

Supplementary Information for

Extracellular Vesicle Fibrinogen Induces Encephalitogenic CD8+ T cells in a Mouse Model of Multiple Sclerosis

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Extended Materials and Methods

Animals. Mice were housed under a 12:12 light/dark cycle, $55 \pm 5\%$ relative humidity, and a temperature of $20 \pm 2^{\circ}$ C with access to standard laboratory chow and water *ad libitum*. They were housed in social groups of a maximum of 5 mice each in standard mouse housing cages and bedding.

Experimental Autoimmune Encephalomyelitis (EAE) was induced in C57B/6 male mice (8-12 week old) by immunizing with a 1:1 ratio of myelin oligodendrocyte glycoprotein (MOG35-55, AnaSpec Inc., Fremont, CA) dissolved in deionized water and complete Freund's adjuvant (CFA, Sigma, St. Louis, MO) containing 0.5 mg of Mycobacterium tuberculosis H37RA (Difco Laboratories: BD Diagnostics, Franklin Lakes, NJ), as described in previous studies (1,2). The MOG-CFA emulsion was administered subcutaneously (s.c.) into the flanks of the hind-limbs (300 μ g/mouse). On days 0 and 2, pertussis toxin (PTX, List Biological, Campbell, CA) was injected intraperitoneally (i.p.) (500 ng/mouse). Weights and clinical scores were recorded daily by an experimenter blinded to experimental treatment of subjects. Clinical signs of disease severity were: 0, no clinical signs; 0.5, distal tail limpness; 1, full tail atony; 2, hind-limb paresis; 3, unilateral hind-limb paralysis; 4, bilateral hind-limb paralysis; 5, moribund.

CD8 and Isotype antibody injections. 500 µg of either **a**CD8 (*InVivo*MAb antimouse CD8 [Lyt 2.1, Clone: 116-13.1 (HB-129)], Bio X Cell, West Lebanon, New Hampshire) or **a**CD8-isotype antibody (*InVivo*MAb mouse IgG2a Isotype control [Clone: C1.18.4], Bio X Cell, West Lebanon, New Hampshire) in sterile PBS was injected intraperitoneally into pEV-injected MOG₃₅₋₅₅-EAE mice at peak clinical EAE and 5 days later. **Blood collection and pEV Isolation**. Whole blood was centrifuged at 2000 x g for 15 min at room temperature and the upper plasma layer was drawn off. Plasma was centrifuged at 1500 x g at room temperature and the supernatant drawn off. Plasma samples were then subjected to a differential ultracentrifugation protocol for extracellular vesicle isolation as previously described (2). Briefly, plasma was spun at 12,000 x g for 30 min at 4°C. The supernatant was collected and equal amounts were subjected to ultracentrifugation at 150,000 x g for 90 min at 4°C. The supernatant was removed and the extracellular vesicle pellets were re-suspended in 150-200 μ l of sterile, 0.22 μ m filtered PBS and stored at -80°C until use. All samples were validated by electron microscopy.

Human Blood Samples. This study was approved by the Office for the Protection of Research Subjects at University of Illinois at Chicago and the Department of Defense Human Research Protection Office. All patients with MS were diagnosed with RRMS according to the revised McDonald criteria. At the time of blood collection, all patients with RRMS were in remission. All patients with MS were under interferon-beta treatment. Three milliliters of blood was collected in tubes with 0.5M ethylenediaminetetraacetic acid (Fisher Scientific, EDTA). Blood was pre-spun at 1500 x *g* for 15 mins at room temperature to isolate plasma. Plasma was then spun at 12,000 x *g* for 30 minutes to remove contaminating microvesicles and flash-frozen on dry ice until extracellular vesicle isolation.

Western Blotting. pEV preparations from either mouse or healthy human subjects or RRMS patient plasma were lysed in RIPA buffer (with protease inhibitor cocktail; Sigma) and separated on a pre-cast 12% Gel (Bio-Rad) by SDS-PAGE. Proteins were transferred to nitrocellulose and immunoblotted using unconjugated antisera against fibrinogen (Dako; catalog ID: A0080; 1:2500), fibrinogen alpha chain (Abnova; catalog ID: H00002243-D01P; 1:1000), and the EV marker flotillin-1 (BD Biosciences; Clone 18/Flotillin-1, catalog ID: 610820, 1:500) that were then visualized by HRP-conjugated secondary antisera (Vector Laboratories, 1:1000-5000) using chemiluminescence (Clarity Western ECL; Bio-Rad). Images were captured using a ChemiDoc XRS+ imaging system (Bio-Rad). Human plasma plasminogen-depleted fibrinogen (Millipore-Sigma, catalog ID: 341578) or mouse plasma plasminogen-depleted plasma fibrinogen (Abcam, catalog ID: ab92791) (100 ng) were used as positive controls for the identification of fibrinogen chains on pEVs.

Quantitative Real-time Polymerase Chain Reaction (qRT-PCR). Total RNA was isolated from saline-perfused unfixed whole brain tissue using TRI Reagent (Sigma) according to the manufacturer's protocol. cDNA was amplified using the iScript kit (BioRad) and qPCR was performed using specific validated primer pairs for *Cxcl10* and *Ccl2* (Integrated DNA Technologies, Coralville, IA) and using the SsoAdvancedTM Universal SYBR® Green Supermix (BioRad) according to the manufacturer's protocol. Target cDNA was amplified and analyzed by the CFX ConnectTM Real-Time PCR Detection System (BioRad). Primers for β-actin were used to assess the general expression level of the housekeeping gene among samples. The relative expression of target RNA was calculated using the comparative cycle threshold analysis (ΔΔCT).

Cytometry by time of flight (CyTOF). The four samples were permeabilized with methanol and incubated with Fc receptor blocking solution and a 31 heavy-metal conjugated antibody panel, including seven signaling markers, as previously described20. DNA was labeled using Cell-ID Intercalator-Ir. The samples were spiked with normalization beads and analyzed by a mass cytometer (HELIOS, Fluidigm) at Jackson Laboratories (Farmington, CT). The data were debarcoded using the Fluidigm Debarcoder v1.04. A single-cell and live-cell gate were identified in each sample. The

samples were downsampled to ensure equal numbers of cells per sample for ViSNE analysis (FlowJo, FlowJo, LLC) (3).

Immunohistochemistry. Spinal cord samples were collected and fixed 4% paraformaldehyde for 24 hours. Tissues were embedded in paraffin and 8 µm sections were applied to superfrost plus glass slides. Antigen retrieval was performed by heating sections to 90°C in 0.1M citrate acid buffer for nine minutes. Slides were blocked in 10% normal goat serum (Millipore-Sigma). Sections were incubated with the following primary antibodies aCD8 (Bio X Cell, [Lyt 2.1, Clone: 116-13.1 (HB-129)], catalog ID: BE0118, 1:1000; Abcam, catalog ID: ab4055, 1:200), CD4 (Abcam, [clone: EPR19514], catalog ID: ab183685, 1:1000), CD68 (Abcam, [clone: FA-11], catalog ID: ab53444, 1:500), and Neurofilament M (Abcam, [clone: NF-09], catalog ID: ab7794, 1:500) in blocking buffer overnight at 4°C. Sections were washed then incubated with the appropriate fluorescence conjugated secondary antibody (Invitrogen, 1:1000) for one hour at room temperature. Sections were washed and stained with FluoroMyelin green fluorescent myelin stain (Invitrogen, catalog ID: F34651, 1:300) for 20 minutes at room temperature. Sections were washed with PBS and counterstained with DAPI (Millipore-Sigma, 1:1000) for 10 minutes at room temperature. Sections were then mounted in Fluoromount-G (Southern Biotech). Quantification of immunopositive cells was performed on at least four spinal cord sections per animal (n = 3 subjects per treatment group / 12 total sections per antibody per subject) by an observer that was blinded to the experimental treatments. Number of positive cells were averaged per experimental subject and statistical comparisons between experimental treatment groups were performed using a Welch's t-test on account of unequal variances. Sections were imaged on an Olympus IX71 and processed using ImageJ software (National Institutes of Health).

Electron Microscopy. For negative staining, 20 µl drops of pEVs (in PBS) were adsorbed onto activated copper grids with carbon coating (Electron Microscopy Sciences) for 15 min, washed by dabbing the grid onto three drops of deionized water, and stained with 1% uranyl acetate (Electron Microscopy Sciences) for 1 min. Grids were imaged under a Hitachi H-7650 transmission electron microscope. For immunogold labeling, 20 µl of isolated pEVs were adsorbed onto activated nickel grids with carbon coating for 15 min. Grids were then blocked for 10 min on 100 µl drops of blocking buffer (1% NGS in PBS). Grids were then incubated for 60 minutes at room temperature on 25 µl drops of primary antibody against fibrinogen (Dako, catalog ID: A0080, 1:10 dilution in 1% NGS) and flotillin-1 (BD Biosciences, Clone 18/Flotillin-1, catalog ID: 610820, 1:10 dilution in 1% NGS). Grids were washed on 100 μ l droplets of PBS three times for 5 min, blocked in 1% NGS for 5 min, and incubated with the appropriate secondary antibody conjugated with 15 nm gold particles or 10 nm gold particles (Electron Microscopy Sciences; 1:15 dilution in blocking solution) for 60 minutes, respectively. Grids were washed three times for 5 min in PBS followed by successive deionized water washes and counter-stained with 25 µl of 1% uranyl-acetate for 1 min. Excess uranyl-acetate was removed by gently blotting the grids which were then left to air dry before imaging under a transmission electron microscope.

In solution Protein Digestion. Extracellular vesicle pellets were resuspended in 1XRIPA buffer containing Halt Protease Inhibitor Cocktail (ThermoScientific, Waltham, MA; Prod# 87786). Samples were homogenized by sonication, and cleared by centrifugation at 14,000 rpm, 4°C, 10 min on a desktop centrifuge. Proteins were extracted by Chloroform/Methanol precipitation using established protocols. Protein pellets were dissolved and denatured in 8M urea, 0.4M ammonium bicarbonate, pH 8. The proteins were reduced by the addition of 1/10 volume of 45mM dithiothreitol (Pierce

ThermoScientific, catalog ID: 20290) and incubation at 37°C for 20 minutes, then alkylated with the addition of 1/10 volume of 100mM iodoacetamide (Millipore-Sigma, catalog ID: 11149) with incubation in the dark at room temperature for 20 minutes. The urea concentration was adjusted to 2M by the addition of water prior to enzymatic digestion at 37°C with LysC (Wako, catalog ID: 125-05061) for 4 hours, then trypsin (Promega; Seq. Grade Mod. Trypsin, catalog ID: V5113) for an additional 16 hours. Protease:protein ratios were estimated at 1:50. Samples were acidified by the addition of 20% trifluoroacetic acid, then desalted using C18 MacroSpin columns (The Nest Group, catalog ID: SMM SS18V) following the manufacturer's directions with peptides eluted with 0.1% TFA, 80% acetonitrile. Eluted sample was speedvaced dry and dissolved in MS loading buffer (2% aceotonitrile, 0.2% trifluoroacetic acid). A nanodrop measurement (Thermo Scientific Nanodrop 2000 UV-Vis Spectrophotometer) determined protein concentrations (A260/A280). Each sample was then further diluted with MS loading buffer to 0.08 μ g/ μ l, with 0.4 μ g (5 μ l) injected for LC-MS/MS analysis.

LC-MS/MS on the Thermo Scientific Q Exactive Plus. LC-MS/MS analysis was performed on a Thermo Scientific Q Exactive Plus with a Waters nanoAcquity UPLC system, using a Waters Symmetry® C18 180 μ m x 20mm trap column and a ACQUITY UPLC PST (BEH) C18 nanoACQUITY Column 1.7 μ m, 75 μ m x 250 mm (37°C) for peptide separation. Trapping was done at 5 μ l/min, 97% Buffer A (100% water, 0.1% formic acid) for 3 min. Peptide separation was performed at 330 nl/min with Buffer A: 100% water, 0.1% formic acid and Buffer B: 100% acetonitrile, 0.1% formic acid. A linear gradient (90 minutes) was run with 3% buffer B at initial conditions; 5% B at 1 minute; 35% B at 50 minutes; 50% B at 60 minutes; 90% B at 65-70; and back to initial conditions at 71 minutes. MS was acquired in profile mode over the 300-1,700 m/z range using 1 microscan; 70,000 resolution; AGC target of 3E6; and a full max ion time of 45

ms. MS/MS was acquired in centroid mode using 1 microscan; 17,500 resolution; AGC target of 1E5; full max IT of 100 ms; 1.7 m/z isolation window; normalized collision energy of 28; and 200-2,000 m/z scan range. Up to 20 MS/MS were collected per MS scan on species with an intensity threshold of 2E4, charge states 2-6, peptide match preferred, and dynamic exclusion set to 20 seconds.

Peptide Identification. Data was analyzed using Proteome Discoverer software v2.2 (Thermo Scientific). Data searching was performed using the Mascot algorithm (version 2.6.0) (Matrix Science) against the SwissProtein database with taxonomy restricted Homo sapiens. The search parameters included tryptic peptides with up to 3 missed cleavages, 10 ppm precursor mass tolerance and 0.02 Da fragment mass tolerance, and variable (dynamic) modifications of methionine oxidation, carbamidomethylated cysteine, deamidated asparagine or glutamine, and citrullination of arginine. Normal and decoy database searches were run, with the confidence level set to 95% (P < 0.05). Scaffold (version Scaffold_4.8.7, Proteome Software Inc., Portland, OR) was used to validate MS/MS based peptide and protein identifications. Peptide identifications were accepted if they could be established at greater than 95.0% probability by the Scaffold Local FDR algorithm. Protein identifications were accepted if they could be established at greater than 99.0% probability and contained at least 2 identified peptides.

Extended Materials and Methods References

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- Svedova J, Menoret A, Mittal P, Ryan JM, Buturla JA, Vella AT. Therapeutic blockade of CD54 attenuates pulmonary barrier damage in T cell-induced acute lung injury. American journal of physiology Lung cellular and molecular physiology. 2017;313(1):L177-I91.



SI Appendix Fig. S1. pEVs induced a spontaneous relapsing-remitting phenotype in wild-type C57BL/6 mice during MOG₃₅₋₅₅-induced EAE. (*A*) Clinical EAE disease courses in individual vehicle (n = 4) and (*B*) pEV-treated mice (n = 6). From grouped data in Fig. 1*D*.



SI Appendix Fig. S2.

SI Appendix Fig. S2. Characterization of increased immune cell infiltrates and axonal injury in spinal cords of pEV-treated R/R EAE mice during spontaneous relapse. (A) Low magnification representative image of spinal cord cross sections from vehicletreated and pEV-treated EAE mice both collected at the same time of the first clinical relapse in pEV-treated mice. Sections were stained with DAPI and clearly indicate (arrows) notable differences in cellular infiltrates in the pEV-treated animals (See Fig. 2H). Dotted line demarcates the dorsal column which was used for immunohistological analyses. (B) Scatter plots of CD3+/CD4+ and CD3+/CD8+ T lymphocytes collected from spinal cord tissues of vehicle and pEV-treated EAE mice analyzed by CyTOF (See Fig. 2C). These analyses indicate that in pEV-treated animals 98.7% of CD8+ cells were also CD3+. CD8+/CD3+ T cells represented 55% of all infiltrating T cells in this treatment group at this time point while, CD8+ cells represented 27% of all CD3+ cells in vehicle treated animals. (C) Immunohistochemistry for CD8+ T cells demonstrated spatial co-localization within the demyelinated spinal cord (See Fig. 2J), and analysis of CD4+ T cells in the dorsal columns of vehicle and pEV-treated indicated a higher proportion of CD4+ immune cells within the infiltrates within this anatomical site in pEV-treated animals. These differences in CD8+ and CD4+ immune cells also reflected a higher ratio of CD8+ T cells in pEV treated animals than observed in vehicle-treated animals. (D) Analysis of CD68+ macrophages in the dorsal column of spinal cord tissues from pEV and vehicle treated animals also revealed a higher abundance of macrophages in the cellular infiltrates of pEV-treated mice. (E) Analysis of Neurofilament M in the dorsal columns of spinal cord tissues from pEV and vehicle treated mice determined comparable numbers of axons in both treatment groups indicating that at this time of the first clinical relapse, axon loss was not a significant pathological feature in the pEV-treated animals in spite of ongoing clinical EAE symptomatology. Scale bars: A = 1 mm; C,D, E = 20 μ m.



SI Appendix Fig. S3. pEVs induce a CD8+ T-cell response responsible for the development of a spontaneous relapsing phenotype in MOG₃₅₋₅₅-EAE. (*A*) Clinical disease courses in individual isotype antisera (n = 4) and (*B*) α CD8 (n = 7) function blocking antibody-treated mice. From grouped data in Fig. 2*F*.



SI Appendix Fig. S4. CyTOF Analysis of spinal cords at time of spontaneous relapses revealed a unique CD8+ T cell population. (*A*) pEV-R/R mice had increases in CD11b/CD8+ immune cell infiltrates during a spontaneous relapse. (*B*) Administration of isotype antisera (n = 3) and α CD8 (n = 3) to MOG₃₅₋₅₅-EAE mice had no effect on clinical disease course and (*C*) disease burden. (Values are mean ± s.e.m., where **P* < 0.05 calculated by two-way ANOVA with uncorrected Fisher's LSD post-hoc test; **P* < 0.05 (Mann-Whitney *U* test.) Grouped data is the result of two independent experiments.



SI Appendix Fig. S5. pEV fibrinogen is necessary to induce a spontaneous relapsingremitting phenotype in wild-type C57BL/6 mice during MOG₃₅₋₅₅-induced EAE. (*A*) Clinical disease courses in individual MOG₃₅₋₅₅-EAE mice administered $Fib^{+/+}$ (n = 5) or (*B*) $Fib^{-/-}$ (n = 6) pEVs. From grouped data in Fig. 3*G*.

Table S1. List of LC-MS/MS peptides identified using PF-2D platform in sample in uniquely identified by Proteome software.

| Expectation | Gene ID | Protein Name | MW | % Coverage | empai |
|-------------|-------------|-----------------------------|--------|------------|-------|
| 0.00054 | FIBA_MOUSE | Fibrinogen alpha chain | 87375 | 12.3 | 0.05 |
| 170 | PZP_MOUSE | Pregnancy zone protein | 165748 | 2.6 | 0.03 |
| 420 | LAMC1_MOUSE | Laminin subunit gamma-1 | 177185 | 0.7 | |
| 480 | CO7A1_MOUSE | Collagen alpha-1(VII) chain | 295054 | 0.8 | |
| 2400 | DACT2_MOUSE | Dapper homolog 2 | 81617 | 1.3 | |

Table S2. LC-MS/MS Identified 265 proteins in pEVs from non-diseased and relapsing-remitting multiple sclerosis patients.

| Entry Name | Protein ID | MW | Alternate ID | Control #3 | Control #13 | Control #40 | MS #39 | MS #10 | MS #2 |
|-------------|--|------------------|------------------|------------|-------------|----------------|----------|----------|---------|
| 1433G_HUMAN | 14-3-3 protein gamma | 28 kDa | YWHAG | 4 | 0 | 0 | 0 | 0 | 0 |
| 1433Z_HUMAN | 14-3-3 protein zeta/delta | 28 kDa | YWHAZ | 5 | 0 | 1 | 3 | 0 | 1 |
| A1AG1_HUMAN | Alpha-1-acid glycoprotein 1 | 24 kDa | ORM1 | 4 | 4 | 1 | 4 | 2 | 1 |
| A1AUZ_NOMAN | Alpha-1-actid giycopi otein 2 | 47 kDa | SERPINA1 | 118 | 86 | 62 | 108 | 96 | 85 |
| A1BG_HUMAN | Alpha-1B-glycoprotein | 54 kDa | A1BG | 23 | 19 | 19 | 25 | 18 | 18 |
| A2AP_HUMAN | Alpha-2-antiplasmin | 55 kDa | SERPINF2 | 17 | 12 | 7 | 14 | 13 | 11 |
| A2GL_HUMAN | Leucine-rich alpha-2-glycoprotein | 38 kDa | LRG1 | 7 | 1320 | 1 | 7 | 3 | 1323 |
| AACT HUMAN | Alpha-1-antichymotrypsin | 48 kDa | SERPINA3 | 38 | 26 | 16 | 33 | 24 | 25 |
| ACTB_HUMAN | Actin, cytoplasmic 1 | 42 kDa | ACTB | 24 | 2 | 14 | 28 | 2 | 17 |
| ACTC_HUMAN | Actin, alpha cardiac muscle 1 | 42 kDa | ACTC1 | 14 | 0 | 8 | 12 | 1 | 6 |
| ACIN1_HUMAN | Alpha-actinin-1 Afamin | 103 kDa | | 18 | 0 | 2 | 15 20 | 12 | 5 |
| ALBU HUMAN | Serum albumin | 69 kDa | ALB | 1498 | 976 | 720 | 960 | 635 | 969 |
| ALS_HUMAN | Insulin-like growth factor-binding protein complex acid labile subunit | 66 kDa | IGFALS | 14 | 6 | 2 | 4 | 1 | 9 |
| AMBP_HUMAN | Protein AMBP | 39 kDa | AMBP | 22 | 14 | 11 | 15 | 20 | 12 |
| ANGI_HUMAN | Angiotensinogen | 53 kDa | AG I SEBPINC1 | 19 29 | 16 22 | 11 | 15 37 | 12 | 20 |
| APOA_HUMAN | Apolipoprotein(a) | 501 kDa | LPA | 4 | 0 | 7 | 37 | 4 | 0 |
| APOA1_HUMAN | Apolipoprotein A-I | 31 kDa | APOA1 | 164 | 51 | 55 | 62 | 43 | 51 |
| APOA2_HUMAN | Apolipoprotein A-II | 11 kDa | APOA2 | 25 | 14 | 19 | 20 | 13 | 15 |
| APOA4_HUMAN | Apolipoprotein A-IV Apolipoprotein B-100 | 45 kDa | | 52 607 | 21 | 253 | 20 | 14 | 18 |
| APOC1 HUMAN | Apolipoprotein C-I | 9 kDa | APOC1 | 5 | 3 | 3 | 7 | 5 | 4 |
| APOC2_HUMAN | Apolipoprotein C-II | 11 kDa | APOC2 | 6 | 3 | 5 | 7 | 4 | 4 |
| APOC3_HUMAN | Apolipoprotein C-III | 11 kDa | APOC3 | 9 | 3 | 2 | 5 | 2 | 3 |
| APOD_HUMAN | Apolipoprotein D | 21 kDa | APOD | 13 | 8 | 6 | 10 | 2 | 6 |
| APOE_HUMAN | Apolipoprotein E | 36 kDa | APOE | 16 | 14 | 12 | 15 | 13 | 13 |
| APOH HUMAN | Beta-2-glycoprotein 1 | 38 kDa | APOP | 39 | 12 | 13 | 20 | 13 | 16 |
| APOL1_HUMAN | Apolipoprotein L1 | 44 kDa | APOL1 | 8 | 8 | 16 | 8 | 19 | 5 |
| APOM_HUMAN | Apolipoprotein M | 21 kDa | APOM | 10 | 1 | 2 | 3 | 0 | 1 |
| ATRN_HUMAN | Attractin | 159 kDa | ATRN | 3 | 2 | 1 | 2 | 0 | 0 |
| C1QA_HUMAN | Complement C1q subcomponent subunit A | 26 KDa | C1QA C1OB | 25 | 25 | <u>5</u> 21 | 10 | / | 15 |
| C1QC HUMAN | Complement C1q subcomponent subunit C | 26 kDa | C1QC | 7 | 11 | 10 | 5 | 10 | 8 |
| C1R_HUMAN | Complement C1r subcomponent | 80 kDa | C1R | 24 | 29 | 25 | 28 | 41 | 25 |
| C1RL_HUMAN | Complement C1r subcomponent-like protein | 53 kDa | C1RL | 0 | 0 | 0 | 0 | 3 | 0 |
| C1S_HUMAN | Complement C1s subcomponent | 77 kDa | C1S | 6 | 6 | 4 | 6 | 9 | 6 |
| C4BPA_HUMAN | C4b-binding protein lipha chain | 28 kDa | C4BPR | 9 | 9 | 9 | 92 10 | 13 | 10 |
| CAP1_HUMAN | Adenylyl cyclase-associated protein 1 | 52 kDa | CAP1 | 0 | 0 | 0 | 3 | 0 | 0 |
| CBG_HUMAN | Corticosteroid-binding globulin | 45 kDa | SERPINA6 | 5 | 4 | 0 | 3 | 0 | 0 |
| CBPB2_HUMAN | Carboxypeptidase B2 | 48 kDa | CPB2 | 1 | 7 | 3 | 0 | 2 | 2 |
| Entry Name | Protein ID | MW | Alternate ID | Control #3 | Control #13 | Control #40 | MS #39 | MS #10 | MS #2 |
| CBPN HUMAN | Carboxypeptidase N catalytic chain | 52 kDa | CPN1 | 7 | 5 | 5 | 4 | 5 | 3 |
| CD5L_HUMAN | CD5 antigen-like | 38 kDa | CD5L | 25 | 19 | 24 | 21 | 29 | 20 |
| CD9_HUMAN | CD9 antigen | 25 kDa | CD9 | 5 | 0 | 4 | 7 | 0 | 6 |
| CERU_HUMAN | Ceruloplasmin | 122 kDa | CP | 91 | 54 | 51 | 73 | 56 | 56 |
| CFAB_HUMAN | Complement factor B | 139 kDa | CFB | 34 80 | 92 | 19 | 96 | 21 | 63 |
| CFAI HUMAN | Complement factor I | 66 kDa | CFI | 12 | 11 | 9 | 13 | 14 | 8 |
| CHLE_HUMAN | Cholinesterase | 68 kDa | BCHE | 3 | 0 | 1 | 0 | 1 | 0 |
| CLH1_HUMAN | Clathrin heavy chain 1 | 192 kDa | CLTC | 0 | 0 | 0 | 4 | 0 | 0 |
| CLUS_HUMAN | Clusterin Rota Ala His disportidoso | 52 kDa | CLU | 24 | 16 | 17 | 26 | 17 | 17 |
| CO2 HUMAN | Complement C2 | 83 kDa | C2 | 3 | 2 | 0 | 1 | 0 | 0 |
| CO3_HUMAN | Complement C3 | 187 kDa | C3 | 500 | 447 | 389 | 388 | 538 | 469 |
| CO4A_HUMAN | Complement C4-A | 193 kDa | C4A | 217 | 157 | 150 | 206 | 273 | 201 |
| CO4B_HUMAN | Complement C4-B | 193 kDa | C4B | 217 | 163 | 143 | 204 | 263 | 199 |
| COS_HUMAN | Complement C5 | 105 kDa | C6 | 61 11 | 12 | 50 10 | 17 | 12 | 16 |
| CO7_HUMAN | Complement component C7 | 94 kDa | 0 | 12 | 19 | 10 | 10 | 18 | 8 |
| CO8A_HUMAN | Complement component C8 alpha chain | 65 kDa | C8A | 12 | 14 | 9 | 13 | 14 | 12 |
| CO8B_HUMAN | Complement component C8 beta chain | 67 kDa | C8B | 28 | 24 | 24 | 16 | 31 | 23 |
| CO8G_HUMAN | Complement component C8 gamma chain | 22 kDa | C8G | 7 | 6 | 8 | 6 | 10 | 5 |
| CO9_HUMAN | Complement component C9 Cofilin-1 | оз кµа 19 kDa | CFI 1 | 3 | 0 | 10 | 6 | ∠o () | 3 |
| COF2_HUMAN | Cofilin-2 | 19 kDa | CFL2 | 0 | 0 | 1 | 2 | 0 | 1 |
| COL11_HUMAN | Collectin-11 | 29 kDa | COLEC11 | 1 | 4 | 0 | 0 | 1 | 2 |
| COR1A_HUMAN | Coronin-1A | 51 kDa | CORO1A | 0 | 0 | 0 | 4 | 0 | 0 |
| CPN2_HUMAN | Carboxypeptidase N subunit 2 Platelet basic protein | 61 kDa | CPN2 | 9 | 7 | 10 | 2 | 12 | 6 |
| ECM1 HUMAN | Extracellular matrix protein 1 | 61 kDa | ECM1 | 3 | 15 | 5 | 3 | 2 | 5 |
| ENOA_HUMAN | Alpha-enolase | 47 kDa | ENO1 | 1 | 0 | 0 | 2 | 0 | 0 |
| F13A_HUMAN | Coagulation factor XIII A chain | 83 kDa | F13A1 | 4 | 20 | 17 | 38 | 7 | 13 |
| F13B_HUMAN | Coagulation factor XIII B chain | 76 kDa | F13B | 0 | 17 | 14 | 26 | 3 | 5 |
| FATZ_HUMAN | Coagulation factor XI | 08 KDa | F12 | 15 | 15 | 14 | 12 | 20 | 18 3 |
| FA9_HUMAN | Coagulation factor IX | 52 kDa | F9 | 2 | 0 | 0 | 0 | 1 | 0 |
| FBLN1_HUMAN | Fibulin-1 | 77 kDa | FBLN1 | 13 | 8 | 2 | 6 | 4 | 6 |

Total Spectral Counts

| FBLN3_HUMAN | EGF-containing fibulin-like extracellular matrix protein 1 | 55 kDa | EFEMP1 | 2 | 2 | 2 | 2 | 3 | 2 |
|----------------------------|---|-------------------|----------------|------------|-------------|-------------|---------|---------|---------|
| FCGBP_HUMAN | IgGFc-binding protein | 572 kDa | FCGBP | 3 | 2 | 6 | 16 | 12 | 2 |
| FCN2_HUMAN | Ficolin-2 | 34 kDa | FCN2 | 2 | 2 | 1 | 1 | 1 | 0 |
| FCN3_HUMAN | Ficolin-3 | 33 kDa | FCN3 | 14 | 11 | 6 | 4 | 20 | 7 |
| FETUA_HUMAN | Alpha-2-HS-glycoprotein | 39 kDa | AHSG | 28 | 19 | 19 | 25 | 19 | 19 |
| FETUB HUMAN | Fetuin-B | 42 kDa | FETUB | 1 | 0 | 1 | 1 | 2 | 1 |
| FHR1 HUMAN | Complement factor H-related protein 1 | 38 kDa | CFHR1 | 5 | 0 | 11 | 12 | 6 | 12 |
| FHR2 HUMAN | Complement factor H-related protein 2 | 31 kDa | CFHR2 | 3 | 1 | 2 | 4 | 1 | 3 |
| FHR3 HUMAN | Complement factor H-related protein 3 | 37 kDa | CFHR3 | 0 | 0 | 0 | 0 | 0 | 6 |
| FIBA HUMAN | Fibringen alpha chain | 95 kDa | FGA | 96 | 379 | 346 | 351 | 225 | 319 |
| FIBB HUMAN | Eibringen beta chain | 56 kDa | FGB | 140 | 853 | 872 | 829 | 612 | 758 |
| FIBG HUMAN | Fibringen gamma chain | 52 kDa | FGG | 123 | 465 | 426 | 388 | 334 | 408 |
| | | 021184 | 1 0 0 | 120 | 100 | 120 | | | 100 |
| Entry Name | Protein ID | MW | Alternate ID | Control #3 | Control #13 | Control #40 | MS #39 | MS #10 | MS #2 |
| | | | | | | | | | |
| FINC_HUMAN | Fibronectin | 263 kDa | FN1 | 209 | 477 | 353 | 282 | 253 | 319 |
| FLNA_HUMAN | Filamin-A | 281 kDa | FLNA | 3 | 0 | 5 | 75 | 1 | 2 |
| FLNC_HUMAN | Filamin-C | 291 kDa | FLNC | 0 | 0 | 0 | 0 | 0 | 0 |
| G3P_HUMAN | Glyceraldehyde-3-phosphate dehydrogenase | 36 kDa | GAPDH | 6 | 0 | 4 | 14 | 1 | 2 |
| GELS_HUMAN | Gelsolin | 86 kDa | GSN | 40 | 45 | 35 | 34 | 42 | 31 |
| GPX3_HUMAN | Glutathione peroxidase 3 | 26 kDa | GPX3 | 0 | 1 | 1 | 0 | 0 | 2 |
| H2A1B_HUMAN | Histone H2A type 1-B/E | 14 kDa | HIST1H2AB | 0 | 0 | 0 | 4 | 0 | 0 |
| H2B1B HUMAN | Histone H2B type 1-B | 14 kDa | HIST1H2BB | 0 | 0 | 0 | 5 | 0 | 0 |
| H4 HUMAN | Histone H4 | 11 kDa | HIST1H4A | 0 | 0 | 0 | 3 | 0 | 1 |
| HABP2 HUMAN | Hvaluronan-binding protein 2 | 63 kDa | HABP2 | 1 | 0 | 0 | 4 | 1 | 2 |
| | Hemoglobin subunit alpha | 15 kDa | HBA1 | /3 | 17 | 23 | 18 | 31 | 23 |
| | | 16 kDa | | 40 | 17 | 20 | - 10 | 26 | 20 |
| | | 10 KDa | | 39 | 17 | 30 | | 30 | 22 |
| HBD_HUMAN | Hemoglobin subunit delta | 16 kDa | HBD | 15 | 4 | 10 | 8 | 12 | 6 |
| HEMO_HUMAN | Hemopexin | 52 KDa | HPX | 55 | 39 | 29 | 37 | 29 | 39 |
| HEP2_HUMAN | Heparin cofactor 2 | 57 kDa | SERPIND1 | 20 | 13 | 10 | 11 | 15 | 14 |
| HGFA_HUMAN | Hepatocyte growth factor activator | 71 kDa | HGFAC | 3 | 2 | 3 | 1 | 7 | 3 |
| HGFL_HUMAN | Hepatocyte growth factor-like protein | 80 kDa | MST1 | 1 | 3 | 0 | 0 | 1 | 0 |
| HPT_HUMAN | Haptoglobin | 45 kDa | HP | 154 | 63 | 73 | 123 | 111 | 125 |
| HPTR_HUMAN | Haptoglobin-related protein | 39 kDa | HPR | 85 | 52 | 63 | 75 | 93 | 77 |
| HRG HUMAN | Histidine-rich glycoprotein | 60 kDa | HRG | 30 | 29 | 30 | 30 | 29 | 25 |
| HV102 HUMAN | Immunoglobulin heavy variable 1-2 | 13 kDa | IGHV1-2 | 1 | 0 | 1 | 2 | 4 | 1 |
| HV103 HUMAN | Immunoglobulin heavy variable 1-3 | 13 kDa | IGHV1-3 | 2 | 5 | 2 | 1 | 1 | 3 |
| | Immunoglobulin hoavy variable 1-8 | 13 kDa | | 0 | 0 | | | | 2 |
| | | 13 kDa | | 0 | 0 | 0 | | | 2 |
| | | 13 KDa | | 2 | E | | 3 | | 2 |
| HV146_HUMAN | Immunogiobulin neavy variable 1-46 | 13 kDa | IGHV1-46 | 3 | 5 | 2 | | 3 | 3 |
| HV205_HUMAN | Immunoglobulin heavy variable 2-5 | 13 kDa | IGHV2-5 | / | 5 | 3 | 4 | 5 | 5 |
| HV226_HUMAN | Immunoglobulin heavy variable 2-26 | 13 kDa | IGHV2-26 | 3 | 0 | 2 | 1 | 2 | 2 |
| HV307_HUMAN | Immunoglobulin heavy variable 3-7 | 13 kDa | IGHV3-7 | 8 | 6 | 8 | 7 | 11 | 0 |
| HV309_HUMAN | Immunoglobulin heavy variable 3-9 | 13 kDa | IGHV3-9 | 12 | 5 | 12 | 5 | 10 | 9 |
| HV311_HUMAN | Immunoglobulin heavy variable 3-11 | 13 kDa | IGHV3-11 | 8 | 0 | 0 | 0 | 0 | 0 |
| HV313_HUMAN | Immunoglobulin heavy variable 3-13 | 13 kDa | IGHV3-13 | 6 | 4 | 8 | 0 | 6 | 6 |
| HV315_HUMAN | Immunoglobulin heavy variable 3-15 | 13 kDa | IGHV3-15 | 4 | 3 | 4 | 2 | 3 | 2 |
| HV321 HUMAN | Immunoglobulin heavy variable 3-21 | 13 kDa | IGHV3-21 | 0 | 6 | 0 | 0 | 0 | 0 |
| HV323 HUMAN | Immunoglobulin heavy variable 3-23 | 13 kDa | IGHV3-23 | 7 | 8 | 7 | 4 | 7 | 8 |
| HV330 HUMAN | Immunoglobulin heavy variable 3-30 | 13 kDa | IGHV3-30 | 8 | 10 | 8 | 6 | 11 | 9 |
| HV349 HUMAN | Immunoglobulin heavy variable 3-49 | 13 kDa | IGHV3-49 | 3 | 2 | 1 | 4 | 5 | 2 |
| | Immunoglobulin heavy variable 3-72 | 13 kDa | IGHV3-72 | 2 | 4 | 6 | 4 | 5 | 2 |
| | | 12 kDa | | 1 | 4 | 1 | 4 | | |
| | | 13 KDa | | 7 | 0 | | | | 0 |
| | | 13 KDa | | / | | 4 | 0 | 0 | 9 |
| | | 13 KDa | IGHV4-4 | 0 | 5 | | 0 | | 0 |
| | | 13 KDa | IGHV4-26 | 2 | 0 | 7 | 0 | | 1 |
| HV432_HUMAN | Immunoglobulin neavy variable 4-30-2 | 13 kDa | IGHV4-30-2 | 8 | 5 | / | 4 | 6 | 0 |
| HV434_HUMAN | Immunoglobulin heavy variable 4-34 | 14 kDa | IGHV4-34 | 11 | 9 | 9 | 7 | 8 | 7 |
| HV551_HUMAN | Immunoglobulin heavy variable 5-51 | 13 kDa | IGHV5-51 | 9 | 10 | 3 | 5 | 6 | 2 |
| HV5X1_HUMAN | Immunoglobulin heavy variable 5-10-1 | 13 kDa | IGHV5-10-1 | 3 | 4 | 2 | 2 | 4 | 2 |
| HV601_HUMAN | Immunoglobulin heavy variable 6-1 | 13 kDa | IGHV6-1 | 1 | 1 | 0 | 0 | 2 | 1 |
| HV64D_HUMAN | Immunoglobulin heavy variable 3-64D | ? | | 3 | 2 | 3 | 1 | 2 | 1 |
| HV741_HUMAN | Immunoglobulin heavy variable 7-4-1 | 13 kDa | IGHV7-4-1 | 0 | 0 | 0 | 0 | 4 | 5 |
| Entry Namo | Protoin ID | M/M | | Control #2 | Control #12 | Control #40 | MC #20 | MS #10 | MC #2 |
| Lindy Name | FIOLEIIIID | IVIVV | Alternate ID | 0011101#3 | 0011101#13 | 0011101#40 | WO#39 | WI3 #10 | W3#2 |
| IC1 HUMAN | Plasma protease C1 inhibitor | 55 kDa | SERPING1 | 19 | 16 | 8 | 18 | 12 | 8 |
| | Immunodobulin aloba-2 heavy chain | 10 100 | 02.11 1101 | 20 | 23 | 15 | 24 | 30 | 15 |
| | | 40 KDd | | 23 | £3 6 | o | 1 | 25 | |
| | Immunoglobulin della nedvy chalin | 30 KDd | | 2 | 107 | 400 | 171 | 20 | 140 |
| | immunogiobulin gamma-i neavy chain | 49 KDa | | 317 | 12/ | 133 | 1/1 | 128 | 140 |
| IGHA1_HUMAN | Immunogiobulin heavy constant alpha 1 | 38 kDa | IGHA1 | 104 | 95 | /8 | 96 | 126 | 64 |
| IGHD_HUMAN | Immunoglobulin heavy constant delta | 42 kDa | IGHD | 0 | 5 | 0 | 0 | 22 | 0 |
| IGHG2_HUMAN | Immunoglobulin heavy constant gamma 2 | 36 kDa | IGHG2 | 194 | 120 | 96 | 108 | 97 | 99 |
| IGHG3_HUMAN | Immunoglobulin heavy constant gamma 3 | 41 kDa | IGHG3 | 101 | 74 | 71 | 60 | 84 | 51 |
| IGHG4_HUMAN | Immunoglobulin heavy constant gamma 4 | 36 kDa | IGHG4 | 62 | 39 | 51 | 34 | 30 | 47 |
| IGHM_HUMAN | Immunoglobulin heavy constant mu | 49 kDa | IGHM | 361 | 264 | 388 | 239 | 484 | 266 |
| IGJ_HUMAN | Immunoglobulin J chain | 18 kDa | JCHAIN | 16 | 11 | 19 | 16 | 20 | 13 |
| IGK HUMAN | Immunoalobulin kappa liaht chain | 23 kDa | | 173 | 124 | 137 | 111 | 137 | 98 |
| IGKC HUMAN | Immunoalobulin kappa constant | 12 kDa | IGKC | 191 | 132 | 149 | 119 | 144 | 111 |
| IGL1 HUMAN | Immunoqlobulin lambda-1 light chain | 23 kDa | | 116 | 70 | 75 | 75 | 109 | 53 |
| | Immunoglobulin lambda constant 2 | 11 100 | ICI Co | 126 | 70 | 96 | 88 | 100 | 23 |
| | Immunoyiobuliin lambda constant 7 | 11 KDd | | 120 | 19 | 30 | 00 | 109 | 02 |
| IGLU/_HUMAN | immunogiobulin lambda constant / | | IGLU/ | 4/ | 39 | 49 | 30 | 3/ | 33 |
| IGM_HUMAN | Immunoglobulin mu heavy chain | 63 kDa | | 303 | 238 | 331 | 211 | 393 | 247 |
| ILK_HUMAN | Integrin-linked protein kinase | 51 kDa | ILK | 2 | 0 | 0 | 6 | 0 | 0 |
| ITA2B_HUMAN | Integrin alpha-IIb | 113 kDa | ITGA2B | 5 | 0 | 5 | 18 | 0 | 10 |
| ITB3_HUMAN | Integrin beta-3 | 87 kDa | ITGB3 | 5 | 0 | 3 | 14 | 0 | 5 |
| ITIH1_HUMAN | Inter-alpha-trypsin inhibitor heavy chain H1 | 101 kDa | ITIH1 | 44 | 32 | 25 | 29 | 28 | 20 |
| ITIH2_HUMAN | Inter-alpha-trypsin inhibitor heavy chain H2 | 106 kDa | ITIH2 | 47 | 31 | 27 | 35 | 28 | 31 |
| ITIH3_HUMAN | Inter-alpha-trypsin inhibitor beavy chain H3 | 100 kDa | ITIH3 | 4 | 0 | 0 | 6 | 0 | 0 |
| | inter-apria-trypoint infibitor fleavy chain fib | | | | | | | | |
| ITIH4 HUMAN | Inter-alpha-trypsin inhibitor heavy chain H4 | 103 kDa | ITIH4 | 35 | 32 | 23 | 46 | 27 | 33 |
| ITIH4_HUMAN K1C10 HUMAN | Inter-alpha-trypsin inhibitor heavy chain H4 Keratin. tvoe I cvtoskeletal 10 | 103 kDa 59 kDa | ITIH4 KRT10 | 35 1 | 32 4 | 23 0 | 46 0 | 27 1 | 33 1 |

| | Keratin, type II cytoskeletal 2 epidermal | 65 kDa | KRT2 | 0 | 3 | 0 | 0 | 0 | 2 |
|---|---|---|---|---|---|---|---|---|--|
| K2C1_HUMAN | Keratin, type II cytoskeletal 1 | 66 kDa | KRT1 | 2 | 5 | 0 | 0 | 0 | 2 |
| KAIN_HUMAN | Kallistatin | 49 kDa | SERPINA4 | 7 | 7 | 3 | 3 | 4 | 6 |
| KLKB1 HUMAN | Plasma kallikrein | 71 kDa | KLKB1 | 18 | 7 | 11 | 4 | 8 | 13 |
| KNG1 HUMAN | Kininogen-1 | 72 kDa | KNG1 | 28 | 29 | 20 | 26 | 18 | 16 |
| KPYM HUMAN | Pyruvate kinase PKM | 58 kDa | PKM | 3 | 0 | 0 | 3 | 0 | 0 |
| KV105 HUMAN | Immunoglobulin kappa variable 1-5 | 13 kDa | IGKV1-5 | 5 | 2 | 3 | 4 | 2 | 2 |
| KV108 HUMAN | Immunoglobulin kappa variable 1-8 | 13 kDa | IGKV1-8 | 7 | 11 | 5 | 4 | 9 | 5 |
| KV112 HUMAN | Immunoglobulin kappa variable 1-12 | 13 kDa | IGKV1-12 | 9 | 3 | 6 | 4 | 8 | 4 |
| KV/113 HUMAN | Immunoglobulin kappa variable 1-12 | 13 kDa | IGKV1-12 | 1 | 0 | 1 | 3 | 0 | |
| | | 12 kDa | | | 0 | 4 | 0 | | |
| | | 13 kDa | IGKV1-17 | 6 | 5 | 9 | 5 | 12 | - 2 |
| | | 13 KDa | | | 5 | 0 | 5 | 12 | 3 |
| | | 13 KDa | IGKV1-27 | / | 13 | 4 | 3 | | 3 |
| | | 13 KDa | IGKV1-39 | 8 | 3 | 6 | 2 | | 4 |
| KV224_HUMAN | Immunoglobulin kappa variable 2-24 | 13 kDa | IGKV2-24 | 3 | 3 | 5 | 2 | 2 | 3 |
| KV228_HUMAN | Immunoglobulin kappa variable 2-28 | 13 KDa | IGKV2-28 | 6 | / | / | 2 | | |
| KV229_HUMAN | Immunoglobulin kappa variable 2-29 | 13 kDa | IGKV2-29 | 0 | 2 | 3 | 0 | 0 | 0 |
| KV230_HUMAN | Immunoglobulin kappa variable 2-30 | 13 kDa | IGKV2-30 | 4 | 4 | 5 | 2 | 3 | 3 |
| KV240_HUMAN | Immunoglobulin kappa variable 2-40 | 13 kDa | IGKV2-40 | 4 | 3 | 5 | 2 | 3 | 2 |
| KV311_HUMAN | Immunoglobulin kappa variable 3-11 | 13 kDa | IGKV3-11 | 9 | 4 | 3 | 4 | 4 | 4 |
| KV315_HUMAN | Immunoglobulin kappa variable 3-15 | 12 kDa | IGKV3-15 | 3 | 2 | 5 | 2 | 4 | 3 |
| KV320_HUMAN | Immunoglobulin kappa variable 3-20 | 13 kDa | IGKV3-20 | 10 | 8 | 11 | 11 | 12 | 7 |
| KV401_HUMAN | Immunoglobulin kappa variable 4-1 | 13 kDa | IGKV4-1 | 8 | 6 | 4 | 5 | 5 | 5 |
| Entry Nama | Brotoin ID | N/1\A/ | | Control #2 | Control #12 | Control #40 | MC #20 | MC #10 | MC #0 |
| Entry Name | Protein ID | IVI VV | Alternate ID | Control #3 | Control #13 | Control #40 | IVI5 #39 | IVIS # 10 | IVI5 #2 |
| KVD15 HUMAN | Immunoqlobulin kappa variable 3D-15 | 13 kDa | IGKV/3D-15 | 3 | 3 | 5 | 3 | 4 | 3 |
| | Immunoglobulin kappa variable 3D-13 | 13 kDa | | 0 | 3 | 7 | 11 | | 6 |
| | Immunoglobulin kappa variable 3D-20 | 13 kDa | | 9 | | 7 | 0 | | 0 |
| | linenek ezeberide hinding pretein | 13 KDa | IGKV2D-29 | 0 | 2 | 3 | 0 | 2 | 0 |
| | Lipopolysacchande-binding protein | 53 KDa | | 3 | 1 | 1 | 4 | 8 | 4 |
| LDHB_HUMAN | L-lactate denydrogenase B chain | 37 kDa | LDHB | 2 | 0 | 0 | 1 | 0 | 0 |
| LG3BP_HUMAN | Galectin-3-binding protein | 65 kDa | LGALS3BP | 21 | 14 | 18 | 19 | 33 | 20 |
| LIMS1_HUMAN | LIM and senescent cell antigen-like-containing domain protein 1 | 37 kDa | LIMS1 | 0 | 0 | 1 | 2 | 0 | 0 |
| LV144_HUMAN | Immunoglobulin lambda variable 1-44 | 12 kDa | IGLV1-44 | 4 | 4 | 1 | 0 | 3 | 0 |
| LV14/_HUMAN | Immunoglobulin lambda variable 1-47 | 12 kDa | IGLV1-47 | 6 | 4 | 3 | 2 | 4 | 2 |
| LV151_HUMAN | Immunoglobulin lambda variable 1-51 | 12 kDa | IGLV1-51 | 2 | 2 | 2 | 2 | 3 | 2 |
| LV211_HUMAN | Immunoglobulin lambda variable 2-11 | 13 kDa | IGLV2-11 | 1 | 3 | 2 | 1 | 2 | 1 |
| LV218_HUMAN | Immunoglobulin lambda variable 2-18 | 12 kDa | IGLV2-18 | 2 | 0 | 1 | 0 | 2 | 0 |
| LV301_HUMAN | Immunoglobulin lambda variable 3-1 | 12 kDa | IGLV3-1 | 0 | 0 | 0 | 0 | 3 | 0 |
| LV310_HUMAN | Immunoglobulin lambda variable 3-10 | 12 kDa | IGLV3-10 | 2 | 4 | 2 | 2 | 3 | 3 |
| LV319_HUMAN | Immunoglobulin lambda variable 3-19 | 12 kDa | IGLV3-19 | 2 | 0 | 1 | 1 | 1 | 1 |
| LV321_HUMAN | Immunoglobulin lambda variable 3-21 | 12 kDa | IGLV3-21 | 3 | 4 | 4 | 1 | 3 | 2 |
| LV39_HUMAN | Immunoglobulin lambda variable 3-9 | ? | | 3 | 4 | 0 | 0 | 2 | 1 |
| LV861_HUMAN | Immunoglobulin lambda variable 8-61 | 13 kDa | IGLV8-61 | 2 | 1 | 3 | 1 | 0 | 1 |
| LV949_HUMAN | Immunoglobulin lambda variable 9-49 | 13 kDa | IGLV9-49 | 0 | 2 | 0 | 0 | 0 | 0 |
| LYSC_HUMAN | Lysozyme C | 17 kDa | LYZ | 1 | 1 | 0 | 1 | 2 | 1 |
| MASP1_HUMAN | Mannan-binding lectin serine protease 1 | 79 kDa | MASP1 | 2 | 0 | 0 | 0 | 0 | 0 |
| MMRN1_HUMAN | Multimerin-1 | 138 kDa | MMRN1 | 0 | 0 | 0 | 2 | 0 | 0 |
| MYH9_HUMAN | Myosin-9 | 227 kDa | MYH9 | 2 | 0 | 1 | 24 | 3 | 0 |
| MYL6_HUMAN | Myosin light polypeptide 6 | 17 kDa | MYL6 | 1 | 0 | 1 | 5 | 0 | 1 |
| PARVB HUMAN | Beta-parvin | 42 kDa | PARVB | 3 | 0 | 0 | 1 | 0 | 0 |
| PDLI1 HUMAN | PDZ and LIM domain protein 1 | 36 kDa | PDLIM1 | 0 | 0 | 0 | 5 | 0 | 0 |
| | Pigment enithelium-derived factor | 46 kDa | SERPINF1 | 7 | 7 | 5 | 4 | 4 | 8 |
| PEDF HUMAN | | | | | | | - | | |
| PEDF_HUMAN | Platelet factor 4 variant | 12 kDa | PF4VI | 5 | 0 | 5 | 4 | 2 | 3 |
| PEDF_HUMAN PF4V_HUMAN PGRP2 HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase | 12 kDa 62 kDa | PGLYRP2 | 5 18 | 0 | 5 15 | 4 | 2 15 | 3 14 |
| PEDF_HUMAN PF4V_HUMAN PGRP2_HUMAN PHLD_HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidvlinositol-glycan-specific phospholipase D | 12 kDa 62 kDa 92 kDa | PF4V1 PGLYRP2 GPLD1 | 5 18 0 | 0 14 4 | 5 15 4 | 4 12 4 | 2 15 2 | 3 14 0 |
| PEDF_HUMAN PF4V_HUMAN PGRP2_HUMAN PHLD_HUMAN PILD_HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoolobulin recentor | 12 kDa 62 kDa 92 kDa 83 kDa | PGLYRP2 GPLD1 PIGR | 5 18 0 1 | 0 14 4 1 | 5 15 4 9 | 4 12 4 3 | 2 15 2 12 | 3 14 0 4 |
| PEDF_HUMAN PF4V_HUMAN PGRP2_HUMAN PHLD_HUMAN PIGR_HUMAN PI FK HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Pleckstrin | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa | PF4V1 PGLYRP2 GPLD1 PIGR PLFK | 5 18 0 1 5 | 0 14 4 1 0 | 5 15 4 9 0 | 4 12 4 3 5 | 2 15 2 12 0 | 3 14 0 4 3 |
| PEDF_HUMAN PF4V_HUMAN PGRP2_HUMAN PHLD_HUMAN PIGR_HUMAN PLEK_HUMAN PLEK_HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Pleckstrin Platelet factor 4 | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa | PF4V1 PGLYRP2 GPLD1 PIGR PLEK PF4 | 5 18 0 1 5 6 | 0 14 4 1 0 0 | 5 15 4 9 0 | 4 12 4 3 5 4 | 2 15 2 12 0 3 | 3 14 0 4 3 4 |
| PEDF_HUMAN PF4V_HUMAN PGRP2_HUMAN PHLD_HUMAN PIGR_HUMAN PLEK_HUMAN PLEK_HUMAN PLF4_HUMAN PI MN, HIIMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Pleckstrin Platelet factor 4 Plateminoren | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa 11 kDa 91 kDa | PGLYRP2 GPLD1 PIGR PLEK PF4 PL G | 5 18 0 1 5 6 65 | 0 14 4 1 0 0 111 | 5 15 4 9 0 6 91 | 4 12 4 3 5 4 79 | 2 15 2 12 0 3 64 | 3 14 0 4 3 4 80 |
| PEDF_HUMAN PF4V_HUMAN PGRP2_HUMAN PHLD_HUMAN PIGR_HUMAN PLEK_HUMAN PLF4_HUMAN PLF4_HUMAN PLTM_HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Plackstrin Platelet factor 4 Plasminogen Phospholipid transfer protein | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa 11 kDa 91 kDa | PGLYRP2 GPLD1 PIGR PLEK PF4 PLG PLTP | 5 18 0 1 5 6 65 | 0 14 4 1 0 0 111 | 5 15 4 9 0 6 91 | 4 12 4 3 5 4 79 0 | 2 15 2 12 0 3 64 0 | 3 14 0 4 3 4 80 0 |
| PEDF_HUMAN PF4V_HUMAN PGRP2_HUMAN PIGR_HUMAN PIGR_HUMAN PLEK_HUMAN PLF4_HUMAN PLTP_HUMAN PON1_HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Pleckstrin Platelet factor 4 Plasminogen Phospholipid transfer protein Serum paraoxonase/arylectorase 1 | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa 11 kDa 91 kDa 55 kDa | PF4VI PGLYRP2 GPLD1 PIGR PLEK PLG PLTP PON1 | 5 18 0 1 5 6 65 4 32 | 0 14 4 1 0 0 111 0 18 | 5 15 4 9 0 6 91 0 22 | 4 12 4 3 5 4 79 0 28 | 2 15 2 12 0 3 64 0 8 | 3 14 0 4 3 4 80 0 22 |
| PEDF_HUMAN PF4V_HUMAN PGRP2_HUMAN PILD_HUMAN PIGR_HUMAN PLEK_HUMAN PLF4_HUMAN PLTP_HUMAN PON1_HUMAN PON1_HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Pleckstrin Platelet factor 4 Plasminogen Phospholipid transfer protein Serum paraoxonase/arylesterase 1 POTE ankvirin domain family member E | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa 11 kDa 91 kDa 55 kDa 40 kDa 121 kDa | PF4VI PGLYRP2 GPLD1 PIGR PLEK PLG PLTP PON1 POTFF | 5 18 0 1 5 6 65 4 32 11 | 0 14 4 1 0 0 111 0 18 0 | 5 15 4 9 0 6 91 0 22 5 | 4 12 4 3 5 4 79 0 28 13 | 2 15 2 12 0 3 64 0 8 0 | 3 14 0 4 3 4 80 0 22 7 |
| PEDF_HUMAN PF4V_HUMAN PGRP2_HUMAN PHLD_HUMAN PIGR_HUMAN PLF4_HUMAN PLF4_HUMAN PLTP_HUMAN PON1_HUMAN POTEE_HUMAN POTEE_HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Pleckstrin Platelet factor 4 Plasminogen Phospholipid transfer protein Serum paraoxonase/arylesterase 1 POTE ankyrin domain family member E POTE ankyrin domain family member .1 | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa 11 kDa 91 kDa 55 kDa 40 kDa 121 kDa | PGLYRP2 GPLD1 PIGR PLEK PF4 PLG PLTP PON1 POTEE POTE1 | 5 18 0 1 5 6 65 4 32 11 0 | 0 14 1 0 0 111 0 18 0 0 | 5 15 4 9 0 6 91 0 22 5 0 | 4 12 4 3 5 4 79 0 28 13 7 | 2 15 2 12 0 3 64 0 8 0 0 0 | 3 14 0 4 3 4 80 0 22 7 0 |
| PEDF_HUMAN PF4V_HUMAN PGRP2_HUMAN PIGR_HUMAN PIGR_HUMAN PLF4_HUMAN PLF4_HUMAN PLTP_HUMAN PON1_HUMAN POTEE_HUMAN POTEJ_HUMAN PDTEJ_HUMAN PDTEJ_HUMAN PDTEJ_HUMAN PDTEJ_HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Platelet factor 4 Platelet factor 4 Plasminogen Phospholipid transfer protein Serum paraoxonase/arylesterase 1 POTE ankyrin domain family member J PantidyLproku cis.trans isomerase 4 | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa 11 kDa 91 kDa 55 kDa 40 kDa 121 kDa 117 kDa 18 kDa | PF4VI PGLYRP2 GPLD1 PIGR PLEK PLG PLTP PON1 POTEE POTEJ PPIA | 5 18 0 1 5 6 65 4 32 11 0 1 | 0 14 4 0 0 0 1111 0 18 0 0 0 | 5 15 4 9 0 6 91 0 22 5 0 1 | 4 12 4 3 5 4 79 0 28 13 7 2 | 2 15 2 0 3 64 0 8 0 0 0 0 | 3 14 0 4 3 4 80 0 22 7 7 0 0 |
| PEDF_HUMAN PF4V_HUMAN PGRP2_HUMAN PIGR_HUMAN PLGK_HUMAN PLF4_HUMAN PLTP_HUMAN PON1_HUMAN POTEE_HUMAN POTE_HUMAN POTE_HUMAN PDTEJ_HUMAN PDTEJ_HUMAN PDTEJ_HUMAN PBG4_HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Pleckstrin Platelet factor 4 Plasminogen Phospholipid transfer protein Serum paraoxonase/arylesterase 1 POTE ankyrin domain family member E POTE ankyrin domain family member J Peptidyl-prolyl cis-trans isomerase A Proteonlycan 4 | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa 11 kDa 91 kDa 55 kDa 40 kDa 121 kDa 117 kDa 18 kDa 151 kDa | PF4VI PGLYRP2 GPLD1 PIGR PLEK PLG PLTP PON1 POTEE POTEJ PPIA PBG4 | 5 18 0 1 5 6 6 6 5 4 32 11 0 1 | 0 14 4 0 0 111 0 111 0 18 0 0 0 0 0 | 5 15 4 9 0 6 91 0 22 5 0 22 5 0 1 3 | 4 12 4 3 5 4 79 0 28 13 7 2 0 | 2 15 2 0 3 64 0 8 0 0 0 1 | 3 14 0 4 3 4 80 0 22 7 0 0 6 |
| PEDF_HUMAN PF4V_HUMAN PGRP2_HUMAN PIGR_HUMAN PIGR_HUMAN PLEK_HUMAN PLF4_HUMAN PLTP_HUMAN POTE_HUMAN POTEL_HUMAN POTEJ_HUMAN PRG4_HUMAN PRG4_HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Plackstrin Platelet factor 4 Plasminogen Phospholipid transfer protein Serum paraoxonase/arylesterase 1 POTE ankyrin domain family member E POTE ankyrin domain family member J Peptidyl-prolyl cis-trans isomerase A Proteoglycan 4 Proteing | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa 11 kDa 91 kDa 55 kDa 121 kDa 117 kDa 18 kDa 15 kDa | PF4VI PGLYRP2 GPLD1 PIGR PLEK PF4 PLG PLTP PON1 POTEE POTEJ PPIA PRG4 PEN1 | 5 18 0 1 5 6 65 4 32 11 0 1 1 2 | 0 14 1 0 0 0 111 0 18 0 0 0 0 0 0 0 0 | 5 15 4 9 0 6 91 0 22 5 0 1 3 0 | 4 12 4 3 5 4 79 0 28 13 7 2 0 3 | 2 15 2 12 0 3 64 0 8 0 0 0 0 0 1 0 | 3 14 0 4 3 4 80 0 222 7 7 0 0 0 6 6 |
| PEDF_HUMAN PF4V_HUMAN PGRP2_HUMAN PIGR_HUMAN PIGR_HUMAN PLEK_HUMAN PLF4_HUMAN PLTP_HUMAN PON1_HUMAN POTEL_HUMAN POTEL_HUMAN POTEL_HUMAN PRG4_HUMAN PRG4_HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Pleckstrin Platelet factor 4 Plasminogen Phospholipid transfer protein Serum paraoxonase/arylesterase 1 POTE ankyrin domain family member J Potteglycan 4 Protein_1 Protein_1 Paraevertin | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa 11 kDa 55 kDa 40 kDa 121 kDa 121 kDa 117 kDa 18 kDa 151 kDa 15 kDa | PGLYRP2 GPLD1 PIGR PLEK PF4 PLG PLTP PON1 POTEE POTEJ PPIA PRG4 PFN1 OEP | 5 18 0 1 5 6 65 4 32 11 0 1 1 2 1 | 0 14 1 0 0 1111 0 111 0 111 0 0 0 0 0 0 | 5 15 4 9 0 6 91 0 22 5 0 1 3 0 2 2 2 5 0 0 1 3 3 | 4 12 4 5 5 4 79 0 28 13 7 2 0 3 3 2 | 2 15 2 12 0 3 64 0 8 0 0 0 0 1 1 0 4 | 3 14 0 4 3 4 80 0 22 7 0 0 0 6 2 2 |
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| PEDF_HUMAN PF4V_HUMAN PGRP2_HUMAN PILD_HUMAN PIGR_HUMAN PLF4_HUMAN PLF4_HUMAN PLTP_HUMAN PON1_HUMAN POTEE_HUMAN POTEJ_HUMAN PRG4_HUMAN PROF1_HUMAN PROF_HUMAN PROS_HUMAN PDS_HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Platelet factor 4 Platelet factor 4 Plasminogen Phospholipid transfer protein Serum paraoxonase/arylesterase 1 POTE ankyrin domain family member E POTE ankyrin domain family member J Peptidyl-prolyl cis-trans isomerase A Proteoglycan 4 Profilin-1 Properdin Vitamin K-dependent protein S Processor Zeno protein | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa 11 kDa 91 kDa 55 kDa 121 kDa 121 kDa 151 kDa 151 kDa 51 kDa 51 kDa 16 kDa | PF4VI PGLYRP2 GPLD1 PIGR PLEK PLG PLTP PON1 POTEE POTEJ PPIA PFN1 CFP PROS1 PZC | 5 18 0 1 5 6 65 4 32 11 0 1 1 2 1 24 260 | 0 14 4 1 0 0 111 0 18 0 0 0 0 0 0 0 0 0 0 0 0 27 225 | 5 15 4 9 0 6 91 0 222 5 0 1 3 0 3 23 106 | 4 12 4 3 5 4 79 0 28 13 7 2 0 3 2 2 0 3 2 2 24 | 2 15 2 0 3 64 0 8 0 0 0 0 0 0 0 0 1 1 0 0 4 34 260 | 3 14 0 4 3 4 80 0 22 7 7 0 0 0 6 6 2 1 30 30 |
| PEDF_HUMAN PF4V_HUMAN PGRP2_HUMAN PGRP2_HUMAN PIGR_HUMAN PLD_HUMAN PLF4_HUMAN PLF4_HUMAN PLTP_HUMAN POTE_HUMAN POTEJ_HUMAN PRG4_HUMAN PROS_HUMAN PROS_HUMAN PACP_HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Pleckstrin Platelet factor 4 Plasminogen Phospholipid transfer protein Serum paraoxonase/arylesterase 1 POTE ankyrin domain family member E POTE ankyrin domain family member J Peptidyl-prolyl cis-trans isomerase A Proteoglycan 4 Profilin-1 Properdin Vitamin K-dependent protein S Pregnancy zone protein | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa 11 kDa 91 kDa 55 kDa 121 kDa 121 kDa 151 kDa 151 kDa 51 kDa 75 kDa 164 kDa | PF4VI PGLYRP2 GPLD1 PIGR PLEK PF4 PLG PLTP PON1 POTEE POTEJ PPIA PRG4 PFN1 CFP PROS1 PZP PAP4 | 5 18 0 1 5 6 65 4 32 11 0 1 1 2 1 24 269 | 0 14 4 1 0 0 1111 0 18 0 0 0 0 0 0 0 4 27 235 0 | | 4 12 4 3 5 4 79 0 28 13 7 2 0 3 2 24 206 | $ \begin{array}{c} 2 \\ 15 \\ 2 \\ 12 \\ 0 \\ 3 \\ 64 \\ 0 \\ 8 \\ 0 \\ 0 \\ 0 \\ 1 \\ 0 \\ 4 \\ 34 \\ 259 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0$ | 3 14 0 4 3 4 80 0 22 7 0 0 0 6 2 1 30 287 4 |
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| PEDE_HUMAN PF4V_HUMAN PGRP2_HUMAN PIGR_HUMAN PIGR_HUMAN PLEK_HUMAN PLF4_HUMAN PLF4_HUMAN PON1_HUMAN PON1_HUMAN POTEE_HUMAN POTEL_HUMAN POTEJ_HUMAN PRG4_HUMAN PROF1_HUMAN PROF_HUMAN PROS_HUMAN RAP1A_HUMAN RAP1A_HUMAN RAP1A_HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Pleckstrin Platelet factor 4 Plasminogen Phospholipid transfer protein Serum paraoxonase/arylesterase 1 POTE ankyrin domain family member E POTE ankyrin domain family member J Peptidyl-prolyl cis-trans isomerase A Proteoglycan 4 Profilin-1 Properdin Vitamin K-dependent protein S Pregnancy zone protein Ras-related protein Rap-1A Retinol-binding protein 4 | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa 11 kDa 55 kDa 40 kDa 121 kDa 121 kDa 151 kDa 151 kDa 151 kDa 151 kDa 21 kDa 21 kDa 21 kDa | PF4VI PGLYRP2 GPLD1 PIGR PLEK PF4 PLG PLTP PON1 POTEE POTEJ PPIA PRG4 PFN1 CFP PROS1 PZP RAP1A RBP4 | 5 18 0 1 5 6 65 4 32 11 0 1 2 1 24 269 2 15 0 | 0 14 1 0 0 1111 0 18 0 0 0 0 0 0 0 0 0 0 0 0 4 27 235 0 6 0 | 5 15 4 9 0 6 91 0 22 5 0 1 3 0 3 23 196 2 7 0 | 4 12 4 5 5 4 79 0 28 13 7 2 0 3 2 24 206 3 4 7 2 2 4 206 3 4 7 2 2 2 4 2 2 3 3 7 2 2 2 3 3 3 7 2 2 3 3 7 2 2 3 3 7 2 2 3 3 7 2 2 3 3 7 2 2 3 3 7 2 2 3 3 7 2 2 3 3 7 2 2 3 3 7 2 2 3 3 7 2 2 3 3 7 2 2 3 3 7 2 2 3 3 7 2 2 3 3 7 2 2 3 3 7 2 2 3 3 7 2 2 2 3 3 3 7 2 2 2 2 3 3 2 2 2 3 3 2 2 2 2 2 3 3 2 2 2 3 3 2 2 3 3 2 2 2 2 2 2 3 3 2 2 2 2 2 2 3 3 2 2 2 2 2 3 3 2 2 2 2 4 2 2 3 3 2 2 2 4 2 2 3 3 2 2 2 4 2 2 2 3 3 2 2 2 4 2 2 2 3 3 2 2 2 4 2 2 2 3 3 2 2 2 4 2 2 2 4 2 2 2 4 2 2 2 3 3 2 2 2 4 2 2 3 3 2 2 2 4 2 2 3 3 2 2 2 4 2 2 2 3 3 2 2 2 4 2 2 2 2 2 2 4 2 2 2 2 3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 | 2 15 2 12 0 3 64 0 0 0 0 0 0 1 0 0 0 1 0 0 0 1 0 0 4 34 259 0 4 259 | 3 14 0 4 3 4 80 0 22 7 0 0 6 2 1 30 287 1 5 |
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| PEDF_HUMAN PF4V_HUMAN PGRP2_HUMAN PIGR_HUMAN PIGR_HUMAN PLF4_HUMAN PLF4_HUMAN PLTP_HUMAN POTE5_HUMAN POTE5_HUMAN PRG4_HUMAN PRG4_HUMAN PROF1_HUMAN PRO5_HUMAN PRO5_HUMAN PRO5_HUMAN PRO5_HUMAN PRO5_HUMAN PRO5_HUMAN PRO5_HUMAN PRO5_HUMAN PRO5_HUMAN PRO5_HUMAN PAD5_HUMAN SAA4_HUMAN SAA4_HUMAN SAMP_HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Pleckstrin Platelet factor 4 Plasminogen Phospholipid transfer protein Serum paraoxonase/arylesterase 1 POTE ankyrin domain family member E POTE ankyrin domain family member J Peptidyl-prolyl cis-trans isomerase A Proteoglycan 4 Profilin-1 Properdin Vitamin K-dependent protein S Pregnancy zone protein Ras-related protein Rap-1A Retinol-binding protein 4 Serum amyloid A-4 protein | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa 11 kDa 55 kDa 40 kDa 121 kDa 121 kDa 151 kDa 151 kDa 51 kDa 164 kDa 21 kDa 23 kDa 15 kDa | PF4VI PGLYRP2 GPLD1 PIGR PLEK PF4 PLG PLTP PON1 POTEE POTEJ PPIA PFN1 CFP PROS1 PZP RAP1A RBP4 SAA4 APCS | 5 18 0 1 5 6 65 4 32 11 0 1 2 1 24 269 2 15 9 13 | 0 14 4 1 0 0 1111 0 188 0 0 0 0 0 0 0 0 0 0 0 0 0 | | 4 12 4 3 5 4 79 0 28 13 7 2 0 3 2 24 206 3 4 7 13 | 2 15 2 0 3 64 0 8 0 0 0 0 0 0 0 0 0 0 0 1 1 0 0 0 0 0 | 3 14 0 4 3 4 80 0 22 7 0 6 2 1 30 287 1 5 1 12 |
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| PEDF_HUMAN PF4V_HUMAN PGRP2_HUMAN PILD_HUMAN PILD_HUMAN PLEK_HUMAN PLF4_HUMAN PLTP_HUMAN PON1_HUMAN POTEE_HUMAN POTEE_HUMAN POTEL_HUMAN PRG4_HUMAN PROF1_HUMAN PROF1_HUMAN PROF1_HUMAN RAP1A_HUMAN RAP1A_HUMAN RAP1A_HUMAN SA44_HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Pleckstrin Platelet factor 4 Plasminogen Phospholipid transfer protein Serum paraoxonase/arylesterase 1 POTE ankyrin domain family member E POTE ankyrin domain family member J Peptidyl-prolyl cis-trans isomerase A Proteoglycan 4 Profilin-1 Properdin Vitamin K-dependent protein S Pregnancy zone protein Ras-related protein Rap-1A Retinol-binding protein 4 Serum amyloid A-4 protein Serum amyloid A-4 protein Serum amyloid P-component Protein ID Selenoprotein P Sex hormone-binding globulin Erythrocyte band 7 integral membrane protein | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa 11 kDa 55 kDa 40 kDa 121 kDa 121 kDa 121 kDa 151 kDa 151 kDa 151 kDa 21 kDa 23 kDa 15 kDa 23 kDa 44 kDa 32 kDa | PF4VI PGLYRP2 GPLD1 PIGR PLEK PF4 PLG PLTP PON1 POTEE POTEJ PPIA PRG4 PFN1 CFP PROS1 PEP RAP1A RBP4 SAA4 APCS Alternate ID SELENOP SHBG STOM | 5 18 0 1 5 6 65 4 32 11 0 1 2 1 2 1 24 269 2 15 9 13 Control #3 6 3 0 | 0 14 4 1 0 0 1111 0 18 0 0 0 0 0 0 0 0 0 0 0 0 0 | 5 15 4 9 0 6 91 0 22 5 0 1 2 5 0 1 3 0 3 23 196 2 7 3 11 Control #40 3 0 0 0 0 0 0 0 0 0 0 0 0 0 | 4 12 4 3 5 4 79 0 28 13 7 2 0 0 3 2 24 206 3 4 7 13 MS #39 2 0 2 2 4 2 2 4 2 2 4 2 2 2 4 2 2 2 2 2 2 2 2 2 2 2 2 2 | 2 15 2 12 0 3 64 0 0 0 0 0 1 0 0 1 0 4 34 259 0 4 0 17 MS #10 0 0 0 0 0 0 0 0 0 0 0 0 0 | 3 14 0 4 3 4 80 0 22 7 0 0 0 6 2 1 1 30 287 1 1 5 1 12 MS #2 3 1 0 |
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| PEDE_HUMAN PF4V_HUMAN PGRP2_HUMAN PIGR_HUMAN PIGR_HUMAN PLD_HUMAN PLEK_HUMAN PLF4_HUMAN PLTP_HUMAN POTEL_HUMAN POTEL_HUMAN POTEL_HUMAN POTEL_HUMAN PROF1_HUMAN PROF1_HUMAN PROF1_HUMAN PROF1_HUMAN PROF1_HUMAN SA44_HUMAN SA | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Pleckstrin Platelet factor 4 Plasminogen Phospholipid transfer protein Serum paraoxonase/arylesterase 1 POTE ankyrin domain family member E POTE ankyrin domain family member J Peptidyl-prolyl cis-trans isomerase A Proteoglycan 4 Proteilin-1 Properdin Vitamin K-dependent protein S Pregnancy zone protein Serum amyloid A-4 protein Serum amyloid P-component Protein ID Selenoprotein P Sex hormone-binding globulin Erythrocyte band 7 integral membrane protein Tubulin alpha-4A chain Tubulin beta-4B chain Tubulin beta-4B chain Tubulin beta-4B chain Tubulin beta-4B chain Transfitonal endoplasmic reticulum ATPase Tetranectin | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa 11 kDa 55 kDa 121 kDa 121 kDa 121 kDa 131 kDa 15 kDa 15 kDa 15 kDa 21 kDa 23 kDa 25 kDa 25 kDa 25 kDa 25 kDa 50 kDa 50 kDa 50 kDa 50 kDa 50 kDa 50 kDa 50 kDa | PF4VI PGLYRP2 GPLD1 PIGR PLEK PF4 PLG PLTP PON1 POTEE POTEJ PPIA PRG4 PFN1 CFP PROS1 PEP RAP1A RBP4 SAA4 APCS Alternate ID SELENOP SHBG STOM TUBA1B TUBA4A TUBB4 | 5 18 0 1 5 6 65 4 32 11 0 1 2 1 2 1 2 4 269 2 15 9 13 Control #3 6 3 0 6 4 3 0 1 1 1 2 4 2 1 1 2 1 1 2 4 2 1 1 2 1 1 2 4 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 2 1 1 2 1 1 2 1 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 3 2 1 1 2 1 2 1 3 1 2 1 3 1 1 2 1 3 1 5 9 1 3 1 5 9 1 3 1 5 9 1 3 1 5 9 1 3 1 5 9 1 3 1 5 9 1 3 1 5 9 1 3 1 1 1 1 5 9 1 3 1 1 1 5 9 1 3 1 1 1 1 1 1 5 9 1 1 1 1 1 1 5 9 1 3 1 1 1 1 1 1 5 9 1 1 1 1 1 1 1 1 1 1 1 1 1 | 0 14 4 1 0 0 0 1111 0 18 0 0 0 0 0 0 4 27 235 0 0 4 27 235 0 0 0 0 13 Control #13 2 0 0 0 0 0 0 0 0 0 0 0 0 0 | 5 15 4 9 0 6 91 0 22 5 0 1 3 0 1 3 23 196 2 7 3 11 Control #40 3 0 0 1 1 1 0 0 1 1 1 0 0 1 1 1 0 0 0 1 1 1 0 0 1 1 1 0 0 1 1 1 0 0 1 1 1 1 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 | 4 12 4 3 5 4 79 0 28 13 7 2 0 0 3 2 24 206 3 4 7 13 MS #39 2 0 2 19 19 13 9 18 21 9 2 0 | 2 15 2 12 0 3 64 0 0 0 0 0 1 0 0 4 259 0 4 34 259 0 4 0 0 17 MS #10 0 0 0 0 0 0 0 0 0 0 0 0 0 | 3 14 0 4 3 4 80 0 22 7 0 0 0 6 2 1 1 5 1 1 2 MS #2 3 1 0 0 0 0 0 0 0 6 2 30 287 1 5 1 1 5 1 0 0 0 0 6 2 2 30 287 1 5 1 0 0 0 0 6 2 2 30 287 1 5 1 1 5 1 1 5 1 0 0 0 6 2 2 30 287 1 5 1 1 5 1 0 0 0 6 2 2 1 30 287 1 5 1 1 5 1 1 5 1 0 0 0 6 2 2 1 1 5 1 1 5 1 0 0 0 6 2 2 1 1 5 1 1 0 0 0 0 6 2 30 287 1 1 5 1 0 0 0 0 6 0 0 0 0 6 2 30 287 1 1 5 1 0 0 0 0 0 0 0 0 0 0 0 0 0 |
| PEDF_HUMAN PF4V_HUMAN PGRP2_HUMAN PIGR_HUMAN PIGR_HUMAN PLD_HUMAN PLD_HUMAN PLTP_HUMAN PON1_HUMAN POTEJ_HUMAN POTEJ_HUMAN POTEJ_HUMAN POTEJ_HUMAN PROS_HUMAN PROS_HUMAN PROS_HUMAN RET4_HUMAN SAMP_HUMAN SAMP_HUMAN SAMP_HUMAN SAMP_HUMAN SAMP_HUMAN TBAL_HUMAN TBAL_HUMAN TBAL_HUMAN TBAL_HUMAN TBAL_HUMAN TBAL_HUMAN TBAL_HUMAN TBAL_HUMAN TBAL_HUMAN TBAL_HUMAN | Platelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Pleckstrin Platelet factor 4 Plasminogen Phospholipid transfer protein Serum paraoxonase/arylesterase 1 POTE ankyrin domain family member E POTE ankyrin domain family member J Peptidyl-prolyl cis-trans isomerase A Proteoglycan 4 Proteoglycan 4 Profilin-1 Properdin Vitamin K-dependent protein S Pregnancy zone protein Ras-related protein Rap-1A Retinol-binding protein 4 Serum amyloid A-4 protein Serum amyloid A-4 protein Serum amyloid P-component Protein ID Selenoprotein P Sex hormone-binding globulin Erythrocyte band 7 integral membrane protein Tubulin alpha-1B chain Tubulin beta-4B chain Tubulin beta-4B chain Tubulin beta-4B chain Tubulin beta-chain Transferin receptor protein 1 Transferin receptor protein 1 Transferin receptor protein 1 Thurwina-binding obbulin | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa 11 kDa 55 kDa 121 kDa 121 kDa 131 kDa 151 kDa 151 kDa 151 kDa 21 kDa 21 kDa 23 kDa 25 kDa 26 kDa 20 | PF4VI PGLYRP2 GPLD1 PIGR PLEK PLG PLTP PON1 POTEE POTEJ POTEJ PPIA PRG4 PFN1 CFP PRO51 PZP RAP1A RBP4 SAA4 APCS Alternate ID SELENOP SHBG STOM TUBA1B TUBA4A TUBB1 TUBB4B TUBB4 TUBA4 TUBB4 TUBA4 TUBB4 TUBA | 5 18 0 1 5 6 65 4 32 11 0 1 1 2 1 2 4 269 2 15 9 13 Control #3 6 3 0 6 4 4 3 1 1 1 5 9 13 Control #3 6 13 Control #3 6 13 Control #3 6 13 Control #3 13 Control #3 13 Control #3 11 1 1 1 1 1 1 1 1 1 1 1 1 | 0 14 4 1 0 0 1111 0 18 0 0 0 0 0 0 4 27 235 0 4 27 235 0 6 0 0 13 Control #13 2 0 0 0 0 0 0 0 0 0 0 0 0 0 | 5 15 4 9 0 6 91 0 22 5 0 1 3 0 1 3 23 196 2 7 3 11 Control #40 3 0 0 1 1 1 0 1 1 0 1 1 0 0 2 2 3 11 Control #40 3 0 0 1 1 1 0 0 2 2 3 1 1 0 0 2 2 3 1 1 0 0 2 2 3 1 1 0 0 0 2 2 3 1 1 0 0 0 1 1 1 1 1 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 | 4 12 4 3 5 4 79 0 28 13 7 2 0 0 3 2 24 206 3 2 24 206 3 4 7 13 MS #39 2 0 2 19 19 19 19 19 19 19 0 2 0 0 2 2 13 13 13 13 13 13 13 13 13 13 | 2 15 2 12 0 3 64 0 0 0 0 0 1 0 4 34 259 0 4 34 259 0 4 0 17 MS #10 4 0 0 0 0 0 0 0 0 0 0 0 0 0 | 3 14 0 4 3 4 80 0 22 7 0 6 2 1 30 287 1 12 MS #2 3 1 0 <tr< td=""></tr<> |
| PEDE_HUMAN PF4V_HUMAN PGRP2_HUMAN PIGR_HUMAN PIGR_HUMAN PLD_HUMAN PLCF4_HUMAN PLTP_HUMAN PON1_HUMAN POTEJ_HUMAN POTEJ_HUMAN POTEJ_HUMAN POTEJ_HUMAN PROS_HUMAN PROS_HUMAN PROS_HUMAN PROS_HUMAN PROS_HUMAN RAP1A_HUMAN SA44_HUMAN SA44_HUMAN SA44_HUMAN SA44_HUMAN SA44_HUMAN SHBG_HUMAN SHBG_HUMAN TBA1B_HUMAN TBA1B_HUMAN TBA1B_HUMAN TBA1B_HUMAN TBA1B_HUMAN TBA1B_HUMAN TBA1B_HUMAN | Piatelet factor 4 variant N-acetylmuramoyl-L-alanine amidase Phosphatidylinositol-glycan-specific phospholipase D Polymeric immunoglobulin receptor Pleckstrin Platelet factor 4 Plasminogen Phospholipid transfer protein Serum paraoxonase/arylesterase 1 POTE ankyrin domain family member E POTE ankyrin domain family member J Petidyl-prolyl cis-trans isomerase A Proteoglycan 4 Proffiln-1 Properdin Vitamin K-dependent protein S Pregnancy zone protein Serum amyloid A-4 protein Serum amyloid A-4 protein Serum amyloid P-component Proteo ID Selenoprotein P Sex hormone-binding globulin Erythrocyte band 7 integral membrane protein Tubulin alpha-4A chain Tubulin alpha-8 chain Tubulin deta-4B chain Transitional endoplasmic reticulum ATPase Tetranectin Proteo ployain 1 Thyroxine-binding globulin Protein 1 Thyroxine-binding globulin Protein 1 Thyroxine-binding globulin | 12 kDa 62 kDa 92 kDa 83 kDa 40 kDa 11 kDa 55 kDa 40 kDa 121 kDa 151 kDa 151 kDa 151 kDa 25 kDa 164 kDa 21 kDa 23 kDa 25 kDa 43 kDa 43 kDa 43 kDa 50 k | PF4V1 PGLYRP2 GPLD1 PIGR PLEK PF4 PLG PLTP PON1 POTEE POTEJ PPIA PRG4 PFN1 CFP PROS1 PZP RAP1A RBP4 SAA4 APCS Alternate ID SELENOP SHBG STOM TUBA1B TUBA4A TUBA4B TUBA4B TUBA4B TUBA4B TUBA4B TUBB4B VCP CLEC3B TFRC SE2 | 5 18 0 1 5 6 65 4 32 11 0 1 1 2 1 2 4 269 2 15 9 13 Control #3 6 3 0 6 4 3 0 6 4 1 1 5 9 13 Control #3 0 6 4 1 1 5 0 1 1 1 2 1 1 1 5 0 1 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 2 1 1 2 4 2 6 9 1 3 Control #3 0 6 3 0 6 6 3 0 6 1 1 1 5 9 1 1 5 9 1 1 5 9 1 1 5 9 1 1 5 9 1 1 5 9 1 1 5 9 1 1 5 9 1 1 5 9 1 1 5 9 1 3 Control #3 1 1 5 9 1 1 5 9 1 1 5 9 1 1 5 9 1 1 5 9 1 1 5 5 0 6 6 1 1 1 1 5 0 0 6 1 1 1 1 5 0 0 6 1 1 1 1 1 1 5 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 | 0 14 1 0 0 111 0 18 0 0 0 0 0 0 0 4 27 235 0 0 0 4 27 235 0 0 0 0 4 27 235 0 0 0 0 0 0 0 0 0 0 0 0 0 | 5 15 4 9 0 6 91 0 22 5 0 1 3 0 3 23 196 2 7 3 10 3 23 196 2 7 3 11 Control #40 3 0 1 1 1 0 1 1 0 1 1 1 0 0 1 1 1 0 0 1 1 1 0 1 1 1 0 1 1 1 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1 | 4 12 4 3 5 4 79 0 28 13 7 2 0 3 2 24 206 3 2 24 206 3 4 7 13 MS #39 2 0 2 13 MS #39 2 0 13 MS #39 2 0 2 0 13 MS #39 2 0 2 0 2 13 MS #39 2 0 2 13 MS #39 2 0 2 0 2 0 2 13 MS #39 2 0 2 0 2 0 2 13 MS #39 2 0 2 0 19 19 13 9 18 21 9 2 0 0 13 9 13 9 13 13 9 13 9 13 13 9 13 13 9 13 13 9 13 13 9 13 13 9 13 13 9 13 13 9 13 13 9 13 13 9 13 13 9 13 13 9 13 13 13 13 13 13 13 13 13 13 | 2 15 2 12 0 3 64 0 0 0 0 0 1 1 0 4 34 259 0 4 0 17 MS #10 4 0 0 0 0 0 0 0 0 0 0 0 0 0 | 3 14 0 4 3 4 80 0 0 22 7 0 0 0 6 2 1 30 287 1 12 MS #2 3 1 12 MS #2 3 1 0 0 0 0 0 6 6 0 0 0 0 0 0 0 0 0 0 0 0 0 |

| TLN1_HUMAN | Talin-1 | 270 kDa | TLN1 | 48 | 0 | 27 | 154 | 4 | 56 |
|------------|--------------------------------|---------|--------|-----|-----|-----|-----|-----|-----|
| TLN2_HUMAN | Talin-2 | 272 kDa | TLN2 | 0 | 0 | 0 | 0 | 0 | 0 |
| TPM4_HUMAN | Tropomyosin alpha-4 chain | 29 kDa | TPM4 | 2 | 0 | 0 | 0 | 0 | 0 |
| TRFE_HUMAN | Serotransferrin | 77 kDa | TF | 179 | 123 | 117 | 151 | 102 | 154 |
| TSP1_HUMAN | Thrombospondin-1 | 129 kDa | THBS1 | 6 | 0 | 2 | 36 | 5 | 11 |
| TTHY_HUMAN | Transthyretin | 16 kDa | TTR | 41 | 24 | 27 | 28 | 24 | 29 |
| URP2_HUMAN | Fermitin family homolog 3 | 76 kDa | FERMT3 | 5 | 0 | 1 | 8 | 0 | 0 |
| VINC_HUMAN | Vinculin | 124 kDa | VCL | 6 | 0 | 1 | 15 | 0 | 1 |
| VTDB_HUMAN | Vitamin D-binding protein | 53 kDa | GC | 61 | 34 | 33 | 49 | 27 | 46 |
| VTNC_HUMAN | Vitronectin | 54 kDa | VTN | 25 | 21 | 17 | 24 | 22 | 20 |
| VWF_HUMAN | von Willebrand factor | 309 kDa | VWF | 3 | 118 | 60 | 77 | 65 | 78 |
| WDR1_HUMAN | WD repeat-containing protein 1 | 66 kDa | WDR1 | 4 | 0 | 0 | 2 | 0 | 0 |
| ZA2G_HUMAN | Zinc-alpha-2-glycoprotein | 34 kDa | AZGP1 | 5 | 2 | 2 | 4 | 2 | 2 |
| ZYX_HUMAN | Zyxin | 61 kDa | ZYX | 3 | 0 | 0 | 4 | 0 | 1 |
| | | | | | | | | | |

| Patient ID | Gender | Age | Disease | EDSS | DMT |
|------------|--------|-----|---------|------|-------|
| 3 | Male | 58 | | | |
| 13 | Female | 48 | | | |
| 40 | Female | 46 | | | |
| 39 | Female | 45 | RRMS | 0 | IFN-β |
| 10 | Male | 53 | RRMS | 5 | IFN-β |
| 2 | Female | 48 | BBMS | 6.5 | IEN-B |

 Table S3. Demographic and Clinical Features of Patients with

 RRMS and Non-Diseased Controls