HUMAN	P04217	54.2/5.58	82/5.3	6	13.3
3	Serum albumin	ALBU_HUMAN	P02768	69.3/5.92	70/6.0	8	15.1
4	Alpha-2-macroglobulin (fragment)	A2MG_HUMAN	P01023	163.3/6.00	150/6.7	2	2.0
5	Serotransferrin	TRFE_HUMAN	P02787	77.0/6.81	90/6.8	25	36.3
8	Alpha-1-antitrypsin A1	A1AT_HUMAN	P01009	46.7/5.37	56/5.2	6	16.8
12	Fibrinogen gamma chain	FIBG_HUMAN	P02679	51.5/5.37	51/5.7	2	4.9
13	Fibrinogen gamma chain	FIBG_HUMAN	P02679	51.5/5.37	51/5.6	5	17.7

24	Serum albumin	ALBU_HUMAN	P02768	69.3/5.92	44/6.5	1	2.8
25	Fibrinogen beta chain	FIBB_HUMAN	P02675	55.9/8.54	56/7.1	9	22.0
26	Fibrinogen beta chain	FIBB_HUMAN	P02675	55.9/8.54	55/7.5	9	24.6
51	Hemoglobin gamma-2 chain	HBG2_HUMAN	P69892	16.1/6.64	16/7.2	1	6.8
52	Hemoglobin beta chain	HBB_HUMAN	P68871	16.0/6.74	16/7.4	3	23.1
	Apolipoproteins						
40	Apolipoprotein A-I (Apo-AI)	APA1_HUMAN	P02647	30.7/5.56	28/5.3	8	31.8
41	Apolipoprotein A-I	APA1_HUMAN	P02647	30.7/5.56	28/5.4	9	28.5
	Transmembrane protein 16B (ApoA1)	T16B_HUMAN	Q9NQ90	113.6/6.01	28/5.4	1	1.4
	Immunoglobulins						
20	Ig mu chain C region	MUC_HUMAN	P01871	49.5/6.35	47/6.3	1	3.5
21	Ig mu chain C region	MUC_HUMAN	P01871	49.5/6.35	52/6.4	2	6.0
22	Ig mu chain C region	MUC_HUMAN	P01871	49.5/6.35	47/6.5	2	5.3
23	Ig mu chain C region	MUC_HUMAN	P01871	49.5/6.35	47/6.8	2	6.0
27	Ig gamma-1 chain C region	GC1_HUMAN	P01857	36.1/8.46	53/7.0	5	25.5
	Ig gamma-2 chain C region	GC2_HUMAN	P01859	35.8/7.66	53/7.0	1	4.9
28	Ig gamma-4 chain C region	GC4_HUMAN	P01861	35.9/7.18	52/7.3	2	8.0
	Ig gamma-1 chain C region	GC1_HUMAN	P01857	36.1/8.46	52/7.3	4	18.8
29	Ig gamma-4 chain C region	GC4_HUMAN	P01861	35.9/7.18	52/7.5	2	8.0
30	Ig gamma-1 chain C region	GC1_HUMAN	P01857	36.1/8.46	52/7.7	6	29.7
	Ig gamma-4 chain C region	GC4_HUMAN	P01861	35.9/7.18	52/7.7	2	8.0
31	Ig gamma-1 chain C region	GC1_HUMAN	P01857	36.1/8.46	51/8.3	4	18.8
44	Ig Kappa chain C region	KAC_HUMAN	P01834	11.6/5.58	30/7.2	3	48.1
45	Ig Kappa chain C region	KAC_HUMAN	P01834	11.6/5.58	30/7.4	2	33.0
47	Ig Kappa chain C region	KAC_HUMAN	P01834	11.6/5.58	28/8.6	1	32.1
48	Ig Kappa chain C region	KAC_HUMAN	P01834	11.6/5.58	28/8.1	1	16.0

49	Ig Kappa chain C region	KAC_HUMAN	P01834	11.6/5.58	28/7.2	4	67.0
	Complement & associated proteins						
6	Complement C3 (fragment)	C03_HUMAN	P01024	187.1/6.02	73/7.7	3	2.8
	Glucose metabolism						
32	Enolase alpha	ENOA_HUMAN	P06733	47.1/7.01	47/7.5	5	15.2
33	Glyceraldehyde-3-phosphate dehydrogenase	G3P_HUMAN	P04406	36.0/8.57	36/8.6	3	13.7
34	Glyceraldehyde-3-phosphate dehydrogenase	G3P_HUMAN	P04406	36.0/8.57	36/8.3	5	22.1
50	Triosephosphate isomerase (TIM)	TPIS_HUMAN	P60174	26.7/6.45	28/7.4	1	5.2
	Annexins						
35	Annexin A2 (AnnexinII) (Lipocortin II)	ANX2_HUMAN	P07355	38.6/7.57	35/8.0	14	44.3
36	Annexin A2 (AnnexinII) (Lipocortin II)	ANX2_HUMAN	P07355	38.6/7.57	35/7.5	8	25.1
38	Annexin A1 (Annexin I) (Lipocortin I)	ANX1_HUMAN	P04083	38.7/6.57	29/5.5	1	4.1
	ER proteins						
1	Calreticulin (CRP55) *	CALR_HUMAN	P27797	48.1/4.29	71/7.3	4	14.6
7	Protein disulfide-isomerase	PDIA1_HUMAN	P07237	57.1/4.76	57/4.8	4	9.1
10	Protein disulfide-isomerase A3	PDIA3_HUMAN	P30101	56.7/5.98	56/5.8	2	4.2
11	Protein disulfide-isomerase A3	PDIA3_HUMAN	P30101	56.7/5.98	56/6.0	7	16.0
	Others						
43	Ferritin light chain (Ferritin L subunit)	FRIL_HUMAN	P02792	20.0/5.51	25/5.7	1	8.6
	Secreted protein						
39	Serum amyloid P-component	SAMP_HUMAN	P02743	25.3/6.10	30/5.7	7	24.2
42	Serum amyloid P-component	SAMP_HUMAN	P02743	25.3/6.10	25/5.5	4	21.5

	Mixtures						
37	Actin, cytoplasmic 1 (Beta-actin)	ACTB_HUMAN	P60709	41.7/5.29	32/5.3	4	13.3
	Actin, alpha cardiac (Alpha-cardiac actin)	ACTC_HUMAN	P68032	42.0/5.23	32/5.3	3	10.9
	Apolipoprotein A-IV (Apo-AIV)	APA4_HUMAN	P06727	45.3/5.28	32/5.3	1	2.3
46	Ig kappa chain C region	KAC_HUMAN	P01834	11.6/5.58	30/7.9	3	48.1
	Serum albumin	ALBU_HUMAN	P02768	69.3/5.92	30/7.9	4	7.4

* denotes proteins not identified in the 1D SDS-PAGE LC-MS/MS experiment (Supplemental Table I)

Supplemental Table V. Clinical characteristics of carotid endarterectomy patients.

Patient No	Carotid artery stenosis	Hypertension	Smoking	Dyslipidemia	Diabetes	Blood group	Rhesus factor
07 3	Asymptomatic	No	No	Yes	No	0	Positive
07 5	Asymptomatic	Yes	No	Yes	No	B	Positive
07 11	Symptomatic	No	No	No	No	A	Positive
07 20	Symptomatic	Yes	Yes	Yes	No	B	Negative
07 22	Asymptomatic	Yes	Yes	Yes	No	0	Positive
07 27	Symptomatic	Yes	Yes	Yes	No	0	Positive

Supplemental Table VI. Details of the printed carbohydrate antigens.

Numbers on x-axis of Figure 8	Catalogue Number	Source	Antigen	Comment
1 / 17 / 33 / 49	B1010	Glycorex	Gal α1-4 Gal β1-4 GlcNAc β (O-spacer)$_n$-BSA	-
2 / 18 / 34 /50	BSA	Dextra	BSA	-
3 / 19 / 35 / 51	Blank	Pronostics	No coat	-
4 / 20 /36 /52	HSA	Dextra	HSA	-
5 /21 / 37 / 53	NGP0501	Dextra	Lacto-N-fucopentaose II-BSA	Lewis A trisaccharide but with additional lactose spacer
6 / 22 / 38 / 54	NGP0502	Dextra	Lacto-N-fucopentaose III-BSA	Lewis X trisaccharide but with additional lactose spacer
7 / 23 / 39 / 55	NGP0503	Dextra	Lacto-N-fucopentaose I-BSA	Blood group H antigen (type I) linked b1-3 onto lactose spacer
8 / 24 / 40 / 56	NGP0601	Dextra	Lacto-N-difucohexaose I-BSA	Lewis B antigen linked to a lactose spacer
9 / 25 / 41 / 57	NGP1201	Dextra	N-Acetyllactosamine-BSA	Core neoglycoprotein antigen
10 / 26 /42 / 58	NGP1305	Dextra	A antigen (20-atom spacer) BSA	Blood group A antigen
11 / 27 / 43 / 59	NGP1323	Dextra	B antigen (20-atom spacer) BSA	Blood group B antigen
12 / 28 / 44 / 60	NGP2202	Dextra (custom)	Gal α1-2 Gal - HSA	-
13/ 29 / 45 / 61	NGP2333	Dextra	Gal α1-3 Gal β1-3 GlcNAc (3-atom spacer) HSA	Alpha-Gal analogue
14 / 30 / 46 / 62	NGP3203	Dextra	Gal α1-3 Gal (14-atom spacer) HSA	Alpha-Gal analogue
15 / 31 / 47 / 63	NGP3334	Dextra	Gal α1-3 Gal β1-4 GlcNAc (14-atom spacer) HSA	Alpha-Gal analogue
16 / 32 / 48 / 64	Penta	BCS (custom)	Gal α1-3 Gal β1-4 GalNAc β1-3 Gal β1-4 Glc β1 - HSA	'PentaGal'

BSA: bovine serum albumin, HSA: human serum albumin

ONLINE REFERENCES

1. Shevchenko A, Wilm M, Vorm O, Mann M. Mass spectrometric sequencing of proteins silver-stained polyacrylamide gels. *Anal Chem*. 1996;68(5):850-858.

2. Wilm M, Shevchenko A, Houthaeve T, Breit S, Schweigerer L, Fotsis T, Mann M. Femtomole sequencing of proteins from polyacrylamide gels by nano-electrospray mass spectrometry. *Nature*. 1996;379(6564):466-469.

3. Keller A, Nesvizhskii AI, Kolker E, Aebersold R. Empirical statistical model to estimate the accuracy of peptide identifications made by MS/MS and database search. *Anal Chem*. 2002;74(20):5383-5392.

4. Nesvizhskii AI, Keller A, Kolker E, Aebersold R. A statistical model for identifying proteins by tandem mass spectrometry. *Anal Chem*. 2003;75(17):4646-4658.

5. Bradford MM. A rapid and sensitive method for the quantitation of microgram quantities of protein utilizing the principle of protein-dye binding. *Anal Biochem*. 1976;72:248-254.

6. Yan JX, Wait R, Berkelman T, Harry RA, Westbrook JA, Wheeler CH, Dunn MJ. A modified silver staining protocol for visualization of proteins compatible with matrix-assisted laser desorption/ionization and electrospray ionization-mass spectrometry. *Electrophoresis*. 2000;21(17):3666-3672.

7. Bergmeyer H. *Methods of enzymatic analysis*. Weinheim, Germany: Verlag Chemie; 1974.