Targeted Synovial Fluid Proteomics for Biomarker Discovery in Rheumatoid Arthritis

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Abstract

Objective Rheumatoid arthritis (RA) is an autoimmune disease that targets the synovium. The autoantigens involved in the autoantibody responses in RA are unknown. A targeted proteomics approach was used to identify proteins in RA synovial fluid (SF) that are recognized by autoantibodies in RA sera.

Methods RA SF, depleted of abundant proteins, was fractionated by two-dimensional liquid chromatography (chromatofocusing followed by reverse phase HPLC). Protein arrays constructed from these fractions were probed with RA and normal control sera, and proteins within reactive fractions were identified by mass spectrometry. The reactivity of RA sera to an identified peptide was confirmed by ELISA.

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Laboratory of Applied Mass Spectrometry, National Heart, Lung and Blood Institute, National Institutes of Health, Bethesda, MD, USA *Results* RA sera specifically reacted to a SF fraction containing fibrin. Mass spectrometry analyses established the presence of a citrullinated arginine at position 271 of the fibrin fragment present in RA SF. A synthetic peptide corresponding to fibrin residues 259–287, containing the citrulline substitution at Arg 271, was recognized by 10 of 12 RA sera, but by two of 18 normal control sera and one of 10 systemic lupus erythematosus sera.

Conclusion Proteomics methodology can be used to directly characterize post-translational modifications in candidate autoantigens isolated from sites of disease activity. The finding that RA sera contain antibodies to the citrullinated fibrin 259–287 peptide may ultimately lead to improved diagnostic tests for RA and/or biomarkers for disease activity.

Keywords Rheumatoid arthritis · Synovial fluid · Clinical proteomics · Biomarker discovery · Citrullination · Fibrinogen · ELISA, protein macroarrays · Autoimmune disease · Autoantibodies · Autoantigens · Mass spectrometry · Post-translational modification

Introduction

Rheumatoid arthritis (RA) is an autoimmune disease that targets the joints and affects 0.8% of the adults worldwide [1, 2]. Chronic joint inflammation leads to cartilage and bone destruction, resulting in loss of function. Many self-antigens have been implicated in the triggering and/or maintenance of autoreactive lymphocyte responses in RA [3–5]. Nevertheless, there remains an uncertainty as to how disease is caused and maintained [6]. Aberrant post-translational modifications of self-proteins may play a role in breaking T and B cell tolerance, leading to autoimmunity [7–9]. Of particular interest to the clinical management of

RA are the anti-citrulline antibodies [10], which can predict both development [11, 12] and severity of disease [13, 14]. Citrullination is the post-translational modification (deimination) of arginine to citrulline catalyzed by protein arginyl deiminase (PAD) enzymes [15]. This conversion changes the charge of the site from a positive to a neutral and increases the mass of the amino acid by 1 Da. The difference in charge may cause protein unfolding [16], thereby exposing novel epitopes.

The current diagnostic test for anti-citrulline antibodies employs a cyclic citrullinated peptide (CCP), yet the citrulline residues on synovial joint proteins that are target(s) of anti-citrulline antibodies in vivo have not been precisely defined. Autoantigens, which exist in citrullinated forms include fibrinogen [17–19] (which was initially thought to be filaggrin [20, 21]), vimentin [22–24], collagen type I [25, 26], collagen type II [26– 28], fibronectin [29], and alpha-enolase [30]. The presence of citrulline-modified fibrinogen alpha (FIBA) and beta chains in RA synovial tissue or fluid has been reported [17, 19].

The goal of this project was to develop a method to discover novel RA autoantigens using a targeted proteomic analysis. We and others have reasoned that autoantigens might be enriched in RA SF and specifically recognized by autoantibodies in RA sera. Previous autoantigen and biomarker discovery projects have employed one of several approaches to fractionate biological sample preparations, including two-dimensional PAGE, miniaturized chips with diverse surfaces to promote differential protein binding, and multidimensional LC-MS/MS [31]. Often these fractionation approaches were combined with immunoblotting with patient sera. Although they yielded some novel information, such methods were complicated by the wide dynamic range of protein concentrations in serum and SF, which obscures identification of potentially informative proteins in minor abundance.

To separate and probe SF proteins, we used a method that was previously used to characterize cancer antigens [32]. which included two-dimensional liquid chromatography, protein arrays, and high-resolution mass spectrometry. Depletion of abundant serum proteins followed by protein fractionation via two-dimensional liquid chromatography increased the likelihood of identifying the lower abundance proteins. Protein arrays constructed from fractionated SF were probed with RA and control sera to identify biologically significant fractions, and further analyses were performed only on those targeted fractions. It is important to note that the arrays were constructed from clinical samples that contain proteins with their post-translational modifications acquired in vivo. Liquid chromatography-tandem mass spectrometry (LC-MS/MS) was then used to identify immunogenic protein fragments and their post-translational modifications. Through this targeted proteomics approach, we have identified a citrulline-modified Arg 271 residue, within a fibrin alphaC domain fragment stably present in RA SF, as a target of autoantibodies in RA sera.

Materials and Methods

Patient Samples

All samples were obtained using IRB approved protocols and all patients consented to be part of the study. SF and sera were obtained from patients receiving care in the outpatient Rheumatology clinics at the Los Angeles County and University of Southern California Medical Center. RA and systemic lupus erythematosus (SLE) patients were diagnosed according to established clinical criteria [33, 34]. All patients had to have a clinical diagnosis of RA as defined by rheumatologists at academic center. The sampling was on consecutive RA patients from LA County hospital who had a joint effusion that was aspirated. Due to use of biologic agents, much less effusions are seen in the clinic. Patient population was mostly Hispanic, approximately 80%, with active RA stage 2 to 4 with most probably falling into 2 or 3 but data not collected so this is speculative. Comorbidities were not examined. All samples processed within 4 h. Control sera were obtained from healthy volunteers at the City of Hope General Clinical Research Center. SF samples were diluted 1:5 in PBS, centrifuged to remove cellular debris, and stored at -80°C. There are no viscosity issues when the SF is diluted 1:5 in PBS. Blood samples were allowed to clot overnight at 4°C. The next day, the blood was centrifuged and the top layer of serum was transferred into new tubes. Serum samples were stored at -80°C until use.

Protein Fractionation

A multiple affinity removal column (Agilent Technologies, Wilmington, DE, USA) was used to remove six abundant proteins (albumin, IgG, antitrypsin, IgA, transferrin, and haptoglobin) from SF. The procedure removed 85–90% of the total protein mass, which increased the probability of detecting the lower abundance proteins. Depletion was performed according to manufacturer's protocol. After the depletion, samples were desalted by use of a 5-kDa MWCO spin filter (Amicon Ultra-15, Millipore Corp., Bedford, MA, USA). Reactivity of RA sera to proteins in the 5-kDa filtrate was not detected. Protein concentration of the desalted SF was determined by RCDC protein assay (BioRad Laboratories, Hercules, CA, USA).

SF proteins were separated by 2D-HPLC, chromatofocusing, and reverse phase (RP) HPLC. A Beckman PF2D System (Beckman Coulter, Inc., Fullerton, CA, USA) with a PF2D kit (column and buffers) was used for the firstdimension separation. Approximately 5 mg of proteins was separated in the pH range 8.5 to 4.0. After loading, the sample was washed in start buffer for 20 min, eluant buffer for 75 min, and then 1 M sodium chloride buffer for 45 min. The column was then washed overnight in water. Fractions were collected in increments of 5 min or 0.2 pH units, whichever came first, into a cooled deep well 96-well plate. This separation was reproducible as performed according to manufacturers' supplied protocol. The second-dimension separation was performed on a Vydac C4 column (5 um, 300 A, 2.1×250 mm) using the following program: hold for 12 min at 5% buffer B; 5% to 95% buffer B in 25 min; hold at 95% buffer B for 8 min. The flow rate was 0.25 ml/min. Fractions were collected between 14 and 45 min at every 2 min into standard 96well plates using a fraction collector.

The pooled SF second-dimension separations were performed on a Vydac C4 column (10 um, 300 A, 4.6× 250 mm) using a gradient of 2% to 98% buffer B in 60 min and a flow rate of 1 ml/min. Corresponding fractions that eluted in the same pH range from four first-dimension runs were combined to ensure enough material was obtained for analysis by mass spectrometry. Buffer A consisted of 0.1% TFA. Buffer B consisted of 0.1% TFA in 90% acetonitrile. A Beckman System Gold 126 equipped with a model 168 diode array detector (Beckman Coulter, Inc.) was used to perform the separations. Fractions were collected every minute. Samples were frozen and lyophilized to dryness.

Protein Arrays

Custom arrays were hand made using a VP 409 replicator with 96 pins each holding 100 nl of fluid (V&P Scientific, Inc., San Diego, CA, USA). The selected HPLC fractions were resuspended in ~200 µl of 6 M urea/sodium bicarbonate pH 8.0. The microtiter plates were slowly rocked for about 30 min to facilitate protein solubility. The replicator was dipped into a 96-well plate, and the fluid (~100 nl) retained on the tips of the pins was transferred to a nitrocellulose membrane. Each fraction was arrayed in triplicate. To serve as a positive control for serum antibody reactivity, an influenza vaccine preparation also was arrayed. After drying overnight in a laminar flow hood, the arrayed membranes were blocked overnight in a non-fat dried milk solution and subsequently were rinsed twice in TBS (20 mM Tris-HCl, 500 mM NaCl, pH 7.5). The arrays were incubated with a 1:200 dilution of RA or control sera for 1 h at room temperature. After rinsing twice in TBS, the arrays were incubated with a 1:100,000 dilution of HRPconjugated F(ab')2 goat anti-human IgG + IgM + IgA secondary antibodies (Jackson ImmunoResearch Laboratories, Inc., West Grove, PA, USA). The arrays were washed twice with 3% newborn calf serum/0.05% Tween/TBS, twice with a 0.05% Tween/TBS, twice with TBS, and twice with water. ECL Plus Western Blotting Detection Reagents (GE Healthcare, Piscataway, NJ, USA) were used as the detection agent. The arrays were imaged on a Typhoon 9410 (GE Healthcare) using the following conditions: Laser (457 nm), Emission filter (520BP40), Focal Plane (Platen), Pixel Size (50 μ m), Sensitivity (Normal). Different voltages were used to scan the images but typically 500v was used for most of the images. To distinguish background noise from foreground signal by a statistical method that complemented the visual inspection of the protein arrays, the median filter smoothing technique was applied to the imaged signals as described [35].

Mass Spectrometry

Approximately 80% of the solubilized RP-HPLC fraction was digested with trypsin (Promega, Madison, WI, USA). Approximately 5% of the digested material was analyzed by LC/MS/MS. Analyses were performed on a Thermo Finnigan LTQ-FT linear ion trap-Fourier transform mass spectrometer (Thermo Electron Corporation, San Jose, CA, USA) coupled to an Eksigent nanoLC-2D capillary HPLC system (Eksigent Technologies, LLC, Dublin, CA, USA). Samples were loaded onto a 300 µm×5 mm C18 trapping column (Dionex Corporation, Sunnyvale, CA, USA) and then eluted through a lab-built 75 µm×10 cm analytical column packed with 3 µm C18 Pursuit resin (Varian, Inc., Palo Alto, CA, USA). The gradient for the trapping column was 100% A for 5 min using a flow rate of 10 μ /min. The gradient for the analytical column was 2% to 35% B in 45 min, 35% to 50% B in 4 min, and 50% to 95% B in 2 min using a flow rate of 0.2 ul/min. High-resolution fullscale mass spectra were acquired in the Fourier transformion cyclotron resonance (FT-ICR) section of the mass spectrometer while fragment ion (MS/MS) spectra were obtained from the linear ion trap section. Fragmentation was performed using a collision energy setting of 35. Dynamic exclusion was set at 15 s.

Monoisotopic peaks and peptide charge states were determined during acquisition by the Xcalibur acquisition software using the high-resolution Fourier transform mass spectrometry (FTMS) spectra. Protein identifications were made by SEQUEST [36]. SEQUEST searches were performed with the following parameters: use of the 10/17/08 release of the SwissProt database (downloaded from ftp://ftp.ncbi.nlm.nih.gov/blast/db), monoisotopic masses, partial trypsin cleavage, 2 amu peptide and fragment tolerance, and automatic charge state determination. The SwissProt database was filtered to include only entries containing _HUMAN as a parameter. Peptide hits were

Synovial Fluid (late RA, early RA, serum from healthy control) Abundant Protein Depletion (Agilent Column, flowthru from 15 runs) 1D-HPLC, Chromatofocusing (Approx. 40 fractions collected into deep well plates) 2D-HPLC, Reverse Phase (Approx 1280 fractions collected into standard 96-well plates) Macroarrays (Screen Fractions with RA Serum to detect Presence of Autoantigens) Identify Autoantigens by Mass Spectrometry Identify Post-translationally Modified Sites

Verify Peptide Epitope Reactivity with RA sera by ELISA

Fig. 1 Proteomic Strategy to Identify autoantigens present in synovial fluid of RA patients

filtered using the following criteria: DeltaCn greater than or equal to 0.08, XC greater than or equal to 1.8 for peptides having +1 charge, 2.5 for peptides with a +2 charge, and 3.5 for peptides having a +3 charge and the peptide must be to a protein with probability score less than 0.0001 used [37]. Peptides meeting these criteria were further analyzed. Although the LTQ-FT has routine mass accuracy of 2 ppm, it is set to perform MS/MS on the most abundant peak in an isotope envelope, rather than the monoisotopic mass. This frequency results in errors of 1 or 2 mass units for large peptides. Because SEQUEST and extract_msn do not correct for this error, it was necessary to set peptide mass tolerance to 2.5 to account for errors in precursor assignment. Fragment ion tolerance was set at 0.0. The searches were performed assuming both trypsin and no enzyme specificity. Spectra were hand sorted to identify and verify post-translational modifications (PTM). All charge states and mass were manually verified using the high-resolution FTMS data. All spectra corresponding to candidate autoantigens were manually verified.

Synthetic Peptides

The FIBA 259–287 peptides with and without the citrulline substitution for arginine 271 (MELERPGGNEITR*GGST-SYGTGSETESPR) were synthesized in the City of Hope Peptide Synthesis Core Facility. The synthesized profilag-grin 619–631 peptide (SSFSQDR*DSQAQS) contained a citrulline for arginine substitution at position 625. Peptides were dissolved in 0.1% TFA and purified two to three times on a C18 reverse phase column. Concentration was determined by amino acid analysis.

ELISA

Maleic anhydride coated ELISA plates (Pierce Biotechnology, Inc., Rockford, IL, USA) were incubated overnight with 100 μ l of 12.5 μ g/ml peptide in PBS. The plates were blocked overnight in a dried milk solution, washed twice in TBS, and incubated overnight in a 1:20 dilution of patient sera. After rinsing two times in TBS, the plates were incubated in a 1:10,000 dilution of HRP-conjugated F(ab')2 goat anti-human IgG + IgM + IgA secondary antibodies for 1 h. The plates were then rinsed 6 times in TBS. For color development 150 μ l ABTS (Pierce Biotechnology) was

Fig. 2 Fraction containing candidate autoantigen detected on second-dimension RP-HPLC. Fractions from the SF separation were spotted in a protein array, which was used to determine which fractions contained an autoantigen. *Arrow* points patient synovial fluid fraction that reacted with RA patient serum



Fig. 3 a Representative HPLC chromatogram for the firstdimension chromatofocusing separation of the abundant protein depleted SF sample. The diagonal line indicates the observed pH gradient. The fractions corresponding to the elution range of pH 5.63-5.45 from four runs were combined for the second-dimension separation. b HPLC chromatogram for the second-dimension reverse phase separation. This sample was separated on a Beckman System Gold HPLC coupled to a diode array detector. The diagonal line indicates the solvent gradient (%B). The fraction (between 20 and 25 min) corresponding to the region that tested positive in the protein array assay was selected for further characterization by mass spectrometry



added to the wells and incubated for 30 min. To stop the reaction, 100 μ l of 1% SDS was added. The absorbance at 405 nm was read on a plate reader.

Results

A targeted proteomic approach was performed to identify autoantigens in RA SF. The experimental design is diagrammed in Fig. 1. An immunodepletion column was first used to remove six abundant serum proteins (albumin, antitrypsin, haptoglobin, IgA, IgG, and transferrin). The depleted SF was then fractionated by chromatofocusing HPLC (provided as Supplement Fig. 1) and reverse phase HPLC (provided as Supplement Fig. 2). This protein fractionation strategy increased the chance of identifying the lower abundance proteins by separating them from the higher abundance proteins. The second-dimension fractions were used to construct protein arrays on nitrocellulose membranes, which were used to test for the presence of autoantigens by analyzing differential reactivity of RA and control sera. We focused on one second-dimension fraction resulting from the separation of the first-dimension fraction eluting at pH 5.63–5.45 (Fig. 2) that tested positive when probed with RA serum but negative when probed with normal control serum. This was the only fraction that tested positive in which a peak was detected on the HPLC chromatographs. Although there was sufficient material for

Table 1 Proteins identified in the B2 second-dimension RP fractions

	P (pro)	Score	MW	Hits
Fraction 13 proteins				
K1C9 HUMAN Keratin, type I cytoskeletal 9	3.93E-13	60.40	62,091.8	6
PRG4 HUMAN Proteoglycan-4	5.32E-13	40.33	15,0,983.2	5
GRP78 HUMAN 78 kDa glucose-regulated protein	1.57E-09	10.25	72,288.5	1
ALBU HUMAN Serum albumin	2.20E-09	40.24	69,321.6	5
TYB4 HUMAN Thymosin beta-4	1.25E-07	30.23	5,049.5	6
K2C1 HUMAN Keratin, type II cytoskeletal 1	2.44E-07	96.26	65,977.9	10
K1C10 HUMAN Keratin, type I cytoskeletal 10	2.80E-07	30.25	59,474.8	3
Fraction 14 proteins			,	
K1C9 HUMAN Keratin, type I cytoskeletal 9	1.00E-30	110.27	62,091.8	13
PRG4 HUMAN Proteoglycan-4	1.22E-14	60.34	150,983.2	11
K2C6C HUMAN Keratin, type II cytoskeletal 6C	1.33E-14	10.31	59,988.4	2
K2C1 HUMAN Keratin type II cytoskeletal 1	2.93E-11	126 39	65,977,9	15
K1C10 HUMAN Keratin type I cytoskeletal 10	7.90E-10	10.26	59,474.8	1
ALBU HUMAN Serum albumin	2.28E-09	10.20	69.321.6	2
TTHY HUMAN Transtbyretin	3 41E-08	20.26	15.877.1	4
BASP HUMAN Brain acid soluble protein 1	5.02E-07	20.20	22 680 0	2
FFHD2 HUMAN FE-hand domain-containing protein D2	1.42E-06	10.19	26,680.5	1
K22E HUMAN Keratin type II cytoskeletal 2 enidermal	1.12E 00	10.19	65 825 4	1
APOA2 HUMAN Anolinoprotein A-II	3 90E-04	10.15	11 167 9	1
Fraction 15 proteins	5.702 04	10.15	11,107.9	1
PRG4 HUMAN Proteoglycan_4	1 13E-11	50.33	150 983 2	8
K1C10 HUMAN Keratin type I cytoskeletal 10	3.63E-10	30.27	59 474 8	3
K1C0 HUMAN Keratin type I cytoskeletal 9	9.80E-08	30.41	62 091 8	3
FIBA HUMAN Eibringen alpha chain	7.51E-07	30.22	02,001.0	6
K2C1 HUMAN Kerstin type II cytoskeletel 1	6.51E-06	70.26	94,914.5 65 977 9	7
PMS2 HUMAN Mismatch rappir and anualogsa PMS2	0.51E 00 2.41E-05	10.10	05,977.9	1
ADOA1 HIIMAN Apolinoprotoin A I	2.41E 05	20.12	20,758,0	7
KOAL HUMAN Keretin true II gyteckeletel 2 enidermel	5.14E-05	10.20	50,738.9	/
S10AC HUMAN Retain, type if cytoskeletal 2 epidemiai	1.43E=04	10.20	10,172,2	1
STOAO_HOMAN FIOIEIII STOO-AO	4.94E ⁻⁰⁴	10.15	10,175.5	1
K2C6C HUMAN Kentin ture II extended to 6	2 02E 12	20.20	50 088 4	2
EIDA HUMAN Eibring ogn alnha shair	3.02E-12	20.30	39,988.4	5 97
FIBA_HUMAN Fibrinogen alpha chain	4.08E-12	408.33	94,914.5	87
ADOAA UUNAAN Keralin angetein A W	2.09E-11	20.25	45 271 5	12
APOA4_HUMAN Apolipoprotein A-IV	4./9E-11	20.23	43,371.3	3 2
K1C10_HUMAN Keratin, type I cytoskeletal 10	1.88E-10	30.23	39,474.8	3
ALDU HUMAN Keratin, type I cytoskeletal 9	4.42E-10	60.31	62,091.8	0
ALBU_HUMAN Serum albumin	5.8/E-08	20.21	69,321.6	3
ABOAL HUMAN Assilia sector A L	7.30E-07	10.22	35,401.5	1
APOAI_HUMAN Apolipoprotein A-I	1.23E-05	20.20	30,758.9	2
K22E_HUMAN Keratin, type II cytoskeletal 2 epidermal	6.83E-05	10.22	65,825.4	1
Fraction 21 proteins	1.005 20	70.21	(2.001.0	0
KIC9_HUMAN Keratin, type I cytoskeletal 9	1.00E-30	70.31	62,091.8	8
K22E_HUMAN Keratin, type II cytoskeletal 2 epidermal	5.55E-15	30.28	65,825.4	4
K2C6C_HUMAN Keratin, type II cytoskeletal 6C	1.11E-14	10.29	59,988.4	2
K2C1_HUMAN Keratin, type II cytoskeletal 1	6.48E-13	100.38	65,977.9	12
FIBA_HUMAN Fibrinogen alpha chain	8.06E-12	428.33	94,914.3	87
USIP_HUMAN Osteopontin	2.97E-09	70.25	35,401.3	14
K1C10_HUMAN Keratin, type I cytoskeletal 10	8.09E-09	40.24	59,474.8	4

	P (pro)	Score	MW	Hits
ADIPO_HUMAN Adiponectin	2.01E-08	10.22	26,397.0	2
APOA1_HUMAN Apolipoprotein A-I	3.54E-08	110.20	30,758.9	15
K2C5_HUMAN Keratin, type II cytoskeletal 5	4.79E-08	10.25	62,340.0	1
HEP2 HUMAN Heparin cofactor 2	1.86E-07	20.26	57,034.3	6
A2MG_HUMAN Alpha-2-macroglobulin	4.97E-07	10.22	163,174.3	2
HPT HUMAN Haptoglobin	2.91E-06	62.22	45,176.6	11
APOB HUMAN Apolipoprotein B-100	1.20E-05	10.17	515,241.6	2
APOA4 HUMAN Apolipoprotein A-IV	1.46E-05	20.19	45,371.5	2
CLUS HUMAN Clusterin	5.35E-05	10.16	52,461.1	1
K2C75 HUMAN Keratin, type II cytoskeletal 75	1.47E-04	16.20	59,468.0	2
CD99 HUMAN CD99 antigen	1.73E-04	10.16	18,836.3	1
Fraction 22 proteins			,	
K22E HUMAN Keratin, type II cytoskeletal 2 epidermal	1.00E-30	130.30	65,825.4	17
K1C9 HUMAN Keratin, type I cytoskeletal 9	6.66E-15	80.38	62.091.8	9
K2C1 HUMAN Keratin, type II cytoskeletal 1	5.66E-14	226.35	65.977.9	34
HPT HUMAN Hantoglobin	1 12E-13	98.26	45,176,6	25
FIBA HUMAN Fibringen alpha chain	1.12E 13	588 31	94 914 3	115
K1C10 HUMAN Keratin type I cytoskeletal 10	2.69E-11	200.34	59 474 8	34
K2C6C HUMAN Keratin type II cytoskeletal 6C	4 30E-11	50.31	59 988 4	7
FETUA HUMAN Alpha 2 HS alveopretein	2.71E-00	10.21	30 200 7	1
DI MN. HI IMAN Diagminagan	2.71E 09	20.28	99,299.7 00 510 2	5
K2C5 HUMAN Karatin tuna II autocholatal 5	7.18E_08	20.28	<i>50,310.2</i>	2
K2C5_HUMAN Keratin, type II cytoskeletal 5	7.16E-08	20.22	62,340.0	3
A DOAL HUMAN Analing restain A L	9.30E-08	20.17	31,389.3	2 79
APOAI_HUMAN Aponpoprotein A-1	1.80E-07	138.21	30,738.9	/8
LBR_HUMAN Lamin-B receptor	7.18E-07	10.18	70,658.2	1
UPAR_HUMAN Urokinase plasminogen activator surface receptor	8.12E-07	10.24	36,953.3	1
FINC_HUMAN Fibronectin	8.99E-07	30.22	262,439.5	4
ECMI_HUMAN Extracellular matrix protein 1	1.83E-06	20.18	60,635.4	2
K2C6A_HUMAN Keratin, type II cytoskeletal 6A	1.85E-06	10.13	60,008.3	1
TMOD3_HUMAN Tropomodulin-3	2.02E-06	10.20	39,570.3	1
K1C24_HUMAN Keratin, type I cytoskeletal 24	3.28E-06	10.16	55,053.5	1
OSTP_HUMAN Osteopontin	9.62E-06	30.24	35,401.3	6
K1C17_HUMAN Keratin, type I cytoskeletal 17	1.05E-05	30.17	48,076.1	3
APOB_HUMAN Apolipoprotein B-100	2.09E-05	10.15	515,241.6	1
K2C75_HUMAN Keratin, type II cytoskeletal 75	2.46E-05	36.21	59,468.0	4
CFAB_HUMAN Complement factor B	2.82E-05	40.22	85,478.6	6
DEF3_HUMAN Neutrophil defensin 3	6.01E-05	10.14	10,238.2	2
HEP2_HUMAN Heparin cofactor 2	2.17E-04	10.25	57,034.3	1
Fraction 23 proteins				
K2C6C_HUMAN Keratin, type II cytoskeletal 6C	1.55E-14	10.35	59,988.4	3
FIBA_HUMAN Fibrinogen alpha chain	2.36E-11	180.27	94,914.3	23
K2C1_HUMAN Keratin, type II cytoskeletal 1	4.97E-11	110.35	65,977.9	12
IBP6_HUMAN Insulin-like growth factor-binding protein 6	6.63E-11	20.26	25,306.2	3
K2C5_HUMAN Keratin, type II cytoskeletal 5	2.42E-10	10.31	62,340.0	1
K1C9_HUMAN Keratin, type I cytoskeletal 9	2.71E-10	110.33	62,091.8	12
K1C10_HUMAN Keratin, type I cytoskeletal 10	2.05E-09	50.30	59,474.8	5
APOA1_HUMAN Apolipoprotein A-I	7.38E-08	100.23	30,758.9	31
TTHY_HUMAN Transthyretin	1.41E-07	40.28	15,877.1	8
APOC3_HUMAN Apolipoprotein C-III	7.99E-07	10.25	10,845.5	1

	P (pro)	Score	MW	Hits
CLUS_HUMAN Clusterin	9.57E-07	30.20	52,461.1	5
K22E_HUMAN Keratin, type II cytoskeletal 2 epidermal	1.13E-06	10.21	65,825.4	1
CFAB_HUMAN Complement factor B	1.29E-06	60.23	85,478.6	10
PLMN_HUMAN Plasminogen	1.69E-06	10.25	90,510.2	1
K2C75_HUMAN Keratin, type II cytoskeletal 75	1.01E-04	16.21	59,468.0	2
ACTS_HUMAN Actin, alpha skeletal muscle	1.21E-04	10.15	42,023.9	1
STP2_HUMAN Nuclear transition protein 2	5.46E-04	10.19	15,630.8	1
Fraction 24 proteins				
K2C6C_HUMAN Keratin, type II cytoskeletal 6C	1.00E-30	10.33	59,988.4	2
K22E_HUMAN Keratin, type II cytoskeletal 2 epidermal	2.22E-15	40.25	65,825.4	4
K2C1_HUMAN Keratin, type II cytoskeletal 1	8.66E-14	170.28	65,977.9	18
K1C9_HUMAN Keratin, type I cytoskeletal 9	5.47E-12	80.34	62,091.8	9
FIBA_HUMAN Fibrinogen alpha chain	4.36E-10	410.31	94,914.3	93
IBP6 HUMAN Insulin-like growth factor-binding protein 6	1.62E-09	10.24	25,306.2	2
APOC3 HUMAN Apolipoprotein C-III	2.04E-09	20.27	10,845.5	4
FHR4 HUMAN Complement factor H-related protein 4	2.82E-09	20.28	37,300.4	10
FINC HUMAN Fibronectin	7.99E-09	110.25	262,439.5	15
CO3 HUMAN Complement C3	1.44E-08	30.23	187,029.3	3
KNG1 HUMAN Kininogen-1	1.81E-08	10.21	71,912.1	3
AHNK HUMAN Neuroblast differentiation-associated protein AHNAK	2.21E-08	144.21	628,705.2	17
CFAI HUMAN Complement factor I	3.09E-08	10.22	65,676.7	1
TTHY HUMAN Transthyretin	3.45E-08	70.27	15,877.1	13
PLMN HUMAN Plasminogen	6.87E-08	20.26	90,510.2	3
CLUS HUMAN Clusterin	1.57E-07	10.21	52,461.1	1
EMIL2 HUMAN EMILIN-2	1.82E-07	10.23	115,544.0	1
UPAR HUMAN Urokinase plasminogen activator surface receptor	2.83E-07	10.25	36,953.3	1
APOA1 HUMAN Apolipoprotein A-I	6.53E-07	100.23	30,758.9	23
PRIO HUMAN Major prion protein	7.31E-07	10.21	27,643.2	2
HRG HUMAN Histidine-rich glycoprotein	1.84E-06	10.19	59,540.9	1
FHR1 HUMAN Complement factor H-related protein 1	2.60E-06	30.17	37,637.0	3
CFAB HUMAN Complement factor B	3.71E-06	80.21	85,478.6	10
HPT HUMAN Haptoglobin	6.41E-06	38.18	45,176.6	7
FHR3 HUMAN Complement factor H-related protein 3	9.61E-06	20.16	37,298.8	2
K1C10 HUMAN Keratin, type I cytoskeletal 10	1.00E-05	20.19	59,474.8	2
RETBP PANTR Plasma retinol-binding protein	1.19E-05	30.18	22,995.3	4
GDIS HUMAN Rho GDP-dissociation inhibitor 2	1.48E-05	20.22	22,973.6	2
NHERF HUMAN Ezrin-radixin-moesin-binding phosphoprotein 50	4.74E-05	20.16	38.844.6	2
IBP3 HUMAN Insulin-like growth factor-binding protein 3	9.03E-05	40.18	31.653.8	7
ACTS HUMAN Actin. alpha skeletal muscle	2.25E-04	10.15	42.023.9	1
K2C75 HUMAN Keratin, type II cytoskeletal 75	2.54E-04	16.21	59.468.0	2
HSPB1 HUMAN Heat shock protein beta-1	3.19E-04	10.15	22,768.5	1
APOC2 HUMAN Apolipoprotein C-II	4.13E-04	10.16	11.276.8	1
ADAM8 HUMAN ADAM 8	5.40E-04	10.15	88.615.7	1
Fraction 30 proteins				-
HEMO HUMAN Hemonexin	5.65E-16	604 31	51,643,3	307
CFAI HUMAN Complement factor I	1.11E-15	300.33	65.676.7	79
FETUB HUMAN Fetuin-B	3.33E-15	80.26	42.028.0	14
AMBP HUMAN AMBP protein	2.00E-14	20.24	38.974 0	2
IGKC HUMAN Ig kappa chain C region	7.99E-14	30.27	11,601.7	11

	P (pro)	Score	MW	Hits
TTHY HUMAN Transthyretin	1.11E-13	150.29	15,877.1	44
TRFE HUMAN Serotransferrin	2.02E-13	40.33	76,999.7	4
RETBP PANTR Plasma retinol-binding protein	4.00E-13	70.32	22,995.3	33
VTDB HUMAN Vitamin D-binding protein	9.50E-13	20.27	52,929.1	3
CO7 HUMAN Complement component C7	3.29E-12	80.22	93,457.3	10
FIBG HUMAN Fibrinogen gamma chain	1.25E-11	120.29	51,478.9	27
FIBA HUMAN Fibrinogen alpha chain	1.75E-11	70.28	94,914.3	8
ITIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H4	2.39E-11	80.29	103,261.2	22
ALBU_HUMAN Serum albumin	4.44E-11	716.29	69,321.6	473
APOC3_HUMAN Apolipoprotein C-III	1.08E-10	38.26	10,845.5	6
FIBB_HUMAN Fibrinogen beta chain	2.14E-10	130.29	55,892.2	25
TENX_HUMAN Tenascin-X	7.70E-10	10.21	464,165.9	1
A2MG_HUMAN Alpha-2-macroglobulin	2.49E-09	10.17	163,174.3	1
HBB_HUMAN Hemoglobin subunit beta	6.11E-09	28.22	15,988.3	3
FETUA_HUMAN Alpha-2-HS-glycoprotein	1.00E-08	20.26	39,299.7	2
APOA1_HUMAN Apolipoprotein A-I	2.09E-08	110.23	30,758.9	34
HPTR_HUMAN Haptoglobin-related protein	3.73E-08	10.18	38,982.7	1
K2C1_HUMAN Keratin, type II cytoskeletal 1	4.44E-08	10.34	65,977.9	2
CERU_HUMAN Ceruloplasmin	4.89E-08	10.22	122,127.6	1
HBA_HUMAN Hemoglobin subunit alpha	6.40E-08	10.23	15,247.9	3
PCOC1_HUMAN Procollagen C-endopeptidase enhancer 1	2.70E-07	30.16	47,942.0	7
CO3A1 HUMAN Collagen alpha-1(III) chain	4.23E-07	20.21	138,479.2	2
LAC HUMAN Ig lambda chain C regions	5.62E-07	20.23	11,229.5	9
HPT_HUMAN Haptoglobin	7.82E-07	38.18	45,176.6	13
CATB_HUMAN Cathepsin B	1.21E-06	20.21	37,796.8	2
MUCB_HUMAN Ig mu heavy chain disease protein	1.89E-06	38.19	43,030.3	4
IGHA2_HUMAN Ig alpha-2 chain C region	4.73E-06	10.13	36,485.1	2
COR1A_HUMAN Coronin-1A	6.19E-06	10.23	50,993.9	1
TETN_HUMAN Tetranectin	9.66E-06	30.24	22,552.3	5
IGHM_HUMAN Ig mu chain C region	1.93E-05	20.26	49,275.6	3
CFAB_HUMAN Complement factor B	2.98E-05	40.18	85,478.6	4
CAPG_HUMAN Macrophage-capping protein	3.70E-05	40.20	38,493.6	6
IGHD_HUMAN Ig delta chain C region	4.73E-05	10.14	42,227.3	1
IGHA1_HUMAN Ig alpha-1 chain C region	1.52E-04	10.18	37,630.7	1
ATS9_HUMAN ADAMTS-9	4.44E-04	10.15	216,415.5	1
Fraction 31 proteins				
CFAB_HUMAN Complement factor B	1.00E-30	296.35	85,478.6	74
CO8A_HUMAN Complement component C8 alpha chain	1.00E-30	104.27	65,121.0	18
TTHY_HUMAN Transthyretin	1.11E-16	340.32	15,877.1	103
CERU_HUMAN Ceruloplasmin	1.11E-16	80.31	122,127.6	10
RETBP_PANTR Plasma retinol-binding protein	1.11E-16	70.31	22,995.3	31
HEMO_HUMAN Hemopexin	2.22E-16	236.31	51,643.3	85
K1C9_HUMAN Keratin, type I cytoskeletal 9	4.44E-16	20.39	62,091.8	2
HBA_HUMAN Hemoglobin subunit alpha	4.44E-15	40.29	15,247.9	5
S10AC_HUMAN Protein S100-A12	6.66E-15	10.30	10,568.5	1
CO8G_HUMAN Complement component C8 gamma chain	7.77E-15	60.26	22,263.6	11
IGKC_HUMAN Ig kappa chain C region	9.99E-15	70.30	11,601.7	53
ITIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H4	1.44E-14	468.31	103,261.2	188
IGHA1_HUMAN Ig alpha-1 chain C region	5.46E-12	80.32	37,630.7	35

	P (pro)	Score	MW	Hits
APOC2_HUMAN Apolipoprotein C-II	5.67E-12	60.28	11,276.8	14
FIBB_HUMAN Fibrinogen beta	7.98E-12	210.39	55,892.2	78
AMBP_HUMAN AMBP protein	8.25E-12	40.25	38,974.0	5
CLUS_HUMAN Clusterin	1.08E-11	148.28	52,461.1	26
HV3P_HUMAN Ig heavy chain V-III region TEI	1.38E-11	10.28	12,794.4	4
ALBU HUMAN Serum albumin	1.48E-11	370.28	69,321.6	160
FIBG HUMAN Fibrinogen gamma chain	1.71E-11	240.30	51,478.9	46
KV1D HUMAN Ig kappa chain V-I region CAR	2.53E-11	10.26	11,696.3	3
AACT HUMAN Alpha-1-antichymotrypsin	3.63E-11	10.21	47,620.6	1
LAC HUMAN Ig lambda chain C regions	5.29E-11	60.26	11,229.5	16
IGHA2 HUMAN Ig alpha-2 chain C region	5.55E-11	120.26	36,485.1	44
HPT HUMAN Haptoglobin	8.17E-11	110.29	45,176.6	25
ENOB HUMAN Beta-enolase	1.28E-10	10.24	46.957.4	1
ENOA HUMAN Alpha-enolase	1.31E-10	30.26	47,139,4	3
APOA1 HUMAN Apolipoprotein A-I	1.45E-10	330.30	30 758 9	111
CFAL HUMAN Complement factor I	1.53E-10	118 28	65 676 7	23
COR1A HUMAN Coronin-1A	1.95E 10	64.25	50 993 9	8
HBD HUMAN Hemoglobin subunit delta	2.66E-10	78.23	16 045 3	12
FETLIA HUMAN Alpha 2 HS glycoprotein	2.00E 10	20.27	30 200 7	12
DIAC HUMAN Di N acetulohitohinga	0.50E 10	20.27	12 721 6	7
A2AD HUMAN Alaba 2 antialogmin	9.02E 10	20.20	43,731.0	2
AZAF_HOMAN Apha-2-antipiasinii	9.02E-10	40.24	14,351.2	4
SUDC HUMAN for homeone binding states	1.01E-09	18.23	14,200.2	4
SHBG_HUMAN Sex normone-binding globulin	2.19E-09	60.24	43,/51.9	6
ENOIB_HUMAN Alpha-enoiase, lung specific	2.99E-09	10.21	49,446.4	2
AIFI_HUMAN Allograft inflammatory factor I	3.56E-09	10.23	16,692.6	1
FRIH_HUMAN Ferritin heavy chain	5.57E-09	60.25	21,212.3	8
FIBA_HUMAN Fibrinogen alpha chain	7.21E-09	98.28	94,914.3	17
IGHD_HUMAN Ig delta chain C region	7.77E-09	30.23	42,227.3	6
LUM_HUMAN Lumican	1.22E-08	60.30	38,404.8	14
GELS_HUMAN Gelsolin	2.34E-08	20.21	85,644.3	2
HBB_HUMAN Hemoglobin subunit beta	2.70E-08	50.22	15,988.3	14
COF1_HUMAN Cofilin-1	3.91E-08	10.26	18,490.7	1
KV1S_HUMAN Ig kappa chain V-I region Wes	4.88E-08	10.21	11,600.7	1
MUCB_HUMAN Ig mu heavy chain disease protein	5.93E-08	56.22	43,030.3	15
LV3B_HUMAN Ig lambda chain V-III region LOI	9.13E-08	20.24	11,927.8	6
FETUB_HUMAN Fetuin-B	9.28E-08	60.27	42,028.0	8
K2C1_HUMAN Keratin, type II cytoskeletal 1	1.53E-07	46.37	65,977.9	6
IGHM_HUMAN Ig mu chain C region	2.18E-07	30.23	49,275.6	5
MMP1_HUMAN Interstitial collagenase	2.78E-07	30.21	53,972.8	3
COTL1_HUMAN Coactosin-like protein	3.14E-07	10.23	15,935.0	1
KV3G_HUMAN Ig kappa chain V-III region GOL	3.86E-07	10.21	11,823.0	4
CATB_HUMAN Cathepsin B	3.96E-07	10.16	37,796.8	1
S10A9_HUMAN Protein S100-A9	4.68E-07	10.19	13,233.5	1
THIO_HUMAN Thioredoxin	4.91E-07	10.18	11,729.7	4
TRFE_HUMAN Serotransferrin	5.57E-07	50.26	136,191	6
A2MG_HUMAN Alpha-2-macroglobulin	6.03E-07	20.21	163,174.3	3
ANT3_HUMAN Antithrombin-III	6.29E-07	10.21	52,569.0	1
KPYM_HUMAN Pyruvate kinase isozymes M1/M2	7.06E-07	10.24	57,900.2	1
PROF1_HUMAN Profilin-1 (Profilin I)	8.10E-07	30.20	15,044.6	3

	P (pro)	Score	MW	Hits
CO8B HUMAN Complement component C8 beta chain	8.76E-07	30.17	67,003.5	3
PCOC1 HUMAN Procollagen C-endopeptidase enhancer 1	1.74E-06	20.19	47,942.0	2
HV3J HUMAN Ig heavy chain V-III region HIL	1.97E-06	10.19	13,557.2	3
SAMP HUMAN Serum amyloid P-component	2.29E-06	10.16	25,371.1	1
KV31 HUMAN Ig kappa chain V–III region VG	2.90E-06	20.25	12,567.3	4
CAPG HUMAN Macrophage-capping protein	3.08E-06	10.20	38,493.6	1
APOC3 HUMAN Apolipoprotein C-III	4.71E-06	20.21	10,845.5	3
CO7 HUMAN Complement component C7	5.24E-06	48.24	93,457.3	6
ADIPO HUMAN Adiponectin	7.98E-06	10.22	26,397.0	1
KV1V HUMAN Ig kappa chain V-I region BAN	9.70E-06	10.21	11,832.8	1
HV1G HUMAN Ig heavy chain V-I region V35	1.01E-05	10.15	13,000.4	1
KV4C HUMAN Ig kappa chain V-IV region B17	2.11E-05	20.16	14,956.5	2
TETN HUMAN Tetranectin	2.36E-05	10.18	22.552.3	1
APOD HUMAN Apolipoprotein D	7.83E-05	20.13	21,261.8	4
IGL1 HUMAN Immunoglobulin lambda-like nolynentide 1	8 60E-05	28.19	22 948 6	3
IGL HUMAN Immunoglobulin I chain	8.94F-05	10.13	15 584 6	1
HV3R HUMAN Ig heavy chain V-III region TUR	1.01E-04	10.13	12 423 3	3
SA AA HUMAN Serum amyloid A-A protein	1.78E-04	10.22	14 797 3	2
HV1C HUMAN Is heavy chain VI region ND	1.78E 04	10.13	16 493 0	1
HPTP HIMAN Ig neavy chain v-i region ND	1.93E 04	10.13	28 082 7	1
IV2A IIIMAN Ia lambda ahain VIII ragion SII	1.94E 04	10.18	11 285 6	1
CO1A1 HUMAN Collagen alpha 1(1) shoin	5.30E-04	10.17	11,363.0	ے 1
MDOA2 HUMAN Conagen appra-1(1) chain	J.80E-04	10.13	50,488.2	1
MBOA2_HUMAN Memorane-bound O-acyltransierase domain-containing	7.03E-04	10.11	39,488.5	1
ZA26_HOMAN Zinc-aipna-z-giycoprotein	8.0/E-04	10.14	33,830.9	1
TTUV IIIMAN Transformation	1.00E 20	250.24	15 977 1	114
ITHY_HUMAN Transtnyretin	1.00E-30	350.34	15,8/7.1	114
HBA_HUMAN Hemoglobin subunit alpha	1.00E-30	90.31	15,247.9	15
CO8B_HUMAN Complement component C8 beta chain	1.00E-30	10.26	67,003.5	1
CFAB_HUMAN Complement factor B	/.//E=15	220.34	85,4/8.6	52
ITIH2_HUMAN Inter-alpha-trypsin inhibitor heavy chain H2	8.88E-15	10.29	106,369.8	I
CO8G_HUMAN Complement component C8 gamma chain	9.99E-15	30.25	22,263.6	5
K1C9_HUMAN Keratin, type I cytoskeletal 9	9.99E-15	20.38	62,091.8	2
CERU_HUMAN Ceruloplasmin	1.11E-14	60.28	122,127.6	7
CLUS_HUMAN Clusterin	1.67E-14	190.29	52,461.1	57
G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase	2.11E-14	50.33	36,030.4	5
CBPN_HUMAN Carboxypeptidase N catalytic chain	3.55E-14	20.26	52,253.4	3
RETBP_PANTR Plasma retinol-binding protein	4.00E-14	60.32	22,995.3	34
AMBP_HUMAN AMBP protein	4.00E-14	30.27	38,974.0	4
ENOA_HUMAN Alpha-enolase	5.33E-14	148.35	47,139.4	43
IGKC_HUMAN Ig kappa chain C region	5.77E-14	60.29	11,601.7	66
HEMO_HUMAN Hemopexin	2.15E-13	136.31	51,643.3	41
ANT3_HUMAN Antithrombin-III	7.48E-13	316.31	52,569.0	59
S10AC_HUMAN Protein S100-A12	1.80E-12	40.36	10,568.5	8
HBD_HUMAN Hemoglobin subunit delta	2.46E-12	206.30	16,045.3	77
KLKB1_HUMAN Plasma kallikrein	2.60E-12	50.24	71,322.8	6
ENOB_HUMAN Beta-enolase	2.71E-12	38.26	46,957.4	9
SHBG_HUMAN Sex hormone-binding globulin	5.08E-12	90.29	43,751.9	23
ITIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H4	6.78E-12	110.29	103,261.2	25
S10A8_HUMAN Protein S100-A8	7.06E-12	20.31	10,827.7	5

	P (pro)	Score	MW	Hits
APOC2_HUMAN Apolipoprotein C-II	9.10E-12	100.29	11,276.8	30
PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase	1.26E-11	60.29	62,178.0	8
KV1D_HUMAN Ig kappa chain V-I region CAR	1.76E-11	10.25	11,696.3	3
KV1S_HUMAN Ig kappa chain V-I region Wes	2.20E-11	10.23	11,600.7	2
APOM_HUMAN Apolipoprotein M	2.21E-11	70.25	21,239.4	11
HBB_HUMAN Hemoglobin subunit beta	2.64E-11	208.31	15,988.3	131
IGHA1_HUMAN Ig alpha-1 chain C region	3.97E-11	80.26	37,630.7	29
LAC_HUMAN Ig lambda chain C regions	6.32E-11	60.27	11,229.5	19
CFAI_HUMAN Complement factor I	6.39E-11	116.28	65,676.7	21
KV4C_HUMAN Ig kappa chain V-IV region B17	7.16E-11	20.26	14,956.5	3
THRB_HUMAN Prothrombin	1.36E-10	40.28	69,992.2	5
APOA1 HUMAN Apolipoprotein A-I	1.44E-10	530.26	30,758.9	302
CFAD HUMAN Complement factor D	2.12E-10	30.22	27,015.9	4
IGHA2 HUMAN Ig alpha-2 chain C region	2.79E-10	118.23	36,485.1	36
FIBB HUMAN Fibrinogen beta chain	2.86E-10	100.27	55,892.2	16
HPT HUMAN Haptoglobin	3.59E-10	130.32	45,176.6	28
SAMP HUMAN Serum amyloid P-component	4.06E-10	60.21	25,371.1	12
KV3H HUMAN Ig kappa chain V-III region CLL	5.94E-10	10.22	14,266.2	2
APOA2 HUMAN Apolipoprotein A-II	7.84E-10	60.31	11,167.9	7
HSP71 PONAB Heat shock 70 kDa protein 1	8.30E-10	10.24	70,009.2	1
CO8A HUMAN Complement component C8 alpha chain	9.20E-10	20.25	65,121.0	2
S10A9 HUMAN Protein S100-A9	1.43E-09	40.25	13,233.5	7
ALBU HUMAN Serum albumin	2.15E-09	262.26	69.321.6	70
VASP HUMAN Vasodilator-stimulated phosphoprotein	2.32E-09	10.23	39,805.1	1
K2C1 HUMAN Keratin, type II cytoskeletal 1	2.40E-09	26.41	65,977.9	4
FIBA HUMAN Fibrinogen alpha chain	2.63E-09	30.23	94,914.3	3
ADIPO HUMAN Adiponectin	3.36E-09	10.22	26,397.0	1
FIBG HUMAN Fibrinogen gamma chain	1.33E-08	70.27	51,478.9	14
ENO1B HUMAN Alpha-enolase, lung specific	1.53E-08	50.29	49,446,4	9
LV4C HUMAN Ig lambda chain V-IV region Hil	1.59E-08	10.25	11,509.6	2
IGHG3 HUMAN Ig gamma-3 chain C region	2.06E-08	10.18	41,260,4	1
COR1A HUMAN Coronin-1A	2.58E-08	10.24	50,993,9	1
CO4A HUMAN Complement C4-A	3.08E-08	20.24	192,649.5	2
KV3G HUMAN Ig kappa chain V-III region GOL	3.61E-08	10.21	11.823.0	3
IGHD HUMAN Ig delta chain C region	3.83E-08	20.19	42,227.3	3
FRIH HUMAN Ferritin heavy chain	3.91E-08	10.21	21,212,3	1
IGHM HUMAN Ig mu chain C region	5.37E-08	20.23	49.275.6	13
LUM HUMAN Lumican	5.61E-08	80.26	38.404.8	17
PSA6 RAT Proteasome subunit alpha type-6	6.04E-08	20.17	27.381.8	2
MUCB HUMAN Ig mu heavy chain disease protein	1.04E-07	58.23	43.030.3	12
LV3B HUMAN Ig lambda chain V-III region LOI	1.17E-07	30.24	11.927.8	6
CO1A1 HUMAN Collagen alpha-1(I) chain	1.76E-07	10.15	138.826.8	1
APOE HUMAN Apolipoprotein E	1.87E-07	20.19	36.131.8	3
CAPG HUMAN Macrophage-capping protein	2.00E-07	10.19	38.493.6	1
LMNA HUMAN Lamin-A/C	2.15E-07	30.20	74,094.8	4
A2MG HUMAN Alpha-2-macroglobulin	3.81E-07	60.19	163.174.3	7
IGLL1 HUMAN Immunoglobulin lambda-like polypeptide 1	4.24E-07	38.22	22,948.6	5
CFAH HUMAN Complement factor H	6.11E-07	10.14	139.004 4	1
GELS HUMAN Gelsolin	1.31E-06	20.23	85,644.3	2

	P (pro)	Score	MW	Hits
HV1G HUMAN Ig heavy chain V-I region V35	1.50E-06	10.16	13,000.4	1
CO3 HUMAN Complement C3	1.59E-06	30.22	187,029.3	3
FETUB HUMAN Fetuin-B	1.64E-06	10.26	42,028.0	1
UBP15 HUMAN Ubiquitin carboxyl-terminal hydrolase 15	3.10E-06	10.20	112,347.6	1
GPX3 HUMAN Glutathione peroxidase 3	3.23E-06	60.20	25,386.0	6
FETUA HUMAN Alpha-2-HS-glycoprotein	4.85E-06	20.18	39,299.7	2
APOA4 HUMAN Apolipoprotein A-IV	5.76E-06	10.19	45,371.5	1
FGFP2 HUMAN Fibroblast growth factor-binding protein 2	1.29E-05	20.18	24,565.2	2
APOC1 HUMAN Apolipoprotein C-I	2.47E-05	10.12	9,326.1	1
APOD HUMAN Apolipoprotein D	2.86E-05	10.12	21,261.8	1
HV3P HUMAN Ig heavy chain V-III region TEI	2.88E-05	10.20	12,794.4	3
GDIS HUMAN Rho GDP-dissociation inhibitor 2	3.11E-05	10.18	22,973.6	1
TENA HUMAN Tenascin	3.65E-05	10.16	240,710.7	1
HV1B HUMAN Ig heavy chain V-I region HG3	3.81E-05	10.17	12,937.3	1
TRFE HUMAN Serotransferrin	4.38E-05	66.22	76,999.7	7
PROF1 HUMAN Profilin-1	4.39E-05	10.22	15,044.6	1
KV3I HUMAN Ig kappa chain V-III region VG	8.00E-05	20.25	12,567.3	3
APOB HUMAN Apolipoprotein B-100	8.41E-05	20.21	515,241.6	2
LV3A HUMAN Ig lambda chain V-III region SH	8.52E-05	10.21	11,385.6	1
APOC3 HUMAN Apolipoprotein C-III	8.88E-05	10.16	10,845.5	1
PRDX6 HUMAN Peroxiredoxin-6	9.49E-05	10.14	25,019.2	1
DOPO HUMAN Dopamine beta-hydroxylase	1.01E-04	20.16	69,020.8	2
KV1V HUMAN Ig kappa chain V-I region BAN	1.47E-04	10.19	11,832.8	2
TRIM7 HUMAN Tripartite motif-containing protein 7	2.81E-04	10.15	56,595.0	6
SAA4 HUMAN Serum amyloid A-4 protein	3.43E-04	20.16	14,797.3	4
Fraction 33 proteins				
HBA HUMAN Hemoglobin subunit alpha	1.00E-30	350.39	15,247.9	127
PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase	1.11E-15	268.33	62,178.0	53
CFAB_HUMAN Complement factor B	1.11E-15	180.34	85,478.6	30
RETBP_PANTR Plasma retinol-binding protein	1.11E-15	70.32	22,995.3	30
APOA1_HUMAN Apolipoprotein A-I	8.88E-15	648.34	30,758.9	410
S10AC_HUMAN Protein S100-A12	1.22E-14	20.35	10,568.5	3
CO3_HUMAN Complement C3	2.11E-14	468.34	187,029.3	76
HEMO_HUMAN Hemopexin	6.33E-14	178.29	51,643.3	30
TTHY_HUMAN Transthyretin	1.45E-13	220.33	15,877.1	49
CFAI_HUMAN Complement factor I	2.96E-13	88.28	65,676.7	14
ENOA_HUMAN Alpha-enolase	3.60E-13	50.33	47,139.4	7
CERU_HUMAN Ceruloplasmin	3.69E-13	60.33	122,127.6	6
K2C1_HUMAN Keratin, type II cytoskeletal 1	3.94E-13	76.34	65,977.9	9
ITIH2_HUMAN Inter-alpha-trypsin inhibitor heavy chain H2	1.32E-12	50.33	106,369.8	6
ENOB_HUMAN Beta-enolase	1.48E-12	10.25	46,957.4	3
CO8G_HUMAN Complement component C8 gamma chain	3.98E-12	20.20	22,263.6	3
ANT3_HUMAN Antithrombin-III	4.03E-12	268.30	52,569.0	39
IGKC_HUMAN Ig kappa chain C region	4.14E-12	100.29	11,601.7	54
IGHA1_HUMAN Ig alpha-1 chain C region	1.07E-11	90.29	37,630.7	32
KV1D_HUMAN Ig kappa chain V-I region CAR	1.20E-11	20.26	11,696.3	3
APOM_HUMAN Apolipoprotein M	1.29E-11	60.25	21,239.4	8
CO4A_HUMAN Complement C4-A	1.48E-11	200.28	192,649.5	25
PSA2_HUMAN Proteasome subunit alpha type-2	1.55E-11	60.29	25,882.3	8

	P (pro)	Score	MW	Hits
HV3R_HUMAN Ig heavy chain V-III region TUR	2.17E-11	20.25	12,423.3	4
KV1R_HUMAN Ig kappa chain V-I region WEA	2.35E-11	26.28	11,832.8	8
HBB_HUMAN Hemoglobin subunit beta	3.15E-11	190.27	15,988.3	85
HBD_HUMAN Hemoglobin subunit delta	4.14E-11	228.29	16,045.3	66
GSTP1_HUMAN Glutathione S-transferase P	7.69E-11	30.25	23,341.0	4
LV4C_HUMAN Ig lambda chain V-IV region Hil	8.74E-11	20.26	11,509.6	4
FIBA_HUMAN Fibrinogen alpha chain	9.51E-11	20.26	94,914.3	2
APOC2_HUMAN Apolipoprotein C-II	1.01E-10	100.28	11,276.8	17
LAC_HUMAN Ig lambda chain C regions	1.09E-10	50.27	11,229.5	14
S10A9_HUMAN Protein S100-A9	1.16E-10	128.28	13,233.5	31
CLUS_HUMAN Clusterin	2.11E-10	218.30	52,461.1	47
SAMP_HUMAN Serum amyloid P-component	2.58E-10	10.19	25,371.1	2
HV3P_HUMAN Ig heavy chain V-III region TEI	4.78E-10	10.26	12,794.4	3
KV3H_HUMAN Ig kappa chain V-III region CLL	6.52E-10	10.21	14,266.2	2
PERM_HUMAN Myeloperoxidase	6.57E-10	10.21	83,815.0	1
ALBU_HUMAN Serum albumin	6.70E-10	190.27	69,321.6	44
SPB10_HUMAN Serpin B10	7.84E-10	30.21	45,374.0	3
CO6A1_HUMAN Collagen alpha-1(VI) chain	7.93E-10	20.26	108,462.0	3
A2GL_HUMAN Leucine-rich alpha-2-glycoprotein	8.29E-10	50.25	38,154.1	8
IGHA2_HUMAN Ig alpha-2 chain C region	1.05E-09	94.24	36,485.1	28
ITIH1_HUMAN Inter-alpha-trypsin inhibitor heavy chain H1	1.10E-09	30.26	101,325.8	3
KV1S_HUMAN Ig kappa chain V-I region Wes	1.21E-09	10.23	11,600.7	1
APOA2_HUMAN Apolipoprotein A-II	1.22E-09	100.28	11,167.9	13
CATD_HUMAN Cathepsin D	1.30E-09	32.22	44,523.7	4
A2MG_HUMAN Alpha-2-macroglobulin	1.34E-09	120.23	163,174.3	16
SHBG_HUMAN Sex hormone-binding globulin	1.66E-09	10.29	43,751.9	1
KV4C_HUMAN Ig kappa chain V-IV region B17	1.69E-09	30.24	14,956.5	5
TRFE_HUMAN Serotransferrin	4.52E-09	20.21	76,999.7	2
ITIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H4	6.22E-09	110.26	103,261.2	16
MUCB_HUMAN Ig mu heavy chain disease protein	6.34E-09	68.25	43,030.3	20
S10A8_HUMAN Protein S100-A8	6.64E-09	20.25	10,827.7	2
HSP71_PONAB Heat shock 70 kDa protein 1	6.79E-09	20.27	70,009.2	2
HPT_HUMAN Haptoglobin	7.42E-09	132.26	45,176.6	24
KV3G_HUMAN Ig kappa chain V-III region GOL	7.50E-09	10.23	11,823.0	2
AFAM_HUMAN Afamin	2.07E-08	70.24	69,024.1	7
FIBB_HUMAN Fibrinogen beta chain	2.09E-08	70.24	55,892.2	8
K1C9_HUMAN Keratin, type I cytoskeletal 9	2.09E-08	40.33	62,091.8	4
TKT_HUMAN Transketolase	2.24E-08	40.21	67,834.9	5
IGHM_HUMAN Ig mu chain C region	2.76E-08	50.25	49,275.6	9
GELS_HUMAN Gelsolin	3.10E-08	10.23	85,644.3	1
FIBG_HUMAN Fibrinogen gamma chain	3.14E-08	50.19	51,478.9	5
IGHD_HUMAN Ig delta chain C region	3.27E-08	20.19	42,227.3	3
ADIPO_HUMAN Adiponectin	4.87E-08	10.23	26,397.0	1
PRDX2_HUMAN Peroxiredoxin-2	5.29E-08	50.21	21,878.2	6
LV3B_HUMAN Ig lambda chain V-III region LOI	7.16E-08	20.22	11,927.8	4
VASP_HUMAN Vasodilator-stimulated phosphoprotein	1.37E-07	30.25	39,805.1	5
PSA6_RAT Proteasome subunit alpha type-6	2.97E-07	10.17	27,381.8	1
ENO1B_HUMAN Alpha-enolase, lung specific	6.65E-07	10.26	49,446.4	1
HPTR_HUMAN Haptoglobin-related protein	6.93E-07	10.20	38,982.7	1

	P (pro)	Score	MW	Hits
IGHG3 HUMAN Ig gamma-3 chain C region	1.04E-06	20.18	41,260.4	2
G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase	1.35E-06	20.22	36,030.4	3
KLKB1_HUMAN Plasma kallikrein	2.39E-06	10.18	71,322.8	1
ANXA1_HUMAN Annexin A1	2.64E-06	10.20	38,690.0	1
ANXA3_HUMAN Annexin A3	3.79E-06	24.18	36,352.7	3
AMPL HUMAN Cytosol aminopeptidase	4.31E-06	10.14	56,130.9	1
S100P HUMAN Protein S100-P	4.65E-06	10.18	10,393.2	1
MMP8_HUMAN Neutrophil collagenase	4.76E-06	30.23	53,378.6	3
APOE_HUMAN Apolipoprotein E	5.02E-06	50.21	36,131.8	6
HBG1_PANTR Hemoglobin subunit gamma-1	8.24E-06	20.16	16,130.3	2
KV1V_HUMAN Ig kappa chain V-I region BAN	9.89E-06	10.22	11,832.8	1
APOA4_HUMAN Apolipoprotein A-IV	1.25E-05	60.19	45,371.5	7
KV3I_HUMAN Ig kappa chain V-III region VG precursor	1.41E-05	20.23	12,567.3	3
HV3A_HUMAN Ig heavy chain V-III region TRO	1.43E-05	10.16	13,463.5	1
THBG HUMAN Thyroxine-binding globulin	1.94E-05	10.20	46,294.7	1
K1C14 HUMAN Keratin, type I cytoskeletal 14	2.73E-05	10.13	51,589.5	1
IGLL1 HUMAN Immunoglobulin lambda-like polypeptide 1	3.37E-05	38.21	22,948.6	5
K1C10 HUMAN Keratin, type I cytoskeletal 10	5.01E-05	30.19	59,474.8	3
LV3A HUMAN Ig lambda chain V-III region SH	8.87E-05	10.18	11,385.6	1
CRP HUMAN C-reactive protein	2.33E-04	20.18	25,022.7	2
CBPN HUMAN Carboxypeptidase N catalytic chain	2.42E-04	10.24	52,253.4	1
CAPG HUMAN Macrophage-capping protein	2.55E-04	20.16	38,493.6	2
SAA4 HUMAN Serum amyloid A-4 protein	2.71E-04	20.14	14,797.3	2
MMP3 HUMAN Stromelysin-1	4.23E-04	10.13	53,943.4	1
GDIS HUMAN Rho GDP-dissociation inhibitor 2	6.94E-04	20.25	22,973.6	2
HV3V HUMAN Ig heavy chain V-III region GAR	8.20E-04	10.13	13,079.2	1
Fraction 34 proteins				
CO3 HUMAN Complement C3	1.00E-30	576.33	187,029.3	99
HBA HUMAN Hemoglobin subunit alpha	1.00E-30	230.37	15,247.9	91
TTHY HUMAN Transthyretin	1.00E-30	150.33	15,877.1	28
CFAB HUMAN Complement factor B	3.33E-15	120.35	85,478.6	20
PGRP2 HUMAN N-acetylmuramoyl-L-alanine amidase	8.88E-15	290.34	62,178.0	52
IGKC HUMAN Ig kappa chain C region	1.11E-14	70.29	11,601.7	40
APOA1 HUMAN Apolipoprotein A-I	1.89E-14	862.32	30,758.9	660
ENOB_HUMAN Beta-enolase	2.34E-13	10.24	46,957.4	1
ENOA HUMAN Alpha-enolase	4.31E-13	40.24	47,139.4	4
RETBP PANTR Plasma retinol-binding protein	7.37E-13	58.31	22,995.3	20
KV4C HUMAN Ig kappa chain V-IV region B17	8.39E-13	20.26	14,956.5	3
IGHA1 HUMAN Ig alpha-1 chain C region	9.03E-13	110.27	37,630.7	28
QSOX1_HUMAN Sulfhydryl oxidase 1	1.02E-12	60.29	82,525.7	6
HV3R HUMAN Ig heavy chain V-III region TUR	1.09E-12	10.28	12,423.3	2
MMP8 HUMAN Neutrophil collagenase	1.19E-12	60.26	53,378.6	9
CO4A_HUMAN Complement C4-A	4.03E-12	190.32	192,649.5	21
ITIH1_HUMAN Inter-alpha-trypsin inhibitor heavy chain H1	4.04E-12	110.34	101,325.8	16
APOL1_HUMAN Apolipoprotein-L1	4.42E-12	10.28	43,947.0	1
CO6A1_HUMAN Collagen alpha-1(VI) chain	8.68E-12	40.32	108,462.0	6
LAC_HUMAN Ig lambda chain C regions	1.47E-11	50.28	11,229.5	20
CFAI_HUMAN Complement factor I	1.60E-11	66.24	65,676.7	10
ALBU_HUMAN Serum albumin	2.54E-11	150.26	69,321.6	27

CBPB2_HUMAN Carboxypeptidase B2 3.13E-11 10.23 48,381.5 1 APOA2_IUMAN Apolipopytein A-II 4.64E-11 118.31 11,167.9 24 HEMO_HUMAN Hemopexin 9.46E-11 10.31 51,643.3 16 S10A9_HUMAN Protein S100-A9 2.64E-10 136.27 13,233.5 33 INY3F IUMAN Ig heavy chain VII region TEI 3.69E-10 10.26 12,794.4 1 TIPL_HUMAN Glutathione S-transferase P 4.12E-10 30.26 83,815.0 10 FRM_HUMAN Nycloperovidase 4.13E-10 30.26 83,815.0 10 FIBB_HUMAN Florinogen beta chain 4.90E-10 60.27 55,892.2 7 HBG1_PANTR Hemoglobin suburit detta 8.76E-10 100.31 51,643.3 20 HED_HUMAN Ilemoglobin suburit detta 8.76E-10 106.31 16,645.3 20 HED_HUMAN Ilemoglobin suburit detta 8.76E-10 10.21 11,832.8 1 MUCB_HUMAN Ig apha-chain Cregion 1.79F-09 98.22 36,645.1 28 APOC_HUMAN Apolipoprotein C-II 2.18E-09 </th <th></th> <th>P (pro)</th> <th>Score</th> <th>MW</th> <th>Hits</th>		P (pro)	Score	MW	Hits
APOA2 JUUMAN Apolipoprotein A-II 4.64E-11 118.21 11,67.9 24 HEMO_HUMAN Hemopexin 9.46E-10 100.31 51,643.3 16 S10A9 HUMAN Protein S100-A9 2.64E-10 102.67 12,32.5 33 GSTP1 HUMAN Ig heavy chain V-III region TEI 3.86E-10 30.20 106,30.88 3 GSTP1 HUMAN Mycloperoxidase 4.13E-10 30.26 23,341.0 3 PERM HUMAN Printers/bin-arrysein inhibitor heavy chain H2 3.86E-10 30.22 16,130.3 4 ANT3 HUMAN Antifrhombin-III 7.22E-10 50.30 52,569.0 8 HBD_HUMAN It hemoglobin subunit delta 8.76E-10 10.83.1 16.60.5.3 20 HED_HUMAN It hemoglobin subunit delta 8.76E-10 10.83.1 16.60.5.3 20 HEV UV-HUMAN Ig tappa chain V-Iregion BAN 1.08E-09 7.82.3 43.00.3 14 KVIV_HUMAN Ig tappa chain V-Iregion CLI 2.18E-09 7.82.3 43.60.6 9 GMCG HUMAN Apolipoprotein C-II 2.18E-09 7.82.3 43.60.7 5 GHAY <t< td=""><td>CBPB2_HUMAN Carboxypeptidase B2</td><td>3.13E-11</td><td>10.23</td><td>48,381.5</td><td>1</td></t<>	CBPB2_HUMAN Carboxypeptidase B2	3.13E-11	10.23	48,381.5	1
HEMO_HUMAN Hemogexin 9.46E-11 100.11 \$1,64.3.3 16 S10A9_HUMAN Protein S100-A9 2.64E-10 136.27 13,233.5 33 HV3P HUMAN Inter-alpha-trypsin inhibitor havy chain H2 3.86E-10 30.29 106,369.8 3 GSTP1_HUMAN Nuter-alpha-trypsin inhibitor havy chain H2 3.86E-10 30.29 683,815.0 10 FRM_HUMAN Nytolperxvidase 4.13E-10 90.26 83,815.0 10 FRM_HUMAN Fibringen beta chain 4.00E-10 60.27 55,892.2 7 HBD, HUMAN Hemoglobin subunit datin 8.76E-10 108.31 16,045.3 20 HEU_HUMAN Leukocyte chatses inhibitor 9.01E-10 10.24 42,71.48 1 KV1V_HUMAN Ig alpha2 chain V1 region BAN 1.08E-09 10.21 11,832.8 1 KU1A_HUMAN Ig alpha2 chain C region 1.74E-09 80.26 11,276.8 3 GICHA_HUMAN AnexinA1 3.24E-09 80.26 11,276.8 3 GICHA_HUMAN AnexinA1 3.24E-09 80.27 15,988.3 18 GICHA_HUMAN AnexinA1 3.2	APOA2_HUMAN Apolipoprotein A-II	4.64E-11	118.31	11,167.9	24
S10A2, HUMAN Protein S100-A9 2.64H-10 136.27 13,233.5 33 HV3P_HUMAN Ig heavy chain VIII region TEI 3.66H-10 30.29 106,369.8 3 GSTP1_HUMAN Clutathines Stransferse P 4.12E-10 30.26 83,815.0 10 FIBB. HUMAN Wyeloperoxidase 4.13E-10 90.26 83,815.0 10 FIBB. HUMAN Nichtenbines Stransferse P 4.13E-10 90.26 83,815.0 10 FIBB. HUMAN Nichtones Stransferse P 4.13E-10 90.26 83,815.0 10 FIBB. HUMAN Nichtones Stransferse P 4.13E-10 90.26 83,815.0 10 FIBB. HUMAN Nichtones Stransferse P 4.13E-10 90.26 15,30.3 4 ANT3 HUMAN Antifree Stransferse P 9.021 10.23.2 16,10.3 4 ANT3 HUMAN Na Antifree Stransferse P 9.91E-10 10.24 42,714.8 1 MUCB HUMAN Ig kappa chain V-largion BAN 1.08E-09 10.21 11.83.2 11 MUCB HUMAN Ig kappa chain V-largion BAN 1.08E-09 10.21 11.83.2 12 MUCB HUMAN Ig anapa-2 chain C region 1.79E-09 9.02.2 52,461.1 2 </td <td>HEMO_HUMAN Hemopexin</td> <td>9.46E-11</td> <td>100.31</td> <td>51,643.3</td> <td>16</td>	HEMO_HUMAN Hemopexin	9.46E-11	100.31	51,643.3	16
IIV3P_IIUMAN Ig heavy chain V-III region TEI 3.69E-10 10.26 12,794.4 1 ITTRE_IUMAN Inter-alpha-trypsin inhibitor heavy chain H2 3.86E-10 30.26 23,341.0 3 SGTP1_HUMAN Molendamic Stransferase P 4.12E-10 90.26 83,815.0 10 FIBB_HUMAN Fibriongen beta chain 4.90E-10 60.27 55,892.2 7 BIG1 PANTR Hemoglobin subunit gamma-1 5.83E-10 108.31 16,045.3 20 ILEU_HUMAN Latkocyte elastase inhibitor 991E-10 10.24 42,714.8 1 KVIV, HUMAN Ig gap a chain V-I region BAN 1.08E-09 10.21 11,832.8 1 MUCB HUMAN Ig tapha chain V-I region BAN 1.08E-09 98.22 36,485.1 28 APOC2, HUMAN A gap a chain V-I region BAN 1.08E-09 98.22 36,485.1 28 APOC2, HUMAN A gapha-chain C region 2.78E-09 90.24 49,275.6 9 APOC2, HUMAN Anchin C region 2.74E-09 40.22 52,461.1 2 KV3H_HUMAN Ig mac chain V-II region CLL 5.07E-09 10.22 52,461.1 2 KV3H_HUMAN Ng gapan chain V-II region CLL 5.07E-09 10.22 <td>S10A9_HUMAN Protein S100-A9</td> <td>2.64E-10</td> <td>136.27</td> <td>13,233.5</td> <td>33</td>	S10A9_HUMAN Protein S100-A9	2.64E-10	136.27	13,233.5	33
ITHE HUMAN Inter-alpha-trypsin inhibitor heavy chain H2 3 862–10 30.29 106,369.8 3 GSTP1 ILLMAN Glutathione S-transferse P 4.12E–10 30.26 23,341.0 3 PIRM HUMAN Myeloperoxidisee 4.13E–10 90.26 83,815.0 10 FIBB_HUMAN Fibrinogen beta chain 4.90F–10 66.27 55,892.2 7 HBGI_PANTR Hemoglobin subunit gamma-1 5.83E–10 30.22 16,103.3 4 ATT3 HUMAN Anthitrombin-TII 7.22E–10 108.31 16,045.3 20 ILEU_HUMAN Ig kappa chain V-I region BAN 108E–09 102.1 11,832.8 1 MUCB_HUMAN Ig tappa-chain Gregion 1.79E–09 98.22 36,485.1 28 APOC2_HUMAN Apolioprotein C-II 2.18E–09 30.26 11,276.8 3 IGHA_HUMAN Ig ma chain C region 2.74E–09 40.24 49,275.6 9 ANXA_HUMAN Anchinoprotein C-II 2.18E–09 30.25 11,276.8 3 IGHM_HUMAN Ig agapa chain V-III region CLL 5.07E–09 10.22 5.246.1.1 2 KV3H_HUMAN Is dealta chain 9.00E–09 20.27 94,914.3 2 <tr< td=""><td>HV3P_HUMAN Ig heavy chain V-III region TEI</td><td>3.69E-10</td><td>10.26</td><td>12,794.4</td><td>1</td></tr<>	HV3P_HUMAN Ig heavy chain V-III region TEI	3.69E-10	10.26	12,794.4	1
GSTP1, HUMAN Glutahione S-transferase P 4,12E-10 30,26 23,341.0 3 PERM, HUMAN Mycloperoxidase 4,13E-10 90,26 83,815.0 10 PIBL JUMAN Fibrinogen beta chain 5,80E-10 30,22 16,130.3 4 ANT3, HUMAN Antimombin-III 7,22E-10 50,30 52,560.0 8 IBD_JIUMAN Itemoglobin subunit denta 7,67E-10 10,24 42,714.8 1 KVIV, HUMAN Ig mappe chain V-Ir groin BAN 1,08E-09 10,21 11,838.8 1 MCGB_IUMAN Ng up bains v-1 groin BAN 1,08E-09 10,24 42,714.8 1 IGHA 2, HUMAN Ig anapha-2 chain C region 1,79E-09 98,22 36,485.1 28 APOC2_HUMAN Ng muchain C region 1,79E-09 30,22 34,430.3 14 IGHA HUMAN Ig muchain C region 2,74E-09 40,24 49,275.6 9 APOC2_HUMAN Ng Igan chain V-III region CLL 507E-09 10,25 24,46.1 2 IGHA HUMAN Ig anapha-2 chain C region 7,74E-09 40,24 46,352.7 5 IGHA HUMAN Ig ganpa-3 chain V-III	ITIH2_HUMAN Inter-alpha-trypsin inhibitor heavy chain H2	3.86E-10	30.29	106,369.8	3
PERM. HUMAN Myeloperoxidase 4.13E-10 90.26 83,815.0 10 FIBB_HUMAN Fibringen beta chain 4.90E-10 60.27 55,892.2 7 BIGD_PANTR Hemoglobin subunit gamma-1 5.83E-10 30.22 16,130.3 4 ANT3_HUMAN Antithrombin-III 7.22E-10 50.30 52,569.0 8 HBD_JIUMAN Hemoglobin subunit delta 8.76E-10 10.24 42,714.8 1 KVIV_HUMAN Ig kappa chain V-I region BAN 1.08E-09 10.21 11,832.8 1 MUCB_HUMAN Ig thu heavy chain disease protein 1.48E-09 78.23 43,030.3 14 GHA2_HUMAN Ig and hear C region 2.18E-09 30.26 11,276.8 3 APOC2_HUMAN Anchin C region 2.74E-09 40.24 49,275.6 9 ANXA1_HUMAN Ig mu chain C region 2.18E-09 30.26 11,276.8 3 IGHM HUMAN Ig dappa chain V-III region CLL 5.07E-09 10.25 14,266.2 1 HBB_HUMAN Ig delta chain C region 7.74E-09 20.27 94,914.3 2 IGHM HUMAN Ig delta chain C region	GSTP1_HUMAN Glutathione S-transferase P	4.12E-10	30.26	23,341.0	3
FIBB_IIUMAN Fibrinogen beta chain 4.90E-10 60.27 55,892.2 7 HBGI_PANTR Hemoglobin subunit gamma-1 5.88E-10 30.22 16,130.3 4 ANT3_HUMAN Anthithrombin-III 7.22E-10 50.30 52,569.0 8 HBD_HUMAN Hemoglobin subunit delta 8.76E-10 108.31 16,045.3 20 ILEU_HUMAN Leukocyte elastase inhibitor 9.91E-10 10.24 42,714.8 1 WICB_HUMAN Ig tapha-2 chain C region 1.08E-09 78.23 43,030.3 14 IGHA2_HUMAN Ig tapha-2 chain C region 1.79E-09 98.22 36,485.1 28 APOC2_HUMAN Ng tapha-2 chain C region 2.74E-09 80.27 38,690.0 13 CLUS_HUMAN Clusterin 4.75E-09 10.22 52,460.1 2 HBB_HUMAN Ng tapha chain V-III region CLL 5.07E-09 10.22 54,461.1 2 KY3H_HUMAN Ju K gapa chain V-III region CLL 6.68E-09 80.27 15,988.3 18 IGHD_HUMAN Ig authan chain 9.00E-09 2.019 42,227.3 2 KY3H_HUMAN Angenyan chain C region 7.4E-09 2.019 42,331.2 3	PERM_HUMAN Myeloperoxidase	4.13E-10	90.26	83,815.0	10
HBGI_PANTR Hemoglobin subunit gamma-1 5.83E-10 30.22 16,130.3 4 ANT3_HUMAN Antihrombin-III 7.22E-10 50.30 52,690.0 8 IBD_JIUMAN Hemoglobin subunit delta 8.76E-10 108.31 16,045.3 20 ILEU_HUMAN Leukocyte elastase inhibitor 9.91E-10 10.24 42,714.8 1 KVIV_HUMAN Ig mappa chain VI region BAN 1.08E-09 78.23 43,030.3 14 IGHA_HUMAN Ig alpha-2 chain C region 1.79E-09 98.22 36,485.1 28 APOC2_HUMAN Aploprotein C-II 2.18E-09 30.26 11,276.8 3 IGHM_HUMAN Ig map chain VI region CLL 5.07E-09 10.22 52,461.1 2 KV3H_HUMAN Rapa chain VI region CLL 5.07E-09 10.22 52,461.1 2 KV3H_HUMAN Rapa chain VI region CLL 5.07E-09 10.22 52,461.1 2 IBB_JIUMAN Fibrinogen alpha chain 9.00E-09 9.027 14,942.57.3 18 IGHD_HUMAN Ig kappa chain C region 1.14E-08 10.19 41,260.4 1 A2AP EHUMAN Fibrinogen alpha chain 9.08E-09 8.23 56,577.9 3 <t< td=""><td>FIBB_HUMAN Fibrinogen beta chain</td><td>4.90E-10</td><td>60.27</td><td>55,892.2</td><td>7</td></t<>	FIBB_HUMAN Fibrinogen beta chain	4.90E-10	60.27	55,892.2	7
ANT3_HUMAN Antithrombin-III 7.22E-10 50.30 52,569,0 8 HBD_HUMAN Hennoglobin subuni delta 8.76E-10 108.31 16,045.3 20 LEU_HUMAN Leukocyte clastase inhibitor 9.01E-10 10.24 42,714.8 1 MUCB_HUMAN Ig kappa chain V-I region BAN 1.08E-09 10.21 11,832.8 1 MUCB_HUMAN Ig alpha-2 chain C region 1.79E-09 98.22 36,485.1 28 POC2_HUMAN Apolipoprotein C-II 2.18E-09 30.26 11,276.8 3 IGHM_HUMAN Ig mu chain C region 2.74E-09 40.24 49,275.6 9 ANXA1_HUMAN Clusterin 3.24E-09 80.27 18,8690.0 13 CLUS_HUMAN Clusterin 4.75E-09 10.25 14,266.2 1 HBB_HUMAN I gapa chain V-III region CLL 5.07E-09 10.25 14,266.2 1 HBB_HUMAN I gapa chain V-III region CLL 5.07E-09 10.25 14,266.2 1 HBB_HUMAN N Ig delta chain C region 7.74E-09 20.27 9,4914.3 2 ANXA3_HUMAN Annexin A3 9.98E-09 48.24 36,352.7 5 IGHA_HUMAN I gamma-3 chai	HBG1_PANTR Hemoglobin subunit gamma-1	5.83E-10	30.22	16,130.3	4
HBD_HUMAN Hemoglobin subunit delta 8.76E-10 108.31 16.045.3 20 LLEU_HUMAN Leukocyte dastase inhibitor 9.91E-10 10.24 42.714.8 1 KVIV_HUMAN Ig kappa chain V-I region BAN 10.88E-09 78.23 43.030.3 14 IGHA2_HUMAN Ig nu heavy chain disease protein 1.48E-09 78.23 43.030.3 14 IGHA2_HUMAN Ig alpha-2 chain C region 1.79E-09 98.22 36.485.1 28 APOC2_HUMAN Apolipoprotein C-II 2.18E-09 80.27 38.690.0 13 ICHM_HUMAN Ig mu chain C region 2.74E-09 10.22 52.461.1 2 KV3H_HUMAN Ig kappa chain V-III region CLL 5.07E-09 10.25 14.266.2 1 HBB_HUMAN Hemoglobin subunit beta 6.68E-09 80.27 15.988.3 18 IGHAD_HUMAN Ig delta chain C region 7.74E-09 20.19 42.227.3 2 FIBA_HUMAN Fibrinogen alpha chain 9.00E-09 20.27 94.914.3 2 ANXA3_HUMAN Apha-2-antiplasmin 1.51E-08 20.24 54.531.2 3 APOM_HUMAN Apl	ANT3_HUMAN Antithrombin-III	7.22E-10	50.30	52,569.0	8
ILEU_HUMAN Leukocyte elastase inhibitor 9.91E-10 10.24 42,714.8 1 KVIV_HUMAN Ig kappa chain V-I region BAN 1.08E-09 78.23 43,030.3 14 MUCB_HUMAN Ig aubha-2 chain C region 1.78E-09 78.23 43,030.3 14 IGHAZ_HUMAN Ig alpha-2 chain C region 2.78E-09 90.26 11,276.8 3 APOC2_HUMAN Apolipoprotein C-II 2.18E-09 30.26 11,276.8 3 IGHM HUMAN Ig un chain C region 2.74E-09 80.27 38,690.0 13 CLUS_HUMAN Clusterin 4.75E-09 10.22 52,461.1 2 KV3H HUMAN Ig kappa chain V-III region CLL 5.07E-09 10.25 14,266.2 1 HBB_HUMAN Hemoglobin subunit beta 6.68E-09 80.27 15,988.3 18 IGHID HUMAN Ig delta chain C region 7.74E-09 20.19 42,227.3 2 FIBA_HUMAN Fly mana-3 chain C region 1.14E-08 10.19 41,260.4 1 AAP HUMAN Alpha-2-antiplasmin 1.51E-08 20.24 54,531.2 3 ACOGAJ_HUMAN Aclage ampha-3(VI) chain 1.68E-08 30.25 65,977.9 3	HBD_HUMAN Hemoglobin subunit delta	8.76E-10	108.31	16,045.3	20
KV1V_HUMAN Ig kappa chain V-I region BAN 1.08E-09 10.21 11.832.8 1 MUCB_HUMAN Ig mu heavy chain disease protein 1.48E-09 78.23 43.030.3 14 IGHA2_HUMAN Ig alpha-2 chain C region 1.79E-09 98.22 36.485.1 28 APOC2_HUMAN Apolipoprotein C-II 2.18E-09 30.26 11.726.8 3 IGHM_HUMAN Ig mu chain C region 2.74E-09 40.24 49.275.6 9 ANXA1_HUMAN Annexin A1 3.24E-09 80.27 38.690.0 13 CLUS_HUMAN Ig kappa chain V-III region CLL 5.07E-09 10.25 14.266.2 1 HBB_HUMAN Ig delta chain C region 7.74E-09 20.19 42.277.3 2 FIBA_HUMAN Ig delta chain C region 7.74E-09 20.27 94.914.3 2 ANXA3_HUMAN Annexin A3 9.08E-09 48.24 36.352.7 5 IGHG3_HUMAN Ig gamma-3 chain C region 1.14E-08 10.19 41.260.4 1 A2AP_HUMAN Apolipoprotein M 1.51E-08 30.25 21.239.4 3 APOM_HUMAN Collagen alpha-3(VI) chain 1.86E-08 34.23 343.337.4 4 K	ILEU_HUMAN Leukocyte elastase inhibitor	9.91E-10	10.24	42,714.8	1
MUCB_HUMAN Ig mu heavy chain disease protein 1.48E-09 78.23 43,030.3 14 IGHA2_HUMAN Ig alpha-2 chain C region 1.79E-09 98.22 36,485.1 28 APOC2_HUMAN Na polipoprotein C-II 2.18E-09 30.26 11,276.8 3 IGHM_HUMAN Ig mu chain C region 2.74E-09 40.24 49,275.6 9 ANXA1_HUMAN Annexin AI 3.24E-09 80.27 38,690.0 13 CLUS_HUMAN Ig mu chain C region 4.75E-09 10.22 52,461.1 2 KV3H_HUMAN Ig delta chain C region 5.07E-09 10.27 14,266.2 1 HBB_HUMAN Hemoglobin subunit beta 6.68E-09 80.27 15,988.3 18 IGHD HUMAN Ig delta chain C region 7.74E-09 20.19 42,227.3 2 FIBA_HUMAN Annexin A3 9.08E-09 48.24 36,352.7 5 IGHG3_HUMAN Apolipoprotein M 1.71E-08 20.24 54,531.2 3 APOM_HUMAN Apolipoprotein M 1.72E-08 30.25 21,239.4 3 APOM_HUMAN Apolipoprotein M 1.72E-08 30.22 51,478.9 2 LV4C HUMAN Keratin, type II cytoskel	KV1V_HUMAN Ig kappa chain V-I region BAN	1.08E-09	10.21	11,832.8	1
IGHA2_HUMAN Ig alpha-2 chain C region 1.79E-09 98.22 36,485.1 28 APOC2_HUMAN Apolipoprotein C-II 2.18E-09 30.26 11,276.8 3 IGHM_HUMAN Ig mu chain C region 2.74E-09 40.24 49,275.6 9 ANXA1_HUMAN Annexin A1 3.24E-09 80.27 38,690.0 13 CLUS_HUMAN Clusterin 4.75E-09 10.22 52,461.1 2 KV3H_HUMAN Ig kappa chain V-III region CLL 5.07E-09 10.25 14,266.2 1 HBB_HUMAN Ig delta chain C region 7.74E-09 20.19 42,227.3 2 FIBA_HUMAN Ig delta chain C region 7.74E-09 20.27 94,914.3 2 ANXA3_HUMAN Annexin A3 9.08E-09 48.24 36,352.7 5 IGHG3_HUMAN Alpha-2-antiplasmin 1.51E-08 20.24 54,531.2 3 APOM_HUMAN Apolipoprotein M 1.22E-08 30.25 21,239.4 3 CO6A3_HUMAN Kollagen alpha-3(VI) chain 1.86E-08 34.23 343,337.4 4 K2C1_HUMAN Kollagen alpha-3(VI) chain 3.23E-08 20.22 51,478.9 2 LV4C_HUMAN Ng lambda chain V-VI re	MUCB HUMAN Ig mu heavy chain disease protein	1.48E-09	78.23	43,030.3	14
APOC2_HUMAN Apolipoprotein C-II 2.18E-09 30.26 11,276.8 3 IGHM_HUMAN Ig mu chain C region 2.74E-09 40.24 49,275.6 9 ANXA1_HUMAN Annexin AI 3.24E-09 80.27 38,690.0 13 CLUS_HUMAN Clusterin 4.75E-09 10.22 52,461.1 2 KV3H_HUMAN Ig kappa chain V-III region CLL 5.07E-09 10.25 14,266.2 1 HBB_HUMAN Hemoglobin subunit beta 6.68E-09 80.27 15,988.3 18 IGHD_HUMAN Ig delta chain C region 7.74E-09 20.19 42,227.3 2 FIBA_HUMAN Nersiningan alpha chain 9.08E-09 48.24 36,352.7 5 IGHG3_HUMAN Apolipoprotein M 1.14E-08 10.19 41,260.4 1 A2AP_HUMAN Apolipoprotein M 1.22E-08 30.25 21,239.4 3 COGA3_HUMAN Kortatin, type II cytoskeletal 1 3.05E-08 20.22 51,478.9 2 LV4C_HUMAN Ig lambda chain V-IV region Hil 3.65E-08 10.26 11,509.6 3 COSG_HUMAN Kortatin, type II cytoskeletal 1 3.05E-08 20.22 22,63.6 4 APOE_HUMAN	IGHA2 HUMAN Ig alpha-2 chain C region	1.79E-09	98.22	36,485.1	28
IGHM_HUMAN Ig mu chain C region 2.74E-09 40.24 49,275.6 9 ANXA1_HUMAN Annexin A1 3.24E-09 80.27 38,690.0 13 CLUS_HUMAN Clusterin 4.75E-09 10.22 52,461.1 2 KV3H_HUMAN Ig kappa chain V-III region CLL 5.07E-09 10.25 14,266.2 1 HBB_HUMAN Hemoglobin subunit beta 6.68E-09 80.27 15,988.3 18 IGHD_HUMAN Ig delta chain C region 7.74E-09 20.19 42,227.3 2 ANXA3_HUMAN Annexin A3 9.98E-09 48.24 36,352.7 5 IGHG3_HUMAN Ig gamma-3 chain C region 1.14E-08 10.19 41,260.4 1 A2AP_HUMAN Napcipoprotein M 1.72E-08 30.25 21,239.4 3 CO6A3_HUMAN Collagen alpha-3(VI) chain 1.86E-08 34.23 343,337.4 4 K2C1_HUMAN Keratin, type II cytoskeletal 1 3.05E-08 20.22 51,478.9 2 LV4C_HUMAN Ig lambda chain V-IV region Hil 3.65E-08 10.26 11,590.6 3 COSG_IUMAN Complement component CS agmma chain 3.28E-08 30.22 22,263.6 4 APO	APOC2 HUMAN Apolipoprotein C-II	2.18E-09	30.26	11,276.8	3
ANXA1_HUMAN Annexin A1 3.24E-09 80.27 38,690.0 13 CLUS_HUMAN Clusterin 4.75E-09 10.22 52,461.1 2 KV3H_HUMAN Ig kappa chain V-III region CLL 5.07E-09 10.25 14,266.2 1 HBB_HUMAN Ig delta chain C region 7.74E-09 20.19 42,227.3 2 FIBA_HUMAN Ig delta chain C region 7.74E-09 20.27 94,914.3 2 ANXA3_HUMAN Annexin A3 9.98E-09 48.24 36,352.7 5 IGHG3 HUMAN Ig gamma-3 chain C region 1.14E-08 10.19 41,260.4 1 A2AP_HUMAN Alpha-2-antiplasmin 1.51E-08 20.24 54,531.2 3 APOM_HUMAN Achipa-2-antiplasmin 1.72E-08 30.25 21,239.4 3 CO6A3_HUMAN Collagen alpha-3(VI) chain 1.86E-08 34.23 343,337.4 4 K2C1_HUMAN Keratin, type II cytoskeletal 1 3.05E-08 20.26 51,478.9 2 LV4C_HUMAN Ig lambda chain V-IV region Hil 3.65E-08 10.26 11,509.6 3 APOE_HUMAN Apolipoprotein E 4.02E-08 60.27 36,131.8 8 APOA4 HUMAN Apolipop	IGHM HUMAN Ig mu chain C region	2.74E-09	40.24	49,275.6	9
CLUS_HUMAN Clusterin 4.75E-09 10.22 52,461.1 2 KV3H_HUMAN Ig kappa chain V-III region CLL 5.07E-09 10.25 14,266.2 1 HBB_HUMAN Hemoglobin subunit beta 6.68E-09 80.27 15,988.3 18 IGHD_HUMAN Ig delta chain C region 7.74E-09 20.19 42,227.3 2 FIBA_HUMAN Fibrinogen alpha chain 9.00E-09 20.27 94,914.3 2 ANXA3_HUMAN Anexin A3 9.98E-09 48.24 36,352.7 5 IGHG3_HUMAN Ig gamma-3 chain C region 1.14E-08 10.19 41,260.4 1 A2AP_HUMAN Alpha-2-antiplasmin 1.51E-08 20.24 54,531.2 3 APOM_HUMAN Apolipoprotein M 1.72E-08 30.25 21,239.4 3 CO6A3_HUMAN Fibrinogen gamma chain 3.05E-08 20.22 51,478.9 2 LV4C_HUMAN Ig lambda chain V-IV region Hil 3.65E-08 10.26 11,509.6 3 CO8G_HUMAN Complement component C8 gamma chain 3.98E-08 30.22 22,63.6 4 APOE_HUMAN Apolipoprotein A-IV 4.26	ANXA1 HUMAN Annexin A1	3.24E-09	80.27	38,690.0	13
KV3H_HUMAN Ig kappa chain V-III region CLL 5.07E-09 10.25 14,266.2 1 HBB_HUMAN Hemoglobin subunit beta 6.68E-09 80.27 15,988.3 18 IGHD_HUMAN Ig delta chain C region 7.74E-09 20.19 42,227.3 2 FIBA_HUMAN Fibrinogen alpha chain 9.09E-09 20.27 94,914.3 2 ANXA3_HUMAN Annexin A3 9.98E-09 48.24 36,352.7 5 IGHG3_HUMAN Ig agamma-3 chain C region 1.14E-08 10.19 41,260.4 1 A2AP_HUMAN Alpha-2-antiplasmin 1.51E-08 20.24 54,531.2 3 APOM_HUMAN Collagen alpha-3(VI) chain 1.86E-08 34.23 343,337.4 4 K2C1_HUMAN Keratin, type II cytoskeletal 1 3.05E-08 20.22 51,478.9 2 LV4C_HUMAN Ig lambda chain V-IV region Hil 3.65E-08 10.26 11,509.6 3 CO8G_HUMAN Complement component C8 gamma chain 3.98E-08 30.22 22,263.6 4 APOE_HUMAN Apolipoprotein A-IV 4.02E-08 60.27 36,131.8 8 APOA4_HUMAN Apolipoprotein A-IV 4.02E-08 10.24 11,927.8 2	CLUS HUMAN Clusterin	4.75E-09	10.22	52,461.1	2
HBB_HUMAN Hemoglobin subunit beta 6.68E-09 80.27 15,988.3 18 IGHD_HUMAN Ig delta chain C region 7.74E-09 20.19 42,227.3 2 FIBA_HUMAN Fibrinogen alpha chain 9.00E-09 20.27 94,914.3 2 ANXA3_HUMAN Annexin A3 9.98E-09 48.24 36,352.7 5 IGHG3_HUMAN Ig gamma-3 chain C region 1.14E-08 10.19 41,260.4 1 A2AP_HUMAN Alpha-2-antiplasmin 1.51E-08 20.24 54,531.2 3 APOM_HUMAN Apolipoprotein M 1.72E-08 30.25 21,239.4 3 CO6A3_HUMAN Collagen alpha-3(VI) chain 1.86E-08 34.23 343,337.4 4 K2C1_HUMAN Keratin, type II cytoskeletal 1 3.05E-08 20.22 51,478.9 2 LV4C_HUMAN Ig lambda chain V-IV region Hil 3.65E-08 10.26 11,509.6 3 CO8G_HUMAN Apolipoprotein E 4.02E-08 60.27 36,131.8 8 APOA4_HUMAN Apolipoprotein A-IV 4.26E-08 146.23 45,371.5 22 A2MG_HUMAN Alpha-2-macroglobulin 4.73E-07 90.22 163,174.3 9 LV3B_HUMA	KV3H HUMAN Ig kappa chain V-III region CLL	5.07E-09	10.25	14,266.2	1
IGHD_HUMAN Ig delta chain C region 7.74E-09 20.19 42,227.3 2 FIBA_HUMAN Fibrinogen alpha chain 9.00E-09 20.27 94,914.3 2 ANXA3_HUMAN Annexin A3 9.98E-09 48.24 36,352.7 5 IGHG3_HUMAN Ig gamma-3 chain C region 1.14E-08 10.19 41,260.4 1 A2AP_HUMAN Alpha-2-antiplasmin 1.51E-08 20.24 54,531.2 3 APOM_HUMAN Apolipoprotein M 1.72E-08 30.25 21,239.4 3 CO6A3_HUMAN Korlain, type II cytoskeletal 1 3.05E-08 20.24 54,577.9 3 FIBG_HUMAN Fibrinogen gamma chain 3.23E-08 20.22 51,478.9 2 LV4C_HUMAN Ig lambda chain V-IV region Hil 3.65E-08 10.26 11,509.6 3 CO8G_HUMAN Apolipoprotein E 4.02E-08 60.27 36,131.8 8 APOA4_HUMAN Apolipoprotein A-IV 4.02E-08 60.22 163,174.3 9 LV4C_HUMAN Apolipoprotein A-IV 4.26E-08 10.24 11,927.8 2 LV4C_HUMAN Apolipoprotein A-IV 4.26E-08 10.24 11,927.8 2 APOA4_HUMAN Apolipopro	HBB HUMAN Hemoglobin subunit beta	6.68E-09	80.27	15,988.3	18
FIBA_HUMAN Fibrinogen alpha chain 9.00E-09 20.27 94,914.3 2 ANXA3_HUMAN Annexin A3 9.98E-09 48.24 36,352.7 5 IGHG3_HUMAN Ig gamma-3 chain C region 1.14E-08 10.19 41,260.4 1 A2AP_HUMAN Alpha-2-antiplasmin 1.51E-08 20.24 54,531.2 3 APOM_HUMAN Apolipoprotein M 1.72E-08 30.25 21,239.4 3 C06A3_HUMAN Collagen alpha-3(VI) chain 1.86E-08 34.23 343,337.4 4 K2C1_HUMAN Keratin, type II cytoskeletal 1 3.05E-08 20.25 65,977.9 3 FIBG_HUMAN Fibrinogen gamma chain 3.23E-08 20.22 21,478.9 2 LV4C_HUMAN Ig lambda chain V-IV region Hil 3.65E-08 10.26 11,509.6 3 C08G_HUMAN Complement component C8 gamma chain 3.98E-08 30.22 22,263.6 4 APOE_HUMAN Apolipoprotein E 4.02E-08 60.27 36,131.8 8 APOA4_HUMAN Apolipoprotein A-IV 4.26E-08 146.23 45,371.5 22 A2MG_HUMAN Ig lambda chain V-III region LOI 6.46E-08 20.24 11,927.8 2 <tr< td=""><td>IGHD HUMAN Ig delta chain C region</td><td>7.74E-09</td><td>20.19</td><td>42,227.3</td><td>2</td></tr<>	IGHD HUMAN Ig delta chain C region	7.74E-09	20.19	42,227.3	2
ANXA3_HUMAN Annexin A3 9.98E-09 48.24 36,352.7 5 IGHG3_HUMAN Ig gamma-3 chain C region 1.14E-08 10.19 41,260.4 1 A2AP_HUMAN Alpha-2-antiplasmin 1.51E-08 20.24 54,531.2 3 APOM_HUMAN Apolipoprotein M 1.72E-08 30.25 21,239.4 3 C06A3_HUMAN Collagen alpha-3(VI) chain 1.86E-08 34.23 343,337.4 4 K2C1_HUMAN Keratin, type II cytoskeletal 1 3.05E-08 20.22 51,478.9 2 LV4C_HUMAN Ig lambda chain V-IV region Hil 3.65E-08 10.26 11,509.6 3 CO8G_HUMAN Complement component C8 gamma chain 3.98E-08 30.22 22,263.6 4 APOE_HUMAN Apolipoprotein E 4.02E-08 60.27 36,131.8 8 APOA_HUMAN Alpha-2-macroglobulin 4.73E-08 90.22 163,174.3 9 LV3B_HUMAN Ig kappa chain V-III region LOI 6.46E-08 20.24 11,927.8 2 LV3G_HUMAN Ig kappa chain V-III region GOL 8.44E-07 10.28 11,600.7 1 LV3G_HUMAN Ig kappa chain V-III region Wes 1.74E-07 10.28 38,982.7 1	FIBA HUMAN Fibrinogen alpha chain	9.00E-09	20.27	94,914.3	2
IGHG3_HUMAN Ig gamma-3 chain C region1.14E-0810.1941,260.41A2AP_HUMAN Alpha-2-antiplasmin1.51E-0820.2454,531.23APOM_HUMAN Apolipoprotein M1.72E-0830.2521,239.43CO6A3_HUMAN Collagen alpha-3(VI) chain1.86E-0834.23343,337.44K2C1_HUMAN Keratin, type II cytoskeletal 13.05E-0820.3565,977.93FIBG_HUMAN Fibrinogen gamma chain3.23E-0820.2251,478.92LV4C_HUMAN Ig lambda chain V-IV region Hil3.65E-0810.2611,509.63CO8G_HUMAN Complement component C8 gamma chain3.98E-0830.2222,263.64APOE_HUMAN Apolipoprotein E4.02E-0860.2736,131.88APOA_HUMAN Apolipoprotein A-IV4.26E-08146.2345,371.522A2MG_HUMAN Ig lambda chain V-III region LOI6.46E-0820.2411,927.82LV3G_HUMAN Ig kappa chain V-III region GOL8.44E-0810.2411,823.01KV1S_HUMAN Ig kappa chain V-III region GOL8.44E-0710.2038,982.71PRDX2_HUMAN Peroxiredoxin-22.32E-0710.2038,982.71PRDX2_HUMAN Peroxiredoxin-24.68E-0740.2221,878.25K1C10_HUMAN Keratin, type I cytoskeletal 107.41E-0720.1959,474.82ITIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H47.44E-07100.25103,261.211A1AT_HUMAN Alpha-1-antitypsin9.34E-0710.1846,707.11 <tr< td=""><td>ANXA3 HUMAN Annexin A3</td><td>9.98E-09</td><td>48.24</td><td>36,352.7</td><td>5</td></tr<>	ANXA3 HUMAN Annexin A3	9.98E-09	48.24	36,352.7	5
A2AP_HUMAN Alpha-2-antiplasmin1.51E-0820.2454,531.23APOM_HUMAN Apolipoprotein M1.72E-0830.2521,239.43CO6A3_HUMAN Collagen alpha-3(VI) chain1.86E-0834.23343,337.44K2C1_HUMAN Keratin, type II cytoskeletal 13.05E-0820.3565,977.93FIBG_HUMAN Fibrinogen gamma chain3.23E-0820.2251,478.92LV4C_HUMAN Ig lambda chain V-IV region Hil3.65E-0810.2611,509.63CO8G_HUMAN Complement component C8 gamma chain3.98E-0830.2222,263.64APOE_HUMAN Apolipoprotein E4.02E-0860.2736,131.88APOA4_HUMAN Apolipoprotein A-IV4.26E-08146.2345,371.522A2MG_HUMAN Alpha-2-macroglobulin4.73E-0890.22163,174.39LV3B_HUMAN Ig lambda chain V-III region GOL8.44E-0810.2411,823.01KV1S_HUMAN Ig kappa chain V-III region GOL8.44E-0710.2038,982.71HPTR_HUMAN Haptoglobin-related protein2.32E-0710.2038,982.71PRDX2_HUMAN Peroxiredoxin-24.68E-0740.2221,878.25K1C10_HUMAN Keratin, type I cytoskeletal 107.41E-07100.25103,261.211A1AT_HUMAN Alpha-1-antitrypsin9.34E-0710.1846,707.11HMOX1_HUMAN Heme oxygenase 11.60E-0610.2032,798.01	IGHG3 HUMAN Ig gamma-3 chain C region	1.14E-08	10.19	41,260.4	1
APOM_HUMAN Apolipoprotein M1.72E-0830.2521,239.43CO6A3_HUMAN Collagen alpha-3(VI) chain1.86E-0834.23343,337.44K2C1_HUMAN Keratin, type II cytoskeletal 13.05E-0820.3565,977.93FIBG_HUMAN Fibrinogen gamma chain3.23E-0820.2251,478.92LV4C_HUMAN Ig lambda chain V-IV region Hil3.65E-0810.2611,509.63CO8G_HUMAN Complement component C8 gamma chain3.98E-0830.2222,263.64APOE_HUMAN Apolipoprotein E4.02E-0860.2736,131.88APOA4_HUMAN Apolipoprotein A-IV4.26E-08146.2345,371.522A2MG_HUMAN Alpha-2-macroglobulin4.73E-0890.22163,174.39LV3B_HUMAN Ig lambda chain V-III region LOI6.46E-0820.2411,927.82KV3G_HUMAN Ig kappa chain V-II region GOL8.44E-0810.2411,823.01KV1S_HUMAN Ig kappa chain V-II region Wes1.74E-0710.2811,600.71HPTR_HUMAN Haptoglobin-related protein2.32E-0710.2038,982.71PRDX2_HUMAN Neratin, type I cytoskeletal 107.41E-0720.1959,474.82ITIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H47.44E-07100.25103,261.211AIAT_HUMAN Alpha-1-antitypsin9.34E-0710.1846,707.11HMOX1_HUMAN Heme oxygenase 11.60E-0610.2032,798.01	A2AP HUMAN Alpha-2-antiplasmin	1.51E-08	20.24	54,531.2	3
CO6A3_HUMAN Collagen alpha-3(VI) chain1.86E-0834.23343,337.44K2C1_HUMAN Keratin, type II cytoskeletal 13.05E-0820.3565,977.93FIBG_HUMAN Fibrinogen gamma chain3.23E-0820.2251,478.92LV4C_HUMAN Ig lambda chain V-IV region Hil3.65E-0810.2611,509.63CO8G_HUMAN Complement component C8 gamma chain3.98E-0830.2222,263.64APOE_HUMAN Apolipoprotein E4.02E-0860.2736,131.88APOA4_HUMAN Apolipoprotein A-IV4.26E-08146.2345,371.522A2MG_HUMAN Alpha-2-macroglobulin4.73E-0890.22163,174.39LV3B_HUMAN Ig kappa chain V-III region GOL8.44E-0810.2411,823.01KV3G_HUMAN Ig kappa chain V-II region Wes1.74E-0710.2811,600.71HPTR_HUMAN Haptoglobin-related protein2.32E-0740.2221,878.25KIC10_HUMAN Keratin, type I cytoskeletal 107.41E-0720.1959,474.82ITIH4_HUMAN Alpha-1-antitrypsin9.34E-0710.1846,707.11HMOX1_HUMAN Heme oxygenase 11.60E-0610.2032,798.01	APOM HUMAN Apolipoprotein M	1.72E-08	30.25	21,239,4	3
K2C1_HUMAN Keratin, type II cytoskeletal 13.05E-0820.3565,977.93FIBG_HUMAN Fibrinogen gamma chain3.23E-0820.2251,478.92LV4C_HUMAN Ig lambda chain V-IV region Hil3.65E-0810.2611,509.63CO8G_HUMAN Complement component C8 gamma chain3.98E-0830.2222,263.64APOE_HUMAN Apolipoprotein E4.02E-0860.2736,131.88APOA4_HUMAN Apolipoprotein A-IV4.26E-08146.2345,371.522A2MG_HUMAN Alpha-2-macroglobulin4.73E-0890.22163,174.39LV3B_HUMAN Ig lambda chain V-III region LOI6.46E-0820.2411,927.82KV3G_HUMAN Ig kappa chain V-III region GOL8.44E-0810.2411,823.01KV1S_HUMAN Ig kappa chain V-I region Wes1.74E-0710.2811,600.71HPTR_HUMAN Haptoglobin-related protein2.32E-0710.2038,982.71PRDX2_HUMAN Irer-alpha-trypsin inhibitor heavy chain H47.44E-07100.25103,261.211A1AT_HUMAN Alpha-1-antitrypsin9.34E-0710.1846,707.11HMOX1_HUMAN Heme oxygenase 11.60E-0610.2032,798.01	CO6A3 HUMAN Collagen alpha-3(VI) chain	1.86E-08	34.23	343,337.4	4
FIBG_HUMAN Fibrinogen gamma chain3.23E-0820.2251,478.92LV4C_HUMAN Ig lambda chain V-IV region Hil3.65E-0810.2611,509.63CO8G_HUMAN Complement component C8 gamma chain3.98E-0830.2222,263.64APOE_HUMAN Apolipoprotein E4.02E-0860.2736,131.88APOA4_HUMAN Apolipoprotein A-IV4.26E-08146.2345,371.522A2MG_HUMAN Alpha-2-macroglobulin4.73E-0890.22163,174.39LV3B_HUMAN Ig lambda chain V-III region LOI6.46E-0820.2411,927.82KV3G_HUMAN Ig kappa chain V-III region GOL8.44E-0810.2411,823.01KV1S_HUMAN Ig kappa chain V-I region Wes1.74E-0710.2811,600.71HPTR_HUMAN Haptoglobin-related protein2.32E-074.68E-0740.2221,878.25K1C10_HUMAN Keratin, type I cytoskeletal 107.41E-0720.1959,474.82ITIH4_HUMAN Alpha-1-antitrypsin9.34E-0710.1846,707.11HMOX1_HUMAN Heme oxygenase 11.60E-0610.2032,798.01	K2C1 HUMAN Keratin, type II cytoskeletal 1	3.05E-08	20.35	65.977.9	3
Liv4C_HUMAN Ig lambda chain V-IV region Hil3.65E-0810.2611,509.63C08G_HUMAN Complement component C8 gamma chain3.98E-0830.2222,263.64APOE_HUMAN Apolipoprotein E4.02E-0860.2736,131.88APOA4_HUMAN Apolipoprotein A-IV4.26E-08146.2345,371.522A2MG_HUMAN Alpha-2-macroglobulin4.73E-0890.22163,174.39LV3B_HUMAN Ig lambda chain V-III region LOI6.46E-0820.2411,927.82KV3G_HUMAN Ig kappa chain V-III region GOL8.44E-0810.2411,823.01KV1S_HUMAN Ig kappa chain V-I region Wes1.74E-0710.2811,600.71HPTR_HUMAN Haptoglobin-related protein2.32E-0710.2038,982.71PRDX2_HUMAN Keratin, type I cytoskeletal 107.41E-0720.1959,474.82ITIH4_HUMAN Alpha-1-antitrypsin9.34E-0710.1846,707.11HMOX1_HUMAN Heme oxygenase 11.60E-0610.2032,798.01	FIBG HUMAN Fibringen gamma chain	3.23E-08	20.22	51.478.9	2
CORSC_HUMAN Complement component C8 gamma chain3.98E-0830.2222,263.64APOE_HUMAN Apolipoprotein E4.02E-0860.2736,131.88APOA4_HUMAN Apolipoprotein A-IV4.26E-08146.2345,371.522A2MG_HUMAN Alpha-2-macroglobulin4.73E-0890.22163,174.39LV3B_HUMAN Ig lambda chain V-III region LOI6.46E-0820.2411,927.82KV3G_HUMAN Ig kappa chain V-III region GOL8.44E-0810.2411,823.01KV1S_HUMAN Ig kappa chain V-I region Wes1.74E-0710.2811,600.71HPTR_HUMAN Haptoglobin-related protein2.32E-0710.2038,982.71PRDX2_HUMAN Keratin, type I cytoskeletal 107.41E-0720.1959,474.82ITIH4_HUMAN Alpha-1-antitrypsin9.34E-0710.1846,707.11HMOX1_HUMAN Heme oxygenase 11.60E-0610.2032,798.01	LV4C HUMAN Ig lambda chain V-IV region Hil	3.65E-08	10.26	11.509.6	3
APOE_HUMAN Apolipoprotein E4.02E-0860.2736,131.88APOA4_HUMAN Apolipoprotein A-IV4.26E-08146.2345,371.522A2MG_HUMAN Alpha-2-macroglobulin4.73E-0890.22163,174.39LV3B_HUMAN Ig lambda chain V-III region LOI6.46E-0820.2411,927.82KV3G_HUMAN Ig kappa chain V-III region GOL8.44E-0810.2411,823.01KV1S_HUMAN Ig kappa chain V-I region Wes1.74E-0710.2811,600.71HPTR_HUMAN Haptoglobin-related protein2.32E-0710.2038,982.71PRDX2_HUMAN Neroxiredoxin-24.68E-0740.2221,878.25K1C10_HUMAN Keratin, type I cytoskeletal 107.41E-0720.1959,474.82ITIH4_HUMAN Alpha-1-antitrypsin9.34E-0710.1846,707.11HMOX1_HUMAN Heme oxygenase 11.60E-0610.2032,798.01	CO8G HUMAN Complement component C8 gamma chain	3.98E-08	30.22	22.263.6	4
APOA4_HUMAN Apolipoprotein A-IV4.26E-08146.2345,371.522A2MG_HUMAN Alpha-2-macroglobulin4.73E-0890.22163,174.39LV3B_HUMAN Ig lambda chain V-III region LOI6.46E-0820.2411,927.82KV3G_HUMAN Ig kappa chain V-III region GOL8.44E-0810.2411,823.01KV1S_HUMAN Ig kappa chain V-I region Wes1.74E-0710.2811,600.71HPTR_HUMAN Haptoglobin-related protein2.32E-0710.2038,982.71PRDX2_HUMAN Peroxiredoxin-24.68E-0740.2221,878.25K1C10_HUMAN Keratin, type I cytoskeletal 107.41E-0720.1959,474.82ITIH4_HUMAN Alpha-1-antitrypsin9.34E-0710.1846,707.11HMOX1_HUMAN Heme oxygenase 11.60E-0610.2032,798.01	APOE HUMAN Apolipoprotein E	4.02E-08	60.27	36.131.8	8
A2MG_HUMAN Alpha-2-macroglobulin4.73E90.22163,174.39LV3B_HUMAN Ig lambda chain V-III region LOI6.46E-0820.2411,927.82KV3G_HUMAN Ig kappa chain V-III region GOL8.44E-0810.2411,823.01KV1S_HUMAN Ig kappa chain V-I region Wes1.74E-0710.2811,600.71HPTR_HUMAN Haptoglobin-related protein2.32E-0710.2038,982.71PRDX2_HUMAN Peroxiredoxin-24.68E-0740.2221,878.25K1C10_HUMAN Keratin, type I cytoskeletal 107.41E-0720.1959,474.82ITIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H47.44E-07100.25103,261.211A1AT_HUMAN Heme oxygenase 11.60E-0610.2032,798.01	APOA4 HUMAN Apolipoprotein A-IV	4 26E-08	146.23	45.371.5	22
LINBE_HOLMENT Higher Endet og for and LV3B_HUMAN Ig lambda chain V-III region LOI6.46E-0820.2411,927.82KV3G_HUMAN Ig kappa chain V-III region GOL8.44E-0810.2411,823.01KV1S_HUMAN Ig kappa chain V-I region Wes1.74E-0710.2811,600.71HPTR_HUMAN Haptoglobin-related protein2.32E-0710.2038,982.71PRDX2_HUMAN Peroxiredoxin-24.68E-0740.2221,878.25K1C10_HUMAN Keratin, type I cytoskeletal 107.41E-0720.1959,474.82ITIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H47.44E-07100.25103,261.211A1AT_HUMAN Alpha-1-antitrypsin9.34E-0710.1846,707.11HMOX1_HUMAN Heme oxygenase 11.60E-0610.2032,798.01	A2MG HUMAN Alpha-2-macroglobulin	4 73E-08	90.22	163,174.3	9
KV3G_HUMAN Ig kanpa chain V-III region GOL8.44E-0810.2411,823.01KV1S_HUMAN Ig kappa chain V-I region Wes1.74E-0710.2811,600.71HPTR_HUMAN Haptoglobin-related protein2.32E-0710.2038,982.71PRDX2_HUMAN Peroxiredoxin-24.68E-0740.2221,878.25K1C10_HUMAN Keratin, type I cytoskeletal 107.41E-0720.1959,474.82ITIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H47.44E-07100.25103,261.211A1AT_HUMAN Alpha-1-antitrypsin9.34E-0710.1846,707.11HMOX1_HUMAN Heme oxygenase 11.60E-0610.2032,798.01	IV3B HUMAN Ig lambda chain V-III region I OI	6 46E-08	20.24	11 927 8	2
KY1S_HUMAN Ig kappa chain V-I region Wes 1.74E-07 10.28 11,600.7 1 HPTR_HUMAN Haptoglobin-related protein 2.32E-07 10.20 38,982.7 1 PRDX2_HUMAN Peroxiredoxin-2 4.68E-07 40.22 21,878.2 5 K1C10_HUMAN Keratin, type I cytoskeletal 10 7.41E-07 20.19 59,474.8 2 ITIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H4 7.44E-07 100.25 103,261.2 11 A1AT_HUMAN Alpha-1-antitrypsin 9.34E-07 10.18 46,707.1 1 HMOX1_HUMAN Heme oxygenase 1 1.60E-06 10.20 32,798.0 1	KV3G HUMAN Ig kanna chain V-III region GOL	8.44E-08	10.24	11,927.0	1
HYTE_HUMAN Haptoglobin-related protein 2.32E-07 10.20 38,982.7 1 PRDX2_HUMAN Haptoglobin-related protein 2.32E-07 10.20 38,982.7 1 PRDX2_HUMAN Peroxiredoxin-2 4.68E-07 40.22 21,878.2 5 K1C10_HUMAN Keratin, type I cytoskeletal 10 7.41E-07 20.19 59,474.8 2 ITIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H4 7.44E-07 100.25 103,261.2 11 A1AT_HUMAN Alpha-1-antitrypsin 9.34E-07 10.18 46,707.1 1 HMOX1_HUMAN Heme oxygenase 1 1.60E-06 10.20 32,798.0 1	KV1S HUMAN Ig kappa chain V-I region Wes	1 74E-07	10.21	11,629.0	1
In Inc. International operation 2.522 of 10.20 56,502.7 1 PRDX2_HUMAN Peroxiredoxin-2 4.68E-07 40.22 21,878.2 5 K1C10_HUMAN Keratin, type I cytoskeletal 10 7.41E-07 20.19 59,474.8 2 ITIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H4 7.44E-07 100.25 103,261.2 11 A1AT_HUMAN Alpha-1-antitrypsin 9.34E-07 10.18 46,707.1 1 HMOX1_HUMAN Heme oxygenase 1 1.60E-06 10.20 32,798.0 1	HPTR HUMAN Hantoglobin-related protein	2 32E-07	10.20	38 982 7	1
K1C10_HUMAN Keratin, type I cytoskeletal 107.41E-0720.1959,474.82ITIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H47.44E-07100.25103,261.211A1AT_HUMAN Alpha-1-antitrypsin9.34E-0710.1846,707.11HMOX1_HUMAN Heme oxygenase 11.60E-0610.2032,798.01	PRDX2 HUMAN Peroxiredoxin-2	2.52E 07	40.22	21 878 2	5
ITIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H4 7.44E-07 100.25 103,261.2 11 A1AT_HUMAN Alpha-1-antitrypsin 9.34E-07 10.18 46,707.1 1 HMOX1_HUMAN Heme oxygenase 1 1.60E-06 10.20 32,798.0 1	K1C10 HIIMAN Keratin type I cytoskeletal 10	7.41E-07	20.19	59 474 8	2
A1AT_HUMAN Alpha-1-antitrypsin 9.34E-07 10.18 46,707.1 1 HMOX1_HUMAN Heme oxygenase 1 1.60E-06 10.20 32,798.0 1	ITIH4 HUMAN Inter-alpha-trynsin inhibitor heavy chain H4	7.44E-07	100.25	103 261 2	11
HMOX1_HUMAN Heme oxygenase 1 1.60E-06 10.20 32,798.0 1	A1AT HUMAN Alpha-1-antitrupsin	9.34E-07	10.18	46 707 1	1
1.00E 00 10.20 52,/98.0 1	HMOX1 HIIMAN Heme oxygenase 1	1.60F-06	10.10	37 798 0	1
IGI HUMAN Immunoglobulin Lehain 1 88E–06 10.15 15.584.6 2	IGI HUMAN Immunoglobulin I chain	1.88E-06	10.20	15 584 6	2
ACTR HUMAN Actin extenlasmic 1 3 50E-06 30.10 41.700.7 2	ACTR HUMAN Actin extenlasmic 1	3 50F-06	30.10	41 700 7	2
$A = D_{1}^{-1} O = M_{1}^{-1} O =$	CEAH HUMAN Complement factor H	5.39E 00	10.15	130 004 4	5
AFAM HUMAN Afamin 5.24E 00 10.10 135,004.4 1 AFAM HUMAN Afamin 5.26E-06 10.19 69.024.1 1	AFAM HUMAN Afamin	5.24E 00	10.10	69.024 1	1

	P (pro)	Score	MW	Hits
TRFE HUMAN Serotransferrin	5.69E-06	10.19	76,999.7	1
A2GL HUMAN Leucine-rich alpha-2-glycoprotein	6.14E-06	20.21	38,154.1	2
CO9 HUMAN Complement component C9	7.89E-06	20.21	63,132.8	2
KV3I HUMAN Ig kappa chain V-III region VG	9.13E-06	20.24	12,567.3	2
KV2F HUMAN Ig kappa chain V-II region RPMI 6410	1.13E-05	10.13	14,697.4	1
MMP3 HUMAN Stromelysin-1	2.47E-05	10.17	53,943.4	1
HPT HUMAN Haptoglobin	2.94E-05	74.19	45,176.6	13
S10A8 HUMAN Protein S100-A8	2.99E-05	10.19	10,827.7	3
HV1B HUMAN Ig heavy chain V-I region HG3	5.54E-05	10.16	12,937.3	1
S11Y HUMAN Putative S100 calcium-binding protein H NH0456N16.1	6.65E-05	10.20	11,501.9	1
GGH HUMAN Gamma-glutamyl hydrolase	7.09E-05	40.19	35,941.2	4
SAMP HUMAN Serum amyloid P-component	2.25E-04	30.14	25,371.1	3
PROF1 HUMAN Profilin-1	3.64E-04	10.23	15,044.6	1
KV1F HUMAN Ig kappa chain V-I region EU	5.68E-04	10.16	11,780.8	1
S100P HUMAN Protein S100-P	6.18E-04	10.18	10,393.2	1
TRIM7 HUMAN Tripartite motif-containing protein 7	8.38E-04	10.16	56,595.0	2
Fraction 35 proteins				
A2AP HUMAN Alpha-2-antiplasmin	1.00E-30	50.30	54,531.2	9
HBA HUMAN Hemoglobin subunit alpha	5.55E-15	50.32	15,247.9	8
APOA1 HUMAN Apolipoprotein A-I	5.83E-15	1,010.32	30,758.9	1,258
CO3 HUMAN Complement C3	1.44E-14	190.35	187,029.3	28
A2MG HUMAN Alpha-2-macroglobulin	1.44E-14	60.37	163,174.3	6
ACTB HUMAN Actin, cytoplasmic 1	2.23E-13	20.34	41,709.7	2
IGKC HUMAN Ig kappa chain C region	2.95E-13	30.25	11,601.7	22
S10A6 HUMAN Protein S100-A6	3.49E-13	30.26	10,173.3	4
K2C1 HUMAN Keratin, type II cytoskeletal 1	1.93E-12	20.25	65,977.9	2
FRIL HUMAN Ferritin light chain	3.90E-12	14.27	20,007.1	3
APOA2 HUMAN Apolipoprotein A-II	1.08E-11	110.31	11,167.9	17
TTHY HUMAN Transthyretin	1.16E-11	70.30	15,877.1	14
LAC HUMAN Ig lambda chain C regions	4.68E-11	20.30	11,229.5	13
PGRP2 HUMAN N-acetylmuramoyl-L-alanine amidase	5.23E-11	30.29	62,178.0	3
HV3P_HUMAN Ig heavy chain V-III region TEI	9.68E-11	10.26	12,794.4	1
HBD_HUMAN Hemoglobin subunit delta	3.71E-10	28.26	16,045.3	3
CO4A HUMAN Complement C4-A	6.90E-10	40.25	192,649.5	4
IGHA2 HUMAN Ig alpha-2 chain C region	1.08E-09	58.22	36,485.1	13
MUCB HUMAN Ig mu heavy chain disease protein	1.21E-09	48.26	43,030.3	6
ILEU HUMAN Leukocyte elastase inhibitor	1.50E-09	30.23	42,714.8	3
KV1D HUMAN Ig kappa chain V-I region CAR	2.61E-09	10.27	11,696.3	3
KAIN HUMAN Kallistatin	3.73E-09	50.22	48,511.2	6
HEMO HUMAN Hemopexin	4.23E-09	30.23	51,643.3	3
S10A8 HUMAN Protein S100-A8	5.29E-09	10.24	10,827.7	1
ALBU HUMAN Serum albumin	7.79E-09	40.24	69,321.6	5
HBB_HUMAN Hemoglobin subunit beta	1.31E-08	30.26	15,988.3	4
APOA4_HUMAN Apolipoprotein A-IV	2.29E-08	40.23	45,371.5	9
IGHA1 HUMAN Ig alpha-1 chain C region	2.35E-08	40.27	37,630.7	5
CFAI_HUMAN Complement factor I	2.62E-08	20.23	65,676.7	2
ITIH1_HUMAN Inter-alpha-trypsin inhibitor heavy chain H1	5.56E-08	20.23	101,325.8	2
KV3H_HUMAN Ig kappa chain V-III region CLL	7.79E-08	10.25	14,266.2	1
APOE_HUMAN Apolipoprotein E	1.90E-07	20.27	36,131.8	3

	P (pro)	Score	MW	Hits
ITIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H4	2.81E-07	30.21	103,261.2	3
CFAB_HUMAN Complement factor B	3.03E-07	30.24	85,478.6	4
IGHM_HUMAN Ig mu chain C region	3.85E-07	30.23	49,275.6	5
LV3B_HUMAN Ig lambda chain V-III region LOI	1.97E-06	10.25	11,927.8	2
CO6A3_HUMAN Collagen alpha-3(VI) chain	2.12E-06	44.24	343,337.4	6
HV3R_HUMAN Ig heavy chain V-III region TUR	2.31E-06	10.20	12,423.3	1
HPT_HUMAN Haptoglobin	4.31E-06	20.18	45,176.6	3
FIBA_HUMAN Fibrinogen alpha chain	1.10E-05	10.21	94,914.3	1
LV4C_HUMAN Ig lambda chain V-IV region Hil	2.21E-05	10.22	11,509.6	1
APOM_HUMAN Apolipoprotein M	3.10E-05	10.24	21,239.4	1
PLMN_HUMAN Plasminogen	4.83E-05	10.22	90,510.2	1
RETBP PANTR Plasma retinol-binding protein	5.79E-05	20.15	22,995.3	3
Fraction 36 proteins				
CO3 HUMAN Complement C3	1.00E-30	220.30	187,029.3	29
IGHA2 HUMAN Ig alpha-2 chain C region	1.00E-30	70.34	36,485.1	20
CO4B HUMAN Complement C4-B	2.22E-15	10.33	192.671.6	1
HBA HUMAN Hemoglobin subunit alpha	5.55E-15	50.33	15.247.9	8
ACTB HUMAN Actin. cytoplasmic 1	7.77E-15	30.32	41,709.7	4
A2MG HUMAN Alpha-2-macroglobulin	2.22E-14	100.32	163.174.3	17
APOA1 HUMAN Apolipoprotein A-I	6.08E-14	1.012.33	30.758.9	1,155
A2AP HUMAN Alpha-2-antiplasmin	1.15E-13	136.34	54,531,2	20
HEMO HUMAN Hemonexin	1.15E-13	50.21	51 643 3	5
ITIH1 HUMAN Inter-alpha-trypsin inhibitor heavy chain H1	1.13E 13	10.24	101 325 8	1
K1C9 HUMAN Keratin type I cytoskeletal 9	3.15E-13	10.38	62 091 8	1
KAIN HUMAN Kallistatin	6.87E-13	140.28	48 511 2	26
PI MN HIIMAN Plasminogen	1 32E-12	30.32	90,510,2	3
APOA2 HUMAN Apolipoprotein A-II	3.83E-12	248.32	11 167 9	167
KVAC HUMAN Is kappa chain VIV region B17	3.05E 12	10.28	14 956 5	107
IGKC HUMAN Is kappa chain C region	3.90E 12	40.26	11,550.5	23
DETED DANTE Discons ratinal hinding protein	5.97E 12	40.20	22 005 2	23
K2C1 HUMAN Kentin tune II esteeleletel 1	1.01E 11	40.31	22,993.3 65.077.0	1
ADOA4 UUMAN Anglingmetein A IV	1.01E 11	70.28	45 271 5	4
APOA4_HUMAN Agonpoprotein A-IV	1./9E=11	70.28	45,571.5	14
LAC_HUMAN Ig lamoda chain C legions	0.00E-11	10.20	11,229.3	15
LW2D LUMAN Ig kappa chain V-1 region CAR	0.09E-11	10.29	12,704.4	1
HV3P_HUMAN Ig neavy chain V-III region TEI	7.38E-11	10.30	12,794.4	1
HBB_HUMAN Hemoglobin subunit beta	3.96E-10	/0.27	15,988.3	13
FRIL_HUMAN Ferritin light chain	4.07E-10	36.27	20,007.1	1
TIHY_HUMAN Iransthyretin	4.79E-10	50.31	15,877.1	6
CFAB_HUMAN Complement factor B	7.78E-10	20.25	85,478.6	2
AMBP_HUMAN AMBP protein	1.37E-09	10.25	38,974.0	l
ALBU_HUMAN Serum albumin	1.37E-09	70.24	69,321.6	9
MUCB_HUMAN Ig mu heavy chain disease protein	3.44E-09	38.22	43,030.3	6
KV3H_HUMAN Ig kappa chain V-III region CLL	4.18E-09	10.24	14,266.2	1
A1AT_HUMAN Alpha-1-antitrypsin	4.96E-09	20.23	46,707.1	2
APOL1_HUMAN Apolipoprotein-L1	5.95E-09	30.29	43,947.0	4
CO6A3_HUMAN Collagen alpha-3(VI) chain	7.12E-09	48.23	343,337.4	6
S10A9_HUMAN Protein S100-A9	8.28E-09	10.26	13,233.5	1
CFAI_HUMAN Complement factor I	1.04E-08	46.24	65,676.7	5
IGHG3 HUMAN Ig gamma-3 chain C region	1.24E-08	10.17	41,260.4	1

	P (pro)	Score	MW	Hits
FIBA HUMAN Fibrinogen alpha chain	1.61E-08	20.22	94,914.3	2
APOE HUMAN Apolipoprotein E	3.40E-08	20.27	36,131.8	3
IGHA1 HUMAN Ig alpha-1 chain C region	6.15E-08	30.24	37,630.7	5
IGHM HUMAN Ig mu chain C region	1.50E-07	40.24	49,275.6	8
ACTS HUMAN Actin, alpha skeletal muscle	2.46E-07	50.23	42,023.9	6
TALDO HUMAN Transaldolase	2.88E-07	20.19	37,516.5	2
ANT3 HUMAN Antithrombin-III	1.16E-06	10.22	52,569.0	1
CO4A_HUMAN Complement C4-A	6.92E-06	26.18	192,649.5	3
CO8G_HUMAN Complement component C8 gamma chain	1.20E-05	10.20	22,263.6	1
HPT_HUMAN Haptoglobin	1.99E-05	28.19	45,176.6	4
ILEU_HUMAN Leukocyte elastase inhibitor	2.13E-05	20.23	42,714.8	2
IGJ_HUMAN Immunoglobulin J chain	2.93E-05	10.16	15,584.6	1
LV3B_HUMAN Ig lambda chain V-III region LOI	3.63E-05	10.20	11,927.8	1
M6PBP_HUMAN Mannose-6-phosphate receptor-binding protein 1	3.95E-04	10.22	47,018.0	1
PROF1_HUMAN Profilin-1	7.14E-04	10.20	15,044.6	1
Fraction 37 proteins				
IGHA1_HUMAN Ig alpha-1 chain C region	1.00E-30	70.29	37,630.7	17
K2C1_HUMAN Keratin, type II cytoskeletal 1	1.11E-16	60.39	65,977.9	7
ACTB_HUMAN Actin, cytoplasmic 1	5.55E-16	150.32	41,709.7	19
K1C9_HUMAN Keratin, type I cytoskeletal 9	1.11E-15	44.38	62,091.8	6
APOB_HUMAN Apolipoprotein B-100	1.33E-15	398.38	515,241.6	53
A2AP_HUMAN Alpha-2-antiplasmin	3.33E-15	222.33	54,531.2	32
PLMN_HUMAN Plasminogen	4.44E-15	50.33	90,510.2	8
CO3_HUMAN Complement C3	9.88E-15	352.35	187,029.3	49
APOE_HUMAN Apolipoprotein E	7.77E-14	50.29	36,131.8	5
IGKC_HUMAN Ig kappa chain C region	1.58E-13	70.30	11,601.7	30
LKHA4_HUMAN Leukotriene A-4 hydrolase	1.75E-13	50.26	69,241.3	5
PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase	3.96E-13	20.27	62,178.0	2
APOL1_HUMAN Apolipoprotein-L1	4.22E-13	150.31	43,947.0	23
A2MG_HUMAN Alpha-2-macroglobulin	5.13E-13	380.37	163,174.3	58
ANGT_HUMAN Angiotensinogen	2.56E-12	50.31	53,120.6	5
CO4A_HUMAN Complement C4-A	5.35E-12	36.27	192,649.5	4
KAIN_HUMAN Kallistatin	6.59E-12	40.30	48,511.2	5
APOA2_HUMAN Apolipoprotein A-II	8.45E-12	174.33	11,167.9	68
APOA1_HUMAN Apolipoprotein A-I	8.67E-12	912.32	30,758.9	918
PLTP_HUMAN Phospholipid transfer protein	2.02E-11	30.26	54,704.7	3
KV4C_HUMAN Ig kappa chain V-IV region B17	2.83E-11	20.26	14,956.5	3
S10A6_HUMAN Protein S100-A6	2.88E-11	10.25	10,173.3	1
CO5_HUMAN Complement C5	2.96E-11	110.25	188,185.3	11
RETBP_PANTR Plasma retinol-binding protein	3.46E-11	50.29	22,995.3	12
HBA_HUMAN Hemoglobin subunit alpha	5.76E-11	30.20	15,247.9	5
ITIH1_HUMAN Inter-alpha-trypsin inhibitor heavy chain H1	6.33E-11	10.30	101,325.8	1
LAC_HUMAN Ig lambda chain C regions	8.48E-11	50.30	11,229.5	15
KV1D_HUMAN Ig kappa chain V-I region CAR	1.34E-10	20.26	11,696.3	4
HEMO_HUMAN Hemopexin	1.43E-10	88.25	51,643.3	11
CO6A3_HUMAN Collagen alpha-3(VI) chain	1.90E-10	38.22	343,337.4	5
HV3R_HUMAN Ig heavy chain V-III region TUR	2.35E-10	10.26	12,423.3	1
ITIH2_HUMAN Inter-alpha-trypsin inhibitor heavy chain H2	3.54E-10	100.25	106,369.8	15
TTHY_HUMAN Transthyretin	3.86E-10	30.34	15,877.1	4

IBD_HUMAN Henoglobin subuni delta 4.49E 10 38.25 16.045.3 6 AMRP_HUMAN AMB protein 7.76F-10 10.24 38,974.0 1 COSG HUMAN Scomplement component CS gamma chain 8.36E-10 30.23 22,26.36 4 ICHA2, HUMAN Fig alpha-2 chain C region 4.57E-09 68.25 36,645.1 13 ALBU HUMAN Scoma abumin 4.66E-09 60.24 60,321.6 7 HBB HUMAN Networks bota chain 7.26E-09 10.24 55,576.7 5 MUCB HUMAN Ig much any chain disease protein 1.38F-08 162.3 41,303.3 11 LV3B HUMAN Ig tambac chain V-III region CLL 2.88F-08 10.24 14,266.2 1 S10.9 FIUMAN Portoris 100-0.9 3.71E 08 20.14 14,227.6 7 KV3G HUMAN Ig kappa chain V-III region CLL 5.84E-08 10.24 14,323.0 1 FIBA, HUMAN Ig muchain C region 4.69F-08 30.24 49,275.6 7 KV3G HUMAN Ig muchain C region 4.69F-08 10.22 13,33.0 1 FIBA		P (pro)	Score	MW	Hits
AMBP HUMAN AMBP protein 7,76E-10 10.24 38,974.0 1 CORG IIUMAN Complement component CS gamma chain 8,36E.10 30.23 22,263.6 4 IGHA2_HUMAN Seum athomin 4,66F-09 662.3 36,485.1 13 AI.BU_HUMAN Seum athomin 4,66F-09 602.4 66,371.6 7 IBB_HUMAN Floringen beta chain 7,26F-09 10.24 55,892.2 1 CFAL_HUMAN Floringen beta chain 1,38F-08 46.21 65,676.7 5 MUCB_HUMAN Floringen beta chain 1,38F-08 10.23 14,927.8 1 CYAL_HUMAN Ig much chain CHI region COL 2,88F-08 10.24 14,266.2 1 S10A9_HUMAN Ig muchain Cregion 4,04P-08 30.24 49,275.6 7 KV3G HUMAN Ig muchain Cregion 4,04P-08 30.24 49,275.6 7 IGMH_HUMAN Ig muchain Cregion 5,54H-08 10.22 14,266.2 1 IDMA Protein S100-A9 10.22 14,323.6 2 1 IDMA HUMAN Ig muchain Cregion 5,54H-08 10.22 16,3	HBD_HUMAN Hemoglobin subunit delta	4.49E-10	38.25	16,045.3	6
CONG_PUIMAN Complement component C8 gamma chain8.36E-1030.2322,63.64IGHA2_HUMAN Ig alpha-2 chain Cregion4.67E-0966.2336,485.113ALBU_HUMAN Serum albumin4.66E-0960.4269,321.67HBB_HUMAN Hemoglobin subuni beta7.58E-0940.2715,598.36CFA1_HUMAN Complement factor I1.06E-0846.2165,576.75MUCB_HUMAN Velmoglobin subuni beta7.38E-0814,927.81CFA1_HUMAN Complement factor I1.38E-0814,259,225.45MUCB_HUMAN Velmoglobin VIII region CLL2.81E-0820.1713,23.52IGHM_HUMAN Protein S100-A93.71E-0820.1714,23.52S10A9_HUMAN Protein S100-A93.71E-0820.2218,23.51S10A9_HUMAN Ig ma chain C region4.69E-0830.2449,275.61IGHM_HUMAN Ig ma chain C region7.08E-0820.2218,23.61VX3G_HUMAN KIg kapa chain VII region GOL5.54E-0810.183.6615.21PEDE_HUMAN Complement C27.13E-0820.2283,21.422C02_HUMAN Complement C27.13E-0710.2725,259.011PEDE_HUMAN Lactate dohydrogenase B chain3.59E-0710.1224,56.41PEDE_HUMAN Lactate dohydrogenase B chain1.37E-0710.2725,559.01PEDE_HUMAN Netrica lipha skeletal mascle2.70E-0710.2224,52.61PEDE_HUMAN Lactate dohydrogenase B chain1.37E-0710.2	AMBP_HUMAN AMBP protein	7.76E-10	10.24	38,974.0	1
IGHA2 HUMAN Ig olpha-2 chain C region 4 57E-09 68.25 36.48.51 1 ALBU HUMAN Serum albumin 4.66E 09 60.24 69.321.6 7 HBB, HUMAN Fibringen beta chain 7.26F-09 10.24 55.892.2 1 CFMI HUMAN Complement factor I 1.06E 4.421 65.676.7 5 MUCB HUMAN Ig mu heavy chain disease protein 1.38E-08 58.24 43.030.3 11 LY3B_HUMAN Ig famba chain VIII region IC1 1.37F-08 10.23 14.235.5 5 KV3H HUMAN Protein S100-A9 7.71E-08 20.17 14.232.5 2 12 S10A9 HUMAN Protein S100-A9 7.71E-08 20.22 83.214.4 2 2 C02 HUMAN Ig kappa chain VIII region CDL 5.54E-08 10.12 14.235.6 7 KV3G HUMAN Ig kappa chain VIII region GOL 5.54E-08 10.18 36.615.2 1 F1BA_HUMAN An Igha-1-antichymotypsin 1.12E-07 10.27 46.31.4 3 ACC_HUMAN Alpha-1-antichymotypsin 1.12E-07 10.22 40.23.5 1 KV1Y H	CO8G_HUMAN Complement component C8 gamma chain	8.36E-10	30.23	22,263.6	4
Al.RU_HUMAN Serum albumin4.666-0960.2460.321.67HBB HUMAN Hemoglobin subuni beta5.88E-0940.2715,898.36FIBH_HUMAN Fibrinogen beta chain7.26E-0910.4255,892.21CFAI IUMAN Complement factor I1.06E.0846.2165,676.75MUCB,HUMAN Ig un baxy chain disease protein1.38Fe-0810.2311,927.81LV3B_HUMAN Ig kanpta chain V-III region LOI1.87E-0810.2311,927.81LV3B_HUMAN Ig kanpta chain V-III region CLL2.88F-0810.2414,266.21SIAO_P IUMAN Protein SIO0-A93.71E-0820.2111,823.01FIBA, IUMAN I Skappa chain V-III region GOL5.44F-0810.2211,823.01FIBA, Complement C27.13E-0820.2694,914.322LDHB_HUMAN L-lactate dehydrogenase B chain8.55E-0810.1836,615.21FIDA, JUMAN N Fleinoure phinklum-derived factor9.32E-0830.1744,503.43ACT IIUMAN Alpha-Jancifuknotrypsin1.12C10.2211,832.81ACT IIUMAN Alpha-Jancifuknotrypsin1.20E-0710.2211,832.81ACT IIUMAN Alpha-Jancifuknotrypsin1.20E-0710.2211,832.81ACT IIUMAN Alpha-Jancifuknotrypsin1.20E-0710.2211,832.81ACT IIUMAN Alpha-Jancifuknotrypsin1.20E-0710.2211,832.81ACT IIUMAN Alpha-Jancifuknotrypsin1.20E-0710.232.57.14HYDA JUMAN Natin, alpha S	IGHA2_HUMAN Ig alpha-2 chain C region	4.57E-09	68.25	36,485.1	13
HBB_HUMAN Henoglobin subunit beta 5.881:-09 40.27 15.988.3 6 FIBD FIIDMAN Fibrinogen beta chain 7.26E-09 10.24 65.670 5 FIBD FILMAN Complement factor I 1.06E-08 84.21 65.677 5 MUCB HUMAN Ig mu bavy chain disease protein 1.38E-08 34.25 93.255.4 5 KY3H_HUMAN Ig lambda chain V-III region I.01 2.8EF-08 10.24 44.266.2 1 S10A9_HUMAN Protein S100-A9 3.71E 08 20.27 13.23.5 2 IGHM_HUMAN Ig un chain C region 4.69E-08 30.24 49.275.6 7 KV3G JIUMAN K lapan chain V-III region GOL 5.34E-08 10.22 83.214.4 2 IDHB_HUMAN I-lactate delydrogenase B chain 7.13E-08 20.22 83.214.4 2 IDHB_HUMAN Alpha-l-antichymotrypsin 1.12E-07 10.27 45.33.4 3 ACT_HUMAN Na Alpha-l-antichymotrypsin 1.29E-07 10.22 10.32.2.4 1 TIHH HUMAN Alpha-lantichymotrypsin 1.29E-07 10.22 40.30.4 1 ACT_HU	ALBU_HUMAN Serum albumin	4.66E-09	60.24	69,321.6	7
FIBB_JIUMAN Fibrinogen beta chain 7.26E-09 10.24 55.892.2 1 CFAL_HUMAN Complement factor I 1.06E-08 66.21 65.076 5 MUCB_HUMAN Ig um bacy bain disease protein 1.38E-08 10.23 11.927.8 1 POSIN_HUMAN Ig kanpad chain V-III region LOI 2.21E-08 34.25 93.255.4 5 KV3H_HUMAN Ig kanpad chain V-III region CLI. 2.88E-08 10.24 14.266.2 1 SI0A9_HUMAN Protein SI06-A9 3.71E-08 20.26 11.823.0 1 KV3G HUMAN Ig kappa chain V-III region GOL 5.44E-08 10.22 11.823.0 1 CO2_HUMAN Complement C2 7.13E-08 20.26 94.914.3 2 2 LDHB_HUMAN 1-lactate dehydrogenase B chain 8.55E-08 10.18 36.615.2 1 PEDT_IUMAN N Pigment epithelium-derived factor 9.52E-08 10.18 36.615.2 1 VIV_IUTMAN A laba-1-andite/portypsin inhibitor heavy chain H4 1.20E-07 10.22 11.82.8 1 ACT HUMAN A lig kappa chiny VIII region TBI 1.79E-07 10.23 26.509.0	HBB_HUMAN Hemoglobin subunit beta	5.88E-09	40.27	15,988.3	6
CFA ^T HUMAN Complement factor I 1.06E-08 4.6.21 65,676.7 5 MUCB, HUMAN Ig mu havy chain disease protein 1.38E-08 58.24 43,030.3 11 LX3B, HUMAN Ig lambda chain V-III region LOI 1.38T-08 10.23 11,232.5 5 VOSTI, HUMAN Protein S100-A9 2.21E-08 34.25 93,255.4 5 S10A9, HUMAN Ig kappa chain V-III region CLI. 2.88E-08 10.24 14,266.2 11 S10A9, HUMAN Ig kappa chain V-III region GOL 5.54E-08 10.22 11,233.5 2 COL HUMAN Complement C2 7.13E-08 20.22 149,275.6 7 SV3G, HUMAN Ig kappa chain V-III region GOL 7.13E-08 20.22 83,214.4 2 LDBH, BUMAN I-lactud chydrogenase B chain 8,55E-08 10.18 33,615.2 1 PEDF_HUMAN Pigment epithelum-derived factor 9,52E-08 30,17 46,313.4 3 AACT_HUMAN Anithorabhin-HII 1.27E-07 10,27 52,560.0 1 KVIV-HUMAN Ig kappa chain V-I region BAN 2,30E-07 10,62 42,037.5 4	FIBB HUMAN Fibrinogen beta chain	7.26E-09	10.24	55,892.2	1
MUCB_HUMAN Ig mu heavy chain disease protein 1.38E-98 \$8.24 43,030.3 11 LV3B_HUMAN Ig hambda chain V-III region LOI 1.87E-98 10.23 11,927.8 1 DOSTN_HUMAN Periosin 2.21E-08 342.55 55 KV3H,JILMAN Ig kappa chain V-III region CLL 2.88E-08 10.24 14,266.2 1 S10A9_HUMAN Proteins S100-A9 3.71E-08 20.24 49,275.6 7 KV3G HUMAN Ig map chain V-III region GOL 5.54E-08 10.22 11,823.0 1 FIBA_HUMAN Fibriogen alpha chain 7.08E-08 20.22 83,214.4 2 LDHB HUMAN I-kiteta dehydrogenase B chain 8.55E-08 10.18 36,615.2 1 PEDF_HUMAN Neigment epithelium-derived factor 9.52E-08 10.17 46,313.4 31 ACT_TILMAN Alpha-I-antichymotrysin 1.12E 07 10.27 47,620.6 1 TITH4 JUMAN I ther-alpha-trysin inhibior heavy chain H4 1.20E-07 10.22 11,832.8 1 ACTS_ILUMAN Achin, alpha skeletal muscle 2.70E-07 96.22 42,023.9 14	CFAI_HUMAN Complement factor I	1.06E-08	46.21	65,676.7	5
LV3B_TUMAN Ig lambda chain V-III region LOI 1.87E-08 10.23 11,927.8 1 POSTN, HUMAN Protein S100-A0 2.21E-08 34.25 03,255.4 5 S10A9_HUMAN Ig kappa chain V-III region CLL 2.88E-08 0.024 44,266.2 1 S10A9_HUMAN Ig kappa chain V-III region GOL 5.54E-08 0.022 11,823.0 1 FIBA_HUMAN Ig kappa chain V-III region GOL 7.13E-08 20.26 94,914.3 2 CO2_HUMAN Complement C2 7.13E-08 20.22 83,214.4 2 DD1B_HUMAN Ishar Lactate delydogenase B chain 8.55E-08 30.17 46,313.4 3 AACT_HUMAN Nuter-dphate-typis in hibitor heavy chain 114 1.20E 07 20.22 13,261.2 3 ANT3_HUMAN Antinter-dphat-spis in hibitor heavy chain 114 1.20E 07 10.27 52,560.0 11 KVIV_HUMAN Ig kappa chain V-I region BAN 2.30E-07 10.23 26,370.0 1 ADFO_HUMAN Advingnetin 8.44E-07 10.18 59,540.0 1 ADFO_HUMAN Advingnetin 8.44E-07 10.23 26,370.0 1 HYD_HUMAN Ig heavy chain V-II region TEI 1.03E-06 10.20 <	MUCB HUMAN Ig mu heavy chain disease protein	1.38E-08	58.24	43,030.3	11
POSTN_HUMAN Periosin 2.21E-08 34.25 93,255.4 5 KV3H_IUMAN Ig kappa chain V-III region CLL 2.88E-08 10.24 14,266.2 1 S10.49 HUMAN Protein S100-A9 3.71E-08 20.17 13.233.5 2 IGHM_HUMAN Ig mu chain C region 4.69E-08 30.24 49,275.6 7 KV3G_HUMAN Ig kappa chain V-III region GOL 5.54E-08 10.22 83,214.4 2 C02_HUMAN Complement C2 7.18E-08 20.22 83,214.4 2 LDIIB_IUMAN I-lactate dehydrogenase B chain 8.55E-08 10.17 46,313.4 3 AACT_HUMAN Alpha-1-antichymotrypsin 1.12E-07 10.27 47,620.6 1 RTIHUMAN Nathere-alpha-trypsin inhibior heavy chain H4 1.20E-07 10.22 11,822.8 1 ACTS_HUMAN Achtin, alpha skeleal muscle 2.70E-07 96.22 42,023.9 14 ACDA_HUMAN Apolipoprotein A-V 3.06E-07 30.18 45,371.5 4 HRG_HUMAN Alphapotentin Muscle 2.70E-07 96.22 42,023.9 14 ADDA_IUMAN Apolipoporotein A-V <td>LV3B HUMAN Ig lambda chain V-III region LOI</td> <td>1.87E-08</td> <td>10.23</td> <td>11,927.8</td> <td>1</td>	LV3B HUMAN Ig lambda chain V-III region LOI	1.87E-08	10.23	11,927.8	1
KV3H HUMAN Ig kappa chain V-III region CLL 2.88E-08 10.24 14,266.2 1 S10A9, HUMAN Protein S100-A9 3.71E-08 20.17 13,233.5 2 IGHM, HUMAN Ig mu chain C region 4.69F-08 30.24 49,275.6 7 KV3G, HUMAN Ig kappa chain V-III region GOL 5.54E-08 10.22 11,823.0 1 FIBA_TIUMAN Fibrinogen alpha chain 7.08E-08 20.26 94,914.3 2 LDJIB, HUMAN Compement C2 7.18F-08 10.18 36,615.2 1 PEDF, JIUMAN Negment epithelium-derived factor 9.52E-08 30.17 46,313.4 3 ACCT, HUMAN Alpha-1-antichymotrypsin 1.12E-07 10.27 47,620.6 1 TITH4_HUMAN Iatr-aphat-typsin inhibitor heavy chain H4 1.20E-07 20.22 103,261.2 3 ANT3 HUMAN Antithrombin-III 1.79E-07 10.27 52,660.0 1 KV1V HUMAN Ia kappa chain V-I region BAN 2.30E-07 30.18 45,371.5 4 ADFO, HUMAN Adtiponectin 8.44E-07 10.18 59,540.9 1 KV1V HUMAN Ia kappa chain V-III region TEI 1.03E-06 10.26 1.2,794.4 <td>POSTN HUMAN Periostin</td> <td>2.21E-08</td> <td>34.25</td> <td>93,255.4</td> <td>5</td>	POSTN HUMAN Periostin	2.21E-08	34.25	93,255.4	5
S10.49 HUMAN Protein S100-A9 3.71E-08 20.17 13,233.5 2 IGHM, HUMAN Ig mu chain C region 4.69E-08 30.24 49,275.6 7 KV3G, HUMAN Ig kappa chain V-III region GOL 5.54E-08 10.22 11,823.0 1 FIBA, IIUMAN Fibrinogen alpha chain 7.08E-08 20.22 83,214.4 2 CO2, HUMAN Complement C2 7.13E-08 20.22 83,214.4 3 ACCT, JIUMAN Negment epithelium-derived factor 9.52E-08 30.17 46,313.4 3 AACT, JIUMAN Anthirombin-III 1.70E-07 10.27 47,620.6 1 RVIV HUMAN Nathrahonbin-III 1.70E-07 10.22 11,832.8 1 ACTS, JIUMAN Anthirombin-III 1.70E-07 10.22 11,832.8 1 ACTS, JIUMAN Andiroportion A-IV 306E-07 30.18 45,371.5 4 ROPA, HUMAN Apolipoprotein A-IV 306E-07 10.28 42,023.9 14 ADIPO, HUMAN Apolipoprotein A-IV 306E-07 10.18 53,540.9 1 HRG_HUMAN Serum anyloid Pcomponent 2.09E-06 10.17 25,371.1 1 VIDT, HUMA	KV3H HUMAN Ig kappa chain V-III region CLL	2.88E-08	10.24	14,266.2	1
IGHM_HUMAN Ig mu chain C region 4.69E-08 30.24 49,275.6 7 KV3G_HUMAN Ig kappa chain V-III region GOL 5.54E-08 10.22 11,823.0 1 CO2_HUMAN Complement C2 7.13E-08 20.22 83,214.4 2 LDBB HUMAN L-lactate dehydrogenase B chain 8.55E-08 10.18 36,615.2 1 PEDF_HUMAN Nigment epithelium-derived factor 9.52E-08 30.17 46,313.4 3 AACT. HUMAN Alpha-1-antichymotrypsin 1.12E-07 10.27 47,620.6 1 ITHH, HUMAN Ig kappa chain V-I region BAN 2.30E-07 10.22 11,832.8 1 ACTS_HUMAN Actin, alpha skeletal muscle 2.70E-07 96.22 42,023.9 14 APOA4_HUMAN Adiponectin 8.44E-07 10.18 59,540.9 1 ADIPO_HUMAN Adiponectin 8.44E-07 10.18 59,540.9 1 ADIPO_HUMAN Nama multiporotin A-IV 306E-07 30.18 45,71.5 5 ANT_HUMAN Adiponectin 8.44E-07 10.18 59,540.9 1 ADIPO_HUMAN Adiponectin 8.44E-07 10.23 26,397.0 1 HV3P_HUMAN Ig havy ch	S10A9 HUMAN Protein S100-A9	3.71E-08	20.17	13,233.5	2
KV3G_IIUMAN lg kappa chain VIII region GOL 5.54E-08 10.22 11,823.0 1 FIBA_HUMAN Fibrinogen alpha chain 7.08E-08 20.26 94,914.3 2 C02_HUMAN Complement C2 7.13E-08 20.22 83,214.4 2 LDHB_HUMAN L-lactate dehydrogenase B chain 8.55E-08 30.17 46,313.4 3 AACT_HUMAN Alpha-1-antichymotrypsin 1.12E-07 20.22 103,261.2 3 ANT3_HUMAN Inter-alpha-trypsin inhibitor heavy chain H4 1.20E-07 20.22 103,261.2 3 ANT3_HUMAN Antitheropsin inhibitor heavy chain H4 1.20E-07 10.27 52,569.0 1 KVIV_HUMAN Actin, alpha skeletal muscle 2.70E-07 10.22 11,832.8 1 ACTF, HUMAN Actin, alpha skeletal muscle 2.70E-07 10.22 42,023.9 14 APOA4_HUMAN Actin, alpha skeletal muscle 2.70E-07 10.23 26,397.0 1 HV3P_HUMAN Ig kappa chain V-III region TEI 1.03E-06 10.26 12,794.4 1 SAMP_HUMAN Ig kapy chain V-III region TEI 1.03E-06 10.23 12,567.3 2 VINC_HUMAN Ig kapy chain V-III region TG 6.88E-06 <td< td=""><td>IGHM HUMAN Ig mu chain C region</td><td>4.69E-08</td><td>30.24</td><td>49,275.6</td><td>7</td></td<>	IGHM HUMAN Ig mu chain C region	4.69E-08	30.24	49,275.6	7
FIBA_HUMAN Fibrinogen alpha chain 7.08E-08 20.26 94,914.3 2 CO2_HUMAN Complement C2 7.13E-08 20.22 83,214.4 2 LDHB_HUMAN Lactate dehydrogenase B chain 8.55E-08 30.17 46,313.4 3 AACT_HUMAN Alpha-1-antichymotrypsin 1.12E-07 10.27 47,620.6 1 ITHH_HUMAN Inter-alpha-trypsin inhibitor heavy chain H4 1.20E-07 10.22 118,832.8 1 ANT3 HUMAN Antithrombin-III 7.99E-07 10.22 118,832.8 1 ACTS_HUMAN Astin, alpha skeletal muscle 2.70E-07 96.22 42,023.9 14 APOA4_HUMAN Adiponectin A-IV 3.06E-07 10.18 49,574.5 4 RIG_HUMAN Histidine-rich glycoprotein 8.44E-07 10.18 49,574.5 4 ADPO_HUMAN Na Agionectin 8.44E-07 10.23 26,397.0 1 HV3P_HUMAN Revay chain V-II region TEI 1.03E-06 10.26 12,794.4 1 SAMP_HUMAN Transaldolase 2.15E-06 30.20 37,516.5 5 KV3_HUMAN Transaldolase 2.15	KV3G HUMAN Ig kappa chain V-III region GOL	5.54E-08	10.22	11,823.0	1
CO2_HUMAN Complement C2 7.13E-08 20.22 83,214.4 2 LDHB_HUMAN L-lactate dehydrogenase B chain 8.55E-08 10.18 36,615.2 1 PEDF_HUMAN Pigment epithelum-derived factor 9.52E-08 30.17 46,313.4 3 AACT_HUMAN Alpha-1-antichymotrypsin 1.12E-07 10.27 47,620.6 1 ITHH_HUMAN Inter-alpha-trypsin inhibitor heavy chain H4 1.20E-07 20.22 103,261.2 3 ANT3_HUMAN Autintrombin-III 1.79E-07 10.27 52,569.0 1 KVIV_HUMAN Ik ghapa chain V-I region BAN 2.30E-07 10.22 11,832.8 1 ACTS_HUMAN Actin, alpha skeletal muscle 2.70E-07 96.22 42,023.9 14 APOA_HUMAN K lig kapat chain V-III region BAN 2.30E-07 30.18 45,371.5 4 HRG_HUMAN Kapha-chain V-III region TEI 1.03E-06 10.26 12,794.4 1 SAMP_HUMAN S kapat chain V-III region TEI 1.03E-06 10.23 12,567.3 2 VINC_HUMAN Ig kapat chain V-III region YG 6.88E-06 10.23 12,567.3 2	FIBA HUMAN Fibrinogen alpha chain	7.08E-08	20.26	94,914.3	2
LDHB_HUMAN L-lactate dehydrogenase B chain 8.55E-08 10.18 36,615.2 1 PEDF_HUMAN Pigment epithelium-derived factor 9.52E-08 30.17 46,313.4 3 AACT_HUMAN Alpha-1-antichymotrypsin 1.12E-07 10.27 47,620.6 1 ITH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H4 1.20E-07 20.22 103,261.2 3 ANT3_HUMAN Antithrombin-III 1.79E-07 10.27 52,569.0 1 KVIV_HUMAN kappa chain V41 region BAN 2.30E-07 30.18 45,371.5 4 APOA4_HUMAN Apolipoprotein A-IV 306E-07 30.18 45,371.5 4 HRG_HUMAN Idphavy chain V411 region TEI 1.03E-06 10.23 26,397.0 1 HV3P_HUMAN Ig heavy chain V411 region TEI 2.09E-06 10.17 25,371.1 1 TALDO_HUMAN Serum amyloid P-component 2.09E-06 10.23 12,567.3 2 VINC_HUMAN Ig kappa chain V411 region TEI 1.03E-06 30.23 37,516.5 5 KV31_HUMAN Ig kappa chain V411 region TEI 2.09E-05 64.24 45,176.6 7 IDHA_HUMAN Nanguapa chain V411 region TRO 1.38E-05 10.15	CO2 HUMAN Complement C2	7.13E-08	20.22	83,214.4	2
PEDF HUMAN Pigment epithelium-derived factor 9.52E-08 30.17 46.313.4 3 AACT_HUMAN Alpha-1-antichymotrypsin 1.12E-07 10.27 47,620.6 1 ITIH4 HUMAN Inter-alpha-trypsin inhibitor heavy chain H4 1.20E-07 20.22 103,261.2 3 ANT3_HUMAN Antithrombin-III 1.79E-07 10.27 52,569.0 1 KVIV_HUMAN Ig kappa chain V-I region BAN 2.30E-07 96.22 42,023.9 14 APOA4_HUMAN Actin, alpha skeletal muscle 2.70E-07 96.22 42,03.9 1 ADIPO_HUMAN Adiponectin 8.44E-07 10.23 26,397.0 1 HY3P_HUMAN Ig heavy chain V-III region TEI 1.03E-06 10.26 12,794.4 1 SAMP_HUMAN Ig kappa chain V-III region VG 6.88E-06 10.23 12,567.3 2 VINC_HUMAN Vinculin 8.61E-06 30.23 123,721.9 3 1 ALDO_HUMAN Vinculin 8.61E-06 30.23 123,721.9 3 1 IDIA_HUMAN Ig kappa chain V-III region TRO 1.88E-05 10.15 36,665.4 1 </td <td>LDHB HUMAN L-lactate dehydrogenase B chain</td> <td>8.55E-08</td> <td>10.18</td> <td>36,615.2</td> <td>1</td>	LDHB HUMAN L-lactate dehydrogenase B chain	8.55E-08	10.18	36,615.2	1
AACT_HUMAN Alpha-1-antichymotrypsin 1.12E-07 10.27 47,620.6 1 ITIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H4 1.20E-07 20.22 103,261.2 3 ANT3_HUMAN Mathirombin-III 1.79E-07 10.27 52,569.0 1 KVIV_HUMAN Ig kappa chain V-I region BAN 2.30E-07 10.22 11,832.8 1 ACTS_HUMAN Actin, alpha skeletal muscle 2.70E-07 96.22 42,023.9 14 APOA4_HUMAN Apolipoprotein A-IV 3.06E-07 30.18 45,371.5 4 AIDPO_HUMAN Adiponectin 8.44E-07 10.23 26,397.0 1 HV3P_HUMAN Serum anyloid P-component 2.09E-06 10.17 25,371.1 1 TALDO_HUMAN Transaldolase 2.15E-06 30.20 37,516.5 5 KV3I_HUMAN Ig kapp achain V-III region VG 6.88E-06 30.23 12,372.19 3 LDHA_HUMAN Nunculin 8.16E-06 30.23 12,372.19 3 LDHA_HUMAN Inprunoglobulin J chain 1.38E-05 10.15 56,665.4 1 LGJ_HUMAN Inmunoglobulin J chain 1.38E-05 10.15 15,884.6 1 H	PEDF HUMAN Pigment epithelium-derived factor	9.52E-08	30.17	46,313.4	3
ITIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H4 1.20E-07 20.22 103,261.2 3 ANT3_HUMAN Antithrombin-III 1.79E-07 10.27 52,569.0 1 KVIV_HUMAN Ig kappa chain V-I region BAN 2.30E-07 96.22 42,023.9 14 APOA4_HUMAN Actin, alpha skeletal muscle 2.70E-07 96.22 42,023.9 14 APOA4_HUMAN Apolipoprotein A-IV 3.06E-07 30.18 45,371.5 4 HRG_HUMAN Histidine-rich glycoprotein 8.44E-07 10.18 59,540.9 1 ADIPO_HUMAN Adiponectin 8.48E-07 10.23 26,397.0 1 HV3P_HUMAN Ig heavy chain V-III region TEI 1.03E-06 10.20 37,516.5 5 KV3_HUMAN Ig kappa chain V-III region VG 6.88E-06 10.23 12,567.3 2 VINC_HUMAN Inductate dehydrogenase A chain 1.07E-05 10.15 36,665.4 1 IGJ_HUMAN Immunoglobulin J chain 1.38E-05 10.15 15,584.6 1 HPT_HUMAN Ig kappa chain V-III region TRO 1.46E-04 10.16 13,463.5 1 IGJ_HUMAN Ig haavy chain V-III region TRO 1.46E-04 10.16 13,463.	AACT HUMAN Alpha-1-antichymotrypsin	1.12E-07	10.27	47,620.6	1
ANT3_HUMAN Antithrombin-III 1.79E-07 10.27 52,569.0 1 KV1V_HUMAN Ig kappa chain V-I region BAN 2.30E-07 10.22 11,832.8 1 ACTS_HUMAN Actin, alpha skeletal muscle 2.70E-07 96.22 42,023.9 14 APOA4_HUMAN Apolipoprotein A-IV 3.06E-07 30.18 45,371.5 4 HRG_HUMAN Histidine-rich glycoprotein 8.44E-07 10.18 59,540.9 1 ADIPO_HUMAN Algioporetin 8.48E-07 10.23 26,397.0 1 HV3P_HUMAN Ig heavy chain V-III region TEI 1.03E-06 10.26 12,794.4 1 SAMP_HUMAN Serum amyloid P-component 2.09E-06 10.17 25,371.1 1 TALDO_HUMAN Transaldolase 2.15E-06 30.20 37,516.5 5 KV3L HUMAN Ig kappa chain V-III region VG 6.88E-06 10.23 123,567.3 2 VINC_HUMAN Ninculin 8.61E-06 30.23 123,721.9 3 LOHA_HUMAN L-lactate dehydrogenase A chain 1.07E-05 10.15 15,584.6 1 IGJ_HUMAN Igaubda chain V-IV region Hill 3.00E-05 10.23 67,774.1 1	ITIH4 HUMAN Inter-alpha-trypsin inhibitor heavy chain H4	1.20E-07	20.22	103,261.2	3
KV1V_HUMAN Ig kappa chain V-I region BAN 2.30E-07 10.22 11,832.8 1 ACTS_HUMAN Actin, alpha skeletal muscle 2.70E-07 96.22 42,023.9 14 APOA4_HUMAN Apolipoprotein A-IV 3.06E-07 30.18 43,371.5 4 HRG_HUMAN Histidine-rich glycoprotein 8.44E-07 10.18 59,540.9 1 ADIPO_HUMAN Adiponectin 8.48E-07 10.23 26,397.0 1 HV3P_HUMAN Ig havy chain V-III region TEI 1.03E-06 10.26 12,794.4 1 SAMP_HUMAN Serum amyloid P-component 2.09E-06 10.17 25,371.1 1 TALDO_HUMAN Transaldolase 2.15E-06 30.20 37,516.5 5 KV3I_HUMAN Ig kappa chain V-III region VG 6.88E-06 10.23 123,667.3 2 VINC_HUMAN Vinculin 8.61E-06 30.23 123,721.9 3 LDHA_HUMAN L-lactate dehydrogenase A chain 1.07E-05 10.15 36,665.4 1 IGJ_HUMAN Ig lambda chain V-IV region Hil 3.06E-05 10.23 67,774.1 1 LV4C_HUMAN Ig lambda chain V-IV region HII 3.06E-05 10.20 11,509.6 1	ANT3 HUMAN Antithrombin-III	1.79E-07	10.27	52,569.0	1
ACTS_HUMAN Actin, alpha skeletal muscle 2.70E-07 96.22 42,023.9 14 APOA4_HUMAN Apolipoprotein A-IV 3.06E-07 30.18 45,371.5 4 HRG_HUMAN Histidine-rich glycoprotein 8.44E-07 10.18 59,540.9 1 ADIPO_HUMAN Adiponectin 8.44E-07 10.23 26,397.0 1 HV3P_HUMAN Ig heavy chain V-III region TEI 1.03E-06 10.26 12,794.4 1 SAMP_HUMAN Serum amyloid P-component 2.09E-06 10.17 25,371.1 1 TALDO_HUMAN Transaldolase 2.15E-06 30.20 37,516.5 5 KV3I_HUMAN Ig kappa chain V-III region VG 6.88E-06 10.23 12,567.3 2 VINC_HUMAN Vinculin 8.61E-06 30.23 123,721.9 3 LDHA_HUMAN Lattet dehydrogenase A chain 1.07E-05 10.15 36,665.4 1 IGJ_HUMAN Immunoglobuin J chain 1.38E-05 10.15 15,584.6 1 IPT_HUMAN Rogulation factor XII 3.00E-05 10.20 11,509.6 1 IV4C_HUMAN Ig havg chain V-III region TRO 1.46E-04 10.16 13,463.5 1 PROF1	KV1V HUMAN Ig kappa chain V-I region BAN	2.30E-07	10.22	11,832.8	1
APOA4_HUMAN Apolipoprotein A-IV 3.06E-07 30.18 45,371.5 4 HRG_HUMAN Histidine-rich glycoprotein 8.44E-07 10.18 59,540.9 1 ADIPO_HUMAN Adiponectin 8.48E-07 10.23 26,397.0 1 HV3P_HUMAN Ig heavy chain V-III region TEI 1.03E-06 10.26 12,794.4 1 SAMP_HUMAN Serum amyloid P-component 2.09E-06 10.17 25,371.1 1 TALDO_HUMAN Transaldolase 2.15E-06 30.20 37,516.5 5 KV31_HUMAN Ig kappa chain V-III region VG 6.88E-06 10.23 12,567.3 2 VINC_HUMAN Vinculin 8.61E-06 30.23 123,721.9 3 LDHA_HUMAN Lactate dehydrogenase A chain 1.07E-05 10.15 36,665.4 1 IGJ_HUMAN Immunoglobulin J chain 1.38E-05 10.15 15,584.6 1 HPT_HUMAN Rogulation factor XII 3.00E-05 10.23 67,774.1 1 LV4C_HUMAN Ig hambda chain V-IV region Hil 3.06E-05 10.20 11,509.6 1 PROF1_HUMAN Transforming growth factor-beta-induced protein ig-h3 1.76E-04 10.16 13,463.5 1 </td <td>ACTS_HUMAN Actin, alpha skeletal muscle</td> <td>2.70E-07</td> <td>96.22</td> <td>42,023.9</td> <td>14</td>	ACTS_HUMAN Actin, alpha skeletal muscle	2.70E-07	96.22	42,023.9	14
HRG_HUMAN Histidine-rich glycoprotein 8.44E-07 10.18 59,540.9 1 ADIPO_HUMAN Adiponectin 8.48E-07 10.23 26,397.0 1 HV3P_HUMAN Ig heavy chain V-III region TEI 1.03E-06 10.26 12,794.4 1 SAMP_HUMAN Serum amyloid P-component 2.09E-06 10.17 25,371.1 1 TALDO_HUMAN Transaldolase 2.15E-06 30.20 37,516.5 5 KV31_HUMAN Ig kappa chain V-III region VG 6.88E-06 10.23 12,567.3 2 VINC_HUMAN Niculin 8.61E-06 30.23 123,721.9 3 LDHA_HUMAN Lactate dehydrogenase A chain 1.07E-05 10.15 36.665.4 1 IGJ_HUMAN Immunoglobulin J chain 1.38E-05 10.15 35.584.6 1 HYT_HUMAN Raptoglobin 2.95E-05 64.24 45,176.6 7 FA12_HUMAN Coagulation factor XII 3.00E-05 10.23 67,774.1 1 LV4C_HUMAN Ig heavy chain V-III region TRO 1.46E-04 10.16 13,463.5 1 BGH3_HUMAN Transforming growth factor-beta-induced protein ig-h3 1.76E-04 10.18 74,634.1 1 <t< td=""><td>APOA4_HUMAN Apolipoprotein A-IV</td><td>3.06E-07</td><td>30.18</td><td>45,371.5</td><td>4</td></t<>	APOA4_HUMAN Apolipoprotein A-IV	3.06E-07	30.18	45,371.5	4
ADIPO_HUMAN Adiponectin 8.48E-07 10.23 26,397.0 1 HV3P_HUMAN Ig heavy chain V-III region TEI 1.03E-06 10.26 12,794.4 1 SAMP_HUMAN Serum amyloid P-component 2.09E-06 10.17 25,371.1 1 TALDO_HUMAN Transaldolase 2.15E-06 30.20 37,516.5 5 KV3I_HUMAN Ig kappa chain V-III region VG 6.88E-06 10.23 123,67.3 2 VINC_HUMAN Vinculin 8.61E-06 30.20 37,516.5 1 IGJ_HUMAN Immunoglobulin J chain 1.07E-05 10.15 36,665.4 1 IGJ_HUMAN Immunoglobulin J chain 2.95E-05 64.24 45,176.6 7 FA12_HUMAN Coagulation factor XII 3.00E-05 10.23 67,774.1 1 LV4C_HUMAN Ig lambda chain V-IV region Hil 3.06E-05 10.20 11,509.6 1 PROFI_HUMAN Transforming growth factor-beta-induced protein ig-h3 1.76E-04 10.16 13,463.5 1 GS2A5_HUMAN Olfactory receptor 52A5 3.20E-04 10.12 35,931.3 1 CSN8_HUMAN Colpa signalosome complex subunit 8 1.78E-04 10.16 23,211.0 1	HRG_HUMAN Histidine-rich glycoprotein	8.44E-07	10.18	59,540.9	1
HV3P_HUMAN Ig heavy chain V-III region TEI 1.03E-06 10.26 12,794.4 1 SAMP_HUMAN Serum amyloid P-component 2.09E-06 10.17 25,371.1 1 TALDO_HUMAN Transaldolase 2.15E-06 30.20 37,516.5 5 KV3I_HUMAN Ig kappa chain V-III region VG 6.88E-06 10.23 12,567.3 2 VINC_HUMAN Vinculin 8.61E-06 30.23 123,721.9 3 LDHA_HUMAN I-lactate dehydrogenase A chain 1.07E-05 10.15 36,665.4 1 IGJ_HUMAN Immunoglobulin J chain 1.38E-05 10.15 15,584.6 1 HPT_HUMAN Kogulation factor XII 3.00E-05 10.23 67,774.1 1 LV4C_HUMAN Ig heavy chain V-IV region Hil 3.00E-05 10.20 11,509.6 1 PROFI_HUMAN Nransforming growth factor-beta-induced protein ig-h3 1.76E-04 10.16 13,463.5 1 GH3_HUMAN COP9 signalosome complex subunit 8 1.78E-04 10.16 23,211.0 1 OS2A_5_HUMAN Olfactory receptor 52A5 3.20E-04 10.12 35,931.3 1 Fraction 38 proteins 1.11E-16 108.31 54,531.2 15	ADIPO_HUMAN Adiponectin	8.48E-07	10.23	26,397.0	1
SAMP_HUMAN Serum amyloid P-component 2.09E-06 10.17 25,371.1 1 TALDO_HUMAN Transaldolase 2.15E-06 30.20 37,516.5 5 KV31_HUMAN Ig kappa chain V-III region VG 6.88E-06 10.23 12,567.3 2 VINC_HUMAN Vinculin 8.61E-06 30.23 123,721.9 3 LDHA_HUMAN L-lactate dehydrogenase A chain 1.07E-05 10.15 36,665.4 1 IGJ_HUMAN Immunoglobulin J chain 1.38E-05 10.15 15,584.6 1 HPT_HUMAN Laptoglobin 2.95E-05 64.24 45,176.6 7 FA12_HUMAN Coagulation factor XII 3.00E-05 10.23 67,774.1 1 LV4C_HUMAN Ig lambda chain V-IV region Hil 3.06E-05 10.20 11,509.6 1 PROFI_HUMAN ransforming growth factor-beta-induced protein ig-h3 1.76E-04 10.16 13,463.5 1 GS2A5_HUMAN COP9 signalosome complex subunit 8 1.78E-04 10.16 23,211.0 1 OS2A5_HUMAN Olfactory receptor 52A5 3.20E-04 10.12 35,931.3 1 Fraction 38 54,531.2 15 242M_HUMAN Alpha-2-antiplasmin 1.11E-16 <td>HV3P_HUMAN Ig heavy chain V-III region TEI</td> <td>1.03E-06</td> <td>10.26</td> <td>12,794.4</td> <td>1</td>	HV3P_HUMAN Ig heavy chain V-III region TEI	1.03E-06	10.26	12,794.4	1
TALDO_HUMAN Transaldolase 2.15E-06 30.20 37,516.5 5 KV3I_HUMAN Ig kappa chain V-III region VG 6.88E-06 10.23 12,567.3 2 VINC_HUMAN Vinculin 8.61E-06 30.23 123,721.9 3 LDHA_HUMAN L-lactate dehydrogenase A chain 1.07E-05 10.15 36,665.4 1 IGJ_HUMAN Immunoglobulin J chain 1.38E-05 10.15 15,584.6 1 HPT_HUMAN Haptoglobin 2.95E-05 64.24 45,176.6 7 FA12_HUMAN Coagulation factor XII 3.00E-05 10.23 67,774.1 1 LV4C_HUMAN Ig lambda chain V-IV region Hil 3.06E-05 10.20 11,509.6 1 PROFI_HUMAN Transforming growth factor-beta-induced protein ig-h3 1.76E-04 10.16 13,463.5 1 HV3A_HUMAN Ig heavy chain V-III region TRO 1.46E-04 10.16 13,463.5 1 GS2A5_HUMAN OP signalosome complex subunit 8 1.78E-04 10.16 23,211.0 1 OS2A5_HUMAN Olfactory receptor 52A5 3.20E-04 10.12 35,931.3 15 A2MQ_HUMAN Alpha-2-antiplasmin 1.11E-16 108.31 54,531.2 15 </td <td>SAMP_HUMAN Serum amyloid P-component</td> <td>2.09E-06</td> <td>10.17</td> <td>25,371.1</td> <td>1</td>	SAMP_HUMAN Serum amyloid P-component	2.09E-06	10.17	25,371.1	1
KV31_HUMAN Ig kappa chain V-III region VG 6.88E-06 10.23 12,567.3 2 VINC_HUMAN Vinculin 8.61E-06 30.23 123,721.9 3 LDHA_HUMAN L-lactate dehydrogenase A chain 1.07E-05 10.15 36,665.4 1 IGJ_HUMAN Immunoglobulin J chain 1.38E-05 10.15 15,584.6 1 HPT_HUMAN Kaptoglobin 2.95E-05 64.24 45,176.6 7 FA12_HUMAN Coagulation factor XII 3.00E-05 10.23 67,774.1 1 LV4C_HUMAN Ig lambda chain V-IV region Hil 3.06E-05 10.20 11,509.6 1 PROF1_HUMAN Ig heavy chain V-III region TRO 1.46E-04 10.16 13,463.5 1 GGH3_HUMAN Transforming growth factor-beta-induced protein ig-h3 1.76E-04 10.18 74,634.1 1 CSN8_HUMAN Olfactory receptor 52A5 3.20E-04 10.12 35,931.3 1 Fraction 38 proteins 1.11E-16 108.31 54,531.2 15 A2AP_HUMAN Alpha-2-macroglobulin 2.22E-15 538.38 163,174.3 88 APOA1_HUMAN Apolipoprotein A-I 2.55E-14 350.33 30,758.9 389	TALDO_HUMAN Transaldolase	2.15E-06	30.20	37,516.5	5
VINC_HUMAN Vinculin 8.61E-06 30.23 123,721.9 3 LDHA_HUMAN L-lactate dehydrogenase A chain 1.07E-05 10.15 36,665.4 1 IGJ_HUMAN Immunoglobulin J chain 1.38E-05 10.15 15,584.6 1 HPT_HUMAN Koagulation factor XII 2.95E-05 64.24 45,176.6 7 FA12_HUMAN Coagulation factor XII 3.00E-05 10.23 67,774.1 1 LV4C_HUMAN Ig lambda chain V-IV region Hil 3.06E-05 10.20 11,509.6 1 PROF1_HUMAN Ig heavy chain V-IV region TRO 1.46E-04 10.16 13,463.5 1 BGH3_HUMAN COP9 signalosome complex subunit 8 1.78E-04 10.16 23,211.0 1 OS2A5_HUMAN Olfactory receptor 52A5 3.20E-04 10.12 35,931.3 1 Fraction 38 proteins 1.11E-16 108.31 54,531.2 15 A2AP_HUMAN Alpha-2-macroglobulin 2.22E-15 538.38 163,174.3 88 APOA1_HUMAN Alpha-2-macroglobulin 3.00E-14 40.25 37,630.7 16 PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase 6.44E-14 10.29 62,178.0 3	KV3I HUMAN Ig kappa chain V-III region VG	6.88E-06	10.23	12,567.3	2
LDHA_HUMAN L-lactate dehydrogenase A chain1.07E-0510.1536,665.41IGJ_HUMAN Immunoglobulin J chain1.38E-0510.1515,584.61HPT_HUMAN Haptoglobin2.95E-0564.2445,176.67FA12_HUMAN Coagulation factor XII3.00E-0510.2367,774.11LV4C_HUMAN Ig lambda chain V-IV region Hil3.06E-0510.2011,509.61PROF1_HUMAN Profilin-11.12E-0410.2115,044.61HV3A_HUMAN Ig heavy chain V-III region TRO1.46E-0410.1613,463.51BGH3_HUMAN Transforming growth factor-beta-induced protein ig-h31.76E-0410.1874,634.11CSN8_HUMAN COP9 signalosome complex subunit 81.78E-0410.1623,211.01O52A5_HUMAN Olfactory receptor 52A53.20E-0410.1235,931.31Fraction 38 proteins1.11E-16108.3154,531.215A2AP_HUMAN Alpha-2-antiplasmin1.11E-16108.3154,531.215A2MG_HUMAN Alpha-2-macroglobulin2.22E-15538.38163,174.388APOA1_HUMAN Alpha-2-macroglobulin3.00E-1430.0230,758.9389IGHA1_HUMAN Ig alpha-1 chain C region3.00E-1440.2537,630.716PGRP2_HUMAN Actin, cytoplasmic 11.98E-1390.3241,709.713	VINC HUMAN Vinculin	8.61E-06	30.23	123,721.9	3
IGJ_HUMAN Immunoglobulin J chain1.38E-0510.1515,584.61HPT_HUMAN Haptoglobin2.95E-0564.2445,176.67FA12_HUMAN Coagulation factor XII3.00E-0510.2367,774.11LV4C_HUMAN Ig lambda chain V-IV region Hil3.06E-0510.2011,509.61PROF1_HUMAN Profilin-11.12E-0410.2115,044.61HV3A_HUMAN Ig heavy chain V-III region TRO1.46E-0410.1613,463.51BGH3_HUMAN COP9 signalosome complex subunit 81.78E-0410.1623,211.01O52A5_HUMAN Olfactory receptor 52A53.20E-0410.1235,931.31Fraction 38 proteins1.11E-16108.3154,531.215A2AP_HUMAN Alpha-2-antiplasmin2.22E-15538.38163,174.388APOA1_HUMAN Apolipoprotein A-I2.55E-14350.3330,758.9389IGHA1_HUMAN Ig alpha-1 chain C region3.00E-1440.2537,630.716PGRP2_HUMAN Actin, cytoplasmic 11.98E-1390.3241,709.713	LDHA_HUMAN L-lactate dehydrogenase A chain	1.07E-05	10.15	36,665.4	1
HPT_HUMAN Haptoglobin2.95E-0564.2445,176.67FA12_HUMAN Coagulation factor XII3.00E-0510.2367,774.11LV4C_HUMAN Ig lambda chain V-IV region Hil3.06E-0510.2011,509.61PROF1_HUMAN Profilin-11.12E-0410.2115,044.61HV3A_HUMAN Ig heavy chain V-III region TRO1.46E-0410.1613,463.51BGH3_HUMAN Transforming growth factor-beta-induced protein ig-h31.76E-0410.1874,634.11CSN8_HUMAN OCP9 signalosome complex subunit 81.78E-0410.1623,211.01O52A5_HUMAN Olfactory receptor 52A53.20E-0410.1235,931.31Fraction 38 proteins1.11E-16108.3154,531.215A2MG_HUMAN Alpha-2-macroglobulin2.22E-15538.38163,174.388APOA1_HUMAN Apolipoprotein A-I2.55E-14350.3330,758.9389IGHA1_HUMAN Ig alpha-1 chain C region3.00E-1440.2537,630.716PGRP2_HUMAN Actin, cytoplasmic 11.98E-1390.3241,709.713	IGJ_HUMAN Immunoglobulin J chain	1.38E-05	10.15	15,584.6	1
FA12_HUMAN Coagulation factor XII3.00E-0510.2367,774.11LV4C_HUMAN Ig lambda chain V-IV region Hil3.06E-0510.2011,509.61PROF1_HUMAN Profilin-11.12E-0410.2115,044.61HV3A_HUMAN Ig heavy chain V-III region TRO1.46E-0410.1613,463.51BGH3_HUMAN Transforming growth factor-beta-induced protein ig-h31.76E-0410.1874,634.11CSN8_HUMAN COP9 signalosome complex subunit 81.78E-0410.1623,211.01O52A5_HUMAN Olfactory receptor 52A53.20E-0410.1235,931.31Fraction 38 proteins1.11E-16108.3154,531.215A2AP_HUMAN Alpha-2-antiplasmin1.11E-16108.3154,531.215A2MG_HUMAN Alpha-2-macroglobulin2.52E-14350.3330,758.9389IGHA1_HUMAN Ig alpha-1 chain C region3.00E-1440.2537,630.716PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase6.44E-1410.2962,178.03ACTB_HUMAN Actin, cytoplasmic 11.98E-1390.3241,709.713	HPT_HUMAN Haptoglobin	2.95E-05	64.24	45,176.6	7
LV4C_HUMAN Ig lambda chain V-IV region Hil 3.06E-05 10.20 11,509.6 1 PROF1_HUMAN Profilin-1 1.12E-04 10.21 15,044.6 1 HV3A_HUMAN Ig heavy chain V-III region TRO 1.46E-04 10.16 13,463.5 1 BGH3_HUMAN Transforming growth factor-beta-induced protein ig-h3 1.76E-04 10.18 74,634.1 1 CSN8_HUMAN COP9 signalosome complex subunit 8 1.78E-04 10.16 23,211.0 1 O52A5_HUMAN Olfactory receptor 52A5 3.20E-04 10.12 35,931.3 1 Fraction 38 proteins 1.11E-16 108.31 54,531.2 15 A2AP_HUMAN Alpha-2-androglobulin 2.22E-15 538.38 163,174.3 88 APOA1_HUMAN Ig alpha-1 chain C region 3.00E-14 40.25 37,630.7 16 PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase 6.44E-14 10.29 62,178.0 3 ACTB_HUMAN Actin, cytoplasmic 1 1.98E-13 90.32 41,709.7 13	FA12 HUMAN Coagulation factor XII	3.00E-05	10.23	67,774.1	1
PROF1_HUMAN Profilin-11.12E-0410.2115,044.61HV3A_HUMAN Ig heavy chain V-III region TRO1.46E-0410.1613,463.51BGH3_HUMAN Transforming growth factor-beta-induced protein ig-h31.76E-0410.1874,634.11CSN8_HUMAN COP9 signalosome complex subunit 81.78E-0410.1623,211.01O52A5_HUMAN Olfactory receptor 52A53.20E-0410.1235,931.31Fraction 38 proteins1.11E-16108.3154,531.215A2AP_HUMAN Alpha-2-antiplasmin1.11E-16108.3154,531.215A2MG_HUMAN Alpha-2-macroglobulin2.22E-15538.38163,174.388APOA1_HUMAN Apolipoprotein A-I2.55E-14350.3330,758.9389IGHA1_HUMAN Ig alpha-1 chain C region3.00E-1440.2537,630.716PGRP2_HUMAN Actin, cytoplasmic 11.98E-1390.3241,709.713	LV4C HUMAN Ig lambda chain V-IV region Hil	3.06E-05	10.20	11,509.6	1
HV3A_HUMAN Ig heavy chain V-III region TRO1.46E-0410.1613,463.51BGH3_HUMAN Transforming growth factor-beta-induced protein ig-h31.76E-0410.1874,634.11CSN8_HUMAN COP9 signalosome complex subunit 81.78E-0410.1623,211.01O52A5_HUMAN Olfactory receptor 52A53.20E-0410.1235,931.31Fraction 38 proteins1.11E-16108.3154,531.215A2AP_HUMAN Alpha-2-antiplasmin1.11E-16108.3154,531.215A2MG_HUMAN Alpha-2-macroglobulin2.22E-15538.38163,174.388APOA1_HUMAN Apolipoprotein A-I2.55E-14350.3330,758.9389IGHA1_HUMAN Ig alpha-1 chain C region3.00E-1440.2537,630.716PGRP2_HUMAN Actin, cytoplasmic 11.98E-1390.3241,709.713	PROF1 HUMAN Profilin-1	1.12E-04	10.21	15,044.6	1
BGH3_HUMAN Transforming growth factor-beta-induced protein ig-h3 1.76E-04 10.18 74,634.1 1 CSN8_HUMAN COP9 signalosome complex subunit 8 1.78E-04 10.16 23,211.0 1 O52A5_HUMAN Olfactory receptor 52A5 3.20E-04 10.12 35,931.3 1 Fraction 38 proteins 1.11E-16 108.31 54,531.2 15 A2AP_HUMAN Alpha-2-antiplasmin 1.11E-16 108.31 54,531.2 15 A2MG_HUMAN Alpha-2-macroglobulin 2.22E-15 538.38 163,174.3 88 APOA1_HUMAN Apolipoprotein A-I 2.55E-14 350.33 30,758.9 389 IGHA1_HUMAN Ig alpha-1 chain C region 3.00E-14 40.25 37,630.7 16 PGRP2_HUMAN Actin, cytoplasmic 1 1.98E-13 90.32 41,709.7 13	HV3A HUMAN Ig heavy chain V-III region TRO	1.46E-04	10.16	13,463.5	1
CSN8_HUMAN COP9 signalosome complex subunit 8 1.78E–04 10.16 23,211.0 1 O52A5_HUMAN Olfactory receptor 52A5 3.20E–04 10.12 35,931.3 1 Fraction 38 proteins 1.11E–16 108.31 54,531.2 15 A2AP_HUMAN Alpha-2-antiplasmin 1.11E–16 108.31 54,531.2 15 A2MG_HUMAN Alpha-2-macroglobulin 2.22E–15 538.38 163,174.3 88 APOA1_HUMAN Apolipoprotein A-I 2.55E–14 350.33 30,758.9 389 IGHA1_HUMAN Ig alpha-1 chain C region 3.00E–14 40.25 37,630.7 16 PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase 6.44E–14 10.29 62,178.0 3 ACTB_HUMAN Actin, cytoplasmic 1 1.98E–13 90.32 41,709.7 13	BGH3 HUMAN Transforming growth factor-beta-induced protein ig-h3	1.76E-04	10.18	74,634.1	1
O52A5_HUMAN Olfactory receptor 52A5 3.20E-04 10.12 35,931.3 1 Fraction 38 proteins 1.11E-16 108.31 54,531.2 15 A2AP_HUMAN Alpha-2-antiplasmin 1.11E-16 108.31 54,531.2 15 A2MG_HUMAN Alpha-2-macroglobulin 2.22E-15 538.38 163,174.3 88 APOA1_HUMAN Apolipoprotein A-I 2.55E-14 350.33 30,758.9 389 IGHA1_HUMAN Ig alpha-1 chain C region 3.00E-14 40.25 37,630.7 16 PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase 6.44E-14 10.29 62,178.0 3 ACTB_HUMAN Actin, cytoplasmic 1 1.98E-13 90.32 41,709.7 13	CSN8 HUMAN COP9 signalosome complex subunit 8	1.78E-04	10.16	23,211.0	1
Fraction 38 proteins 1.11E-16 108.31 54,531.2 15 A2AP_HUMAN Alpha-2-antiplasmin 1.11E-16 108.31 54,531.2 15 A2MG_HUMAN Alpha-2-macroglobulin 2.22E-15 538.38 163,174.3 88 APOA1_HUMAN Apolipoprotein A-I 2.55E-14 350.33 30,758.9 389 IGHA1_HUMAN Ig alpha-1 chain C region 3.00E-14 40.25 37,630.7 16 PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase 6.44E-14 10.29 62,178.0 3 ACTB_HUMAN Actin, cytoplasmic 1 1.98E-13 90.32 41,709.7 13	O52A5 HUMAN Olfactory receptor 52A5	3.20E-04	10.12	35,931.3	1
A2AP_HUMAN Alpha-2-antiplasmin1.11E-16108.3154,531.215A2MG_HUMAN Alpha-2-macroglobulin2.22E-15538.38163,174.388APOA1_HUMAN Apolipoprotein A-I2.55E-14350.3330,758.9389IGHA1_HUMAN Ig alpha-1 chain C region3.00E-1440.2537,630.716PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase6.44E-1410.2962,178.03ACTB_HUMAN Actin, cytoplasmic 11.98E-1390.3241,709.713	Fraction 38 proteins				
A2MG_HUMAN Alpha-2-macroglobulin2.22E-15538.38163,174.388APOA1_HUMAN Apolipoprotein A-I2.55E-14350.3330,758.9389IGHA1_HUMAN Ig alpha-1 chain C region3.00E-1440.2537,630.716PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase6.44E-1410.2962,178.03ACTB_HUMAN Actin, cytoplasmic 11.98E-1390.3241,709.713	A2AP_HUMAN Alpha-2-antiplasmin	1.11E-16	108.31	54,531.2	15
APOA1_HUMAN Apolipoprotein A-I2.55E-14350.3330,758.9389IGHA1_HUMAN Ig alpha-1 chain C region3.00E-1440.2537,630.716PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase6.44E-1410.2962,178.03ACTB_HUMAN Actin, cytoplasmic 11.98E-1390.3241,709.713	A2MG_HUMAN Alpha-2-macroglobulin	2.22E-15	538.38	163,174.3	88
IGHA1_HUMAN Ig alpha-1 chain C region 3.00E-14 40.25 37,630.7 16 PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase 6.44E-14 10.29 62,178.0 3 ACTB_HUMAN Actin, cytoplasmic 1 1.98E-13 90.32 41,709.7 13	APOA1_HUMAN Apolipoprotein A-I	2.55E-14	350.33	30,758.9	389
PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase 6.44E-14 10.29 62,178.0 3 ACTB_HUMAN Actin, cytoplasmic 1 1.98E-13 90.32 41,709.7 13	IGHA1_HUMAN Ig alpha-1 chain C region	3.00E-14	40.25	37,630.7	16
ACTB_HUMAN Actin, cytoplasmic 1 1.98E–13 90.32 41,709.7 13	PGRP2 HUMAN N-acetylmuramoyl-L-alanine amidase	6.44E-14	10.29	62,178.0	3
	ACTB_HUMAN Actin, cytoplasmic 1	1.98E-13	90.32	41,709.7	13

	P (pro)	Score	MW	Hits
K2C1_HUMAN Keratin, type II cytoskeletal 1	3.56E-13	130.36	65,977.9	16
APOL1 HUMAN Apolipoprotein-L1	1.43E-12	80.29	43,947.0	10
PLMN_HUMAN Plasminogen	1.47E-12	20.31	90,510.2	3
IGKC HUMAN Ig kappa chain C region	5.07E-12	60.29	11,601.7	43
HV3R HUMAN Ig heavy chain V-III region TUR	5.17E-12	10.29	12,423.3	2
K1C10 HUMAN Keratin, type I cytoskeletal 10	5.49E-12	80.31	59,474.8	9
TLN1 HUMAN Talin-1	5.71E-12	40.28	269,596.3	5
APOB_HUMAN Apolipoprotein B-100	6.46E-12	498.35	515,241.6	82
HBA HUMAN Hemoglobin subunit alpha	2.90E-11	50.30	15,247.9	8
CO3 HUMAN Complement C3	2.99E-11	480.30	187,029.3	69
KV4C HUMAN Ig kappa chain V-IV region B17	5.13E-11	40.24	14,956.5	5
LV4C HUMAN Ig lambda chain V-IV region Hil	7.27E-11	10.24	11,509.6	1
LAC HUMAN Ig lambda chain C regions	1.33E-10	20.28	11,229.5	17
APOA2 HUMAN Apolipoprotein A-II	1.34E-10	120.32	11,167.9	20
TTHY HUMAN Transthvretin	2.49E-10	60.23	15,877.1	8
HEMO HUMAN Hemopexin	2.93E-10	60.25	51.643.3	15
S10A6 HUMAN Protein S100-A6	4.78E-10	20.22	10.173.3	2
ACTS HUMAN Actin alpha skeletal muscle	1.07E-09	28.20	42.023.9	4
RETBP PANTR Plasma retinol-binding protein	1 47E-09	100.30	22 995 3	31
ENOA HUMAN Alpha-enolase	1 49E-09	30.24	47 139 4	3
ANT3 HUMAN Antithrombin-III	2 72E-09	20.25	52 569 0	2
HBB HUMAN Hemoglobin subunit beta	3.32E-09	50.25	15 988 3	12
CEAB HUMAN Complement factor B	3.52E 09	40.23	85 478 6	12
S1049 HUMAN Protein S100-49	3.63E-09	20.21	13 233 5	7 2
K1C0 HUMAN Kerztin tune Loutockeletal 0	4.51E-09	90.40	62 001 8	13
COSC HUMAN Complement component C8 gamma chain	5.21E-09	30.21	22,071.8	3
COS HUMAN Complement C5	5.21E 09	160.23	188 185 3	17
DCTN2 HUMAN Dynastin subunit 2	0.03E 09	20.20	100,105.5	2
CO642 HIMAN Collagon alpha 2(VI) shain	9.83E 09	10.10	242,203.9	1
MUCD HUMAN Lo my boom sheir disease metain	1.00E-08	10.19	343,337.4	1
MOCB_HOMAN Ig mu neavy chain disease protein	1.38E-08	68.23	43,030.3	23
CO4A_HOMAN Complement C4-A	1.6/E-08	62.23	192,649.5	20
IGHA2_HUMAN Ig alpha-2 chain C region	1.83E-08	100.23	36,485.1	20
IGHM_HOMAN Rechame: Full=1g mu chain C region	2.08E-08	30.23	49,273.0	9
HRG_HUMAN Histiane-rich glycoprotein	2.20E-08	20.23	59,540.9	2
6PGD_HUMAN 6-phosphogluconate denydrogenase, decarboxylating	2.72E-08	10.23	53,106.0	1
SAMP_HUMAN Serum amyloid P-component	2.99E-08	30.20	25,371.1	4
IIIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H4	5.84E-08	30.22	103,261.2	3
TKT_HUMAN Transketolase	7.66E-08	20.19	67,834.9	3
BGH3_HUMAN Transforming growth factor-beta-induced protein ig-h3	1.10E-07	40.20	74,634.1	4
ALBU_HUMAN Serum albumin	1.25E-07	130.25	69,321.6	18
SPB9_HUMAN Serpin B9	1.27E-07	80.19	42,376.4	8
HBD_HUMAN Hemoglobin subunit delta	1.52E-07	28.19	16,045.3	3
APOA4_HUMAN Apolipoprotein A-IV	2.42E-07	40.20	45,371.5	4
APOE_HUMAN Apolipoprotein E	2.58E-07	20.25	36,131.8	2
HPT_HUMAN Haptoglobin	2.74E-07	102.23	45,176.6	18
CFAI_HUMAN Complement factor I	2.85E-07	56.23	65,676.7	8
ADIPO_HUMAN Adiponectin	4.68E-07	10.23	26,397.0	1
ANGT_HUMAN Angiotensinogen	4.90E-07	30.22	53,120.6	3
IGLL1_HUMAN Immunoglobulin lambda-like polypeptide 1	7.41E-07	10.19	22,948.6	1

	P (pro)	Score	MW	Hits
ENO1B_HUMAN Alpha-enolase, lung specific	9.50E-07	20.24	49,446.4	2
PEDF_HUMAN Pigment epithelium-derived factor	9.80E-07	46.18	46,313.4	5
KV3G_HUMAN Ig kappa chain V-III region GOL	1.03E-06	10.19	11,823.0	2
KAIN_HUMAN Kallistatin	1.10E-06	10.20	48,511.2	1
ENOB_HUMAN Beta-enolase	1.18E-06	10.23	46,957.4	2
S10A8_HUMAN Protein S100-A8	1.41E-06	10.22	10,827.7	1
KV1D_HUMAN Ig kappa chain V-I region CAR	2.42E-06	20.24	11,696.3	2
LV3B_HUMAN Ig lambda chain V-III region LOI	2.43E-06	30.24	11,927.8	4
IGJ_HUMAN Immunoglobulin J chain	3.40E-06	10.16	15,584.6	1
ITIH2_HUMAN Inter-alpha-trypsin inhibitor heavy chain H2	4.00E-06	40.20	106,369.8	4
K22E_HUMAN Keratin, type II cytoskeletal 2 epidermal	6.60E-06	20.23	65,825.4	2
HV3P_HUMAN Ig heavy chain V-III region TEI	8.90E-06	10.26	12,794.4	3
PSME1_HUMAN Proteasome activator complex subunit 1	9.97E-06	20.15	28,705.0	2
PLTP_HUMAN Phospholipid transfer protein	1.10E-05	40.20	54,704.7	5
CO2_HUMAN Complement C2	1.43E-05	10.23	83,214.4	1
KV3H_HUMAN Ig kappa chain V-III region CLL	1.66E-05	20.19	14,266.2	2
TETN_HUMAN Tetranectin	1.82E-05	10.18	22,552.3	1
LV3A_HUMAN Ig lambda chain V-III region SH	1.87E-05	10.21	11,385.6	2
LDHA_HUMAN L-lactate dehydrogenase A chain	1.89E-05	10.19	36,665.4	1
LDHB_HUMAN L-lactate dehydrogenase B chain	2.04E-05	30.22	36,615.2	3
C1QB_HUMAN Complement C1q subcomponent subunit B	3.63E-05	10.23	26,442.4	1
ILEU_HUMAN Leukocyte elastase inhibitor	5.71E-05	10.17	42,714.8	1
IPSP_HUMAN Plasma serine protease inhibitor	7.70E-05	10.16	45,672.8	1
IGHD_HUMAN Ig delta chain C region	1.11E-04	10.17	42,227.3	1
FIBB_HUMAN Fibrinogen beta chain	2.02E-04	10.18	55,892.2	1
IGHG3_HUMAN Ig gamma-3 chain C region	2.10E-04	10.16	41,260.4	1
HV3V_HUMAN Ig heavy chain V-III region GAR	2.52E-04	10.17	13,079.2	1
HPTR_HUMAN Haptoglobin-related protein	2.62E-04	10.20	38,982.7	1
C1QC_HUMAN Complement C1q subcomponent subunit C	2.92E-04	10.19	25,757.1	1
KV3I_HUMAN Ig kappa chain V-III region VG	3.01E-04	10.20	12,567.3	1
PROF1_HUMAN Profilin-1	3.49E-04	10.17	15,044.6	1
K1C25_HUMAN Keratin, type I cytoskeletal 25	7.85E-04	10.15	49,287.4	1

the protein array analysis, the mass spectrometry analysis did not yield a protein identification. Both the protein arrays and HPLC chromatographs appear to be more sensitive at detecting proteins than the mass spectrometry.

In order to obtain enough material for mass spectrometry analysis, SF from nine different patients was pooled (total volume of 50 ml) and used for a large-scale procedure. After protein depletion, approximately 20 mg of depleted SF material was used to perform four first-dimension chromatofocusing runs (Fig. 3a). The fractions that eluted at pH 5.63–5.45 were combined to perform one second-dimension RP-HPLC run (Fig. 3b). Fractions corresponding to the region that tested positive for RA serum binding in the protein array were digested with trypsin and analyzed by LC/ MS/MS. SEQUEST searches were performed using the SwissProt database limiting the search to tryptic peptides. Table 1 lists the proteins found in these fractions and the corresponding peptides are included as supplementary material (Supplement Table 1).

The candidate autoantigen specifically detected by the RA serum was estimated to be in fractions 20–22. Amongst other proteins, these fractions contained fibrinogen, a known autoantigen that can be citrullinated in vivo. Fibrinogen alpha (FIBA_HUMAN, SwissProt Accession # P02671) was identified in fraction 20 with nine unique peptide hits (15% sequence coverage) and in fraction 22 with 18 unique peptides (24% sequence coverage). Altogether, peptides were only found originating from the center of the FIBA protein (amino acids 250–599) corresponding to the alphaC domain of fibrin (amino acids 239–629). Figure 4 shows the sequence of the fibrin alphaC domain with the amino acids identified by mass spectrom-

Fig. 4 The fibrin alphaC domain (239–629) with the regions identified by mass spectrometry in *bold* and the FIBA 259–287 *underlined. Arrows* point to modifications 1

 \downarrow

RGSCSRALAR 181	EVDLKDYEDQ	QKQLEQVIAK	DLLPSRDRQH	LPLIKMKPVP	DLVPGNFKSQ 240
LQKVPPEWK A 241	$\begin{array}{ccc} 2 & 3 \\ \downarrow & \downarrow \\ \texttt{LTDMPQMRME} \end{array}$	$\begin{array}{c} \textbf{4} \\ \downarrow \\ \textbf{LERPGGNEIT} \end{array}$	5 ↓ RGGSTSYGTG	<u>SETESPR</u> NPS	6 ↓ SAGSWNSGSS 300
7 ↓ GPGSTGNRNP 301	$\begin{array}{c} \textbf{8} \\ \downarrow \downarrow \\ \textbf{GSSGTGGTAT} \end{array}$	9 : ↓ WKPGSSGPGS	LO ↓ TGSWNSGSSG	11 ↓ TGSTGNQNPG	SPRPGSTGTW 360
12 ↓ NPGSSERGSA 361	GHWTSESSVS	$\begin{array}{c} \textbf{13} \\ \downarrow \\ \textbf{GSTGQWHSES} \end{array}$	GSFRPDSPGS	14 ↓ GNARPNNPDW	GTFEEVSGNV 420
SPGTRREYHT 421	EKLVTSKGDK	15 ↓ ELRTGKEKVT	16 17 18 ↓ ↓ ↓ SGSTTTTTRRS	19 ↓ CSKTVTKTVI	GPDGHKEVTK 480
EVVTSEDGSD 481	20 21 ↓ ↓ CPEAMDLGTL	SGIGTLDGFR	HRHPDEAAFF	22 ↓ DTASTGKTFP	GFFSP MLGEF 540
23 ↓ VSETESRGSE 541	$\begin{array}{c} \textbf{24} \\ \downarrow \\ \textbf{SGIFTNTKES} \end{array}$	SSHHPGIAEF	25-29 ↓ ↓↓↓↓↓ PSRGKSSSYS	30 ↓ KQFTSSTSYN	31 32 ↓ ↓ RGDSTFESKS 600

3334↓↓YKMADEAGSE ADHEGTHSTK RGHAKSRPVRDCDDVLQTHP601660

etry in bold and arrows pointing to any modifications. Peptides from the center region were not identified due a lysine-/arginine-rich area followed by two cross-linked amino acids (Ser461–Ser491).

Careful examination of the mass spectra assigned to arginine-containing FIBA peptides led to the assignment of a citrullinated peptide corresponding to FIBA 259–287. The calculated mass obtained from the mass spectrum (Fig. 5) was 1 Da higher than the calculated mass for the unmodified peptide. The lower resolution MS/MS spectrum obtained with the ion trap part of the LTQ-FT did not allow determination of the exact location of the modification. However, a number of other fragments corresponding to parts of the peptide (Table 2) were observed in the spectra obtained with the ion cyclotron resonance (ICR) analyzer of the LTQ-FT, which provided precise mass measurements. There are four sites on the FIBA 259–287 peptide that could possibly be modified resulting in a mass shift of +1 Da. The peptide contains three arginines that can be citrullinated and an asparagine that can be deaminated to form aspartic acid (Fig. 5). All fragments that did not show the expected tryptic cleavage at Arg 271 showed observed masses that were 1 Da higher than the expected mass for the unmodified form. This is consistent with the known failure of trypsin to cleave citrullinated Arg residues. Thus, only conversion of Arg 271 to citrulline is

Fig. 4 (continued)

- 1. Cys184, disulfide link to Cys223 in FIBB
- 2. Met254, oxidized
- 3. Met259, oxidized
- 4. Asn267, methylation
- 5. Arg271, citrullination
- 6. Ser299 -> G conflict
- 7. Ser304 -> G conflict
- 8. Gly317,Thr318 -> SG
- 9. Lys322, link to Gln41 in alpha-2- antiplasmin
- 10. Thr331 -> A
- 11. Gln347. link to Lys
- 12. Ser364, phosphorylation
- 13. Gln385, link to Lys 14. Asn406, methylated
- 14. AS1400, met
- 15. Lys446 -> E
- 16. Ser453 glycosylation site a. S -> N
 - b. N-Linked (GLCNAC...)
- 17. Thr456 -> A
- 18. Ser460, phosphorylation
- 19. Ser461 linked to Ser491
- 20. Ser491 linked to Ser461
- 21. Met495, oxidized
- 22. Lys527 linked to GIn
- 23. E545 -> V
- 24. Lys558 linked to GIn
- 25. Arg573 -> C
 - a. R -> L
- 26. Lys575 linked to Gln
- 27. Ser576 phosphorylation
- 28. Ser577 phosporylation
- 29. Ser 578 phosphorylation
- 30. Lys581 linked to GIn
- 31. Arg591 cleavage site tryptase beta1
- 32. Lys599 linked to Gln
- 33. Splicing variant, DCDDVLQTHPSGTQ -> GIHTSPLGKPSLSP
- 34. Splicing variant, Missing

consistent with observed mass values of this FIBA fragment in RA SF and the failure of trypsin to cleave at that site.

As a final proof that the citrullination site was correctly assigned, the peptide corresponding to residues 259–287 was synthesized with and without the citrulline in position 271 (designated 271X and 271R, respectively). Both the charge state distribution in the electrospray spectrum and the fragment masses in the MS/MS spectrum of the 3+ charge state of 271X matched spectral data obtained with the sample isolated from RA SF.

To establish that the citrullinated FIBA 259–287 peptide was recognized specifically by RA patient sera, the two FIBA 259–287 synthetic peptides were tested in an ELISA. An additional citrullinated synthetic peptide, corresponding to profilaggrin 619–631 (FIL) with a citrulline substitution at Arg 625, was included as a control. The immobilized peptides were incubated with sera from RA, SLE, or healthy controls, followed by detection of bound antibodies by HRP-conjugated anti-human IgG, IgA, and IgM antibodies and a colorimetric assay. Graphs depicting the

ELISA optical density readings are shown in Fig. 6. Of 18 healthy control sera tested, two reacted to the 271R peptide, two reacted to the 271X peptide, and one reacted to the FIL peptide. Of the 12 RA sera tested, four reacted to the 271R peptide, 10 reacted to the 271X peptide, and three reacted to the FIL peptide. Of the 10 SLE sera tested, one patient reacted to all three peptides. The number of sera that reacted exclusively to the 271X peptide, and not with the 271R nor FIL peptides, was 5/12 RA sera, 0/18 healthy sera, and 0/10 SLE sera. These results provide evidence that antibodies in a subset of RA sera bind specifically to the citrulline residue at position 271 of the FIBA alphaC domain found in RA SF.

Discussion

Biomarker analysis consists of three phases: discovery, verification, and validation [38, 39]. Discovery is performed by a thorough analysis of a few samples with hopes of identifying many candidate biomarkers to be used for



Fig. 5 Electrospray mass spectra of the citrullinated FIBA 259–287 peptide. The *upper spectrum* shows the observed mass value for each of the indicated charge states. The *inset* shows the isotope distribution for the 3+ charge state

z	M(obs)	M(pep)	dM	Т	Peptide	aa#	Mods
2	1500.742	1500.74	0	F	MELERPGGNEITR	259-271	
3	1516.743	1500.74	16	F	MELERPGGNEITR	259-271	oxidation
2	1344.644	1344.63	0	Ρ	MELERPGGNEIT	259-270	
2	1360.634	1344.63	16	Ρ	MELERPGGNEIT	259-270	oxidation
4	3053.396	3054.39	1	F	MELERPGGNEITRGGSTSYGTGSETESPR	259-287	citrullination
3	3055.38	3054.39	1	F	MELERPGGNEITRGGSTSYGTGSETESPR	259-287	citrullination
2	1240.66	1240.66	0	Ρ	LERPGGNEITR	261-271	
2	1240.66	1240.66	0	Р	LERPGGNEITR	261-271	
3	2795.29	2794.31	1	Ρ	LERPGGNEITRGGSTSYGTGSETESPR	261-287	citrullination
2	1127.576	1127.57	0	Ρ	ERPGGNEITR	262-271	
2	2398.044	2396.08	2	F	PGGNEITRGGSTSYGTGSETESPR	264-287	deamindation & citrullination
3	2423.088	2299.03	124	Ρ	GGNEITRGG <mark>STS</mark> YGTG <mark>S</mark> ETESPR	265-287	acetylation
2	2071.926	2070.95	1	Ρ	EITRGGSTSYGTGSETESPR	268-287	citrullination
3	2071.935	2070.95	1	Ρ	EITRGGSTSYGTGSETESPR	268-287	citrullination
2	1571.67	1571.67	0	F	GGSTSYGTGSETESPR	272-287	

Table 2 The sequence for the citrullinated peptide along with other fragments for which high-resolution MS and MS/MS spectra were obtained

The dM indicates the nominal mass difference between the expected and observed mass for the unmodified precursor ion. Possible sites of posttranslational modification are indicated in red. Only citrullination of the Arg residue is consistent with the observed mass values and the failure of trypsin to cleave at that site



further study. Verification is performed by determining the presence of select candidate biomarker in a large number of clinical samples to estimate sensitivity and specificity. Sensitivity is defined as the percentage of patients with

Fig. 6 RA sera contain antibodies that specifically bind FIBA peptides bearing a citrulline substitution at Arg 271. In an ELISA, RA, SLE or control (C) sera were incubated with plate-immobilized peptides corresponding to FIBA 259–287 with (271X) or without (271R) a citrulline at position 271, or to filaggrin 619–631 (fil) with a citrulline at position 625. Sera that reacted with 271R include: two out of 18 normals, four out of 12 RA, one out of 10 SLE. Sera that reacted with fil include: one out of 18 normals, three out of 12 RA, one out of 10 SLE

the specified disease that test positive for the biomarker. Specificity is defined as the percentage of people that do not have the specified disease that test negative for the biomarker. Candidate biomarkers that have a high sensitivity and high specificity are further analyzed in the validation phase. Validation is performed by analyzing the presence of the candidates in a patient pool that is expected to be present in a clinical setting where patients with the specific disease will be diagnosed. The purpose of validation is to test whether the candidate can be used for diagnosis. After validation, the biomarkers may be used to develop a diagnostic test. This study represents the discovery phase of biomarker analysis.

We have used a proteomic method to fractionate RA SF proteins, determine their reactivity to autoantibodies in RA sera, and identify immunogenic antibody epitopes. This method involves depletion of abundant serum proteins, twodimensional liquid chromatography, protein macroarrays probed with RA and control sera to identify fractions containing potential autoantigens, and mass spectrometric analyses of those fractions via high-resolution LC-MS/MS. We identified a portion of a SF protein, the fibrin alphaC domain fragment, whose immunogenicity depended upon an Arg to citrulline post-translational modification that had occurred in vivo. We have shown that RA autoantibodies specifically target an epitope containing citrulline at position 271 of FIBA and that this post-translational modification of Arg 271 is present in RA SF. This approach is a feasible strategy that can be used to identify or confirm other autoantigens in RA SF as well as self-proteins that are targets of autoreactive B cell responses in other autoimmune diseases.

Citrullinated fibrinogen is a known autoantigen in RA [17, 40]. Experiments using purified fibrinogen and PAD enzymes in vitro identified 22 possible citrullination sites in FIBA [41, 42]; the Arg 271 identified in our study was citrullinated by both PADI4 and PADI2 enzymes in vitro. Several groups have reported reactivity of RA sera to synthetic FIBA peptides [19, 43, 44] and fibrinogen present in synovial exosomes [18]. Another report showed that mAbs specific for the same citrullinated FIBA peptide identified in our study detected the peptide epitope's presence in RA SF but not RA plasma [19]. The results from our study confirm the presence and reactivity

of citrullinated fibrin/fibrinogen in SF. If our study had been performed using RA plasma as the source of autoantigens, we would not have been successful at identifying autoantigens. Identifying the best biomarker source is crucial in biomarker discovery.

It is possible that our study failed to detect additional immunogenic citrulline sites on FIBA as well as other molecules. The failure of trypsin to cleave at citrulline residues often results in large peptides that are difficult to characterize by mass spectrometry. Other autoantigens could be present at very low concentrations, lost due to non-specific binding during chromatography, did not bind to the nitrocellulose, did not bind in the right conformation to the nitrocellulose, are heavily modified or glycosylated, were undetected by the antibodies in the macroarrays, and/ or were not completely digested by trypsin. For these and many more reasons, the proteins could have escaped detection by the macroarray or mass spectrometry experiments. This study was designed to identify proteins so if the autoantigens are carbohydrate, lipid, or another type of molecule then they would have also been undetected. The chromatographs are more sensitive at detecting proteins than the mass spectrometry. However, since small chromatography peaks yielded no protein identifications, the nature of the molecule that produced the peak is unknown.

The role for the fibrin alphaC domain fragment in RA pathogenesis may be complex. Soluble citrullinated fibrinogen and fibrin degradation products have been found in RA SF but not RA plasma, suggesting that there are high levels of active PAD enzymes in RA SF [19, 45]. Fibrin deposits in the joints of RA patients are widely observed and have been hypothesized to be the cause of pannus formation [46]. The fibrin deposits in the joints allow the fibrin molecules to remain in an inflammatory environment for a prolonged period of time, which could facilitate posttranslational citrulline modification [5]. The alphaC domain fragments are the first to be released during fibrinolysis so they are constantly being generated [47]. If stably present, such degraded alphaC fragments could readily be taken up by antigen presenting cells and chronically displayed to the immune system. Hence, a degradation product of an aberrantly modified self-protein may be an RA autoantigen.

This discovery of post-translationally modified immunogenic epitopes present on self-proteins in vivo may contribute to improved diagnostic tests for RA. With the data obtained from a limited number of patients, the citrullinated 271X peptide seems to have similar sensitivity (83.3%) as the commercially available CCP2 test. Since antibodies to CCP have been shown to be present prior to disease-onset development [11, 12], there is a possibility that the citrullinated 271X peptide can also predict disease. Studies determining when autoantibodies to the citrullinated 271X are produced need to be conducted. Whether a test using the native peptide offers any improvement over the commercially available tests remains to be shown. Irreversible joint damage can occur early in the disease process [48], so early diagnosis and aggressive treatment is vital to the preservation of joint function. Autoantibodies specific for citrullinated epitopes are predominant in early RA patients with high-grade joint inflammation and clinical manifestations predicting development of severe erosive disease [43, 49]. One promising diagnostic tool to define clinically distinct subsets of RA patients is antigen microarray profiling of autoantibodies, an assay in which known autoantigens are arrayed on slides, which are probed with patient sera [43]. The method described here, which can be used to identify epitopes on proteins that are modified in inflamed synovial tissue in situ, will lead to additional information about autoantigens that will help to increase the power of such diagnostic autoantigen arrays.

In summary, proteomic analysis defined an immunogenic citrulline-containing epitope, within the fibrin alphaC domain fragment, as an autoantigen present in RA SF. This study provides further validation that citrullinated fibrinogen is an autoantigen in RA. The strategy used in this project should be useful for identification of novel autoantigens in RA and other autoimmune diseases.

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