**Supplementary Information**

**Material and Methods**

**Clinical characterization**

Homozygous proband is a 41 year-old male with TD characterized by HDL deficiency, low plasma cholesterol concentration, hyperplastic orange tonsils and other clinical features such as hepatosplenomegaly, hematologic abnormalities and premature coronary and peripheral vascular disease. The proband's father (Heterozygous) has intermediate HDL and apoA-I levels as compared to unaffected and TD patient and had suffered from premature coronary heart disease.

A detailed clinical description of patients as well as proband's kindred and the plasma lipoprotein profiles of the proband and his family members are reported in Sampietro et al. [1] and in Puntoni et al. [2].

**Sample Preparations**

All reagents were purchased from Sigma-Aldrich (USA) unless otherwise specified.

**Monocyte proteome and secretome**

Monocytes were isolated and cultured as described in Bocchi et al. [3]. For secretome collection, cells were incubated in 6-well plates with 2 ml of Eagle’s Minimum Essential Medium (EMEM) supplemented with Penicillin/Streptomycin (P/S) (both from Lonza Bioscience, Switzerland), without phenol red and FBS, at 37°C in a humidified atmosphere of 5% CO2. After 24 h the conditioned medium was harvested, centrifuged at 300 g for 10 min and concentrated by centrifugal devices Amicon Ultra-3 (Merck Millipore, Germany).

For proteome analysis, cells were pelleted at 1200 g for 10 min, lysed using a buffer containing TRIS HCl 5 mM pH=8, ACN 3% and protease Inhibitors (Roche, Germany) and sonicated.

**Plasma samples**

50 µl of plasma/EDTA from both patients were immuno-depleted from Albumin and Immunoglobulins with Proteoprep (Sigma-Aldrich, USA) according to manufacturer’s instructions.

Protein concentrations were determined by bicinchoninic acid assay (Pierce, Thermo Scientific, USA).

**Reduction, Alkylation and Digestion**

50 mM of ammonium hydrogen carbonate (pH=8) were added to sample proteins in order to reach 1mg/mL concentration. Reduction was obtained in 5 mM dithiothreitol at 80°C for 20 min and alkylation was carried on with 10 mM iodoacetamide and incubating for 30 min at 37°C. Digestion was performed incubating overnight at 37°C trypsin (Roche, Germany) in a concentration trypsin to substrate 1:100. Before MS analysis peptide mixtures were centrifuged for 15 min at 10000 g in order to eliminate debris and filtered with 0.22 μm filters.

**LC-MS/MS Analysis**

Chromatographic separation of peptides was performed using an Ultimate 3000 nano-HPLC system (Thermo Scientific, USA). The loading pump pre-concentrated the sample in a pre-column cartridge (PepMap-100 C18 5 mm 100 A, 30 mm id x 5 mm). Chromatographic separation of peptides was obtained using a C18 PepMap-100 column (15 cm x 75 µm id, Thermo Scientific, USA) equilibrated at 45°C with a solvent A (water/acetonitrile 98/2 vol/vol, 0.1% formic acid) at a flow rate of 300 nL min-1. Runs were performed under 60 min linear gradient from 10 to 45% of solvent B (water/acetonitrile 2/98 vol/vol, 0.1% formic acid) followed by 10 min of a purge step and 20 min re-equilibration step. The column was directly coupled to TripleTOFTM5600 System (ABSciex, USA), equipped with a DuoSprayTM ion source (ABSciex, USA).

Peptides eluted from chromatography were directly processed using TripleTOFTM 5600 mass spectrometer (ABSciex, USA). The mass spectrometer was controlled by Analyst® 1.6.1 software (ABSciex, USA). For Information Dependent Acquisition (IDA) analysis, survey scans were acquired in 250 ms and 25 production scans were collected if exceeding a threshold of 125 counts per second (counts/s). Dynamic exclusion was set for 1/2 of peak width (∼8 s), and then the precursor was refreshed off the exclusion list.

**Data Processing and Statistical Analysis**

MS/MS data were processed with ProteinPilotTM Software (ABSciex, USA), using the ParagonTM and Pro GroupTM Algorithms and SwissProt as protein database for *Homo sapiens* specie. The False Discovery Rate (FDR) analysis was done using the integrated tools in ProteinPilot software and a confidence level of 95% was set.

The statistical comparative analysis was performed using MarkerViewTMSoftware 1.2.1 (ABSciex, USA). The ion chromatograms of high confidence peptides identified by ProteinPilot were extracted using PeakViewTM Software and then MS peak areas and identifications were imported into MarkerViewTM Software. Normalization of the total plaque area (plaque size) was done using a global normalization of profiles (total protein content) in the Marker View 1.2 software.

Principal Component Analysis (PCA) was performed in order to evidence groupings among the data set. The two groups (Homozygote and Heterozygous) were compared with t-test using a threshold of 95% (p value=0.05) and fold change > 2**.**

Pathways and protein connections were investigated with the database String (http://string-db.org) [4].

**References**

1. [Sampietro T, Puntoni M, Bigazzi F, Pennato B, Sbrana F, Dal Pino B, et al. Tangier Disease in Severely Progressive Coronary and Peripheral Artery Disease. Circulation. 2009; 119: 2741-2742.](http://circ.ahajournals.org/content/119/20/2741.short)
2. [Puntoni M, Sbrana F, Bigazzi F, Sampietro T. TangierDisease. Epidemiology, Pathophysiology, and Management. Am J Cardiovasc Drugs. 2012; 12: 303-311.](http://www.ncbi.nlm.nih.gov/pubmed/22913675)
3. [Bocchi L, Pisciotta L, Fasano T, Candini C, Puntoni MR, Sampietro T, et al. Multiple abnormally spliced ABCA1 mRNAs caused by a novel splice site mutation of ABCA1 gene in a patient with Tangier disease. Clinica Chimica Acta. 2010; 411: 524–530.](http://www.sciencedirect.com/science/article/pii/S0009898110000215)
4. [Franceschini A, Szklarczyk D, Frankild S, Kuhn M, Simonovic M, Roth A, et al. STRING v9.1: protein-protein interaction networks,with increased coverage and integration. Nucleic Acids Research. 2013; 41: 808-815.](http://www.ncbi.nlm.nih.gov/pubmed/23203871)

**Table S1:** Identified proteins list from plasma.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Paragon Score** | **%Cov (95)** | **Accession** | **Entry name** | **Name** | **Peptides (95%)** |
| 325.28 | 85.87 | P01024 | CO3\_HUMAN | Complement C3 | 418 |
| 275.39 | 85.82 | P02787 | TRFE\_HUMAN | Serotransferrin | 506 |
| 229.1 | 75.85 | P01023 | A2MG\_HUMAN | Alpha-2-macroglobulin | 314 |
| 214.12 | 32.46 | P04114 | APOB\_HUMAN | Apolipoprotein B-100 | 172 |
| 193.12 | 73.8 | P0C0L5 | CO4B\_HUMAN | Complement C4-B | 203 |
| 182.72 | 59.09 | P02751 | FINC\_HUMAN | Fibronectin | 179 |
| 177.21 | 68.13 | P02671 | FIBA\_HUMAN | Fibrinogen alpha chain | 303 |
| 175.26 | 84.07 | P02768 | ALBU\_HUMAN | Serum albumin | 254 |
| 157.28 | 80.65 | P02675 | FIBB\_HUMAN | Fibrinogen beta chain | 295 |
| 127.14 | 86.36 | P02790 | HEMO\_HUMAN | Hemopexin | 173 |
| 115.52 | 65.35 | P00450 | CERU\_HUMAN | Ceruloplasmin | 142 |
| 113.62 | 60.84 | P08603 | CFAH\_HUMAN | Complement factor H | 98 |
| 110.15 | 63.46 | P00747 | PLMN\_HUMAN | Plasminogen | 108 |
| 103.43 | 86.21 | P00738 | HPT\_HUMAN | Haptoglobin | 221 |
| 102.8 | 86.6 | P01009 | A1AT\_HUMAN | Alpha-1-antitrypsin | 196 |
| 95.63 | 83.22 | P02679 | FIBG\_HUMAN | Fibrinogen gamma chain | 204 |
| 92.85 | 83.29 | P01876 | IGHA1\_HUMAN | Ig alpha-1 chain C region | 175 |
| 92.32 | 67.41 | P00751 | CFAB\_HUMAN | Complement factor B | 86 |
| 85.48 | 41.47 | P01031 | CO5\_HUMAN | Complement C5 | 52 |
| 84.46 | 49.89 | Q14624 | ITIH4\_HUMAN | Inter-alpha-trypsin inhibitor heavy chain H4 | 90 |
| 82.19 | 82.91 | P02774 | VTDB\_HUMAN | Vitamin D-binding protein | 107 |
| 79.48 | 76.78 | P02647 | APOA1\_HUMAN | Apolipoprotein A-I | 118 |
| 74.82 | 70.71 | P06727 | APOA4\_HUMAN | Apolipoprotein A-IV | 96 |
| 63.17 | 56.75 | P00734 | THRB\_HUMAN | Prothrombin | 57 |
| 59.73 | 70.02 | P04003 | C4BPA\_HUMAN | C4b-binding protein alpha chain | 47 |
| 57.89 | 45.23 | P19827 | ITIH1\_HUMAN | Inter-alpha-trypsin inhibitor heavy chain H1 | 86 |
| 55.67 | 57.97 | P01008 | ANT3\_HUMAN | Antithrombin-III | 65 |
| 55.57 | 44.1 | P01042 | KNG1\_HUMAN | Kininogen-1 | 78 |
| 51.64 | 52.94 | P06396 | GELS\_HUMAN | Gelsolin | 58 |
| 50.57 | 58.39 | P01011 | AACT\_HUMAN | Alpha-1-antichymotrypsin | 51 |
| 49.91 | 41.65 | P19823 | ITIH2\_HUMAN | Inter-alpha-trypsin inhibitor heavy chain H2 | 68 |
| 47.86 | 59.42 | P02749 | APOH\_HUMAN | Beta-2-glycoprotein 1 | 65 |
| 47.77 | 46.9 | P13671 | CO6\_HUMAN | Complement component C6 | 37 |
| 47.21 | 57.3 | P01871 | IGHM\_HUMAN | Ig mu chain C region | 54 |
| 46.1 | 67.3 | P02765 | FETUA\_HUMAN | Alpha-2-HS-glycoprotein | 99 |
| 45.73 | 63.84 | P04217 | A1BG\_HUMAN | Alpha-1B-glycoprotein | 75 |
| 45.57 | 51.43 | P04196 | HRG\_HUMAN | Histidine-rich glycoprotein | 57 |
| 41.31 | 41.24 | P43652 | AFAM\_HUMAN | Afamin | 36 |
| 41.1 | 47.8 | P00736 | C1R\_HUMAN | Complement C1r subcomponent | 31 |
| 39.24 | 32.29 | P10909 | CLUS\_HUMAN | Clusterin | 42 |
| 38.72 | 97.17 | P01834 | IGKC\_HUMAN | Ig kappa chain C region | 80 |
| 38.18 | 47.24 | P09871 | C1S\_HUMAN | Complement C1s subcomponent | 30 |
| 37.24 | 48.66 | P02748 | CO9\_HUMAN | Complement component C9 | 25 |
| 37.22 | 64.06 | Q96PD5 | PGRP2\_HUMAN | N-acetylmuramoyl-L-alanine amidase | 35 |
| 37.2 | 58.39 | P25311 | ZA2G\_HUMAN | Zinc-alpha-2-glycoprotein | 37 |
| 35.39 | 41.4 | P10643 | CO7\_HUMAN | Complement component C7 | 32 |
| 35.34 | 46.44 | P04004 | VTNC\_HUMAN | Vitronectin | 30 |
| 35.23 | 47.04 | P07358 | CO8B\_HUMAN | Complement component C8 beta chain | 27 |
| 34.8 | 63.33 | P01857 | IGHG1\_HUMAN | Ig gamma-1 chain C region | 41 |
| 33.11 | 49.69 | P01019 | ANGT\_HUMAN | Angiotensinogen | 26 |
| 32.96 | 42.79 | P03952 | KLKB1\_HUMAN | Plasma kallikrein | 26 |
| 32.84 | 45.62 | P08697 | A2AP\_HUMAN | Alpha-2-antiplasmin | 35 |
| 31.6 | 95.24 | P68871 | HBB\_HUMAN | Hemoglobin subunit beta | 59 |
| 31.36 | 44.3 | P35858 | ALS\_HUMAN | Insulin-like growth factor-binding protein complex acid labile subunit | 20 |
| 28.9 | 77 | P02652 | APOA2\_HUMAN | Apolipoprotein A-II | 65 |
| 28.61 | 39.23 | P36955 | PEDF\_HUMAN | Pigment epithelium-derived factor | 19 |
| 27.42 | 22.78 | P07225 | PROS\_HUMAN | Vitamin K-dependent protein S | 17 |
| 27.32 | 36.61 | P05160 | F13B\_HUMAN | Coagulation factor XIII B chain | 15 |
| 27.01 | 28.99 | P05156 | CFAI\_HUMAN | Complement factor I | 18 |
| 26.61 | 51.1 | P02649 | APOE\_HUMAN | Apolipoprotein E | 19 |
| 25.46 | 50.25 | P02763 | A1AG1\_HUMAN | Alpha-1-acid glycoprotein1 | 48 |
| 25.32 | 93.66 | P69905 | HBA\_HUMAN | Hemoglobin subunit alpha | 51 |
| 24.91 | 28.8 | P05155 | IC1\_HUMAN | Plasma protease C1 inhibitor | 25 |
| 24.66 | 47.71 | P22792 | CPN2\_HUMAN | Carboxypeptidase N subunit 2 | 16 |
| 24.03 | 47.78 | Q16610 | ECM1\_HUMAN | Extracellular matrix protein1 | 14 |
| 23.55 | 42.48 | P05546 | HEP2\_HUMAN | Heparin cofactor 2 | 23 |
| 23.5 | 63.11 | O43866 | CD5L\_HUMAN | CD5 antigen-like | 18 |
| 23.21 | 93.4 | P0CG05 | LAC2\_HUMAN | Ig lambda-2 chain C regions | 48 |
| 21.88 | 42.17 | P02654 | APOC1\_HUMAN | Apolipoprotein C-I | 15 |
| 21.06 | 24.34 | P06681 | CO2\_HUMAN | Complement C2 | 18 |
| 20.96 | 24.04 | Q06033 | ITIH3\_HUMAN | Inter-alpha-trypsin inhibitor heavy chain H3 | 18 |
| 20.27 | 69.39 | P02766 | TTHY\_HUMAN | Transthyretin | 18 |
| 20.18 | 49.15 | P02760 | AMBP\_HUMAN | Protein AMBP | 26 |
| 19.4 | 6.683 | P04275 | VWF\_HUMAN | Von Willebrand factor | 12 |
| 18.76 | 10.64 | O75882 | ATRN\_HUMAN | Attractin | 10 |
| 18.72 | 30.73 | P23142 | FBLN1\_HUMAN | Fibulin-1 | 12 |
| 18.61 | 39.58 | P01880 | IGHD\_HUMAN | Ig delta chain C region | 14 |
| 30.81 | 20.45 | P20742 | PZP\_HUMAN | Pregnancy zone protein | 33 |
| 18.05 | 47.03 | P05452 | TETN\_HUMAN | Tetranectin | 10 |
| 18.03 | 59.72 | P27169 | PON1\_HUMAN | Serum paraoxonase/arylesterase1 | 25 |
| 17.72 | 31.38 | P29622 | KAIN\_HUMAN | Kallistatin | 9 |
| 17.28 | 60.89 | P07360 | CO8G\_HUMAN | Complement component C8 gamma chain | 11 |
| 17.02 | 68.16 | P02753 | RET4\_HUMAN | Retinol-binding protein4 | 29 |
| 16.62 | 37.35 | Q96IY4 | CBPB2\_HUMAN | Carboxypeptidase B2 | 10 |
| 15.34 | 65.12 | P18136 | KV313\_HUMAN | Ig kappa chain V-III region HIC | 15 |
| 15.34 | 65.12 | P18135 | KV312\_HUMAN | Ig kappa chain V-III region HAH | 15 |
| 16.64 | 36.82 | P19652 | A1AG2\_HUMAN | Alpha-1-acid glycoprotein 2 | 21 |
| 14.54 | 32.03 | P00748 | FA12\_HUMAN | Coagulationfactor XII | 13 |
| 13.98 | 27.51 | P51884 | LUM\_HUMAN | Lumican | 8 |
| 58.9 | 83.33 | P00739 | HPTR\_HUMAN | Haptoglobin-related protein | 96 |
| 13.7 | 51.12 | P02743 | SAMP\_HUMAN | Serum amyloid P-component | 11 |
| 16.5 | 44.44 | P36980 | FHR2\_HUMAN | Complement factor H-related protein 2 | 10 |
| 13.45 | 15.24 | P80108 | PHLD\_HUMAN | Phosphatidylinositol-glycan-specific phospholipase D | 9 |
| 13.01 | 37.75 | P02750 | A2GL\_HUMAN | Leucine-rich alpha-2-glycoprotein | 15 |
| 23.66 | 53.37 | P01859 | IGHG2\_HUMAN | Ig gamma-2 chain C region | 26 |
| 12.39 | 57.86 | P01591 | IGJ\_HUMAN | Immunoglobulin J chain | 11 |
| 12.34 | 19.31 | P00740 | FA9\_HUMAN | Coagulation factor IX | 7 |
| 62.72 | 82.65 | P01877 | IGHA2\_HUMAN | Ig alpha-2 chain C region | 117 |
| 12.12 | 25.37 | P27918 | PROP\_HUMAN | Properdin | 8 |
| 12.07 | 23.63 | P07357 | CO8A\_HUMAN | Complement component C8 alpha chain | 12 |
| 11.62 | 14.81 | Q04756 | HGFA\_HUMAN | Hepatocyte growth factor activator | 7 |
| 11.44 | 20 | Q14520 | HABP2\_HUMAN | Hyaluronan-bindingprotein 2 | 8 |
| 11.32 | 18.46 | Q12805 | FBLN3\_HUMAN | EGF-containing fibulin-like extracellular matrix protein 1 | 7 |
| 11.31 | 39.68 | P05090 | APOD\_HUMAN | Apolipoprotein D | 12 |
| 13.28 | 41.48 | P08185 | CBG\_HUMAN | Corticosteroid-binding globulin | 13 |
| 10.87 | 11.73 | P48740 | MASP1\_HUMAN | Mannan-binding lectin serine protease 1 | 6 |
| 10.52 | 47.47 | P02656 | APOC3\_HUMAN | Apolipoprotein C-III | 15 |
| 10.09 | 23.67 | Q96KN2 | CNDP1\_HUMAN | Beta-Ala-His dipeptidase | 7 |
| 9.9 | 12.1 | P26927 | HGFL\_HUMAN | Hepatocyte growth factor-like protein | 6 |
| 9.78 | 11.34 | P00488 | F13A\_HUMAN | Coagulation factor XIII A chain | 7 |
| 186.58 | 71.44 | P0C0L4 | CO4A\_HUMAN | Complement C4-A | 193 |
| 8.46 | 29.9 | O14791 | APOL1\_HUMAN | Apolipoprotein L1 | 8 |
| 34.2 | 54.73 | P04220 | MUCB\_HUMAN | Ig mu heavy chain disease protein | 47 |
| 8.01 | 24.78 | P22352 | GPX3\_HUMAN | Glutathione peroxidase3 | 6 |
| 7.82 | 43.56 | P02655 | APOC2\_HUMAN | Apolipoprotein C-II | 10 |
| 7.6 | 33.07 | P08571 | CD14\_HUMAN | Monocyte differentiation antigen CD14 | 8 |
| 9.62 | 67.83 | P04433 | KV309\_HUMAN | Ig kappa chain V-III region VG (Fragment) | 5 |
| 7.56 | 35.04 | P01764 | HV303\_HUMAN | Ig heavy chain V-III region VH26 | 11 |
| 6 | 26.09 | P01765 | HV304\_HUMAN | Ig heavy chain V-III region TIL | 9 |
| 7.36 | 34.11 | O75636 | FCN3\_HUMAN | Ficolin-3 | 8 |
| 7.2 | 19.43 | P15169 | CBPN\_HUMAN | Carboxypeptidase N catalytic chain | 7 |
| 7.02 | 19.46 | P05154 | IPSP\_HUMAN | Plasma serine protease inhibitor | 6 |
| 6.75 | 20.39 | P04070 | PROC\_HUMAN | Vitamin K-dependent protein C | 5 |
| 6.61 | 12.79 | P06276 | CHLE\_HUMAN | Cholinesterase | 4 |
| 7.05 | 22.41 | P05543 | THBG\_HUMAN | Thyroxine-binding globulin | 8 |
| 6.51 | 14.87 | Q08380 | LG3BP\_HUMAN | Galectin-3-binding protein | 6 |
| 6.38 | 30.83 | P00746 | CFAD\_HUMAN | Complement factor D | 4 |
| 7.46 | 47.86 | P06309 | KV205\_HUMAN | Ig kappa chain V-II region GM607 (Fragment) | 13 |
| 4.26 | 38.94 | P01617 | KV204\_HUMAN | Ig kappa chain V-II region TEW | 9 |
| 6.24 | 8.197 | P00742 | FA10\_HUMAN | Coagulation factor X | 3 |
| 6.17 | 29.12 | P00915 | CAH1\_HUMAN | Carbonic anhydrase1 | 5 |
| 6.14 | 15.59 | P18428 | LBP\_HUMAN | Lipopolysaccharide-binding protein | 4 |
| 21.81 | 65.31 | P02042 | HBD\_HUMAN | Hemoglobin subunit delta | 34 |
| 6.05 | 63.96 | P80748 | LV302\_HUMAN | Ig lambda chain V-III region LOI | 10 |
| 5.93 | 16.44 | Q9UK55 | ZPI\_HUMAN | Protein Z-dependent protease inhibitor | 5 |
| 5.71 | 18.16 | P04278 | SHBG\_HUMAN | Sex hormone-binding globulin | 4 |
| 5.71 | 23.28 | P01781 | HV320\_HUMAN | Ig heavy chain V-III region GAL | 4 |
| 4 | 15 | P01782 | HV321\_HUMAN | Ig heavy chain V-III region DOB | 2 |
| 6.02 | 25 | P01766 | HV305\_HUMAN | Ig heavy chain V-III region BRO | 15 |
| 4.01 | 15.97 | P01777 | HV316\_HUMAN | Ig heavy chain V-III region TEI | 11 |
| 5.35 | 28.57 | P20851 | C4BPB\_HUMAN | C4b-binding protein beta chain | 5 |
| 4.87 | 4.868 | P02786 | TFR1\_HUMAN | Transferrin receptorprotein1 | 3 |
| 5.93 | 49.25 | P06314 | KV404\_HUMAN | Ig kappa chain V-IV region B17 | 12 |
| 4.8 | 32.33 | P06313 | KV403\_HUMAN | Ig kappa chain V-IV region JI | 10 |
| 4.8 | 35.54 | P06312 | KV401\_HUMAN | Ig kappa chain V-IV region (Fragment) | 10 |
| 4.78 | 36.84 | P01625 | KV402\_HUMAN | Ig kappa chain V-IV region Len | 7 |
| 4.58 | 26.67 | P63261 | ACTG\_HUMAN | Actin, cytoplasmic 2 | 6 |
| 4.58 | 26.67 | P60709 | ACTB\_HUMAN | Actin, cytoplasmic1 | 6 |
| 6.52 | 8.419 | Q9NZP8 | C1RL\_HUMAN | Complement C1r subcomponent-like protein | 5 |
| 4.29 | 22.09 | Q13790 | APOF\_HUMAN | Apolipoprotein F | 3 |
| 4.26 | 34.19 | P01601 | KV109\_HUMAN | Ig kappa chain V-I region HK101 (Fragment) | 8 |
| 4.07 | 13.09 | Q9UGM5 | FETUB\_HUMAN | Fetuin-B | 3 |
| 4.07 | 8.864 | P04180 | LCAT\_HUMAN | Phosphatidylcholine-sterol acyltransferase | 2 |
| 4.05 | 10.96 | P06331 | HV209\_HUMAN | Ig heavy chain V-II region ARH-77 | 3 |
| 4.01 | 13.68 | P01825 | HV207\_HUMAN | Ig heavy chain V-II region NEWM | 3 |
| 4.05 | 7.5 | P22891 | PROZ\_HUMAN | Vitamin K-dependent protein Z | 3 |
| 4.03 | 21.37 | P01743 | HV102\_HUMAN | Ig heavy chain V-I region HG3 | 8 |
| 4.02 | 9.071 | Q6UXB8 | PI16\_HUMAN | Peptidase inhibitor 16 | 2 |
| 4.02 | 25.23 | P01717 | LV403\_HUMAN | Ig lambda chain V-IV region Hil | 4 |
| 4.01 | 4.724 | P49908 | SEPP1\_HUMAN | Selenoprotein P | 2 |
| 4.01 | 6.446 | P43251 | BTD\_HUMAN | Biotinidase | 2 |
| 4.01 | 26.79 | P01700 | LV102\_HUMAN | Ig lambda chain V-I region HA | 3 |
| 19.85 | 48.32 | P01861 | IGHG4\_HUMAN | Ig gamma-4 chain C region | 25 |
| 4.01 | 59.26 | P01719 | LV501\_HUMAN | Ig lambda chain V-V region DEL | 9 |
| 4.01 | 16.52 | P01780 | HV319\_HUMAN | Ig heavy chain V-III region JON | 4 |
| 4 | 2.965 | P16070 | CD44\_HUMAN | CD44 antigen | 2 |
| 4 | 12.7 | P01772 | HV311\_HUMAN | Ig heavy chain V-III region KOL | 4 |
| 1.36 | 31.93 | P01770 | HV309\_HUMAN | Ig heavy chain V-III region NIE | 5 |
| 3.86 | 22.34 | O95445 | APOM\_HUMAN | Apolipoprotein M | 5 |
| 3.77 | 23.33 | P01344 | IGF2\_HUMAN | Insulin-like growth factor II | 4 |
| 3.19 | 7.467 | Q15582 | BGH3\_HUMAN | Transforming growth factor-beta-induced protein ig-h3 | 4 |
| 2.95 | 25.21 | P01773 | HV312\_HUMAN | Ig heavy chain V-III region BUR | 3 |
| 2.84 | 23.08 | P35542 | SAA4\_HUMAN | Serumamyloid A-4 protein | 2 |
| 22.04 | 48.6 | B9A064 | IGLL5\_HUMAN | Immunoglobulin lambda-like polypeptide 5 | 45 |
| 21.53 | 90.57 | P0CG04 | LAC1\_HUMAN | Ig lambda-1 chain C regions | 44 |
| 2.56 | 6.873 | P17936 | IBP3\_HUMAN | Insulin-like growth factor-binding protein 3 | 2 |
| 2.52 | 29.41 | P61769 | B2MG\_HUMAN | Beta-2-microglobulin | 2 |
| 2.44 | 12.3 | Q15848 | ADIPO\_HUMAN | Adiponectin | 2 |
| 2.48 | 37.96 | P01609 | KV117\_HUMAN | Ig kappa chain V-I region Scw | 5 |
| 2 | 11.11 | P01595 | KV103\_HUMAN | Ig kappa chain V-I region Bi | 1 |
| 2.3 | 50.39 | P04207 | KV308\_HUMAN | Ig kappa chain V-III region CLL | 4 |
| 1.46 | 8.333 | P01605 | KV113\_HUMAN | Ig kappa chain V-I region Lay | 1 |
| 1.46 | 8.257 | P01624 | KV306\_HUMAN | Ig kappa chain V-III region POM | 1 |
| 2.13 | 2.055 | P13645 | K1C10\_HUMAN | Keratin, type I cytoskeletal10 | 1 |
| 2.11 | 3.043 | P55058 | PLTP\_HUMAN | Phospholipid transfer protein | 1 |
| 2.04 | 13.08 | P06316 | LV107\_HUMAN | Ig lambda chain V-I region BL2 | 3 |
| 2 | 15.32 | P01701 | LV103\_HUMAN | Ig lambda chain V-I region NEW | 3 |
| 2.03 | 2.332 | O00187 | MASP2\_HUMAN | Mannan-binding lectin serine protease 2 | 1 |
| 18.43 | 52.73 | Q03591 | FHR1\_HUMAN | Complement factor H-related protein 1 | 13 |
| 2 | 2.285 | Q9BXR6 | FHR5\_HUMAN | Complement factor H-related protein 5 | 1 |
| 4.02 | 15.65 | P69892 | HBG2\_HUMAN | Hemoglobin subunit gamma-2 | 5 |
| 4.02 | 15.65 | P69891 | HBG1\_HUMAN | Hemoglobin subunit gamma-1 | 5 |
| 2.01 | 2.599 | P11021 | GRP78\_HUMAN | 78 kDa glucose-regulated protein | 1 |
| 19.57 | 40.58 | P01860 | IGHG3\_HUMAN | Ig gamma-3 chain C region | 21 |
| 4.01 | 26.09 | P01767 | HV306\_HUMAN | Ig heavy chain V-III region BUT | 5 |
| 4 | 27.52 | P04208 | LV106\_HUMAN | Ig lambda chain V-I region WAH | 3 |
| 2 | 15.32 | P01699 | LV101\_HUMAN | Ig lambda chain V-I region VOR | 1 |
| 2.08 | 31.48 | P01593 | KV101\_HUMAN | Ig kappa chain V-I region AG | 5 |
| 2 | 14.29 | P01613 | KV121\_HUMAN | Ig kappa chain V-I region Ni | 2 |
| 2.01 | 9.091 | P01771 | HV310\_HUMAN | Ig heavy chain V-III region HIL | 3 |
| 2.01 | 10.09 | P01708 | LV205\_HUMAN | Ig lambda chain V-II region BUR | 1 |
| 2.01 | 26.85 | P04430 | KV122\_HUMAN | Ig kappa chain V-I region BAN | 3 |
| 2.01 | 16.5 | P01703 | LV105\_HUMAN | Ig lambda chain V-I region NEWM | 2 |
| 2 | 1.276 | P33151 | CADH5\_HUMAN | Cadherin-5 | 1 |
| 2 | 3.629 | P11226 | MBL2\_HUMAN | Mannose-binding protein C | 1 |
| 2 | 5.534 | P02746 | C1QB\_HUMAN | Complement C1q subcomponent subunit B | 1 |
| 2 | 8.73 | Q99880 | H2B1L\_HUMAN | Histone H2B type 1-L | 1 |
| 2 | 8.73 | Q99879 | H2B1M\_HUMAN | Histone H2B type 1-M | 1 |
| 2 | 8.73 | Q99877 | H2B1N\_HUMAN | Histone H2B type 1-N | 1 |
| 2 | 8.661 | Q96A08 | H2B1A\_HUMAN | Histone H2B type 1-A | 1 |
| 2 | 8.73 | Q93079 | H2B1H\_HUMAN | Histone H2B type 1-H | 1 |
| 2 | 8.73 | Q5QNW6 | H2B2F\_HUMAN | Histone H2B type 2-F | 1 |
| 2 | 8.73 | P62807 | H2B1C\_HUMAN | Histone H2B type 1-C/E/F/G/I | 1 |
| 2 | 8.73 | P58876 | H2B1D\_HUMAN | Histone H2B type 1-D | 1 |
| 2 | 8.73 | O60814 | H2B1K\_HUMAN | Histone H2B type 1-K | 1 |
| 2 | 8.73 | Q8N257 | H2B3B\_HUMAN | Histone H2B type 3-B | 1 |
| 2 | 8.73 | Q16778 | H2B2E\_HUMAN | Histone H2B type 2-E | 1 |
| 2 | 8.73 | P57053 | H2BFS\_HUMAN | Histone H2B type F-S | 1 |
| 2 | 8.73 | P33778 | H2B1B\_HUMAN | Histone H2B type 1-B | 1 |
| 2 | 8.73 | P23527 | H2B1O\_HUMAN | Histone H2B type 1-O | 1 |
| 2 | 8.73 | P06899 | H2B1J\_HUMAN | Histone H2B type 1-J | 1 |
| 2 | 1.932 | Q6EMK4 | VASN\_HUMAN | Vasorin | 1 |
| 2 | 7.534 | P01034 | CYTC\_HUMAN | Cystatin-C | 1 |
| 2 | 23.58 | P06889 | LV405\_HUMAN | Ig lambda chain V-IV region MOL | 1 |
| 2 | 16.67 | P01714 | LV301\_HUMAN | Ig lambda chain V-III region SH | 1 |
| 1.83 | 12.24 | P02747 | C1QC\_HUMAN | Complement C1q subcomponent subunit C | 2 |
| 1.81 | 19.53 | P02775 | CXCL7\_HUMAN | Platelet basic protein | 2 |
| 1.64 | 16.39 | P0DJI8 | SAA1\_HUMAN | Serum amyloid A-1 protein | 1 |
| 1.57 | 11.56 | P68871 | HBB\_HUMAN | REVERSED Hemoglobin subunit beta | 1 |
| 1.57 | 11.56 | P02042 | HBD\_HUMAN | REVERSED Hemoglobin subunit delta | 1 |
| 1.57 | 6.589 | P22692 | IBP4\_HUMAN | Insulin-like growth factor-binding protein 4 | 1 |
| 1.5 | 5.108 | P14151 | LYAM1\_HUMAN | L-selectin | 2 |

**Table S2:** Identified proteins list from monocytes proteome.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Paragon Score** | **%Cov**  **(95)** | **Accession** | **Entry** | **Name** | **Pep (95%)** | **Localization** | **Functions** |
| 6,21 | 22,83 | A6NIZ1 | RP1BL\_HUMAN | Ras-related protein Rap-1b-like protein | 3 | Cell membrane |  |
| 2,12 | 11,2 | O00299 | CLIC1\_HUMAN | Chloride intracellular channel protein 1 | 1 | Cell membrane | Chloride trasport |
| 5,74 | 6,98 | P05106 | ITB3\_HUMAN | Integrin beta-3 | 3 | Cell membrane | Negative regulation of lipid transport/storage |
| 2,01 | 7,345 | P14770 | GPIX\_HUMAN | Platelet glycoprotein IX | 1 | Cell membrane | Platelet activation; blood coagulation |
| 2 | 1,287 | Q0VD83 | APOBR\_HUMAN | Apolipoprotein B receptor | 1 | Cell membrane |  |
| 2 | 2,311 | Q9H4M7 | PKHA4\_HUMAN | Pleckstrin homology domain-containing family A member 4 | 1 | Cell membrane | PtdIn-binding |
| 9,49 | 9,047 | P08514 | ITA2B\_HUMAN | Integrin alpha-IIb | 7 | Cell membrane | Platelet aggregation |
| 2,08 | 31,11 | P06703 | S10A6\_HUMAN | Protein S100-A6 | 1 | Cell membrane and associated. | Calcium binding; actin reorganization; cell motility |
| 4,39 | 12,84 | Q01518 | CAP1\_HUMAN | Adenylyl cyclase-associated protein 1 | 3 | Cell membrane and associated. | Acting binding, cytoskeleton reorganization |
| 3,79 | 7,059 | O95810 | SDPR\_HUMAN | Serum deprivation-response protein | 2 | Cell membrane caveola. Cytoplasm | PRKCA transport to caveole |
| 2,69 | 4,878 | P13473 | LAMP2\_HUMAN | Lysosome-associated membrane glycoprotein 2 | 2 | Cell membrane. | Shuttle between lysosome, endosome and cell membrane |
| 2,13 | 1,086 | P46940 | IQGA1\_HUMAN | RasGTPase-activating-like protein IQGAP1 | 1 | Cell membrane. | Acting cytoskeleton reorganization (bind cdc42) |
| 8,23 | 28,8 | P61224 | RAP1B\_HUMAN | Ras-related protein Rap-1b | 4 | Cell membrane. |  |
| 13,28 | 9,877 | P18206 | VINC\_HUMAN | Vinculin | 7 | Cell membrane. Cell junction. Cytoskeleton. | Actin-binding, cell adhesion; migration |
| 3,3 | 10,95 | Q15286 | RAB35\_HUMAN | Ras-related protein Rab-35 | 2 | Cell membrane. Clathrin | Endocytosis; recycling pathway |
| 2 | 5,597 | P04632 | CPNS1\_HUMAN | Calpain small subunit 1 | 1 | Cell membrane. Cytoplasm | Calcium-regulated protease |
| 29,46 | 48,16 | P06733 | ENOA\_HUMAN | Alpha-enolase | 19 | Cell membrane. Cytoplasm | Plasminogen activator; glycolysis |
| 7,77 | 7,972 | P26038 | MOES\_HUMAN | Moesin | 4 | Cell membrane. Cytoskeleton. | Cytoskelton to cell membrane connection |
| 15,39 | 22,24 | P07237 | PDIA1\_HUMAN | Protein disulfide-isomerase | 8 | Cell membrane. ER | Chaperone |
| 4,94 | 7,273 | Q15084 | PDIA6\_HUMAN | Protein disulfide-isomerase A6 | 2 | Cell membrane. ER | Chaperone |
| 4,25 | 18,54 | P62820 | RAB1A\_HUMAN | Ras-related protein Rab-1A | 3 | Cell membrane. Lipid-anchor. | Vescicular trafficking |
| 6,21 | 20,65 | P62834 | RAP1A\_HUMAN | Ras-related protein Rap-1A | 3 | Cell membrane. Lipid-anchor. | Vescicular trafficking |
| 5,14 | 31,18 | P05109 | S10A8\_HUMAN | Protein S100-A8 | 3 | Cell membrane. Secreted. Cytoskeleton. | Adhesion and migration; pro-inflammatory |
| 14,4 | 56,14 | P06702 | S10A9\_HUMAN | Protein S100-A9 | 11 | Cell membrane. Secreted. Cytoskeleton. | Pro-inflammatory cascades |
| 2 | 8,901 | P60953 | CDC42\_HUMAN | Cell division control protein 42 homolog | 1 | Cell membrane; Cytoskeleton | Migration; filopodia formation |
| 3,3 | 10,38 | P59190 | RAB15\_HUMAN | Ras-related protein Rab-15 | 2 | Cell membrane; Lipid-anchor | Vescicular trafficking |
| 5,37 | 17,39 | P61006 | RAB8A\_HUMAN | Ras-related protein Rab-8A | 3 | Cell membrane; Lipid-anchor | Vescicular trafficking |
| 5,37 | 16,5 | P61026 | RAB10\_HUMAN | Ras-related protein Rab-10 | 3 | Cell membrane; Lipid-anchor | Vescicular trafficking |
| 20,06 | 23,69 | Q86UX7 | URP2\_HUMAN | Fermitin family homolog 3 | 10 | Cell projection | Cell adhesion; integrin meditated platelet adhesion |
| 78,54 | 25,3 | Q9Y490 | TLN1\_HUMAN | Talin-1 | 41 | Cell projection. Cytoskeleton. | Membrane-cytoskeleton connections |
| 9,41 | 23,53 | P08311 | CATG\_HUMAN | Cathepsin G | 6 | Cell surface. | ECM disassembly; cell defence |
| 6,06 | 61,36 | A8MW06 | TMSL3\_HUMAN | Thymosin beta-4-like protein 3 | 5 | Cytoplasm | Actin-regulator |
| 6,06 | 7,705 | P29401 | TKT\_HUMAN | Transketolase | 3 | Cytoplasm | Energy metabolism |
| 4,37 | 12,91 | P04075 | ALDOA\_HUMAN | Fructose-bisphosphatealdolase A | 3 | Cytoplasm | Actin-binding, glycolis |
| 2 | 10,43 | P05387 | RLA2\_HUMAN | 60S acidic ribosomal protein P2 | 1 | Cytoplasm | Ribosome structure; protein synthesis |
| 9,1 | 9,658 | P08133 | ANXA6\_HUMAN | Annexin A6 | 5 | Cytoplasm | Calcium homeostasis |
| 6,42 | 9,53 | P08238 | HS90B\_HUMAN | Heat shock protein HSP 90-beta | 4 | Cytoplasm | Chaperone |
| 2 | 16,3 | P08708 | RS17\_HUMAN | 40S ribosomal protein S17 | 1 | Cytoplasm | Ribosome structure; protein synthesis |
| 2 | 16,3 | P0CW22 | RS17L\_HUMAN | 40S ribosomal protein S17-like | 1 | Cytoplasm | Ribosome structure; protein synthesis |
| 12,59 | 16,25 | P11142 | HSP7C\_HUMAN | Heat shock cognate 71 kDa protein | 14 | Cytoplasm | Chaperone |
| 2 | 1,22 | Q96MI9 | CBPC4\_HUMAN | Cytosolic carboxypeptidase 4 | 1 | Cytoplasm | Proteinase |
| 7,11 | 18,44 | P08758 | ANXA5\_HUMAN | Annexin A5 | 4 | Cytoplasm, exosomes | Blood coagulation |
| 6,18 | 16,31 | P00558 | PGK1\_HUMAN | Phosphoglycerate kinase 1 | 4 | Cytoplasm. | Glycoslysis glucose metabolism |
| 5,42 | 11,68 | P07195 | LDHB\_HUMAN | L-lactate dehydrogenase B chain | 3 | Cytoplasm. | Glycoslysis glucose metabolism |
| 2,51 | 1,515 | P13639 | EF2\_HUMAN | Elongation factor 2 | 1 | Cytoplasm. | Protein synthesis |
| 2,35 | 2,902 | P30740 | ILEU\_HUMAN | Leukocyte elastase inhibitor | 1 | Cytoplasm. | Regulation proteolysis |
| 4,9 | 15,04 | P31946 | 1433B\_HUMAN | 14-3-3 protein beta/alpha | 4 | Cytoplasm. | Signaling cascades |
| 8,84 | 27,64 | P37802 | TAGL2\_HUMAN | Transgelin-2 | 5 | Cytoplasm. | Marker SMC |
| 2 | 3,736 | P40121 | CAPG\_HUMAN | Macrophage-capping protein | 2 | Cytoplasm. | Actin-binding |
| 2 | 9,434 | P47914 | RL29\_HUMAN | 60S ribosomal protein L29 | 1 | Cytoplasm. | Ribosome structure; protein synthesis |
| 3,8 | 15,2 | P52565 | GDIR1\_HUMAN | Rho GDP-dissociation inhibitor 1 | 2 | Cytoplasm. | Rho protein signal transduction |
| 2,42 | 8,458 | P52566 | GDIR2\_HUMAN | Rho GDP-dissociation inhibitor 2 | 1 | Cytoplasm. | Rho protein signal transduction |
| 6,27 | 16,87 | P60174 | TPIS\_HUMAN | Triosephosphate isomerase | 3 | Cytoplasm. | Glycolisis |
| 2 | 2,463 | P60842 | IF4A1\_HUMAN | Eukaryotic initiation factor 4A-I | 1 | Cytoplasm. | Protein synthesis |
| 2,03 | 7,237 | P62269 | RS18\_HUMAN | 40S ribosomal protein S18 | 1 | Cytoplasm. | Protein synthesis |
| 2 | 4,819 | P62753 | RS6\_HUMAN | 40S ribosomal protein S6 | 1 | Cytoplasm. | Ribosome structure; protein synthesis |
| 2 | 17,39 | P62857 | RS28\_HUMAN | 40S ribosomal protein S28 | 1 | Cytoplasm. | Ribosome structure; protein synthesis |
| 8,47 | 33,06 | P63104 | 1433Z\_HUMAN | 14-3-3 protein zeta/delta | 8 | Cytoplasm. | Signaling cascades |
| 4,01 | 31,17 | P63241 | IF5A1\_HUMAN | Eukaryotic translation initiation factor 5A-1 | 3 | Cytoplasm. | Protein synthesis |
| 11,48 | 18,4 | P68104 | EF1A1\_HUMAN | Elongation factor 1-alpha 1 | 9 | Cytoplasm. | Protein synthesis |
| 2 | 2,457 | Q14240 | IF4A2\_HUMAN | Eukaryotic initiation factor 4A-II | 1 | Cytoplasm. | Protein synthesis |
| 2,02 | 1,445 | Q6ZRR7 | LRRC9\_HUMAN | Leucine-rich repeat-containing protein 9 | 2 | Cytoplasm. |  |
| 25,98 | 42,09 | P04406 | G3P\_HUMAN | Glyceraldehyde-3-phosphate dehydrogenase | 19 | Cytoplasm. Cytoskeleton. | Glycolysis; cytoskeleton organization |
| 3,04 | 8,276 | Q01105 | SET\_HUMAN | Protein SET | 2 | Cytoplasm. Nucleus | Transcription; apoptosis |
| 15,63 | 31,79 | P04083 | ANXA1\_HUMAN | Annexin A1 | 10 | Cytoplasm; Cell membrane and projection. | Exocytosis, membrane fusion |
| 3,46 | 6,991 | O00151 | PDLI1\_HUMAN | PDZ and LIM domain protein 1 | 2 | Cytoskeleton | Cytoskeleton organization |
| 57,38 | 53,22 | P08670 | VIME\_HUMAN | Vimentin | 32 | Cytoskeleton | Structural component of cytoskeleton |
| 10,24 | 46,31 | P62158 | CALM\_HUMAN | Calmodulin | 9 | Cytoskeleton | Platelet activation; glucose metabolism |
| 8,07 | 65,91 | P62328 | TYB4\_HUMAN | Thymosin beta-4 | 6 | Cytoskeleton | Cytoskeleton organization |
| 40,2 | 56,5 | P62736 | ACTA\_HUMAN | Actin, aortic smooth muscle | 53 | Cytoskeleton | Structural component of cytoskeleton |
| 10,3 | 45,93 | O14950 | ML12B\_HUMAN | Myosin regulatory light chain 12B | 6 | Cytoskeleton. | Cytoskeleton organization; contraction |
| 2 | 4,839 | O15143 | ARC1B\_HUMAN | Actin-related protein 2/3 complex subunit 1B | 1 | Cytoskeleton. | Cytoskeleton organization |
| 2 | 7,947 | O15511 | ARPC5\_HUMAN | Actin-related protein 2/3 complex subunit 5 | 1 | Cytoskeleton. | Cytoskeleton organization |
| 13,19 | 20,77 | P06753 | TPM3\_HUMAN | Tropomyosin alpha-3 chain | 8 | Cytoskeleton. | Cytoskeleton organization; contraction |
| 11,63 | 27,25 | P07437 | TBB5\_HUMAN | Tubulin beta chain | 8 | Cytoskeleton. | Structural component of cytoskeleton |
| 10,51 | 60 | P07737 | PROF1\_HUMAN | Profilin-1 | 8 | Cytoskeleton. | Cytoskeleton organization; platelet activation |
| 13,17 | 20,42 | P09493 | TPM1\_HUMAN | Tropomyosin alpha-1 chain | 8 | Cytoskeleton. | Cytoskeleton organization; contraction |
| 18,56 | 11,77 | P12814 | ACTN1\_HUMAN | Alpha-actinin-1 | 8 | Cytoskeleton. | Acting cytoskeleton reorganization |
| 2,01 | 1,034 | P12883 | MYH7\_HUMAN | Myosin-7 | 1 | Cytoskeleton. | Structural component of cytoskeleton contraction |
| 10,3 | 46,2 | P19105 | ML12A\_HUMAN | Myosin regulatory light chain 12A | 6 | Cytoskeleton. | Cytoskeleton organization; contraction |
| 90,79 | 27,43 | P21333 | FLNA\_HUMAN | Filamin-A | 50 | Cytoskeleton. | Cytoskeleton organization; actin binding |
| 6,86 | 14,32 | P31146 | COR1A\_HUMAN | Coronin-1A | 4 | Cytoskeleton. | Cytoskeleton organization; actin binding; motility |
| 82,35 | 28,37 | P35579 | MYH9\_HUMAN | Myosin-9 | 51 | Cytoskeleton. | Structural component of cytoskeleton contraction |
| 2,03 | 3,497 | P47755 | CAZA2\_HUMAN | F-actin-capping protein subunit alpha-2 | 1 | Cytoskeleton. | Cytoskeleton organization; actin binding |
| 4 | 9,79 | P52907 | CAZA1\_HUMAN | F-actin-capping protein subunit alpha-1 | 2 | Cytoskeleton. | Cytoskeleton organization |
| 12,87 | 52,32 | P60660 | MYL6\_HUMAN | Myosin light polypeptide 6 | 9 | Cytoskeleton. | Contraction |
| 69,49 | 62,93 | P60709 | ACTB\_HUMAN | Actin, cytoplasmic 1 | 75 | Cytoskeleton. | Structural component of cytoskeleton |
| 71,68 | 63,2 | P63261 | ACTG\_HUMAN | Actin, cytoplasmic 2 | 77 | Cytoskeleton. | Structural component of cytoskeleton |
| 40,13 | 53,19 | P63267 | ACTH\_HUMAN | Actin, gamma-enteric smooth muscle | 51 | Cytoskeleton. | Structural component of cytoskeleton |
| 18,18 | 37,5 | P67936 | TPM4\_HUMAN | Tropomyosin alpha-4 chain | 11 | Cytoskeleton. | Cytoskeleton organization; contraction |
| 41,24 | 59,68 | P68032 | ACTC\_HUMAN | Actin, alpha cardiac muscle 1 | 54 | Cytoskeleton. | Structural component of cytoskeleton |
| 25,41 | 35,03 | P68363 | TBA1B\_HUMAN | Tubulin alpha-1B chain | 16 | Cytoskeleton. | Structural component of cytoskeleton |
| 17,24 | 35,27 | P68366 | TBA4A\_HUMAN | Tubulin alpha-4A chain | 15 | Cytoskeleton. | Structural component of cytoskeleton |
| 2,27 | 5,634 | Q14019 | COTL1\_HUMAN | Coactosin-like protein | 1 | Cytoskeleton. | Cytoskeleton organization; actin binding |
| 25,41 | 35,03 | Q71U36 | TBA1A\_HUMAN | Tubulin alpha-1A chain | 15 | Cytoskeleton. | Structural component of cytoskeleton |
| 8,56 | 11,97 | Q9H4B7 | TBB1\_HUMAN | Tubulin beta-1 chain | 4 | Cytoskeleton. | Structural component of cytoskeleton |
| 5,06 | 23,29 | Q9NZT1 | CALL5\_HUMAN | Calmodulin-like protein 5 | 3 | Cytoskeleton. | Platelet activation; glucose metabolism |
| 13,34 | 49,4 | P23528 | COF1\_HUMAN | Cofilin-1 | 7 | Cytoskeleton. Cell projection | Cytoskeleton organization; actin binding |
| 14,53 | 21,05 | P13796 | PLSL\_HUMAN | Plastin-2 | 9 | Cytoskeleton. Cell projection. | Cytoskeleton organization; actin binding; memblocaliz of CD25 and CD69 R modulator |
| 4,03 | 21,09 | P06748 | NPM\_HUMAN | Nucleophosmin | 3 | Cytoskeleton. Nucleus. | Chaperone; proliferation regulation, histon assembly |
| 18,53 | 10,51 | P07996 | TSP1\_HUMAN | Thrombospondin-1 | 9 | ECM | Cell-cell and cell-matrix interactions |
| 2,02 | 13,65 | P39687 | AN32A\_HUMAN | Acidic leucine-rich nuclear phosphoprotein 32 family member A | 1 | ER. Nucleus. | Transcription; apoptosis |
| 2,01 | 1,977 | P04843 | RPN1\_HUMAN | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 | 1 | ER | Protein gycosilation |
| 8,08 | 6,849 | P14625 | ENPL\_HUMAN | Endoplasmin | 4 | ER | Chaperone (HSP90) |
| 3,72 | 4,223 | P16615 | AT2A2\_HUMAN | Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 | 3 | ER | Calcium homeostasis |
| 2 | 6,019 | P23284 | PPIB\_HUMAN | Peptidyl-prolylcis-trans isomerase B | 1 | ER | Chaperone |
| 2,75 | 7,939 | P27824 | CALX\_HUMAN | Calnexin | 2 | ER | Chaperone |
| 18,62 | 32,28 | P30101 | PDIA3\_HUMAN | Protein disulfide-isomerase A3 | 10 | ER | Chaperone |
| 21,05 | 22,78 | P11021 | GRP78\_HUMAN | 78 kDa glucose-regulated protein | 17 | ER, membrane | Chaperone (HSP70) |
| 5,04 | 15,59 | P27797 | CALR\_HUMAN | Calreticulin | 3 | ER, secreted | Chaperone |
| 2,88 | 13,26 | P84077 | ARF1\_HUMAN | ADP-ribosylation factor 1 | 2 | Golgi apparatus. | Protein trafficking |
| 2 | 5,556 | P84085 | ARF5\_HUMAN | ADP-ribosylation factor 5 | 1 | Golgi apparatus. | Protein trafficking |
| 2,88 | 13,26 | P61204 | ARF3\_HUMAN | ADP-ribosylation factor 3 | 2 | Golgi apparatus. Cytoplasm | Protein trafficking |
| 34,03 | 30,6 | P05164 | PERM\_HUMAN | Myeloperoxidase | 21 | Lysosome. | Cell defence |
| 4,25 | 6,298 | P07602 | SAP\_HUMAN | Proactivator polypeptide | 3 | Lysosome. | Cell defence; platelet activation |
| 4 | 13,39 | P30041 | PRDX6\_HUMAN | Peroxiredoxin-6 | 2 | Lysosome. | Redox regulation |
| 17,07 | 21,34 | P25705 | ATPA\_HUMAN | ATP synthase subunit alpha, mitochondrial | 11 | Mitochondrion | ATP production |
| 4,31 | 16,18 | P35232 | PHB\_HUMAN | Prohibitin | 2 | Mitochondrion | Apoptosis and DNA synthesis regulation |
| 4,05 | 13,09 | P05141 | ADT2\_HUMAN | ADP/ATP translocase 2 | 2 | Mitochondrion | Membrane transport; ATP metabolism |
| 3,5 | 17,83 | P10606 | COX5B\_HUMAN | Cytochrome c oxidase subunit 5B, mitochondrial | 2 | Mitochondrion | Respiratory chain |
| 12,46 | 15,36 | P10809 | CH60\_HUMAN | 60 kDa heat shock protein, mitochondrial | 7 | Mitochondrion | Chaperone |
| 4 | 13,09 | P12235 | ADT1\_HUMAN | ADP/ATP translocase 1 | 2 | Mitochondrion | Membrane transport; energy metabolism |
| 4,08 | 13,09 | P12236 | ADT3\_HUMAN | ADP/ATP translocase 3 | 2 | Mitochondrion | Membrane transport; ATP metabolism |
| 2 | 5,728 | P17540 | KCRS\_HUMAN | Creatine kinase S-type, mitochondrial | 1 | Mitochondrion | Energy metabolism |
| 4 | 6,19 | P28331 | NDUS1\_HUMAN | NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial | 3 | Mitochondrion | Energy metabolism |
| 6,99 | 10,65 | P40926 | MDHM\_HUMAN | Malate dehydrogenase, mitochondrial | 3 | Mitochondrion | Energy metabolism |
| 4,69 | 31,37 | P61604 | CH10\_HUMAN | 10 kDa heat shock protein, mitochondrial | 3 | Mitochondrion | Chaperone |
| 4,22 | 14,54 | Q07021 | C1QBP\_HUMAN | Complement component 1 Q subcomponent-binding protein, mitochondrial | 2 | Mitochondrion | Inflammation |
| 2 | 1,105 | Q13423 | NNTM\_HUMAN | NAD(P) transhydrogenase, mitochondrial | 1 | Mitochondrion | Energy metabolism |
| 2,96 | 20,06 | Q16836 | HCDH\_HUMAN | Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial | 2 | Mitochondrion | Lipid metabolism |
| 2 | 2,75 | P09622 | DLDH\_HUMAN | Dihydrolipoyldehydrogenase, mitochondrial | 1 | Mitochondrion. | Redox homeostasis |
| 11,05 | 10,8 | P54652 | HSP72\_HUMAN | Heat shock-related 70 kDa protein 2 | 10 | Mitochondrion, cell surface | Chaperone |
| 2,1 | 13,04 | O75947 | ATP5H\_HUMAN | ATP synthase subunit d, mitochondrial | 1 | Mitochondrion. | Energy metabolism |
| 2,02 | 6,306 | P04179 | SODM\_HUMAN | Superoxide dismutase [Mn], mitochondrial | 1 | Mitochondrion. | Cytocrome release; respiratory chain transport |
| 25,49 | 43,48 | P06576 | ATPB\_HUMAN | ATP synthase subunit beta, mitochondrial | 25 | Mitochondrion. | Energy metabolism |
| 2,39 | 5,469 | P30048 | PRDX3\_HUMAN | Thioredoxin-dependent peroxide reductase, mitochondrial | 1 | Mitochondrion. | Redox regulation |
| 2,17 | 4,124 | P38646 | GRP75\_HUMAN | Stress-70 protein, mitochondrial | 2 | Mitochondrion. | Chaperone |
| 2 | 6,573 | P48047 | ATPO\_HUMAN | ATP synthase subunit | 1 | Mitochondrion. | Energy metabolism |
| 2 | 4,878 | Q13011 | ECH1\_HUMAN | Delta(3,5)-Delta(2,4)-dienoyl-CoAisomerase, mitochondrial | 1 | Mitochondrion. | Lipid metabolism |
| 2,42 | 9,048 | P09211 | GSTP1\_HUMAN | Glutathione S-transferase P | 1 | Mitochondrion. Nucleus. | Regulation inflammatory response |
| 7,41 | 8,169 | P19338 | NUCL\_HUMAN | Nucleolin | 4 | Nucleus | Transcription |
| 7,06 | 11,88 | P61978 | HNRPK\_HUMAN | Heterogeneous nuclear ribonucleoprotein K | 4 | Nucleus | RNA maturation |
| 23,36 | 44,66 | P62805 | H4\_HUMAN | Histone H4 | 20 | Nucleus | Chromatin structure |
| 15,96 | 35,71 | P62807 | H2B1C\_HUMAN | Histone H2B type 1-C/E/F/G/I | 18 | Nucleus | Chromatin structure |
| 2,14 | 10,26 | P62979 | RS27A\_HUMAN | Ubiquitin-40S ribosomal protein S27a | 2 | Nucleus | Ribosome structure; protein synthesis |
| 2,14 | 12,5 | P62987 | RL40\_HUMAN | Ubiquitin-60S ribosomal protein L40 | 2 | Nucleus | Ribosome structure; protein synthesis |
| 27,28 | 41,26 | P16104 | H2AX\_HUMAN | Histone H2A.x | 22 | Nucleus. | Chromatin structure |
| 12,95 | 22,12 | P16401 | H15\_HUMAN | Histone H1.5 | 12 | Nucleus. | Chromatin structure |
| 15,37 | 24,43 | P16402 | H13\_HUMAN | Histone H1.3 | 10 | Nucleus. | Chromatin structure |
| 21,46 | 28,17 | P16403 | H12\_HUMAN | Histone H1.2 | 16 | Nucleus. | Chromatin structure |
| 2 | 2,752 | O43929 | ORC4\_HUMAN | Origin recognition complex subunit 4 | 1 | Nucleus. | DNA replication |
| 15,96 | 35,71 | O60814 | H2B1K\_HUMAN | Histone H2B type 1-K | 18 | Nucleus. | Chromatin structure |
| 7,19 | 11,83 | O75367 | H2AY\_HUMAN | Core histone macro-H2A.1 | 5 | Nucleus. | Chromatin structure |
| 15,52 | 35,71 | P06899 | H2B1J\_HUMAN | Histone H2B type 1-J | 18 | Nucleus. | Chromatin structure |
| 15,52 | 35,71 | P23527 | H2B1O\_HUMAN | Histone H2B type 1- | 18 | Nucleus. | Chromatin structure |
| 2 | 15,24 | P31949 | S10AB\_HUMAN | Protein S100-A11 | 1 | Nucleus. | DNA replication regulation |
| 3,39 | 7,125 | P41218 | MNDA\_HUMAN | Myeloid cell nuclear differentiation antigen | 2 | Nucleus. | Monocyte response to interferon |
| 15,96 | 35,71 | P57053 | H2BFS\_HUMAN | Histone H2B type F-S | 18 | Nucleus. | Chromatin structure |
| 15,96 | 35,71 | P58876 | H2B1D\_HUMAN | Histone H2B type 1-D | 18 | Nucleus. | Chromatin structure |
| 36,81 | 9,626 | Q09666 | AHNK\_HUMAN | Neuroblast differentiation-associated protein AHNAK | 23 | Nucleus. |  |
| 15,52 | 35,71 | Q16778 | H2B2E\_HUMAN | Histone H2B type 2-E | 18 | Nucleus. | Chromatin structure |
| 15,96 | 35,71 | Q5QNW6 | H2B2F\_HUMAN | Histone H2B type 2-F | 18 | Nucleus. | Chromatin structure |
| 8,47 | 35,29 | Q71DI3 | H32\_HUMAN | Histone H3.2 | 6 | Nucleus. | Chromatin structure |
| 2 | 10,51 | Q86V81 | THOC4\_HUMAN | THO complex subunit 4 | 1 | Nucleus. | RNA processing |
| 15,51 | 35,71 | Q8N257 | H2B3B\_HUMAN | Histone H2B type 3-B | 18 | Nucleus. | Chromatin structure |
| 2 | 4,695 | Q92522 | H1X\_HUMAN | Histone H1x | 1 | Nucleus. | Chromatin structure |
| 15,96 | 35,71 | Q93079 | H2B1H\_HUMAN | Histone H2B type 1-H | 18 | Nucleus. | Chromatin structure |
| 15,96 | 35,71 | Q99877 | H2B1N\_HUMAN | Histone H2B type 1-N | 18 | Nucleus. | Chromatin structure |
| 15,96 | 35,71 | Q99879 | H2B1M\_HUMAN | Histone H2B type 1-M | 18 | Nucleus. | Chromatin structure |
| 15,96 | 35,71 | Q99880 | H2B1L\_HUMAN | Histone H2B type 1-L | 18 | Nucleus. | Chromatin structure |
| 2 | 1,978 | Q9H0S4 | DDX47\_HUMAN | Probable ATP-dependent RNA helicase DDX47 | 1 | Nucleus. | RNA processing |
| 4 | 31,18 | Q9H299 | SH3L3\_HUMAN | SH3 domain-binding glutamic acid-rich-like protein 3 | 2 | Nucleus. | Redox homeostasis |
| 2 | 1,326 | Q9HBT7 | ZN287\_HUMAN | Zinc finger protein 287 | 1 | Nucleus. | Trancriptional regulation |
| 2,89 | 6,989 | Q9P0M6 | H2AW\_HUMAN | Core histone macro-H2A.2 | 2 | Nucleus. | Chromatin structure |
| 2,14 | 20,96 | P0CG47 | UBB\_HUMAN | Polyubiquitin-B | 2 | Nucleus. Cytoplasm. | Ubiquitin pathway |
| 2,14 | 21,02 | P0CG48 | UBC\_HUMAN | Polyubiquitin-C | 2 | Nucleus. Cytoplasm. | Ubiquitin pathway |
| 34,47 | 46,89 | P14618 | KPYM\_HUMAN | Pyruvate kinase isozymes M1/M2 | 23 | Nucleus. Cytoplasm. | Glucose matabolism |
| 11,87 | 20,68 | P22626 | ROA2\_HUMAN | Heterogeneous nuclear ribonucleoproteins A2/B1 | 7 | Nucleus. Cytoplasm. | RNA processing |
| 2,93 | 5,375 | P23246 | SFPQ\_HUMAN | Splicing factor, proline- and glutamine-rich | 2 | Nucleus. Cytoplasm. | RNA processing |
| 18,27 | 24,06 | P20700 | LMNB1\_HUMAN | Lamin-B1 | 10 | Nucleus. Lipid-anchor | Nucleus structure |
| 4,81 | 8,159 | P04040 | CATA\_HUMAN | Catalase | 3 | Peroxisome. | Antioxidant |
| 3,61 | 5,021 | P04004 | VTNC\_HUMAN | Vitronectin | 3 | Secreted ECM | ECM structure |
| 3,24 | 3,448 | P05154 | IPSP\_HUMAN | Plasma serine protease inhibitor | 2 | Secreted ECM | Lipid transport |
| 2,32 | 3,079 | O00391 | QSOX1\_HUMAN | Sulfhydryl oxidase 1 | 2 | Secreted ECM. | Chaperone; disulphide bonds |
| 13,15 | 25,96 | P07355 | ANXA2\_HUMAN | Annexin A2 | 7 | Secreted ECM. | Collagen organization |
| 2,78 | 2,578 | P01023 | A2MG\_HUMAN | Alpha-2-macroglobulin | 3 | Secreted. | Platelet activation; blood coagulation |
| 3,06 | 7,865 | P02647 | APOA1\_HUMAN | Apolipoprotein A-I | 2 | Secreted. | Reverse transport of colesterol from tissue |
| 2,65 | 5,995 | P02765 | FETUA\_HUMAN | Alpha-2-HS-glycoprotein | 3 | Secreted. | Regulation inflammatory response |
| 4 | 19,53 | P02775 | CXCL7\_HUMAN | Platelet basic protein | 2 | Secreted. | Platelet activation |
| 4,02 | 16,34 | P05452 | TETN\_HUMAN | Tetranectin | 2 | Secreted. | Plasminogen activation |
| 2 | 7,5 | P12724 | ECP\_HUMAN | Eosinophil cationic protein | 1 | Secreted. | RNAse |
| 2 | 3,349 | P36955 | PEDF\_HUMAN | Pigment epithelium-derived factor | 1 | Secreted. | Angiogenesis and proteolysis regulator |
| 4,29 | 20,27 | P61626 | LYSC\_HUMAN | Lysozyme C | 3 | Secreted. | Inflammatory response, defense against bacteria |
| 10,25 | 30,3 | P62937 | PPIA\_HUMAN | Peptidyl-prolylcis-trans isomerase A | 7 | Secreted. | Chaperone, ERK1 pathway |
| 6,14 | 12,73 | P81605 | DCD\_HUMAN | Dermcidin | 3 | Secreted. | Pathogens defence |
| 7,33 | 4,153 | Q13201 | MMRN1\_HUMAN | Multimerin-1 | 3 | Secreted. | Platelet activation |
| 5,66 | 9,014 | P02788 | TRFL\_HUMAN | Lactotransferrin | 5 | Secreted. Cytoplasm. Nucleus. | Iron transport |
| 22,55 | 21,99 | P06396 | GELS\_HUMAN | Gelsolin | 15 | Secreted. Cytoskeleton. | Actin-binding |

**Table S3:** Identified proteins list from monocytes secretome.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Paragon Score** | **%Cov (95)** | **Accession** | **Entry** | **Name** | **Pept (95%)** | **Secret P** | **Sub cellular location** | **Functions** |
| 2,71 | 12,45 | O00299 | CLIC1\_HUMAN | Chloride intracellular channel protein 1 | 2 |  | Cell membrane | Chloride transport |
| 8,09 | 16,18 | P50395 | GDIB\_HUMAN | Rab GDP dissociation inhibitor beta | 6 |  | Cell Membrane | Signaling cascade |
| 1,47 | 0,9852 | Q2M3G0 | ABCB5\_HUMAN | ATP-binding cassette sub-family B member 5 | 1 |  | Cell membrane | Cell membrane transporter |
| 11,9 | 29,05 | Q01518 | CAP1\_HUMAN | Adenylyl cyclase-associated protein 1 | 8 |  | Cell membrane and associated. | Cytoskeleton reorganiz |
| 34,19 | 31,21 | P04264 | K2C1\_HUMAN | Keratin, type II cytoskeletal 1 | 19 |  | Cell membrane. | Cytoskeleton organiz |
| 8,08 | 8,408 | P12814 | ACTN1\_HUMAN | Alpha-actinin-1 | 5 |  | Cell membrane. Cell projection. Cytoskeleton. | Cytoskeleton reorganiz |
| 5,87 | 19,1 | P04406 | G3P\_HUMAN | Glyceraldehyde-3-phosphate dehydrogenase | 4 |  | Cell membrane. Cytoskeleton. | Glycolysis; cytoskeleton organization |
| 45,23 | 77,65 | P06733 | ENOA\_HUMAN | Alpha-enolase | 27 | Non classic | Cell membrane. Cytoskeleton. | Receptor and activator of plasminogen on the cell surface; glycolysis, |
| 3,44 | 6,584 | P14317 | HCLS1\_HUMAN | Hematopoietic lineage cell-specific protein | 2 |  | Cell membrane. Mitochondrion. | Antigen receptor signaling; regulation gene expression |
| 28,52 | 30,68 | P26038 | MOES\_HUMAN | Moesin | 15 | Non classic | Cell membrane; Cytoskeleton. | Cytoskeleton to cell membrane connection |
| 2 | 3,704 | O95497 | VNN1\_HUMAN | Pantetheinase | 1 | Classic | Cell membrane; Lipid-anchor | Inflammatory response |
| 2,08 | 6,18 | O15145 | ARPC3\_HUMAN | Actin-related protein 2/3 complex subunit 3 | 1 | Non classic | Cell projection. Cytoskeleton. | Cytoskeleton organization |
| 3,68 | 21,19 | O15511 | ARPC5\_HUMAN | Actin-related protein 2/3 complex subunit 5 | 2 | Non classic | Cell projection. Cytoskeleton. | Cytoskeleton organization |
| 23,88 | 69,28 | P23528 | COF1\_HUMAN | Cofilin-1 | 17 | Non classic | Cell projection. Cytoskeleton. | Cytoskeleton organization; actin binding |
| 1,9 | 13,1 | P59998 | ARPC4\_HUMAN | Actin-related protein 2/3 complex subunit 4 | 2 | Non classic | Cell projection. Cytoskeleton. | Cytoskeleton organization |
| 5,42 | 20,57 | P61158 | ARP3\_HUMAN | Actin-related protein 3 | 5 |  | Cell projection. Cytoskeleton. | Cytoskeleton organization |
| 3,8 | 7,36 | P61160 | ARP2\_HUMAN | Actin-related protein 2 | 2 |  | Cell projection. Cytoskeleton. | Cytoskeleton organization |
| 2,03 | 2,401 | Q9Y490 | TLN1\_HUMAN | Talin-1 | 3 |  | Cell projection. Cytoskeleton. | Membrane-cytoskeleton connections |
| 30,3 | 39,71 | P13796 | PLSL\_HUMAN | Plastin-2 | 16 | Non classic | Cell projection.Cytoskeleton. | Cytoskeleton organization; actin binding; it modulates memblocaliz of CD25 and CD69 R |
| 2,02 | 9,155 | O60234 | GMFG\_HUMAN | Glia maturation factor gamma | 1 | Non classic | Cytoplasm | Protein phosphorylation |
| 7,34 | 27,78 | P32119 | PRDX2\_HUMAN | Peroxiredoxin-2 | 4 | Non classic | Cytoplasm | Redox regulation |
| 2,09 | 5,195 | P68104 | EF1A1\_HUMAN | Elongation factor 1-alpha 1 | 1 |  | Cytoplasm | Protein synthesis |
| 24,67 | 26,78 | P11142 | HSP7C\_HUMAN | Heat shock cognate 71 kDa protein | 13 |  | Cytoplasm | Chaperone |
| 1,18 | 12,5 | P61088 | UBE2N\_HUMAN | Ubiquitin-conjugating enzyme E2 N | 1 | Non classic | Cytoplasm. | Proteasome |
| 8,79 | 21,39 | P00338 | LDHA\_HUMAN | L-lactate dehydrogenase A chain | 5 | Non classic | Cytoplasm. | Glycoslysisglucose metabolism |
| 3,22 | 39,61 | P00441 | SODC\_HUMAN | Superoxide dismutase [Cu-Zn] | 3 | Non classic | Cytoplasm. | Antioxidant |
| 9,57 | 24,85 | P07195 | LDHB\_HUMAN | L-lactate dehydrogenase B chain | 6 | Non classic | Cytoplasm. | Glycolysis glucose metabolism |
| 44,12 | 59,87 | P08670 | VIME\_HUMAN | Vimentin | 28 | Non classic | Cytoplasm. | Structural component of cytoskeleton |
| 2 | 4,407 | P08865 | RSSA\_HUMAN | 40S ribosomal protein SA | 1 | Non classic | Cytoplasm. | Ribosome structure; protein synthesis |
| 2 | 7,558 | P13693 | TCTP\_HUMAN | Translationally-controlled tumor protein | 1 | Non classic | Cytoplasm. | Calcium transport; cytoskeleton organization |
| 1,64 | 3,112 | P19971 | TYPH\_HUMAN | Thymidine phosphorylase | 1 | Non classic | Cytoplasm. | PDGFR binding |
| 7,36 | 16,62 | P30740 | ILEU\_HUMAN | Leukocyte elastase inhibitor | 5 | Non classic | Cytoplasm. | Regulation proteolysis |
| 2 | 11,65 | P55854 | SUMO3\_HUMAN | Small ubiquitin-related modifier 3 | 1 | Non classic | Cytoplasm. | Proteasome |
| 7,81 | 52,61 | P60174 | TPIS\_HUMAN | Triosephosphateisomerase | 8 | Non classic | Cytoplasm. | Glycolysis |
| 2,35 | 5,911 | P60842 | IF4A1\_HUMAN | Eukaryotic initiation factor 4A-I | 2 | Non classic | Cytoplasm. | Protein synthesis |
| 2 | 9,286 | Q56UQ5 | TPT1L\_HUMAN | TPT1-like protein | 1 | Non classic | Cytoplasm. |  |
| 2 | 12,63 | Q6EEV6 | SUMO4\_HUMAN | Small ubiquitin-related modifier 4 | 1 | Non classic | Cytoplasm. | Proteasome |
| 11,37 | 11,31 | O43707 | ACTN4\_HUMAN | Alpha-actinin-4 | 7 |  | Cytoplasm. | Actin-binding |
| 1,23 | 5,645 | O14818 | PSA7\_HUMAN | Proteasome subunit alpha type-7 | 1 |  | Cytoplasm. | Proteasome |
| 35,29 | 65,47 | P00558 | PGK1\_HUMAN | Phosphoglycerate kinase 1 | 18 |  | Cytoplasm. | Glycoslysis glucose metabolism |
| 20,58 | 38,74 | P04075 | ALDOA\_HUMAN | Fructose-bisphosphatealdolase A | 10 |  | Cytoplasm. | Actin-binding, glycolis |
| 7,42 | 10,45 | P08107 | HSP71\_HUMAN | Heat shock 70 kDa protein 1A/1B | 5 |  | Cytoplasm. | Chaperone |
| 2,55 | 1,632 | P13639 | EF2\_HUMAN | Elongation factor 2 | 1 |  | Cytoplasm. | Protein synthesis |
| 15,07 | 35,83 | P18669 | PGAM1\_HUMAN | Phosphoglyceratemutase 1 | 7 |  | Cytoplasm. | Glycoslysis glucose metabolism |
| 2 | 8,974 | P25787 | PSA2\_HUMAN | Proteasome subunit alpha type-2 | 1 |  | Cytoplasm. | Proteasome |
| 6,79 | 18,37 | P27348 | 1433T\_HUMAN | 14-3-3 protein theta | 4 |  | Cytoplasm. | Signaling cascade |
| 2 | 7,884 | P28066 | PSA5\_HUMAN | Proteasome subunit alpha type-5 | 1 |  | Cytoplasm. | Proteasome |
| 15,32 | 24,08 | P29401 | TKT\_HUMAN | Transketolase | 8 |  | Cytoplasm. | Energy metabolism |
| 7,52 | 40,24 | P31946 | 1433B\_HUMAN | 14-3-3 protein beta/alpha | 8 |  | Cytoplasm. | Signaling cascade |
| 17,87 | 31,75 | P37837 | TALDO\_HUMAN | Transaldolase | 9 |  | Cytoplasm. | Glucose matabolism |
| 2,1 | 17,07 | P40925 | MDHC\_HUMAN | Malate dehydrogenase, cytoplasmic | 3 |  | Cytoplasm. | Energy metabolism |
| 2,03 | 6,211 | P52209 | 6PGD\_HUMAN | 6-phosphogluconate dehydrogenase, decarboxylating | 2 |  | Cytoplasm. | NADP binding |
| 2,68 | 30,88 | P52565 | GDIR1\_HUMAN | Rho GDP-dissociation inhibitor 1 | 3 |  | Cytoplasm. | Rho protein signal transduction |
| 11,66 | 55,22 | P52566 | GDIR2\_HUMAN | Rho GDP-dissociation inhibitor 2 | 7 |  | Cytoplasm. | Rho protein signal transduction |
| 5,59 | 22,27 | P61981 | 1433G\_HUMAN | 14-3-3 protein gamma | 4 |  | Cytoplasm. | Signaling cascade |
| 3,61 | 18,82 | P62258 | 1433E\_HUMAN | 14-3-3 protein epsilon | 3 |  | Cytoplasm. | Signaling cascade |
| 21,55 | 65,71 | P63104 | 1433Z\_HUMAN | 14-3-3 protein zeta/delta | 14 |  | Cytoplasm. | Signaling cascade |
| 1,23 | 5,469 | Q8TAA3 | PSA7L\_HUMAN | Proteasome subunit alpha type-7-like | 1 |  | Cytoplasm. | Proteasome |
| 1,8 | 2,171 | Q9NY33 | DPP3\_HUMAN | Dipeptidyl peptidase 3 | 1 |  | Cytoplasm. | Proteolysis |
| 6,29 | 17,15 | Q9UL46 | PSME2\_HUMAN | Proteasome activator complex subunit 2 | 3 |  | Cytoplasm. | Proteasome |
| 7,25 | 16,34 | O75083 | WDR1\_HUMAN | WD repeat-containing protein 1 | 4 | Non classic | Cytoskeleton. | Actin-binding; cytoskeleton organization |
| 4,02 | 16,2 | P06753 | TPM3\_HUMAN | Tropomyosin alpha-3 chain | 3 | Non classic | Cytoskeleton. | Cytoskeleton organization; contraction |
| 4,57 | 26,85 | P16949 | STMN1\_HUMAN | Stathmin | 3 | Non classic | Cytoskeleton. | Cytoskeleton organization |
| 1,09 | 5,848 | P19105 | ML12A\_HUMAN | Myosin regulatory light chain 12A | 1 | Non classic | Cytoskeleton. | Cytoskeleton organization; contraction |
| 4,15 | 25,63 | P37802 | TAGL2\_HUMAN | Transgelin-2 | 3 | Non classic | Cytoskeleton. | Marker SMC |
| 19,4 | 97,73 | P62328 | TYB4\_HUMAN | Thymosin beta-4 | 17 | Non classic | Cytoskeleton. | Cytoskeleton organization |
| 63,55 | 79,2 | P63261 | ACTG\_HUMAN | Actin, cytoplasmic 2 | 66 | Non classic | Cytoskeleton. | Structural component of cytoskeleton |
| 13 | 97,73 | P63313 | TYB10\_HUMAN | Thymosin beta-10 | 8 | Non classic | Cytoskeleton. | Cytoskeleton organization |
| 4 | 12,68 | Q14019 | COTL1\_HUMAN | Coactosin-like protein | 2 | Non classic | Cytoskeleton. | Cytoskeleton organization; actin binding |
| 2 | 4,559 | O00151 | PDLI1\_HUMAN | PDZ and LIM domain protein 1 | 1 |  | Cytoskeleton. | Cytoskeleton organization |
| 1,09 | 5,814 | O14950 | ML12B\_HUMAN | Myosin regulatory light chain 12B | 1 |  | Cytoskeleton. | Cytoskeleton organization; contraction |
| 2,95 | 12,37 | O15143 | ARC1B\_HUMAN | Actin-related protein 2/3 complex subunit 1B | 3 |  | Cytoskeleton. | Cytoskeleton organization |
| 2 | 2,178 | O95678 | K2C75\_HUMAN | Keratin, type II cytoskeletal 75 | 1 |  | Cytoskeleton. | Cytoskeleton organization |
| 4 | 4,025 | P02533 | K1C14\_HUMAN | Keratin, type I cytoskeletal 14 | 2 |  | Cytoskeleton. | Cytoskeleton organization |
| 2,01 | 2,128 | P02538 | K2C6A\_HUMAN | Keratin, type II cytoskeletal 6A | 1 |  | Cytoskeleton. | Cytoskeleton organization |
| 4,01 | 3,901 | P04259 | K2C6B\_HUMAN | Keratin, type II cytoskeletal 6B | 2 |  | Cytoskeleton. | Cytoskeleton organization |
| 13,35 | 28,38 | P07437 | TBB5\_HUMAN | Tubulin beta chain | 8 |  | Cytoskeleton. | Structural component of cytoskeleton |
| 24,2 | 72,14 | P07737 | PROF1\_HUMAN | Profilin-1 | 18 |  | Cytoskeleton. | Cytoskeleton organization; platelet activation |
| 4 | 4,017 | P08779 | K1C16\_HUMAN | Keratin, type I cytoskeletal 16 | 2 |  | Cytoskeleton. | Cytoskeleton organization |
| 12 | 13,87 | P13645 | K1C10\_HUMAN | Keratin, type I cytoskeletal 10 | 7 |  | Cytoskeleton. | Cytoskeleton reorganization |
| 6 | 6,55 | P13646 | K1C13\_HUMAN | Keratin, type I cytoskeletal 13 | 3 |  | Cytoskeleton. | Cytoskeleton reorganization |
| 2 | 2,034 | P13647 | K2C5\_HUMAN | Keratin, type II cytoskeletal 5 | 1 |  | Cytoskeleton. | Cytoskeleton reorganization |
| 4 | 4,167 | P19012 | K1C15\_HUMAN | Keratin, type I cytoskeletal 15 | 2 |  | Cytoskeleton. | Cytoskeleton organization |
| 29,02 | 9,898 | P21333 | FLNA\_HUMAN | Filamin-A | 16 |  | Cytoskeleton. | Cytoskeleton organization; actin binding |
| 8,81 | 14,93 | P35527 | K1C9\_HUMAN | Keratin, type I cytoskeletal 9 | 6 |  | Cytoskeleton. | Cytoskeleton organization |
| 2,01 | 2,128 | P48668 | K2C6C\_HUMAN | Keratin, type II cytoskeletal 6C | 1 |  | Cytoskeleton. | Cytoskeleton organization |
| 5,27 | 28,32 | P52907 | CAZA1\_HUMAN | F-actin-capping protein subunit alpha-1 | 4 |  | Cytoskeleton. | Cytoskeleton organization |
| 4,52 | 19,21 | P60660 | MYL6\_HUMAN | Myosin light polypeptide 6 | 2 |  | Cytoskeleton. | Contraction |
| 60,41 | 79,2 | P60709 | ACTB\_HUMAN | Actin, cytoplasmic 1 | 74 |  | Cytoskeleton. | Structural component of cytoskeleton |
| 7,29 | 19,29 | P68363 | TBA1B\_HUMAN | Tubulin alpha-1B chain | 6 |  | Cytoskeleton. | Structural component of cytoskeleton |
| 2 | 2,243 | Q5XKE5 | K2C79\_HUMAN | Keratin, type II cytoskeletal 79 | 1 |  | Cytoskeleton. | Cytoskeleton organization |
| 7,29 | 19,29 | Q71U36 | TBA1A\_HUMAN | Tubulin alpha-1A chain | 6 |  | Cytoskeleton. | Structural component of cytoskeleton |
| 7,29 | 19,38 | Q9BQE3 | TBA1C\_HUMAN | Tubulin alpha-1C chain | 6 |  | Cytoskeleton. | Structural component of cytoskeleton |
| 12,2 | 28,63 | P31146 | COR1A\_HUMAN | Coronin-1A | 8 | Non classic | Cytoskeleton. Phagosome membrane. | Cytoskeleton organization; actin binding; motility |
| 6,06 | 5,128 | P07996 | TSP1\_HUMAN | Thrombospondin-1 | 4 | Classic | ECM | Cell-cell and cell-matrix interactions |
| 4,45 | 4,049 | Q8NHM4 | TRY6\_HUMAN | Putative trypsin-6 | 3 | Classic | ECM | Cell migration |
| 3,57 | 5,545 | P30101 | PDIA3\_HUMAN | Protein disulfide-isomerase A3 | 2 | Classic | ER | Chaperone |
| 2,14 | 7,113 | P54819 | KAD2\_HUMAN | Adenylate kinase 2, mitochondrial | 1 | Non classic | Mitochondrion | Energy metabolism |
| 3,96 | 30,16 | Q99497 | PARK7\_HUMAN | Protein DJ-1 | 3 |  | Mitochondrion | Inflammation; redox stress |
| 7,55 | 52,38 | P09211 | GSTP1\_HUMAN | Glutathione S-transferase P | 6 | Non classic | Mitochondrion. | Regulatione inflammatory response |
| 2,5 | 11,18 | P22392 | NDKB\_HUMAN | Nucleoside diphosphate kinase B | 1 |  | Nucleus. Cytoplasm. | Nucleotide metabolism |
| 17,29 | 29,46 | P22626 | ROA2\_HUMAN | Heterogeneous nuclear ribonucleoproteins A2/B1 | 9 |  | Nucleus. Cytoplasm. | RNA maturation |
| 1,85 | 1,98 | P23246 | SFPQ\_HUMAN | Splicing factor, proline- and glutamine-rich | 1 |  | Nucleus. Cytoplasm. | RNA processing |
| 11,5 | 15,36 | P20700 | LMNB1\_HUMAN | Lamin-B1 | 7 |  | Nucleus; Lipid-anchor | Nucleus structure |
| 4 | 21,54 | P20671 | H2A1D\_HUMAN | Histone H2A type 1-D | 2 | Non classic | Nucleus. | Chromatin structure |
| 2 | 2,507 | Q13394 | MB211\_HUMAN | Protein mab-21-like 1 | 1 |  | Nucleus. | Cell proliferation |
| 2 | 2,507 | Q9Y586 | MB212\_HUMAN | Protein mab-21-like 2 | 1 |  | Nucleus. | Cell proliferation |
| 2 | 16,67 | O00479 | HMGN4\_HUMAN | High mobility group nucleosome-binding domain-containing protein 4 | 1 | Non classic | Nucleus. | Regulation gene expression |
| 4 | 21,54 | P04908 | H2A1B\_HUMAN | Histone H2A type 1-B/E | 2 | Non classic | Nucleus. | Chromatin structure |
| 2 | 7,031 | P0C0S5 | H2AZ\_HUMAN | Histone H2A.Z | 1 | Non classic | Nucleus. | Chromatin structure |
| 4 | 21,54 | P0C0S8 | H2A1\_HUMAN | Histone H2A type 1 | 2 | Non classic | Nucleus. | Chromatin structure |
| 4 | 19,58 | P16104 | H2AX\_HUMAN | Histone H2A.x | 2 | Non classic | Nucleus. | Chromatin structure |
| 4 | 33,68 | P61956 | SUMO2\_HUMAN | Small ubiquitin-related modifier 2 | 2 | Non classic | Nucleus. | Proteasome |
| 2 | 7,031 | Q71UI9 | H2AV\_HUMAN | Histone H2A.V | 1 | Non classic | Nucleus. | Chromatin structure |
| 4 | 21,54 | Q8IUE6 | H2A2B\_HUMAN | Histone H2A type 2-B | 2 | Non classic | Nucleus. | Chromatin structure |
| 4 | 21,54 | Q93077 | H2A1C\_HUMAN | Histone H2A type 1-C | 2 | Non classic | Nucleus. | Chromatin structure |
| 4 | 21,88 | Q96KK5 | H2A1H\_HUMAN | Histone H2A type 1-H | 2 | Non classic | Nucleus. | Chromatin structure |
| 4 | 21,37 | Q96QV6 | H2A1A\_HUMAN | Histone H2A type 1-A | 2 | Non classic | Nucleus. | Chromatin structure |
| 4 | 21,88 | Q99878 | H2A1J\_HUMAN | Histone H2A type 1-J | 2 | Non classic | Nucleus. | Chromatin structure |
| 4 | 21,71 | Q9BTM1 | H2AJ\_HUMAN | Histone H2A.J | 2 | Non classic | Nucleus. | Chromatin structure |
| 4,85 | 29,37 | O60814 | H2B1K\_HUMAN | Histone H2B type 1-K | 3 |  | Nucleus. | Chromatin structure |
| 14,25 | 33,79 | P10412 | H14\_HUMAN | Histone H1.4 | 10 |  | Nucleus. | Chromatin structure |
| 5,76 | 21,68 | P16401 | H15\_HUMAN | Histone H1.5 | 5 |  | Nucleus. | Chromatin structure |
| 12,87 | 35,21 | P16403 | H12\_HUMAN | Histone H1.2 | 10 |  | Nucleus. | Chromatin structure |
| 6,85 | 42,86 | P23527 | H2B1O\_HUMAN | Histone H2B type 1-O | 4 |  | Nucleus. | Chromatin structure |
| 6,85 | 42,86 | P33778 | H2B1B\_HUMAN | Histone H2B type 1-B | 4 |  | Nucleus. | Chromatin structure |
| 1,35 | 4,762 | P51991 | ROA3\_HUMAN | Heterogeneous nuclear ribonucleoprotein A3 | 1 |  | Nucleus. | RNA maturation |
| 4,85 | 29,37 | P57053 | H2BFS\_HUMAN | Histone H2B type F-S | 3 |  | Nucleus. | Chromatin structure |
| 6,88 | 42,86 | P58876 | H2B1D\_HUMAN | Histone H2B type 1-D | 4 |  | Nucleus. | Chromatin structure |
| 6,43 | 38,83 | P62805 | H4\_HUMAN | Histone H4 | 3 |  | Nucleus. | Chromatin structure |
| 6,88 | 42,86 | P62807 | H2B1C\_HUMAN | Histone H2B type 1-C/E/F/G/I | 4 |  | Nucleus. | Chromatin structure |
| 4 | 21,71 | Q16777 | H2A2C\_HUMAN | Histone H2A type 2-C | 2 |  | Nucleus. | Chromatin structure |
| 6,85 | 42,86 | Q16778 | H2B2E\_HUMAN | Histone H2B type 2-E | 4 |  | Nucleus. | Chromatin structure |
| 6,88 | 42,86 | Q5QNW6 | H2B2F\_HUMAN | Histone H2B type 2-F | 4 |  | Nucleus. | Chromatin structure |
| 4 | 21,54 | Q6FI13 | H2A2A\_HUMAN | Histone H2A type 2-A | 2 |  | Nucleus. | Chromatin structure |
| 4 | 21,54 | Q7L7L0 | H2A3\_HUMAN | Histone H2A type 3 | 2 |  | Nucleus. | Chromatin structure |
| 6,88 | 42,86 | Q93079 | H2B1H\_HUMAN | Histone H2B type 1-H | 4 |  | Nucleus. | Chromatin structure |
| 6,88 | 42,86 | Q99877 | H2B1N\_HUMAN | Histone H2B type 1-N | 4 |  | Nucleus. | Chromatin structure |
| 6,88 | 42,86 | Q99879 | H2B1M\_HUMAN | Histone H2B type 1-M | 4 |  | Nucleus. | Chromatin structure |
| 6,88 | 42,86 | Q99880 | H2B1L\_HUMAN | Histone H2B type 1-L | 4 |  | Nucleus. | Chromatin structure |
| 2 | 6,481 | P62826 | RAN\_HUMAN | GTP-binding nuclear protein Ran | 1 | Non classic | Nucleus. Cytoplasm. | Transcription regulation |
| 2 | 16,67 | P05204 | HMGN2\_HUMAN | Non-histone chromosomal protein HMG-17 | 1 | Non classic | Nucleus. Cytoplasm. | Chromatin structure |
| 1,8 | 8,146 | Q15365 | PCBP1\_HUMAN | Poly(rC)-binding protein 1 | 2 | Non classic | Nucleus. Cytoplasm. | RNA processing |
| 1,45 | 20,43 | Q9H299 | SH3L3\_HUMAN | SH3 domain-binding glutamic acid-rich-like protein 3 | 1 | Non classic | Nucleus. Cytoplasm. | Redox homeostasis |
| 22,76 | 27,12 | P14618 | KPYM\_HUMAN | Pyruvate kinase isozymes M1/M2 | 11 |  | Nucleus. Cytoplasm. | Glucose metabolism |
| 2,5 | 11,18 | P15531 | NDKA\_HUMAN | Nucleoside diphosphate kinase A | 1 |  | Nucleus. Cytoplasm. | Nucleotide metabolism |
| 8,24 | 13,61 | P61978 | HNRPK\_HUMAN | Heterogeneous nuclear ribonucleoprotein K | 4 |  | Nucleus. Cytoplasm. | RNA maturation |
| 1,19 | 3,662 | Q14103 | HNRPD\_HUMAN | Heterogeneous nuclear ribonucleoprotein D0 | 1 |  | Nucleus. Cytoplasm. | RNA maturation |
| 5,66 | 19,54 | P04040 | CATA\_HUMAN | Catalase | 6 |  | Peroxisome. | Antioxidant |
| 1,09 | 6,78 | Q6ZVS6 | YK025\_HUMAN | Putative uncharacterized protein FLJ42147 | 1 | Classic | Secreted |  |
| 1,66 | 1,398 | P01042 | KNG1\_HUMAN | Kininogen-1 | 1 | Classic | Secreted ECM | Inflammatory response |
| 4,81 | 11,57 | P05120 | PAI2\_HUMAN | Plasminogen activator inhibitor 2 | 3 | Non classic | Secreted ECM | Blood coagulation |
| 1,23 | 11,11 | P09382 | LEG1\_HUMAN | Galectin-1 | 1 |  | Secreted ECM | T cell stimulation |
| 7,64 | 4,749 | P01023 | A2MG\_HUMAN | Alpha-2-macroglobulin | 8 | Classic | Secreted. | Platelet activation; blood coagulation |
| 1,77 | 0,5412 | P01024 | CO3\_HUMAN | Complement C3 | 1 | Classic | Secreted. | Complement cascade |
| 3,96 | 11,94 | P02753 | RET4\_HUMAN | Retinol-binding protein 4 | 2 | Classic | Secreted. | Glucose metabolism |
| 10,78 | 13,63 | P02771 | FETA\_HUMAN | Alpha-fetoprotein | 9 | Classic | Secreted. | Fatty acid binding |
| 2,16 | 14,84 | P02775 | CXCL7\_HUMAN | Platelet basic protein | 1 | Classic | Secreted. | Platelet activation |
| 1,12 | 8,911 | P02776 | PLF4\_HUMAN | Platelet factor 4 | 1 | Classic | Secreted. | Platelet activation |
| 1,35 | 3,152 | P02787 | TRFE\_HUMAN | Serotransferrin | 3 | Classic | Secreted. | Ion transport and homeostasis |
| 1,12 | 8,654 | P10720 | PF4V\_HUMAN | Platelet factor 4 variant | 1 | Classic | Secreted. | Platelet activation |
| 9,32 | 12,9 | P06744 | G6PI\_HUMAN | Glucose-6-phosphate isomerase | 6 |  | Secreted. | Glycolysis; stimulation cell motility |
| 12,34 | 51,52 | P62937 | PPIA\_HUMAN | Peptidyl-prolyl cis-trans isomerase A | 8 |  | Secreted. | Chaperone, ERK1 pathway |
| 1,35 | 1,268 | P02788 | TRFL\_HUMAN | Lactotransferrin | 1 | Classic | Secreted. Cytoplasm. Nucleus. | Iron transport |
| 1,48 | 1,407 | P06396 | GELS\_HUMAN | Gelsolin | 1 | Classic | Secreted. Cytoskeleton. | Actin-binding |
| 10,44 | 7,928 | P19823 | ITIH2\_HUMAN | Inter-alpha-trypsin inhibitor heavy chain H2 | 8 | Classic | Secreted; ECM | ECM structure |
| 2 | 1,573 | Q06033 | ITIH3\_HUMAN | Inter-alpha-trypsin inhibitor heavy chain H3 | 2 | Classic | Secreted; ECM | ECM structure |