Universidade de Aveiro Departamento de Química

2015

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CARACTERIZAÇÃO PROTEÓMICA DE CÉLULAS MONONUCLEARES DO SANGUE

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PROTEOMIC CHARACTERIZATION OF PERIPHERAL BLOOD MONONULEAR CELLS

Dissertação apresentada à Universidade de Aveiro para cumprimento dos requisitos necessários à obtenção do grau de Mestre em Biotecnologia, Ramo de Biotecnologia Molecular, realizada sob a orientação científica do Doutor Bruno José Fernandes Oliveira Manadas, Investigador Auxiliar do Centro de Neurociências e Biologia Celular da Universidade de Coimbra, e do Doutor Francisco Manuel Lemos Amado, Professor Associado do Departamento de Química da Universidade de Aveiro.

o júri

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palavras-chave Células mononucleares do sangue, proteómica, LC-MS/MS, análise SWATH.

resumo

As células mononucleares do sangue (CMS) desempenham diversos e importantes papéis na monitorização da homeostasia do sistema imunitário. Assim sendo, esta subpopulação de células sanguíneas pode providenciar acesso a potenciais biomoléculas relevantes a nível fisiológico, nomeadamente proteínas. Por esta razão, as CMS representam uma amostra biológica promissora na investigação científica, particularmente na descoberta de potenciais marcadores biológicos de diversas doenças.

Estudos anteriores de caracterização proteómica das CMS de indivíduos saudáveis falharam quer na identificação de um grande número de proteínas, quer na sua quantificação, de forma compatível com a pesquisa de potenciais biomarcadores. Portanto, este estudo teve como objectivo providenciar uma caracterização proteómica abrangente, bem como a criação de uma biblioteca SWATH. Foi igualmente avaliado se usando tubos CPT™ disponíveis na BD Vacutainer® para o isolamento das CMS, seria possível identificar um maior número de proteínas imunologicamente relevantes comparativamente a amostras de plasma.

O teste de enriquecimento revelou que é possível identificar mais proteínas associadas ao sistema imunitário em CMS isoladas do que em amostras de plasma. Também se verificou que a maioria das proteínas quantificadas com ontologia genética “sistema imunitário” estão presentes em maior quantidade nas amostras de CMS.

2D LC-MS/MS mostrou ser a melhor abordagem na análise qualitativa das CMS e na elaboração da biblioteca SWATH, uma vez que o número de proteínas identificadas e quantificadas apresentou um aumento de 66,3% e 16,9%, respectivamente, comparativamente à 1D LC-MS/MS.

No total foram identificadas 2071 proteínas e foi possível quantificar 922 proteínas diferentes em seis amostras distintas. Destas, 445 proteínas eram comuns a todos os indivíduos.

Em conclusão, este trabalho disponibiliza um amplo conjunto de dados do proteoma das CMS que será útil a estudos futuros que pretendam centrar-se na pesquisa de potenciais marcadores biológicos, nas CMS, das mais diversas patologias. Além disso, comprovou-se que o método de aquisição SWATH-MS é reprodutível e eficaz na quantificação das proteínas das CMS.

keywords Peripheral blood mononuclear cells, proteomics, LC-MS/MS, SWATH analysis.

abstract

Peripheral blood mononuclear cells (PBMCs) play quite diverse and important roles in monitoring immune homeostasis. Thus, these subset of blood cells may provide access to potential physiological relevant biomolecules, namely proteins. For this reason, PBMCs represent a promising biological sample in scientific research, particularly as a source of potential biological markers discovery of the most diverse diseases.

Prior studies of proteomic characterization of PBMCs from healthy individuals lack either the identification of a large number of proteins or its quantification in a way that is compatible with the search of potential biomarker candidates. Therefore, this study aimed to provide a comprehensive PBMCs proteome characterisation as well as to create a SWATH library.

It was also evaluated if by using the BD Vacutainer® CPT™ tubes for PBMCs isolation, it would be possible to identify a larger number of immunologically relevant proteins in comparison to plasma samples.

The enrichment test assay revealed that it is possible to identify more immune-related proteins from isolated PBMCs than from plasma. Moreover, the majority of the quantified proteins with an “immune system” GO term assigned is present in higher amounts in PBMCs samples.

2D LC-MS/MS proved to be the best approach to use in qualitative analysis of PBMCs and in the construction of a SWATH library, since it resulted in an increase of both identified and quantified proteins (66.3% and 16.9%, respectively) in comparison to 1D LC-MS/MS.

A total of 2071 proteins were identified and it was possible to quantify 922 different proteins among six distinct samples. From these proteins, 445 were commom between all individuals.

In conclusion, this work provides a comprehensive PBMCs proteome dataset that will be useful in further studies that focus on the search for potential biological markers of various pathologies in these cells. Additionally, SWATH-MS proved to be a reproducible and effective acquisition method to quantify PBMCs proteins.

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List of Abbreviations

A	ACN	Acetonitrile
B	BSA	Bovine serum albumin
	BMI	Body mass index
C	CD	Cluster of differentiation
	CHAPS	3-[(3-cholamidopropyl)dimethylammonio]-1-propanesulfonate
	CID	Collision-induced dissociation
	CNS	Central nervous system
	CPT	Cell preparation tube
	CSF	Cerebrospinal fluid
	CV	Coefficient of variantion
D	Da	Dalton
	DC	Direct current
	DCs	Dendritic cells
	DDA	Data dependent acquisition
	ddH_2O	Double deionized water
	DMEM	Dulbecco's modified Eagle's medium
	DMSO	Dimethyl sulfoxide
	DSM	Diagnostic and statistical manual of mental disorders
	DTT	Dithiothreitol
E	EDTA	Ethylenediamine tetraacetic acid
	EL	Exclusion list
	ELISA	Enzyme-linked immunosorbent assay
	ESI	Electrospray ionization
F	FA	Formic acid
	FBS	Fetal bovine serum
	FDR	False discovery rate
G	GFP	Green fluorescent protein
	GO	Gene ontology
	GWAS	Genome wide association studies
H	HPLC	High-performance liquid chromatography
I	ICAT	Isotope-coded affinity tag
	ICD	International classification of diseases
	IDA	Information dependent acquisition
	IFN	Interferon
	iRT	Indexed retention time
	iTRAQ	Isobaric tags for relative and absolute quantitation
K	KEGG	Kyoto encyclopedia of genes and genomes

L	LC	Liquid chromatography
	LC-MS/MS	Liquid chromatography coupled to tandem mass spectrometry
M	MALDI	Matrix-assisted laser desorption/ionization
	mDC	Myeloid dendritic cells
	MHC	Major histocompatibility complex
	MS	Mass spectrometry
	MS/MS	Tandem mass spectrometry
	m/z	Mass-to-charge ratio
N	NCM	Non-classical monocytes
	NK	Natural killer
P	PBC	Potential biomarker candidate
	PBS	Phosphate buffered saline
	PBMCs	Peripheral blood mononuclear cells
	PCA	Principal component analysis
	pDC	Plasmacytoid dendritic cells
	PMSF	Phenylmethylsulfonyl fluoride
	PTM	Post translational modification
Q	QqTOF	Hybrid quadrupole time-of-flight spectrometer
R	RBC	Red blood cells
	RF	Radiofrequency
	RNA	Ribonucleic acid
	RPC	Reversed phase chromatography
	RPMI	Roswell park memorial institute medium
	RT	Room temperature
S	SCX	Strong cation exchange
	SCZ	Schizophrenia
	SDS	Sodium dodecyl sulphate
	SDS-PAGE	Sodium dodecyl sulphate-polyacrylamide gel electrophoresis
	SILAC	Stable isotope labelling by amino acids in cell culture
	SNP	Single nucleotide polymorphism
	SRM	Selected reaction monitoring
	SWATH	Sequential window acquisition of all theoretical fragmentation spectra
T	TCA	Trichloroacetic acid
	TEAB	Triethylammonium bicarbonate
	TOF	Time-of-flight
V	v/v	Volume/volume
W	WB	Whole blood
	WBC	White blood cells
	w/v	Weight/volume

X	XIC	Extracted-ion chromatogram
	1D	One-dimensional
	2D	Two-dimensional
	2-DE	Two-dimensional electrophoresis

I. Introduction

I.1. Master Thesis' context

Schizophrenia (SCZ) is a complex and chronic psychiatric disorder that affects 0.72% of world's population[1,2]. Patients with SCZ exhibit quite severe and diverse symptoms (*e.g.* hallucinations, apathy, and disorganised speech, among others) that cause a considerable burden on patients, their families and society[1], and place SCZ in the top 10 of the most disabling diseases worldwide[3]. Although SCZ is highly heritable, the genetic component does not fully explain its aetiology. Environmental factors such as pregnancy and delivery complications, urbanicity, and migration also play a role in its pathogenesis[4]. Due to the lack of a biochemical test that allows SCZ's diagnosis, currently this process is based on an interview-based evaluation of patients' symptoms, which onset can vary among patients and through the course of the disease, according to international guidelines (*e.g.* DSM and ICD)[5]. The subjective and empirical diagnosis is mostly due to SCZ's heterogenic phenotype and the ambiguous boundaries among other mental illnesses[5]. The existing treatment includes psychosocial interventions and medication with the aim of alleviating some of the symptoms, reducing both the frequency and the severity of psychosis and improving quality of life[6]. Although there is a wide range of antipsychotics available for SCZ treatment, the selection of the best medication is also a challenge for clinicians and involves a long trial and error process[6] in which a considerable number of patients (>70%) have to interrupt the initial treatment due to its inefficacy or intolerable side effects[7]. The identification of a biological marker (or a set of them) that could provide a SCZ's molecular fingerprint may help clinicians to differentiate between psychiatric disorders or to distinguish between SCZ subtypes[8]. That is, the identification of differential biological markers would not only improve its diagnosis, but also the stratification of patients[8]. Moreover, it could help the establishment of treatment strategies, monitoring therapeutic response, predicting its progression, and eventually understanding the pathophysiological mechanisms underlying the disease[8]. Thus, the identification of a SCZ molecular fingerprint is a step forward in the improvement of patients' mental health.

The pathophysiological mechanisms involved in SCZ remain unclear[9], however it is known that both the structure and the functioning of the brain are altered[10–12]. Moreover, there are several hypotheses involving different neurotransmission systems (*e.g.* dopaminergic, glutamatergic and cholinergic systems) that have been proposed based on decades of research[13]. In addition to the neurotransmission systems' hypotheses, there are also strong arguments that the immune system is altered in SCZ and perhaps it underlies its aetiology[14]. GWAS revealed significant single nucleotide polymorphisms (SNPs) spanning the major histocompatibility complex (MHC) region on

chromosome 6p21.3-22.1[15,16]; several studies found alterations in different cytokines, cytokine receptors and antagonists in both blood and cerebrospinal fluid (CSF)[17–20], with some of the observed alterations being associated with different SCZ status; abnormalities in peripheral lymphocyte and monocyte levels[21,22]; some patents with SCZ showed microglia activation[23]; and the antibody production in these patients is higher when comparing to healthy controls[24], specifically antibodies against specific brain regions, and against neurotransmitter receptors[25,26] which can provide an important connection between immune impairments and altered neurotransmissions.

I.2. Peripheral blood mononuclear cells

As the name suggests, peripheral blood mononuclear cells (PBMCs) concern the blood cells that have a round nucleus, in contrast to those that have a multilobed nucleus. This subpopulation consists of lymphocytes (T lymphocytes, B lymphocytes and natural killer (NK) cells) (70-90%), monocytes (10-30%), and dendritic cells (≈1%)[27].

Lymphocytes consist of diverse subsets that differ in how they recognize antigens and in their function. T and B lymphocytes are the unique cells of the adaptive immunity. Once naive B cells recognise antigens by membrane-bound antibodies, they undergo a humoral immune response, become active, and differentiate into plasma cells that segregate antibodies of the same specificity as the antigen receptor. T lymphocytes form a group of functionally distinct cells comprising helper T cells (Th cells), cytotoxic cells (Tc cells), and regulatory T cells (Tregs). The $CD4^+$ Th cells are the orchestrating cells of the immune response and play an important role helping phagocytic cells. Tc cells ($CD8^+$) are responsible for killing body cells infected with virus or bacteria, or that are eventually damaged or dysfunctional, and the function of $CD4^+$ Tregs is to inhibit immune responses (*i.e.* maintenance of self-tolerance). NK cells are involved in the innate immune response and their major function is to kill infected cells and produce interferon-gamma (IFN-γ) which activates macrophages to destroy phagocytised microbes. These cells can be identified by expression of CD56 and the absence of the T cell marker CD3[22,27].

Monocytes can be divided into two classes: the so-called classic monocytes that produce abundant inflammatory mediators and are rapidly recruited to sites of infection or tissue injury, and the non-classical monocytes (NCM) that contribute to tissue repair after injury. These cells are identifiable by high cell surface expression of CD14 and lack of CD16 ($CD14^{++}CD16^-$), and $CD14^+CD16^{++}$, respectively[27].

Dendritic cells (DCs) are the most specialised antigen-presenting cells and play a crucial role in the interphase between the innate and adaptive immune system. Classic or conventional dendritic cells carry antigens from the infection site to the lymph nodes and present it to the adaptive immune system's cells. DCs in cooperation with the MHC class II molecules and the co-stimulatory CD80 and CD86 molecules stimulate the naïve cells of the adaptive immune system, which will consequently proliferate and become active[22,27]. Plasmacytoid dendritic cells (pDC) are responsible for an early response to viral infections. This subpopulation of DCs recognize nucleic acids of intracellular viruses and produce soluble proteins, type I interferons, which have an effective antiviral activity[27].

I.2.1. PBMCs as a source of biomarkers

A biomarker is a measurable feature that allows to distinguish between normal biological processes, pathological processes or pharmacologic responses to a therapeutic intervention[28]. This feature can be a gene, RNA, protein, its post-translational modifications (PTM), lipid or metabolite, what means that practically any human body molecule is a potential biomarker candidate (PBC) as long as it can be associated with a disease[8,29]. However, some authors suggest that PBCs pursuit should focus on proteins, once they are the true effectors of physiological functions[8], and it is also claimed that the proteome is more related to the phenotype of an organism than genes are[30]. As a pathological state modifies the protein levels of a normal physiological state the study of such alterations can provide new insights into the pathophysiological pathways underlying a given disease[8]. Therefore, proteomics is an extremely valuable tool to study different diseases and to search for PBC, namely SCZ[31,32], since it can provide a molecular characterisation of a given sample (*e.g.* cells or tissues) in a large-scale and in a high-throughput manner[33]. Indeed, this approach has been providing molecular signatures of this illness[34,35]. However, to my knowledge, these two studies have not yet been applied in clinical practice, probably because they did not provide a high-quality biomarker. Moreover, these studies used a target proteomic approach, more specifically an immunoassay. This approach limits the discovery of biomarkers since the study was performed against proteins for which the immunoassay was developed. Using a non-targeted approach such as shotgun proteomics it is possible to identify thousands of proteins and thus to provide a better biological fingerprinting for SCZ, however with a more complex and time-consuming data analysis[36].

In PBCs discovery, it is important to know not only what to look for (*e.g.* proteins, metabolites, etc.) but also where to look for, that is, what type of sample use as a source of PBCs.

Plasma has been widely used in PBCs discovery since it is easily obtained from living patients in large amounts[37]. Its proteome comprises 22 highly abundant proteins (*e.g.* albumin, immunoglobulins, among others) that make up 99% of total protein abundance in plasma. This wide dynamic range in protein abundance (greater than 10 orders of magnitude) makes it impossible to detect low abundant proteins without a depletion step of the most abundant proteins[38], and low abundant proteins might be the key to understand pathophysiological pathways of some diseases (*e.g.* psychiatric disorders)[39]. As PBMCs play different and important roles in the immune system, monitoring and responding in an inflammatory manner, they provide access to potential physiological relevant biomolecules[40,41]. Moreover, PBMCs are also easily and rapidly isolated from whole blood (WB), which means that they can be obtained through a low-invasive method of collection (*i.e.* blood drawing) without the interference of human plasma due to the presence of highly abundant proteins[38]. For this reason, PBMCs have been used in scientific research to study the most diverse diseases such as stroke[42], amyotrophic lateral sclerosis[43] and psychiatric disorders[32,44,45]. Therefore, PBMCs may be a source of PBC for diagnosis and monitoring of many diseases, representing an alternative to plasma samples. Regarding psychiatric disorders, specifically SCZ, the first thing that comes to mind when thinking of biomarkers source is living brain tissue, but the use of this biopsies in scientific research is impracticable, thus *post-mortem* brain tissue has been widely used in SCZ studies[46]. However, artefacts arising from chronic medication, the cause of death and the *post-mortem* interval[47,48] may hinder the interpretation of the obtained results, once the observed alterations might be due to the disease itself or a consequence of the chronic therapy. Therefore, the use of peripheral samples (*e.g.* blood, urine and others) provides a valuable alternative once it can be obtained from living patients, through the course of the disease, and in large amounts[44,49]. Furthermore, searching for biomarkers on blood allows the use of a standardized low invasive sample collection procedure[49]. Different studies have been conducted to find out if CNS alterations can actually be observed in the blood stream and it was discovered that brain is integrated in fundamental biological functions of the whole body which is confirmed by modifications in blood molecular composition[50]. Different authors compared the gene expression in blood and in brain, and found out that blood gene expression is significantly identical to that of CNS tissues[51,52], namely approximately 50% of the so-called SCZ susceptibility genes are shared by these tissues[51]. Particularly, PBMCs can be a valuable source of biomarkers for SCZ[40,45,52] and since they represent an important cellular component of the immune system, they can provide a suitable model to study SCZ-related immune impairments[44]. Indeed, Gladkevich *et al.* argue that lymphocytes, a PBMCs subpopulation, may actually be a neuronal probe in the investigations of

CNS pathology in psychiatric disorders, once they play a fundamental role in the interactions between CNS and the immune system. Such affirmation is supported by three observations: i) impaired lymphocyte functions in psychiatric diseases; ii) expression of neuroactive proteins in lymphocytes; and iii) similarities of hormonal effects on the CNS processes and lymphocytes physiology[45].

In biomarker discovery, it is essential to know not only which proteins are present in a given sample, but also its expression levels that is, it is crucial to quantify the difference among different samples (*i.e.* disease *vs.* control samples). Therefore, besides the qualitative protein analysis, it is equally important if not more, a quantitative analysis of the identified proteins[53]. After the identification of a PBC (or a set), it is mandatory to validate it in repeated studies and in a large number of samples so that it can be used in clinical environment. Immuno-based assays, such as Western blot and enzyme-linked immunosorbent assay (ELISA) are the most frequently used techniques, but both methods require the availability of specific antibodies. Another possibility is to perform a mass spectrometry (MS)-based technique, selective reaction monitoring (SRM), which allows an accurate measurement of the relative or absolute concentration of the previous identified PBC[31].

I.3. Proteomics

In 1995 Wilkins *et al.* proposed the concept of proteome defining it as "the entire PROTEin complement expressed by the geneOME, or by a cell or tissue type"[54,55] and consequently emerged a new field of science: *proteomics*. As the word suggests, proteomics is the study of the proteome, that is the study of different protein characteristics (*i.e.* expression level, PTMs and others) on a large scale to characterise biological processes (*e.g.* diseases)[56,57].

Nowadays, there are two fundamental approaches used in proteomics: bottom-up and top-down. Bottom-up proteomics (also known as shotgun proteomics) requires simple or complex protein mixtures to be digested, the resulting peptides are then separated by liquid chromatography (LC) and analysed by MS (Figure I.1.). In top-down strategy, intact proteins are directly analysed by MS and subjected to fragmentation in the mass spectrometer. In both approaches proteins are identified by comparing the mass spectra obtained with theoretical spectra based on protein databases[53].

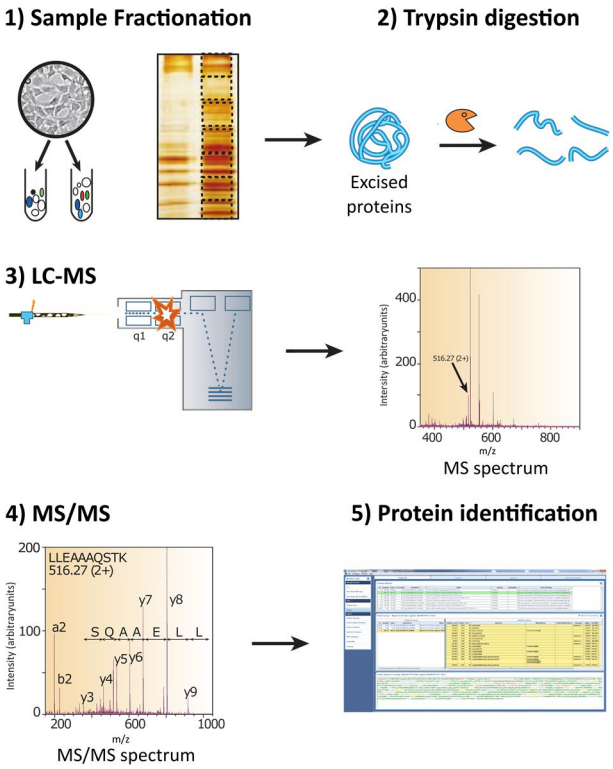

Figure I.1. Generic MS-based proteomics experiment. The classic proteomics approach consists of five stages. In stage 1, the proteins to be analysed are isolated from cell lysate or tissue, which usually includes a final step of one-dimensional gel electrophoresis. After that, the proteins are enzymatically digested, typically with trypsin (stage 2). The resulting peptide mixture is separated by high-performance liquid chromatography and its molecular weight determined by mass spectrometry (stage 3). In stage 4, the software generates a prioritized list of the peptides for fragmentation in a series of tandem mass spectrometric (MS/MS) experiments. Finally, the resulting spectra are matched against protein sequence databases so it is possible to identify the peptides and thus the proteins (stage 5). Adapted from[58].

Since biomarkers discovery is based on proteomic differences between samples (*i.e.* control and disease samples), besides proteins identification it is also extremely important to perform a quantitative approach[53]. Protein quantification can be performed by label-free strategies, such as SRM and SWATH[59]. Both approaches require previous generation of reference spectral maps to perform quantification however, SRM is based on a target data acquisition whereas SWATH is based on an untargeted data acquisition and targeted data extraction[59]. Another way to quantify proteins by MS is to label the samples. Techniques like ICAT, iTRAQ, SILAC and $H_2{}^{18}O$ labelling can be employed yet, all of these methods are quite expensive due to the use of isotopic reagents, or require protein labelling during protein synthesis (SILAC) not amenable for use with human samples[53].

I.3.1. Sample preparation

In proteomics, the most important step is sample preparation as it determines the coverage of the target proteome achieved. As protein classes differ between different types of tissues/cells it is mandatory to adjust the extraction protocol to the tissue/cells in the study[31].

The protein concentration range in a complex biological sample typical exceeds the dynamic range of any currently available analytical method, therefore it is useful to decrease its complexity by prefractionation of the sample, or to perform an enrichment step of the target proteins[60]. In this master's thesis project, the BD Vacutainer® cell preparation tube (CPT™) will be used in order to sub fractionate blood and isolate PBMCs. As described by the manufacturer, CPT™ is an evacuated tube that allows both the collection of WB and the separation of PBMCs in a single centrifugation step. The tube contains sodium citrate as anticoagulant, a FICOLL™ Hypaque™ density solution, and a polyester gel barrier. During centrifugation, the gel fraction moves and forms a barrier separating PBMCs and plasma from denser blood cells (erythrocytes and granulocytes). The use of this simplified procedure is an advantage for inexperienced operators in Ficoll density gradient handling and results in improved consistency among different operators[61].

After prefractionation, the cells must be disrupted either by mechanical or chemical methods so then the proteins can be solubilised[60]. If proteins are not properly extracted and solubilised, they will not be identified nor quantified, hence this step may compromise the whole experiment[31]. Protein solubilisation may involve the use of detergents (*e.g.* SDS, Triton X-100 or CHAPS) which disrupt hydrophobic interactions, reducing agents (*e.g.* DTT or TCEP) to break disulphide bonds between cysteine residues, and protease inhibitors (*e.g.* PMSF or EDTA) to prevent protein degradation[60].

In shotgun proteomics approach, there are two main strategies that can be used to simplify a complex biological sample and obtain a peptide solution proper to MS analysis: in-gel and in-solution digestion[62]. The so-called in-gel digestion consists in the separation of proteins by gel electrophoreses (usually SDS-PAGE) to decrease sample's complexity[53]. After that, the gel-trapped proteins must be digested, usually with trypsin, an enzyme that cleaves the C-terminal side of lysine and arginine residues[63]. The other strategy consists in performing protein extraction with strong chaotropic reagents (*e.g.* urea and thiourea), precipitate them and then digest proteins under denaturing conditions (in-solution digestion)[62].

I.3.2. LC-MS/MS

Liquid chromatography coupled with tandem mass spectrometry (LC-MS/MS) has increasingly become the method of choice in proteomic studies[31]. Chromatography is a powerful tool for the separation of different compounds in a complex mixture, but it clearly lacks unequivocal identification of such molecules, even when retention times are different. On the other hand, mass

spectrometry allows the identification of many compounds with a high degree of confidence, although analysing a complex mixture by MS can be problematic, especially in the identification of molecules present in low concentration. Thus the combination of LC, which allows the separation of peptides reducing sample complexity, with the identification potential of mass spectrometry is extremely advantageous, mostly because different compounds with close retention times can have different mass spectra making it possible to distinguish and identify them[64].

As the system that was used in the development of this project is a high-performance liquid chromatograph coupled to a hybrid quadrupole time-of-flight (QqTOF) mass spectrometer with an electrospray ionization source, only features related to this instrument will be discussed in the following sections.

I.3.2.1. High-Performance Liquid Chromatography

High-performance liquid chromatography (HPLC) is currently established as the leading technique for the separation and purification of a wide range of molecules including peptides and proteins. The success of HPLC is due to a vast number of inherent characteristics related to reproducibility, simplicity of selectivity manipulation, and usually high recoveries[65].

In a chromatographic separation, the compounds present in a complex mixture are resolved according to their interaction with the stationary phase and depending on the extent of the interaction, it takes different times for them to move from the initial position to the detector. To ensure a constant flow rate and therefore a reproducible chromatography, the mobile phase is a liquid delivered under high pressure (usually up to 400 bar), whereas the stationary phase is packed into a column capable of withstanding the high pressures[64].

Reversed-phase chromatography (RPC) is perhaps the most commonly used method for peptides separation. This category of chromatography depends on the hydrophobic interaction of the solute molecule from the mobile phase to the immobilized hydrophobic ligands attached to the stationary phase (*i.e.* the sorbent). The sorbent consists of a functional group (usually n-alkyl groups, such as C18 molecules which is widely used for the fractionation of peptides) bound to silica from which the solutes are eluted with a gradient of increasing concentrations of an organic solvent (*e.g.* acetonitrile) containing an ionic modifier (*e.g.* formic acid)[65].

Proteomic analysis of peptide mixtures from complex biological samples largely exceeds the capacity of 1D chromatography, making it necessary to adopt multidimensional separation approaches, once increasing peptides separation results is the identification of more peptides and

consequently more proteins[66]. Several approaches can be applied to improve proteome coverage however, RPC at high pH coupled with RPC at low pH has proved to give best orthogonality over other 2D-LC combinations (*e.g.* SCX with pH gradient followed by RPC at low pH)[67].

I.3.2.2. Mass Spectrometry

Mass spectrometry is an analytic technique that allows both qualitative and quantitative information of a molecule, by separation of ions according to their mass-to-charge (m/z) ratio. The principle of MS analysis consists of three major steps: i) ionization of the molecules that are converted into gas-phase ions; ii) resolving ions according to their m/z ratio; and iii) detection of the ions, which consists in the conversion of the registration of the number of ions at each m/z value into a mass spectrum (*i.e.* a plot of ions relative abundance versus m/z ratio). In proteomic approaches there are two main classes of ions detected in MS experiments, molecular ions, which contain the entire analyte molecule, and fragment ions, which contain a portion of the structure. The molecular weight of an analyte is determined by the m/z of a molecular ion – if z is known – while some structural information can be determined by the fragmentation spectra[58,64].

In Figure I.2. it is shown the basic components of a mass spectrometer, which includes a sample inlet (*e.g.* a liquid chromatograph or a direct insertion probe), an ion source, a mass analyser, a detector, the instrument control, data and vacuum systems. The mass spectrometer must operate under vacuum conditions so that the generated ions reach the detector, because the

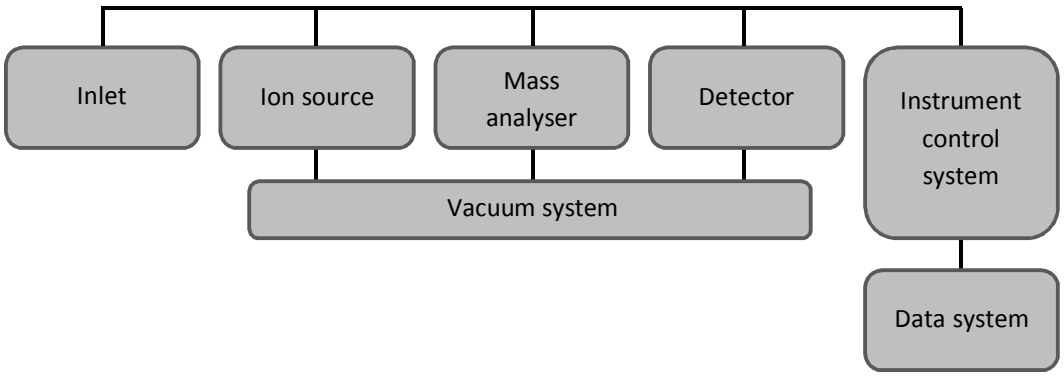

Figure I.2. Basic components of a mass spectrometer. The mass analyser, the detector and some parts of the ion source are kept under vacuum conditions. The instrument control system monitors and controls the whole instrument. The produced data are recorded by the data system. Adapted from[63].

average distance travelled by an ion between collisions (*i.e.* the mean free path) at atmospheric pressure is about 10^{-8} m. Reducing the pressure results in an increased mean free path around 10 m, and so the ions reach the mass spectrometer detector[64].

I.3.2.2.1. Ionization

There are different methods that allow the ionization of molecules including electron ionization (EI), chemical ionization (CI), fast-atom bombardment (FAB), electrospray (ESI), MALDI, and others. However, ESI (Figure I.3.) is the most suitable ionization method for LC-MS analysis of peptides[64]. This method consists in an acidic, aqueous solution containing the peptides to be sprayed through a metallic capillary to which a potential difference (2-5kV) is applied. This results in the production of a Taylor cone from which droplets of the solution are sputtered. Protons from the acidic conditions confer a positive charge to the droplets, causing them to move from the needle towards the instrument, which is negatively charged in relation to the needle. The size of the charged droplets decreases by desolvation, which is assisted by a continuous counter flow of a drying gas, usually nitrogen, that goes in the opposite direction to that of the droplets. As a result, the repulsive forces between equal charges on the surface of the droplets overcome the cohesive forces of surface tension and a Coulombic explosion occurs, producing charged microdroplets. This process is repeated until ions of the peptides are desorbed into the gas-phase, where they can be directed into the mass spectrometer by appropriate electric fields[63,64].

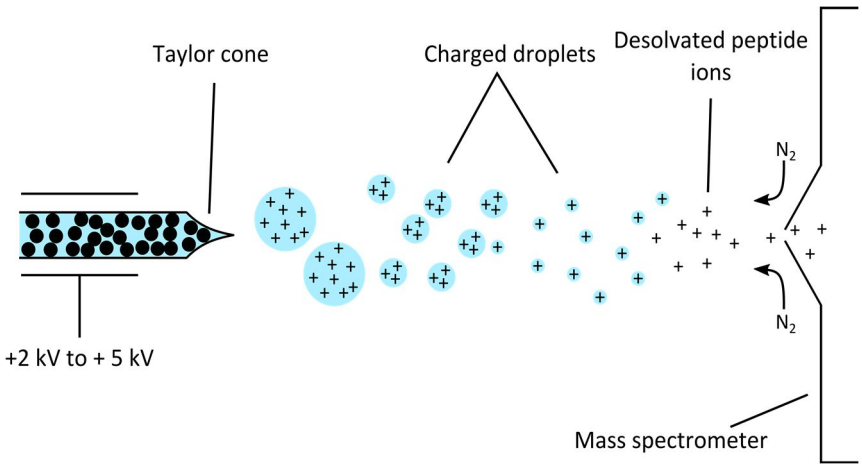

Figure I.3. A generalized view of the electrospray ionization process. Sputtered charged droplets from a Taylor cone are desolved by a continuous flow of N_2, leading to the formation of ions that enter the mass spectrometer. Adapted from[63].

I.3.2.2.2. Mass Analyser

The mass analyser determines the m/z of the generated ions and there is a variety of mass analysers available, mainly quadrupole, ion trap, orbitrap, time-of-flight (TOF), magnetic sector, and Fourier transform ion cyclotron resonance (FT-ICR). Parameters such as resolution, accuracy, precision, speed of data acquisition, sensitivity, and m/z range of the mass analyser should be taken into account when choosing the instrument. Regarding the above mentioned features, quadrupole, ion trap, orbitrap and TOF mass analysers are the most frequently used in high-throughput proteomics experiments because they outperform the other mass analysers[63].

Quadrupole analysers are composed of four rods (poles) arranged as two sets of two electrically connected rods (Figure I.4.). A combination of radiofrequency (RF) and direct current (DC) is applied to each pair of rods. At a specific value of RF and DC, ions of a particular m/z follow a stable trajectory from the beginning of the mass analyser until the end of the mass analyser, while ions with other m/z have unstable trajectories and do not reach the end of the mass analyser. If a detector is available after the quadrupole, the mass spectrum is acquired by varying the RF and DC voltages such that an increasing m/z is selected to pass through the quadrupole and reach the detector. This analyser can also be set up to contain and transmit ions of all m/z by applying an RF-only field[63,64].

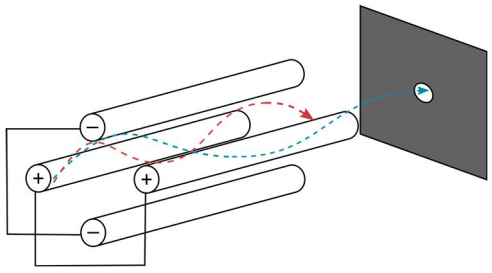

Figure I.4. Schematic representation of a quadrupole mass analyser. Four poles are arranged in two sets of opposing rods. An electric field with RF and DC components is applied in one set of rods, and according to the symmetric equation in the second set of rods. Ions of a given m/z follow a stable trajectory and reach the end of the mass analyser (blue), while ions with other m/z values do not reach the end of the mass analyser (red). Adapted from[63].

As the name suggests, a TOF analyser (Figure I.5.) measures the time required for an ion to travel the length of the flight tube. A fixed amount of kinetic energy is given to an ion by acceleration in an electric field that is generated by the application of a high voltage (typically between +20 kV and +30 kV for positive ions such as peptides). After acceleration, the ion enters a field-free region, travelling at a velocity that is inversely proportional to the square root of its mass. This means that ions with low m/z travel faster than ions with a higher m/z[63]. The initial velocities of the ions as they are accelerated may differ and therefore the resolution of the TOF analyser is compromised. It is

possible to reduce the effects of such initial energy spread using longer flight tubes and higher accelerating voltages. Another method is to use an ion reflector (also referred as a reflectron). It consists of an ion mirror that reverses the flight path of the ion in order to focus ions with the same m/z but different velocities. Ions with the same m/z but different velocities penetrate the reflectron to different levels (*i.e.* higher velocity ions penetrate farther than lower velocity ions), adjusting velocity differences[63].

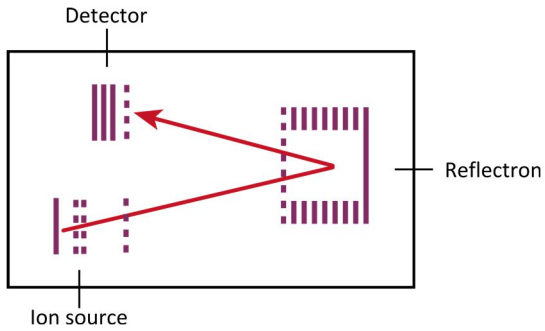

Figure I.5. Schematic representation of a reflector time-of-flight instrument. Ions are accelerated to high kinetic energy and are separated along a flight tube because of their different velocities. The ions are reflected in a reflectron, which compensates for slight differences in kinetic energy, and reach the detector that amplifies and counts the ions. Adapted from[58].

I.3.2.2.3. Tandem Mass Spectrometry

Tandem mass spectrometry (MS/MS) is a two-step mass analysis. A first analyser is used to isolate an ion with a specific m/z that is then fragmented and the m/z of the fragment ions (also known as product ions) is determined in a second stage of mass analysis (Figure I.6.). The acquired MS/MS spectrum is thus a record of m/z values and relative intensities of all the resulting fragment ions generated from an isolated precursor ion. It is the information derived from the product ions spectra that allows structure characterization of an analyte[63]. Collision-induced dissociation (CID) is the most common process to fragment ions. The mass-selected ion in the first analyser is transmitted to a high-pressure region (*i.e.* collision cell) where it undergoes a number of collisions with the neutral gas molecules (usually nitrogen or a noble gas) contained in that region. When the ion collides with the gas molecules part of the kinetic energy of the ion is converted into internal energy. It turns into an unstable ion inducing fragmentation reactions and the resulting fragment ions are analysed in the second stage of mass analysis[63].

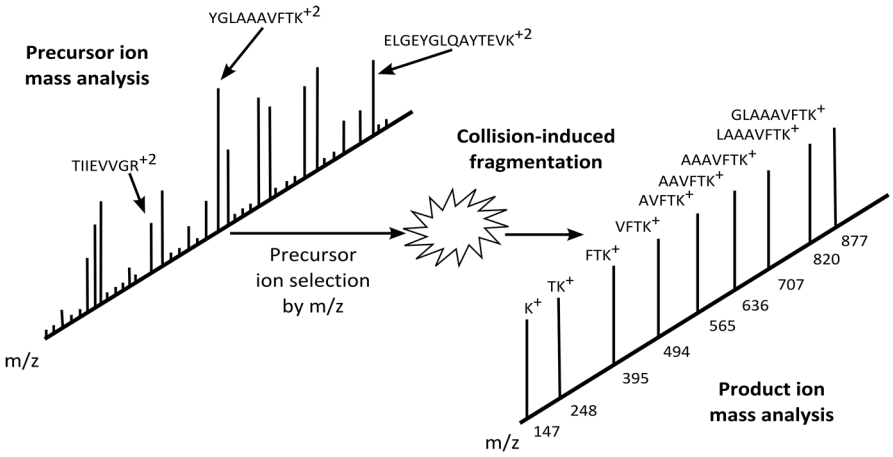

Figure I.6. Tandem mass spectrometry experiment. A precursor ion is selected in the first mass analyser and fragmented by collision with a neutral gas. The fragment ions are analysed in the second stage of mass analysis to produce a product ion spectrum. Adapted from[63].

A QqTOF instrument (Figure I.7.) is widely used in protein identification. The first mass analyser is a quadrupole and the second mass analyser is a TOF. The collision cell is surrounded by lens system so that it is possible for collisions to occur while it contains and transmits ions of all m/z to the second stage of mass analysis. In this type of tandem mass spectrometer both mass and product ion spectra are recorded by the TOF analyser[63].

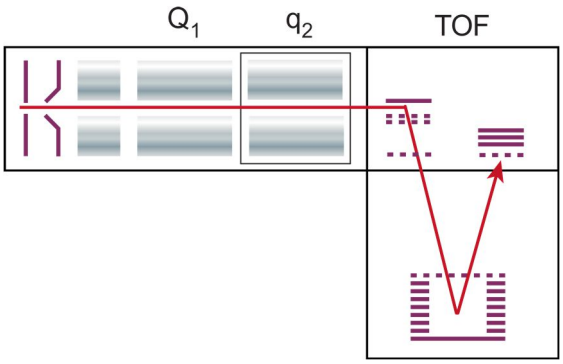

Figure I.7. Schematic representation of a hybrid quadrupole-time-of-flight instrument. Ions of a certain m/z are selected in a first section (Q_1), fragmented in a collision cell (q_2), and the fragments are separated in a reflector TOF. Adapted from[58].

The tandem mass spectrometer can operate in different scan modes. In the standard mode of mass analysis, the first mass analyser and the collision cell transmit all ions that are analysed in the second mass analyser. To determine the amino acid sequence of a peptide a product ion scan is performed: the chosen ion is mass-selected in the first mass analyser and fragmented in the collision cell. The generated ions are scanned in the second mass analyser[63].

I.3.2.2.4. SWATH-MS

As mentioned above, protein quantification by MS can be done either by label or label-free methods[53,59]. In this project, a recently developed method of label-free quantification designated as SWATH (sequential window acquisition of all theoretical fragmentation spectra) was used. This approach requires the use of a fast-scanning, high resolution QqTOF mass spectrometer (TripleTOF 5600^{TM}, AB Sciex®) and combines high specificity of the data-independent acquisition (DIA) method with a novel targeted data extraction strategy[59,68].

SWATH consists in the selection of overlapped sequential precursor ion mass windows of a specific width covering an m/z range (Figure I.8.). The precursor ions selected are then fragmented and the ensemble of these fragment ion spectra as complex fragment ion maps is recorded. The peptides are converted into a high-resolution digital map consisting of fragment ion spectra, which derived from the fragmentation of all precursor ions present in the sample in a determined m/z ratio at a certain time. The use of such scans increases the complexity of the analysis of the acquired data sets, once the link between the fragment ions and the precursors from which they derive is lost[59,68].

The acquired fragment ion maps are queried for the presence and quantity of specific peptides of interest, using *a priori* information contained in reference spectral libraries (*i.e.* the fragment ion signals, their relative intensities, retention time, etc.)[68]. The quantification is based on the peak areas of extracted ion chromatograms (XIC), which are computationally reconstituted from the merged spectra on the basis of both experimental and *in silico* generated spectral information[69].

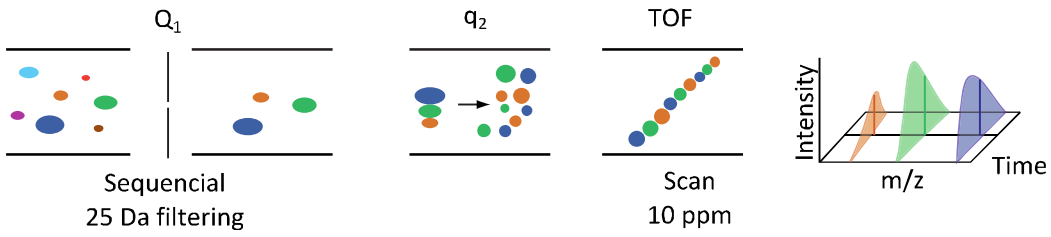

Figure I.8. Schematic representation of SWATH-MS acquisition. In this data-independent acquisition method data are acquired by repeatedly scan through sequential precursor ion mass windows of 25 Da width in a quadrupole mass analyser (Q_1). The selected ions are then fragmented in the collision cell (q_2) and transmitted to the TOF analyser where the fragment ions are measured. The quantification is achieved through the peak areas of XICs of each precursor ion. Adapted from[59].

I.3.3. Bioinformatics

Proteomics studies generate large data sets so manual interpretation of the acquired spectra is not practicable. Thus, it requires the use of software tools that compares experimental spectra with theoretical ones, generated by protein sequences stored in protein databases as well as by *in silico* digestions, to find a match. The software overlaps experimental and theoretical spectra and gives a score based on the similarity of the spectra. This results in a sorted list of the candidate proteins. The score awarded must take into account several features such as dissimilarities in the peak position due to internal or calibration errors, modified amino acids, expected peak intensities, noise, contaminants, missing peaks and others. There are different score schemes used in various algorithms, resulting in different software available to protein assignment (*e.g.* Mascot, SEQUEST, ProteinPilot, etc.), that resort to protein databases (*e.g.* UniProt, NCBI, etc.)[70,71].

Once identified and quantified the altered proteins it is crucial to proceed to their biological interpretation. The Gene Ontology (GO) project provides controlled and structured vocabulary (*i.e.* ontologies) and classifications to describe key domains of molecular and cellular biology that can be used in the annotation of genes, gene products, and sequences. GO classifies gene products according to three categories: i) molecular function, which describes activities that occur at the molecular level (*e.g.* kinase activity); ii) biological process, which describes series of biological events accomplished by one or more organized assemblies of molecular functions (*e.g.* cell proliferation); and iii) cellular component, which describes subcellular locations and macromolecule complexes (*e.g.* nucleus)[72]. GO vocabulary is widely used in enrichment analysis (*i.e.* the identification of GO terms that are significantly over or under represented in a given set of proteins) and there are different tools available to carry out this analysis including, Gene Ontology enRIchment anaLysis and visuaLizAtion tool (GOrilla)[73], GoMiner[74], Database for Annotation Visualization and Integrated Discovery (DAVID)[75], AmiGO[76], etc. Another useful bioinformatic tool for biological interpretation is the Protein Analysis Through Evolutionary Relationships (PANTHER) classification system which provides proteins classification according to their function[77].

I.3.4. Proteomic studies of PBMCs

The search of “peripheral blood mononuclear cells” AND “proteomics” terms on PubMed database turned into 106 results. The majority of the studies are related to different diseases (e.g.

stroke[42], amyotrophic lateral sclerosis[43], and systemic lupus erythematosus[78] among others) and only four aimed to characterise PBMCs' proteome of healthy individuals. One of these studies yielded 174 proteins identified by MS/MS analysis of 246 two-dimension electrophoresis (2-DE) gel spots[79]. Maccarrone *et al.* used a shotgun-MS approach resulting in the identification of about 1090 proteins, but only approximately 685 were identified by at least two non-redundant peptides with maximum false identification rate set to 5%[80]. In the latest study the authors tried different LC-MS/MS analyses with or without strong cation exchange chromatography (SCX) fractionation, reaching a total of 49 different runs, that leaded to the identification of 4129 protein groups[40]. In this article, the authors claim that the stablished method is proper to significantly extend the molecular markers of specific activation states of PBMCs however, it is not compatible with PBC discovery since the amount of protein needed per sample (300 µg) may not be possible to obtain. Moreover, running a sample in 49 different methods drastically increases both the time and the costs of the analysis. Haudek-Prinz *et al.* characterised the proteome signature of inflammatory activated PBMCs by 2D-PAGE or SDS-PAGE followed LC-MS/MS analysis, comprising 1497 proteins[41]. Furthermore, when looking to references of articles from related topics another one was found. In this study the authors identified 1168 proteins, from which 678 were identified by shotgun-MS and 490 by LC-MS/MS preceded by 2-DE[81].

Regarding proteomic studies of PBMCs of schizophrenic patients, 65 results were obtained after searching on PubMed database the terms "peripheral blood mononuclear cells" AND "schizophrenia". Of these, only twelve articles were related to proteins study and three of those studies aimed to uncover the effects of antipsychotic medication on PBMC[82–84]. From the remaining nine, eight of them intended to verify the levels of specific proteins and were based on immunoassays (*e.g.* ELISA, Western blot, and others)[85–92]. In the remaining study a shotgun proteomic approach was used resulting in the identification of 185 cytosolic proteins by LC-MS/MS[93].

It is clear that prior studies of PBMCs proteomic characterisation, from both healthy controls and schizophrenic patients, lack either in the identification of a large set of proteins or in its quantification. This highlights the need for a wider proteomic characterisation of PBMCs proteome. Such improvement would result in a better understanding of the normal physiological protein state of these cells, so it can be later compared to that of different patients, namely patients with SCZ, and thus contribute to a deeper knowledge of the immune impairments in patients with SCZ.

I.4. Flow cytometry

Flow cytometry is a technique that measures optical and fluorescence properties of particles (*e.g.* single cells, nuclei, chromosomes, and other particles that can be suspended in a fluid) flowing in a liquid stream through a beam of light[94,95]. The characteristics measured (*e.g.* relative size, internal complexity, and relative fluorescence intensity) are determined by an optical-to-electronic coupling system that records how the particle scatters incident light (typically from a laser) and emits fluorescence[94]. A flow cytometer (Figure I.10.) is made of four main elements: i) a fluid system to transport particles in a stream to the focused light beam; ii) an optical system that consists of light to illuminate the particles in the sample stream and optical filters to direct the resulting light signals to the appropriate detectors; iii) an electric system to detect light signals and converting it to electronic signals that are proportional to light intensity, and iv) a computer for data recording and analysis[94,96]. Once inside the flow cytometer, the sample is drawn into a stream created by a surrounding sheath fluid that creates laminar flow, allowing the particles in suspension to pass individually through an analysis point. At the analysis point, a beam of monochromatic light intersects the particles that emit light in all directions, and then the light is collected via optics that direct the light to a series of filters and dichroic mirrors that isolate particular wavelength bands. The light signals are detected by photomultiplier tubes and converted to electronic signals that are recorded and analysed in a computer. The resulting data is commonly displayed in univariate histogram or 2D dot-plot formats (to show correlation between two parameters)[94–96].

Blood cells, namely PBMCs, express certain surface proteins that can be used in its immunophenotyping. These proteins are known as cluster of differentiation (CD) and allow distinguishing between different blood cells. This powerful technology has increasingly become the method of choice for the analysis of cellular phenotype and function of the immune system. Typically, in immune phenotyping, antibodies conjugated to fluorescent dyes bind specific proteins on cell surface. As labelled cells pass through the light source, fluorescent molecules are exited and when returning to the stationary state the emitted fluorescence is recorded[95]. The use of multiple fluorochromes (with similar excitation wavelengths and different emission wavelengths) allows several cell properties to be measured simultaneously. This peculiarity permits the characterization of subsets of cells in a complex mixture (*e.g.* blood) in a way that is not possible using bulk assays (*e.g.* Western blot and ELISA)[95,97].

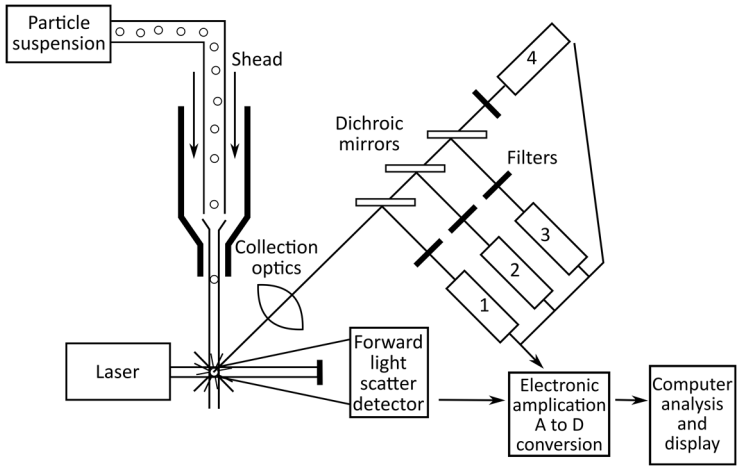

Figure I.10. Schematic representation of a flow cytometer. A particle suspension is hydrodynamically focused with sheath fluid to intersect a laser. Signals are collected by a forward angle light scatter detector, a side-scatter detector (1), and multiple fluorescence emission detectors (2– 4). The signals are amplified and converted to digital form for analysis and display on a computer screen.

II. Objectives

PBMCs correspond to an important part of the immune system that play different and important roles in monitoring immune homeostasis. Therefore, these subset of blood cells may provide access to potential physiological relevant biomolecules, particularly proteins. Moreover they are easily isolated from WB, which in turn can be obtained through a non-invasive method and in large amounts. For this reason, PBMCs represent a promising biological sample in scientific research, namely as a source of PBC discovery of the most diverse diseases.

Prior studies of proteomic characterization of PBMCs from healthy individuals lack either the identification of a large set of proteins or the quantification of those proteins in a way that is compatible with the seach of PBCs. Thus, the aim of this master's thesis project is to provide a comprehensive proteome characterisation of PBMCs contributing to improve the existing databases and the creation of a SWATH library. In addition, it will be assessed if there is an enrichment of immune system proteins in isolated PBMCs comparing to plasma, and it is also suggested the analysis of the main PBMCs subpopulations by flow cytometry to supplement the biological information obtained by the proteomic screening.

In order to achieve it, the following tasks are proposed: i) comparing PBMCs and plasma proteomes, ii) identifying PBMCs proteins by LC-MS/MS and creating a SWATH library, and iii) analysing PBMCs subpopulations by flow cytometry.

III. Methods & Materials

III.1. Samples collection and processing

III.1.1. Samples for the enrichment test

To evaluate if there is an enrichment of immune system proteins in isolated PBMCs three different samples were analysed: PBMCs, plasma depleted from PBMCs, and plasma still with PBMCs (P+C). Blood from healthy volunteers was collected into 8 ml Vacutainer® CPT™ (BD) containing sodium citrate as anticoagulant and the CPTs were processed according to the manufacturer's instructions. After blood drawing and gently inversion of the CPTs, the tubes were centrifuged at 1650×g for 30 minutes (Centrifuge 5810 R, Eppendorf) at RT within two hours of blood collection. CPTs were gently inverted and the mixture of PBMCs and plasma was transferred into a centrifuge tube (VWR). From the mixture of PBMCs with plasma 500 µL were collected into a microcentrifuge tube (Eppendorf) and precipitated with trichloroacetic acid (TCA) (P+C samples). The remaining mixture was centrifuged at 1650×g for 30 minutes (Centrifuge 5810 R, Eppendorf) at RT. The supernatant was collected and proteins were precipitated with TCA (plasma samples). The cell pellet (PBMCs samples) was washed with PBS and centrifuge at 300×g for 5 minutes (the process was repeated). All samples were resuspended in Laemmli Sample Buffer (Bio-Rad).

Protein concentration was determined using the 2-D Quant Kit (GE Healthcare). The assay was performed according to the manufacturer protocol using bovine serum albumin (BSA) as a standard.

III.1.2. Samples for qualitative and quantitative analysis

Blood from healthy volunteers was collected into 8 ml Vacutainer® CPT™ (BD) containing sodium citrate as anticoagulant and the CPTs were processed according to the manufacturer's instructions. After blood drawing and gently inversion of the CPTs, the tubes were centrifuged at 1650×g for 30 minutes (Centrifuge 5810 R, Eppendorf) at RT within two hours of blood collection. PBMCs were collected from the processed CPT by drawing off PBMCs layer with a pipette. Lastly, the PBMCs were washed with PBS and centrifuge at 300×g for 5 minutes (the process was repeated), precipitated with methanol (VWR) and the pellet was resuspended in Laemmli Sample Buffer (Bio-Rad) and sonicated on a SONICS Vibracell 130 W using a 2 mm probe at 20% of amplitude for 30 seconds (1 second on 1 second off cycle). Protein concentration was determined as described above.

III.2. Samples preparation for LC-MS/MS

For the library identification (IDA acquisition) 20 µg of protein of each biological replicate of every single sample (PBMCs, P+C and plasma), were pooled together, and for the SWATH analysis 100 µg of each sample was used (2.1 µg of GFP was added all to samples). All samples were denatured with Laemmli Sample Buffer (Bio-Rad) and boiled at 95˚C during 5 min followed by addition of 2 µL of acrylamide [40% acrylamide/bis solution (Bio-Rad)] per 30 µL of sample to alkylate cysteine residues. The samples were loaded in a 4-20% Mini-PROTEAN® TGX™ Precast Gel (Bio-Rad) and electrophoretically resolved at 110 V for 15 min using a Mini-PROTEAN® Tetra Electrophoresis System (Bio-Rad).

Proteins were visualised with Colloidal Coomassie Brilliant Blue G-250 (Bio-Rad) staining. Shortly, the gel was rinsed with double deionized water (ddH_2O) and immersed in the staining solution [10% (v/v) of an 80% solution of phosphoric acid, 10% (w/v) ammonium sulphate, 20% (v/v) methanol] to which Coomassie was added[98].

Each gel lane was sliced into 9 bands of equal size using a disposable GridCutter (2 mm × 7 mm lanes, 25 rows, 1 column). The bands of each lane were grouped three by three, sliced into smaller pieces, and transferred to microcentrifuge tubes with 1 mL of ultrapure water (VWR) to prevent band pieces to dry. The gel pieces were destained with a destaining solution (50 mM ammonium bicarbonate, 30% acetonitrile (ACN)) by shaking in a thermomixer (Comfort, Eppendorf) at 850 rpm for 15 min at 25˚C. This step was repeated until no Coomassie staining was observed and then the gel pieces were washed with ddH_2O in a thermomixer at 850 rpm for 15 min at 25˚C. After water removal, the gel pieces were dehydrated on a Concentrator Plus (Eppendorf) at 60˚C for 1 hour. A trypsin (Roche) solution (0.01 mg/mL in 10 mM ammonium bicarbonate) was added to each tube until all dried pieces were covered and left for 15 min, on ice, to rehydrate the gel pieces. After this period 20 µL of 10 mM ammonium bicarbonate were added and in-gel digestion was performed in the dark, overnight at RT. After the digestion, the tryptic solution from gel pieces was collected to low binding microcentrifuge tubes (LoBind®, Eppendorf). The peptides were extracted from gel pieces by sequential addition of solutions with an increase concentration of ACN (30%, 50%, and 98%, respectively) in 1% FA. After the addition of each solution, the tubes were shaken in the thermomixer (Comfort, Eppendorf) at 1050 rpm for 15 min and the solution was collected to the tube containing the previous fraction. At this stage, peptides extracted from different bands were pooled together into one peptide mixture per sample, whereas peptides from pool samples were kept separated. The peptide mixtures were concentrated on the Concentrator

Plus (Eppendorf) at 60˚C. Peptides were resuspended to a final volume of 100 µL in a solution of 2% ACN and 1% FA, and sonicated on a SONICS Vibracell 750 W using a cup-horn at 20% of amplitude for 2 min (1 second on 1 second off cycle).

The extracted peptides were desalted using C18 Bond Elut OMIX solid phase extraction pipette tips (Agilent technology). Briefly, the tip column was hydrated with 200 µL of 50% ACN and equilibrated with 300 µL of 2% ACN with 1% FA. The peptides were loaded into the column five times followed a wash step with 100 µL of 2% ACN with 1% FA (the washed is saved until LC-MS/MS analysis of the peptides). Peptides were then eluted to a low binding microcentrifuge tubes (LoBind®, Eppendorf) with 400 µL of 70% ACN and 0.1% FA and the eluates were concentrated using the Concentrator Plus (Eppendorf) at 60°C. The peptide mixtures were resuspended to 30 µL in a solution of 2% ACN and 0.1% FA, spiked with iRTs peptides (Biognosys AG), and sonicated on a SONICS Vibracell 750 W using a cup-horn at 20% of amplitude for 2 min (1 second on 1 second off cycle). After centrifugation at 14,000×g for 5 minutes (MiniSpin® plus, Eppendorf) the supernatants were transferred into vials for posterior LC-MS/MS analysis.

III.3. LC-MS/MS data acquisition

Tryptic peptides were analysed on a TripleTOF 5600™ mass spectrometer (AB Sciex®) in two different acquisition modes: IDA and SWATH. Peptides (from the enrichment test's samples and for the SWATH analysis) were analysed by LC-MS/MS both in IDA and SWATH acquisition modes.

The peptide mixtures were separated by LC (NanoLC Ultra 2D, Eksigent) on a ChromXP™ C18 reverse phase column (300 µm ID × 15 cm length, 3 µm particles, 120 Å pore size, Eksigent) at 5 µL/min with a linear gradient of 2% to 30% ACN in 0.1% FA for 45 min. Peptides were eluted into the mass spectrometer using an ESI source (DuoSpray™ Source, AB Sciex®) in positive mode.

IDA experiments were performed for each fraction (10 µL) to create the identification library. The mass spectrometer was set for IDA scanning full spectra (350-1250 m/z) for 25 ms, followed by up to 20 MS/MS scans (100-1500 m/z for 100 ms each). Candidate ions with a charge state between +2 and +5 and counts above a minimum threshold of 70 counts per second were isolated for fragmentation and one MS/MS spectrum was collected before adding those ions to the exclusion list for 20 seconds (mass spectrometer operated by Analyst® TF 1.6, AB Sciex®). Rolling collision energy was used with a collision energy spread of five. For the exclusion analysis, an

exclusion list (EL) with previous identified peptides was created and LC-MS/MS analysis was performed as described above excluding those peptides in the new acquisition.

Ten µL of each sample were used for quantitative analysis by acquisition in SWATH mode. The SWATH setup was essentially as in Gillet *et al.*[68], with the same chromatographic conditions used as in the IDA analysis described above. For SWATH-MS–based experiments, the mass spectrometer was operated in a looped product ion mode. The instrument was specifically tuned to allow a quadrupole resolution of 25 m/z mass selection. Using an isolation width of 26 m/z (containing 1 m/z for the window overlap), a set of 30 overlapping windows was constructed covering the precursor mass range of 350–1100 m/z. A 50 ms survey scan (350-1250 m/z) was acquired at the beginning of each cycle for instrument calibration and SWATH MS/MS spectra were collected from 100–1500 m/z for 100 ms resulting in a cycle time of 3.25 sec from the precursors ranging from 350 to 1100 m/z. The collision energy for each window was determined according to the calculation for a charge 2+ ion centred upon the window with a collision energy spread of 15.

III.4. Sample preparation for 2D LC-MS/MS

For 2D LC-MS/MS analysis, samples were prepared as described in III.2. with minor modifications: 300 µg of protein was used for library identification (IDA acquisition), and after peptide extraction and concentration on a Concentrator Plus (Eppendorf) at 60˚C , they were resuspended to a final volume of 90 µL in 72 mM TEAB for posterior 2D-LC-MS/MS analysis.

III.5. 2D LC-MS/MS data acquisition

Peptides were analysed by 2D LC-MS/MS, with a high pH RPC as first dimension and then analyzed by LC-MS as described above. The first dimension chromatography was performed in Ultimate™ 3000 LC, LC packing, Dionex with a C18 Acclaim® Polar Advantage II column (2.1 × 150 mm length, 3 µm particles, 120 Å pore size, Dionex), using 72 mM TEAB pH 8.5 as mobile phase A and 72 mM TEAB in ACN pH 8.5 as mobile phase B at 150 µL/min. The peptides were fractionated by a multistep gradient: 0-32 min linear gradient to 45% B, 32-34 min linear gradient from 45% to 100% B, 34-40 100% B, 40-41 min linear gradient from 100% to 0% B, and 41-45 min 0% B.

The 28 collected fractions throughout the chromatographic run were joined into 8 samples (Figure IV.10.), evaporated, resuspended to 30 µL in a solution of 2% ACN and 0.1% FA, spiked with iRTs peptides (Biognosys AG), and sonicated on a SONICS Vibracell 750 W using a cup-horn at 20% of amplitude for 2 min (1 second on 1 second off cycle). After centrifugation at 14,000×g for 5 minutes (MiniSpin® plus, Eppendorf) the supernatants were transferred into vials for posterior LC-MS/MS analysis, as described above.

III.6. Protein identification and library generation

Protein identification for each IDA method was obtained using ProteinPilot™ software (v5, AB Sciex®) with the following search parameters: search against *homo sapiens* from SwissProt database (last update in May 2015); trypsin digestion; acrylamide as cysteine alkylating reagent; special focus option for gel based, thorough ID search effort, and 0.05 unused ProtScore (10% confidence score) as detected protein threshold. Data analysis was based on an independent False Discovery Rate (FDR) analysis using the target-decoy approach. Positive identifications were considered when proteins present 95% confidence (5% local FDR) with more than one peptide hit with individual confidence above 95%. When a protein was identified with a single peptide, an Unused above 1.3 was considered as positive identification or the peptide has to present an individual confidence above 95% and a minimum sequence tag of 3 amino acids (4 consecutive peaks in the MS/MS spectrum). The reverse proteins and peptides, as well as, the peptides with zero contribution were removed.

A specific library of precursor masses and fragment ions was created combining all files from IDA experiments and used for subsequent SWATH processing. The library was obtained using ProteinPilot™ software (v5, AB Sciex®) with similar parameters as above, but including GFP protein and iRTs peptides in the database.

III.7. SWATH data file processing

Prior to data processing, peptides were selected automatically from the library using the following criteria: (i) the unique peptides for a specific targeted protein were ranked by the intensity of the precursor ion from the IDA analysis as estimated by the ProteinPilot™ software, and (ii)

peptides that contained biological modifications and/or were shared between different protein entries/isoforms were excluded from selection. Up to 15 peptides were chosen per protein, and SWATH quantitation was attempted for all proteins in library files that were identified below 1% global FDR from ProteinPilot™ search. In SWATH™ acquisition data, peptides are confirmed by finding and scoring peak groups, which are a set of fragment ions for the peptide.

Up to 5 target fragment ions were automatically selected following the criteria described in Lambert *et al.*[99]: (i) fragment ions for a selected peptide were ranked according to ion intensity; (ii) ions higher in m/z than the y4 fragment ion for each selected peptide were ranked highest; (iii) ions within the SWATH isolation window were excluded from selection; (iv) if insufficient target ions were found, ions lower than y4 but outside of the SWATH window were chosen; and (v) if there were still insufficient ions, then fragment ions from within the SWATH window region were chosen.

Peak groups were scored following the criteria described in Lambert *et al.*[99], briefly, each target fragment ion was scored based on the retention time adjustment, peak width overlap, peak intensity ratio, correct isotopic state, m/z error and MS/MS score. The individual peak group scores were combination of all subscores (scores from fragment ions) and the peak group with the best score was taken forward. Peak group confidence threshold was determined based on a FDR analysis using the target-decoy approach and 1% extraction FDR threshold was used for all the analyses. Peptide features (i.e. peptides in a given charge state) that met the 1% FDR threshold in all the replicates were retained, and the peak areas of the target fragment ions of those peptides were extracted across the experiment using a extracted-ion chromatogram (XIC) window of 5 min with a 0.02 Da width.

Protein levels were estimated by summing all the transitions from all the peptides for a given protein (adapted from[100]). The protein levels were normalized for the most stable internal standards spiked into the samples.

III.8. Bioinformatics

The BioVenn diagram tool[101] (http://www.cmbi.ru.nl/cdd/biovenn/) from Centre for Molecular and Biomolecular Informatics was used to compare the number of proteins that are shared or unique between different samples. The lists containing the proteins from the desired samples to be compared were uploaded and the tool generates area-proportional Venn diagrams of the inserted proteins and a text file containing the accession numbers of the analysed proteins

as well as the distribution of these proteins within the different samples. As this software only analyse a maximum of three data sets at the same time, VENNTURE tool[102] (http://www.irp.nia.nih.gov/branches/lci/nia_bioinformatics_software.html) was used to obtain a Venn diagram of six datasets. This software provides the distribution of the proteins within the different samples, as well as non-proportional Venn diagram.

PANTHER Classification System[77] (http://www.pantherdb.org/tools/) was performed for the lists of identified and quantified proteins. This tool creates map lists of cellular component, biological process, and molecular function ontologies. All the analyses were done for *Homo sapiens*, and the results were viewed as pie charts.

To compare the quantified proteins with an immune system process GO term among the three different samples (PBMCs, P+C and plasma) a heat map with standardized values was generated by the Graphical Proteomics Data Explorer (GProX) tool version 1.1.15[103].

In order to visualise in which metabolic pathways the identified proteins are involved in, the KEGG database[104,105] (http://www.genome.jp/kegg/tool/map_pathway2.html) was used. This displays metabolic pathway maps where the proteins play roles in and highlight the uploaded proteins.

III.9. Multivariate analysis

The principal components analysis (PCA) was performed in the MarkerView™ software (version 1.2.1, AB Sciex) without weighting and using Pareto as the scaling method.

III.10. Flow cytometric data acquisition and analysis

In flow cytometric analysis both PBMCs and WB samples were used. WB samples were collected from healthy volunteers into 2 ml Vacutainer® Blood Collection Tube (BD) containing K_2EDTA as anticoagulant and tubes were inverted to ensure mixing of anticoagulant with blood to prevent clotting. PBMCs were isolated and washed as described in section III.2. The cell pellet was then resuspended in 1 mL PBS and cells were counted on a COULTER® Ac·T diff2™ (Beckman Coulter).

The distribution of PBMCs and WB subsets was evaluated using the following combination of monoclonal antibodies: anti-HLA-DR-FITC (clone Immu-357), anti-CD45-KO (clone J.33), anti-CD56-Pc7 (clone N901 (NKH-1)), anti-CD123-PE (clone SSDCLY107D2), anti-CD8-APC (clone B9.11), anti-CD33-APC (clone D3HL60.251) from Beckman Coulter; anti-CD3-PerCP-Cy5.5 (clone SK7), and anti-CD14-APCH7 (clone MϕP9) from BD Biosciences; anti-CD20-PB (clone 2H7) from BioLegend; and anti-CD4-PB (clone RPA-T4) from BD Pharmingen.

For staining purposes, samples were incubated for 15 minutes in the dark at room temperature in the presence of the above-mentioned monoclonal antibodies. Then, 2 ml of FACS lysing solution (BD) diluted 1/10 (v/v) in distilled water was added and after gentle vortex, samples were incubated for another 15 minutes under the same conditions as those mentioned above to lyse the non-nucleated red cells. After that, cells were centrifuged for 5 min at 430×g (in WB samples this step was repeated) and the cell pellet was resuspended in 250 µl of PBS. Data acquisition was performed in a FACSCanto™II flow cytometer (BD) and data was analysed using the software Infinicyt™ (v1.6, Cytonos SL, Salamanca, Spain).

IV. Results & Discussion

IV.1.Enrichment test

Plasma is perhaps the most studied sample for PBCs discovery[37]. However, due to the wide dynamic range in abundance of plasma proteins, its proteome is very difficult to characterize without a previous depletion step of the most abundant proteins[38]. PBMCs represent a significant part of the immune system, providing access to potential physiological relevant proteins[40,41], thus representing an alternative to plasma samples as valuable source of PBC of the most diverse illnesses[42–45].

The first part of this master thesis project intended to verify if there is an enrichment of immune system proteins in isolated PBMCs comparing to plasma samples using BD Vacutainer® CPT™ for this purpose. Thereby, three different samples were analysed by LC-MS/MS: isolated PBMCs, plasma depleted from PBMCs (plasma samples) and plasma still with PBMCs (P+C samples). Blood was collected from four healthy individuals (Supplementary Table VII.1.) and the samples were processed as described in section III.1.1. For library creation of each sample, the four biological samples were pooled together and protein identification was performed by LC-MS/MS (sections III.3. and III.6.).

IV.1.1. Protein identification

As expected, the number of proteins identified in each sample was very different (Figure IV.1.). In PBMCs samples it was possible to identify 671 proteins while in P+C and plasma samples only 115 and 143 proteins were identified, respectively. At least 74% of the proteins were identified with at least two peptides with a confidence of 95% (496, 100, and 106 in PBMCs, P+C and plasma samples, respectively). It is clear that the isolation step of PBMCs resulted in a decrease of highly abundant proteins present in plasma and consequently in the identification of a higher number of proteins. The low number of identified proteins in plasma and P+C samples (143 and 115, respectively) is due to the lack of a depletion step of the most abundant proteins, making it nearly impossible to identify proteins present in low concentrations.

The comparison between the three different samples using a Venn diagram (Figure IV.2.) revealed that from the 761 proteins identified only 53 were shared by all samples. Six hundred proteins were found to be unique of PBMCs, 34 of plasma and 12 of P+C samples. The higher number of unique proteins in PBMCs is undoubtedly a result of the increased number of proteins identified in this sample by LC-MS/MS.

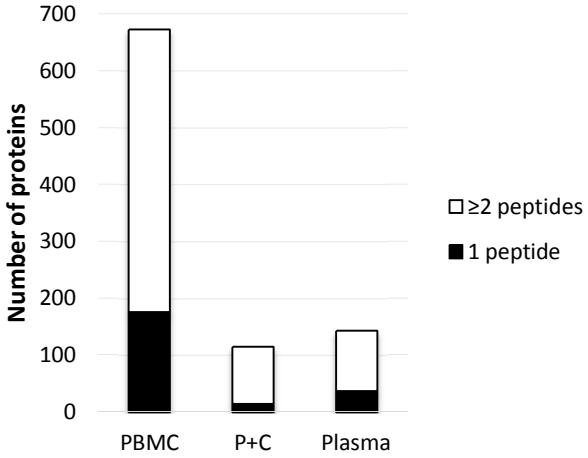

Figure IV.1. Number of proteins identified in PBMCs, P+C and plasma samples by LC-MS/MS. Bar chart of the identified proteins in each sample with at least two peptides (white) and with one peptide (black).

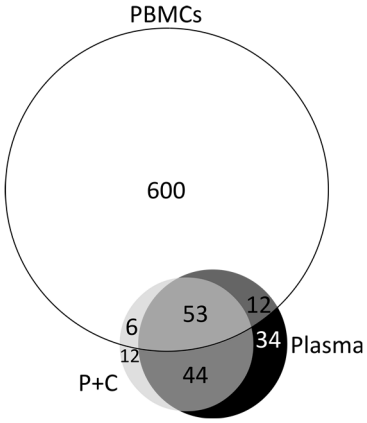

Figure IV.2. Venn diagram illustrating the number of shared and unique confidently identified proteins in each sample. The total number of proteins identified was 761 with only 53 being common to all samples.

Proteins coming from plasma and platelets (*e.g.* albumin and platelet glycoprotein 4) were identified in PBMCs samples, probably due to their adherence to lymphocytes surface during the isolation or their collection along with the buffy coat[79,106].

IV.1.2. GO analysis

For the biological interpretation of the identified proteins, a GO analysis was performed using the PANTHER tool to visualise proteins according to their cellular component, biological process, and molecular function (section III.8.).

Regarding the cellular component of the identified proteins (Figure IV.3.) in PBMCs it is possible to see that P+C and plasma the more expressive cellular component is extracellular region (48% and 52%, respectively). The low representation of membrane proteins (7.2%, 4.5%, and 2.9% in PBMCs, P+C, and plasma samples, respectively) is most likely because their isolation requires adequate protocols to their hydrophobicity, basic pH, and low abundance[67].

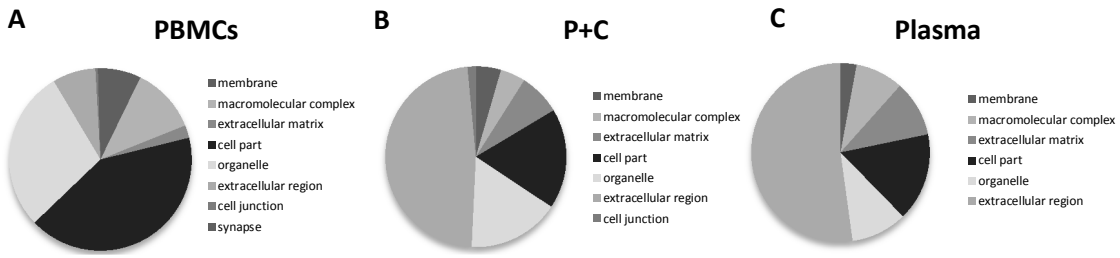

Figure IV.3. Pie charts illustrating the cellular component of the proteins identified in the three different samples: (A) PBMCs, (B) plasma with PBMCs and (C) plasma depleted from PBMCs.

When looking to the biological processes where the identified proteins are involved in (Figure IV.4.), it is clear that all samples comprise proteins that take part in very general processes such as cellular process, apoptotic process, and biological regulation, with metabolic processes being the most represented in the three samples. Proteins involved in immune system processes represent 4.4%, 8.7%, and 10.3% in PBMCs, P+C and plasma, respectively. However, in absolute numbers there are more immune system-related proteins in PBMCs (59) than in P+C and plasma samples (25 and 35, respectively) (Figure IV.5. and Supplementary Tables VII.2, 3, and 4). That is, PBMCs provide access to more immune-relevant proteins than plasma do.

The molecular functions of the identified proteins can be seen in figure IV.6. The first thing that stands out is that PBMCs proteins are involved in more molecular functions than P+C and plasma ones. This may be a consequence of the higher number of identified proteins in PBMCs samples but on the other hand, it shows that isolated PBMCs provide access to a more diverse set of proteins, comparing to plasma and P+C samples without a previous depletion step. However, in all samples catalytic activity is the most represented molecular function.

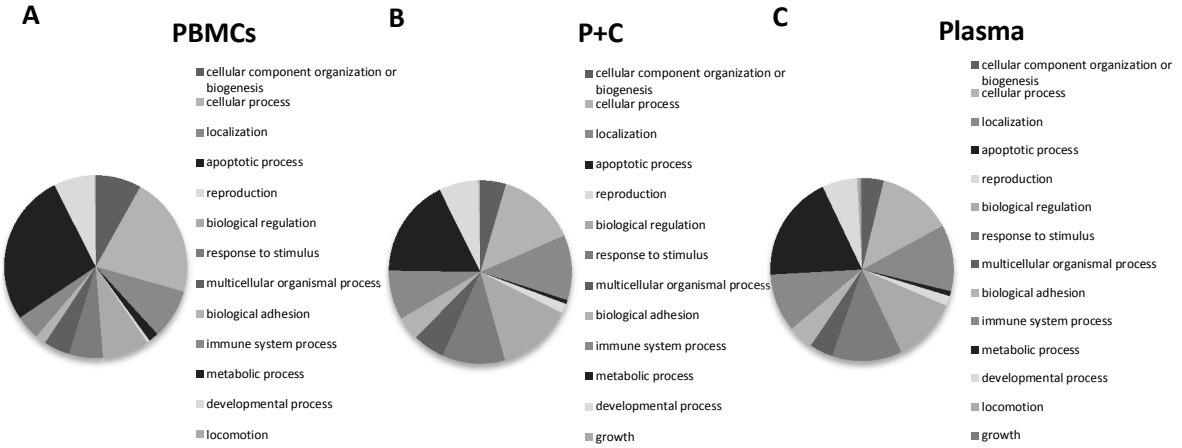

Figure IV.4. Pie charts illustrating the biological process of the proteins identified in the three different samples: (A) PBMCs, (B) plasma with PBMCs and (C) plasma depleted from PBMCs.

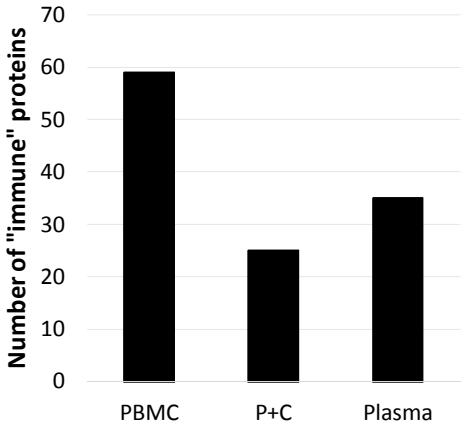

Figure IV.5. Number of identified proteins with an "immune system" GO term assigned in PBMCs, P+C and plasma samples.

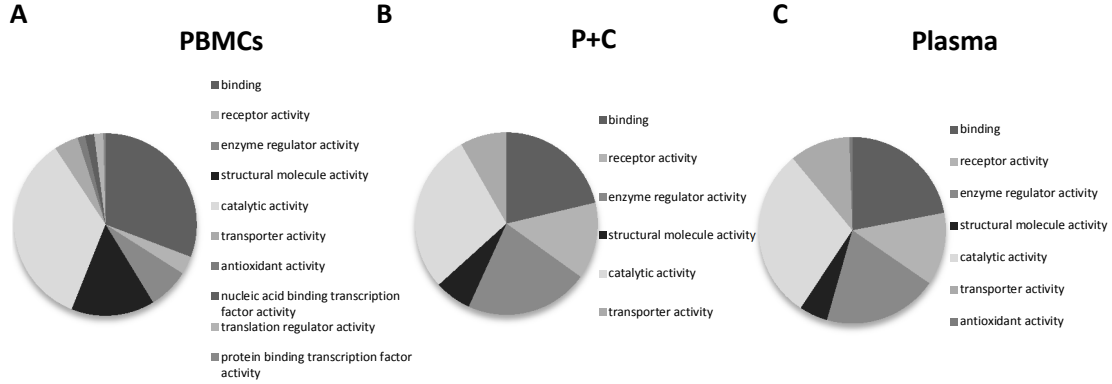

Figure IV.6. Pie charts illustrating the molecular functions of the proteins identified in the three different samples: (A) PBMCs, (B) plasma with PBMCs and (C) plasma depleted from PBMCs.

Regarding the three GO classifications (cellular component, biological process and molecular function), it is possible to observe that the pie charts of P+C and plasma samples are almost indistinguishable, which was already expected considering that at least 68% of the identified proteins in these two samples is shared between them (Figure IV.2.). This possibly occurs because P+C samples still contain the high amounts of the most abundant proteins present in plasma therefore it is less likely to identify PBMCs-related proteins, probably because high abundant plasmatic proteins masked them.

IV.1.3. SWATH analysis

To verify the quantitative distribution of immune-related proteins among the three samples a SWATH analysis was performed. Briefly, this analysis generates a complete recording of the fragment ion spectra of all analytes in a sample within a determined m/z window, and then acquired data from XICs of each peptide is used to determine the relative quantity of a given protein.

Since the aim of this quantitative analysis was to understand if proteins involved in the immune system are present in higher amounts in PBMCs samples, a GO analysis of biological processes was performed and only proteins with a GO term of “immune system” assigned were considered in the following results (42 out of the 363 quantified proteins).

By the analysis of SWATH files in PeakView® it is possible to see that XICs intensity of a given albumin peptide (Figure IV.7. A) is higher in P+C and plasma samples than in PBMCs samples. On the other hand, XICs intensities of a given peptide of C-C motif chemokine 5 and MHC class I antigen B 55 (proteins involved in immune system) (Figures IV.7. B and C, respectively) are increased in PBMCs samples. After normalisation of protein levels to total intensity (Figure IV.8.) the relative intensity of these two proteins in PBMCs samples is higher than in the two other samples. In contrast, albumin (the most abundant plasma protein) intensity is decreased in PBMCs and it almost quadruples in plasma and P+C samples. Meaning that PBMCs isolation resulted in a decrease of albumin and in an increase of MHC class I antigen and C-C motif chemokine 5. However, comparing to MHC class I antigen and C-C motif chemokine 5, the relative intensity of albumin in PBMCs samples is 36 and 500 times higher, respectively.

When looking to all proteins with an “immune system” GO term assigned (Supplementary Table VII.5.), it is possible to verify that the majority of the immune system-related quantified proteins are present in higher amounts in PBMCs samples than in the P+C and plasma samples (Figure IV.9.). Meaning that in PBMCs samples there is an enrichment of immune-related proteins.

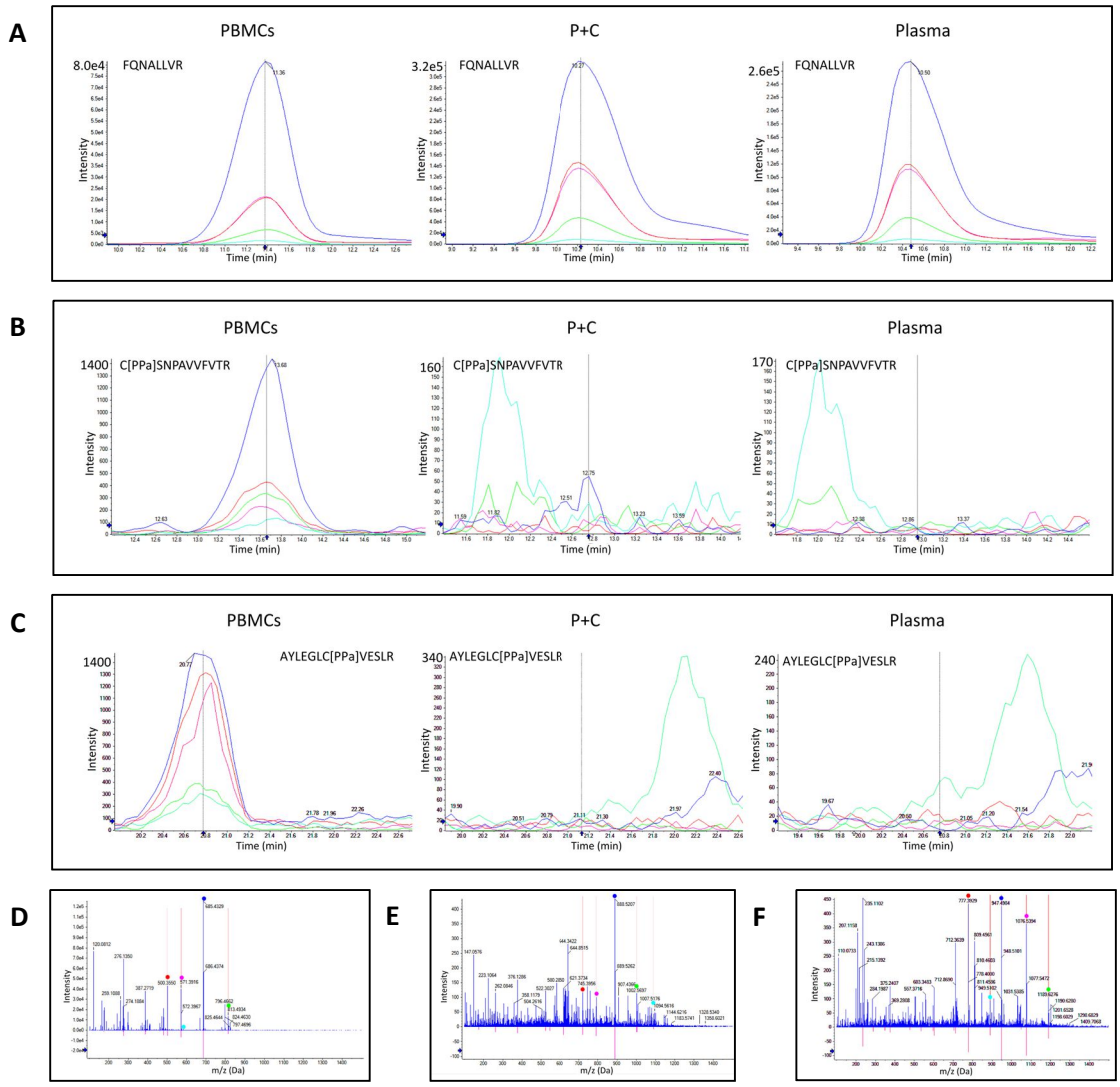

Figure IV.7. Peptide profile of albumin, C-C motif chemokine 5, and MHC class I antigen B55 among the three different samples. Peak groups (XICs of a chosen peptide) of (A) albumin, (B) C-C motif chemokine 5 and (C) MHC class I antigen B 55 peptides previously identified in IDA experiments of each sample**.** For each peak group it is presented the MS/MS fragmentation spectrum of the identified peptides of (D) albumin, (E) C-C motif chemokine 5 and (F) MHC class I antigen B 55. The transitions used are indicated with coloured balls according with its respective extracted ion trace colour.

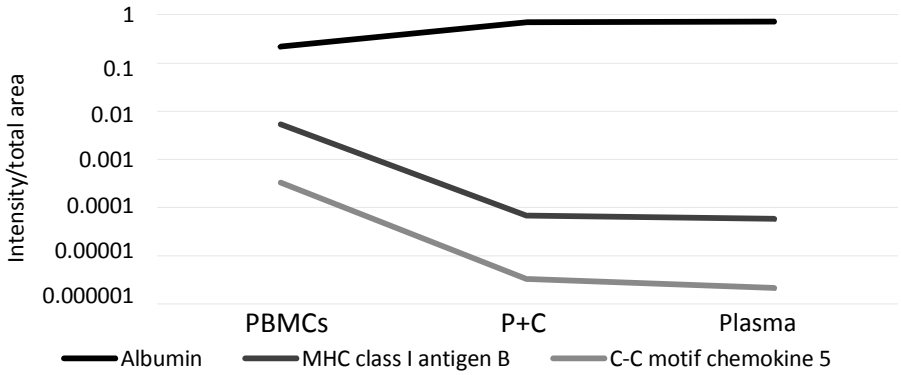

Figure IV.8. Relative intensity of albumin, MHC class I antigen B 55 and C-C motif chemokine 5 in PBMCs, P+C and plasma samples. The summed intensity of each protein was normalised to the total intensity. The vertical axis is shown in logarithmic scale.

Figure IV.9. Heat map analysis of quantified proteins involved in immune system processes. Heat map generated from SWATH data comparing the immune system-related proteins among the three different samples.

IV.2. 1D LC-MS/MS vs. 2D LC-MS/MS

In proteomic analysis of complex peptide mixtures, such as the ones that result from tryptic digestion of mammalian samples, it is difficult to obtain a good proteome coverage by 1D LC-MS/MS[66]. Therefore, it becomes necessary to adopt multidimensional separation approaches to increase peptide separation, its identification, and consequently protein identification[66]. Several approaches can be used to increase 2D LC-MS/MS orthogonality and thus improve the number of identified proteins however, RPC at high pH coupled with RPC at low pH has proved to perform better than other 2D-LC combinations (*e.g.* SCX with pH gradient followed by RPC at low pH)[67].

Thus, after the enrichment test assay, the next step was to try to increase the number of identified proteins by different LC-MS/MS approaches: 1D LC-MS/MS, 1D LC-MS/MS with exclusion list (EL) (*i.e.* excluding previous identified peptides) and 2D LC-MS/MS (sections III.3. and III.4.). The approach that results in more identifications will be use in subsequent qualitative analysis of PBMCs proteins as well as in SWATH library creation.

IV.2.1. Protein identification

One dimensional LC-MS/MS analysis resulted in the identification of 6021 peptides with a confidence of 95% and 1067 proteins (Figure IV.10.). Out of the 1067 proteins, 787 (73.8%) were identified with at least two peptides. Comparing to the number of PBMCs' proteins identified in the enrichment test (671) (section IV.1.2), this analysis yielded more identifications. As the acquisition parameters were the same it was not expected such increase in the number of identifications however, in this test, PBMCs proteins were precipitated with methanol before solubilisation with Laemmli Sample Buffer, which clearly resulted in improvement of protein solubilisation and identification.

In EL analysis peptides identified in previous 1D LC-MS/MS analysis were excluded from data acquisition, resulting in the identification of 2144 and 665 peptides and proteins, respectively. After searching 1D LC-MS/MS and EL analyses together, a total of 6609 peptides with a confidence of 95% were identified corresponding to 1160 proteins (Figure IV.10). Although EL analysis increased the number of identified proteins in 8.7%, the percentage of those identified with at least two peptides remains the same.

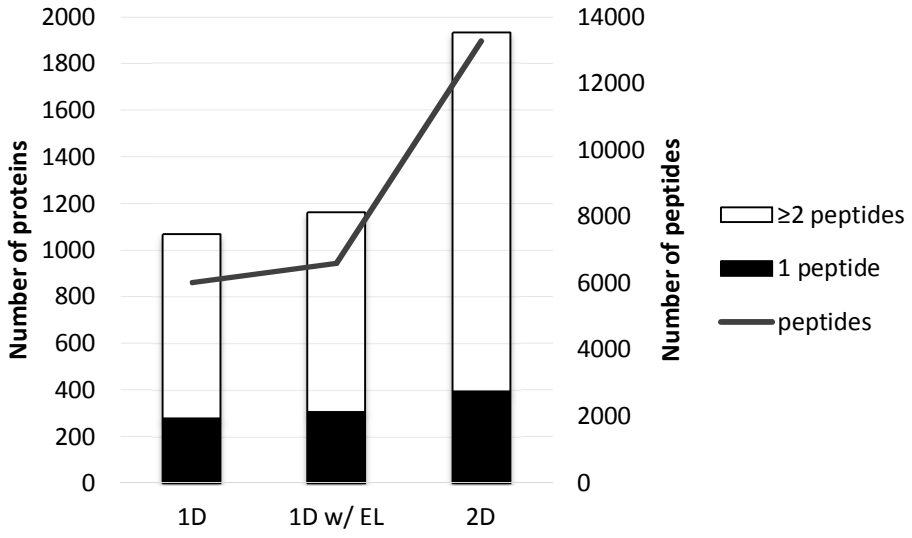

Figure IV.10. Number of peptides and proteins identified by 1D LC-MS/MS (1D), 1D LC-MS/MS with EL (1D w/ EL) and 2D LC-MS/MS (2D) approaches. Bar chart of the identified proteins by the three different approaches with at least two peptides (white) and with one peptide (black). The line chart shows the number of the identified peptides.

In 2D LC-MS/MS analysis, peptides were resolved by RPC at high pH in the first LC dimension throughout which 28 fractions were collected and joined into eight final fractions (F1 to F8) as

shown in figure IV.11. Fractions 1 and 28 were kept separated since as it is possibly to see in the chromatogram, the number of peptides being eluted in time ranges 0-9 min and 35-45 min, respectively, is low. The peptides from final fraction pools were then separated by RPC at low pH and identified by MS/MS. For each fraction, m/z of all identified peptides was plotted against retention time so it can be confirmed the orthogonality of this 2D-LC approach. In F2 to F8, five or four fractions collected with a 6-minute difference were joined, and it can be seen that there are peptides being identified along the entire second LC dimension run, meaning that co-eluted peptides in first LC dimension are resolved in second LC dimension. With the exception of F1, F4 and F8 where 15, 1763 and 963 peptides were identified, respectively, in all fractions more than 3000 peptides were identified.

This approach resulted in the identification of 13281 peptides with a confidence of 95% corresponding to 1929 identified proteins, of which 1534 were identified with at least two peptides (79.5%) (Figure IV.10). Therefore, in 2D-LC, there was a 66.3% increase of the identified proteins and a 79.6% increase of the proteins identified with at least two peptides with 95% of confidence, comparing to 1D-LC approach (1D LC-MS/MS combined with EL analysis). Nevertheless, there are peptides (1014) and proteins (18) only identified in 1D-LC samples (Figure IV.12.).

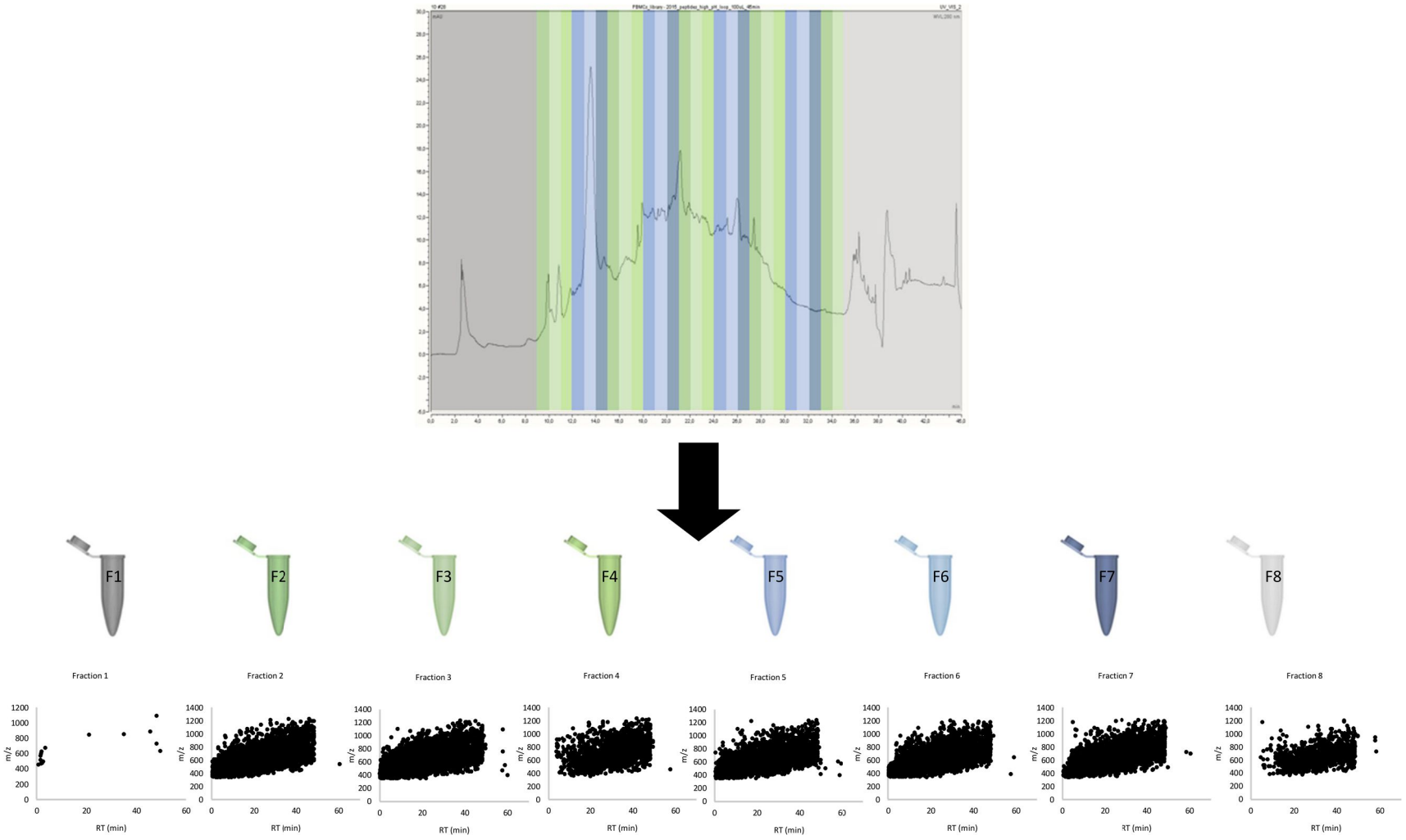

Figure IV.11. Schematic representation of the 2D LC-MS/MS analysis. Throughout the first LC dimension, 28 fractions were collected (colour bars over the chromatogram). The fractions represented in grey (1 and 28) were kept separated, whereas fractions of the same colour shade (2 to 27) were joined for subsequent LC-MS/MS analysis. For each fraction, m/z of all identified peptides was plotted against retention time.

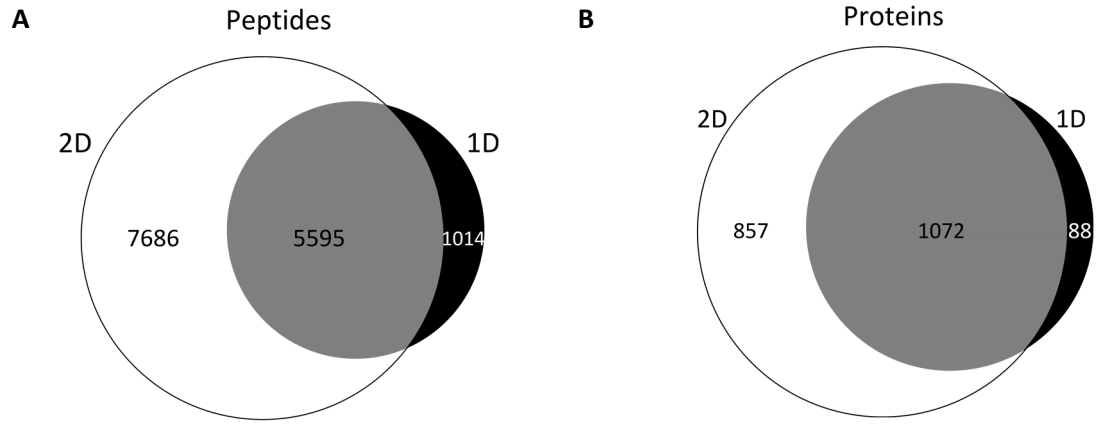

Figure IV.12. Venn diagrams illustrating the number of shared and unique (A) peptides and (B) proteins identified by MS/MS preceded by 1D or 2D-LC fractionation.

In addition, looking to the 1072 common proteins identified by the two approaches, those identified by 2D LC-MS/MS show an increased coverage (with 95% of confidence) of their sequence (Figure IV.13), as a result of the increase in the number of identified peptides. Thus, this approach outperform 1D LC-MS/MS not only in the number of identified proteins, but also in proteins coverage, what makes these results more interesting.

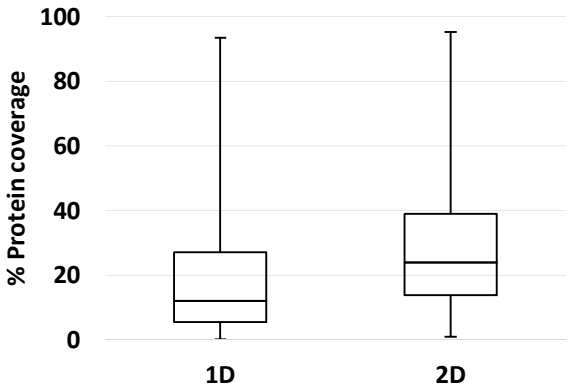

Figure IV.13. Box plots illustrating the percentage of protein coverage with 95% of confidence of the 1072 common proteins identified by 1D and 2D LC-MS/MS analyses.

IV.2.2. SWATH analysis

To quantify the proteins previously identified by the different approaches a SWATH analysis was performed (section III.6.). In this quantitative analysis, only one SWATH acquisition was performed (section III.3), but three different libraries were used: 1D LC-MS/MS, 1D LC-MS/MS with EL and 2D LC-MS/MS.

Out of the 1067 confidently identified proteins by 1D LC-MS/MS, 857 were quantified (80.3%), corresponding to 3087 peptides (Figure IV.14). Combining the 1D LC-MS/MS with EL library (1D-LC approach) it was possible to quantify 918 out of 1160 identified proteins (79.1%), using 3213 peptides. In both cases, the percentage of quantified proteins with at least two peptides was 65%.

In the quantification using the 2D LC-MS/MS library 3356 peptides were used. From the 1924 identified proteins 1077 were quantified (55.0%), of which 654 were quantified with at least two peptides (60.7%) (Figure IV.14.). As expected, the number of quantified proteins was higher using 2D LC-MS/MS library once the number of identified proteins increased 66.3%. However, the increase of quantified proteins was not that high (16.9%) possibly because the SWATH acquisition was performed after a 1D-LC peptide separation instead of 2D-LC. Contrary to protein identification where the number of identified peptides was 101% higher in 2D-LC approach, that was not observed in protein quantification.

Using a Venn diagram to illustrate the unique and shared peptides used in the quantification of 1D-LC with 2D-LC approaches (Figure IV.15. A) it is possible to see that from the 4573 peptides used in quantification only 2013 are shared by both libraries. The number of unique peptides used in each of the approaches is similar (1208 in 1D-LC and 1350 in 2D-LC), and the same happens in proteins; 286 are exclusive of 2D-LC library whereas 127 are only quantified using 1D-LC library. Out of 1204 quantified proteins, 791 are common to both approaches (Figure IV.15. B).

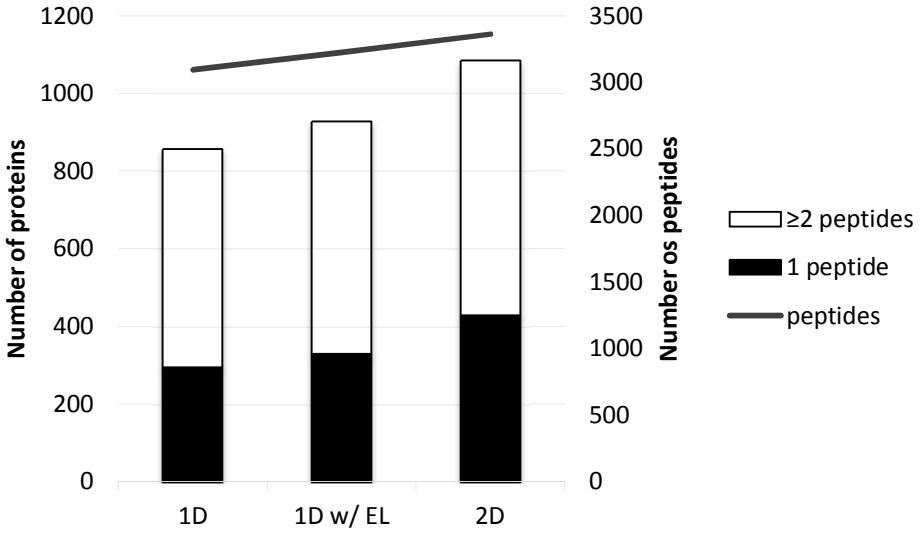

Figure IV.14. Number of peptides and proteins quantified by SWATH-MS analysis using three different libraries: 1D LC-MS/MS (1D), 1D LC-MS/MS with EL (1D w/ EL), and 2D LC-MS/MS (2D). Bar chart of the quantified proteins using the three different libraries with at least two peptides (white) and with one peptide (black). The line chart shows the number of quantified peptides.

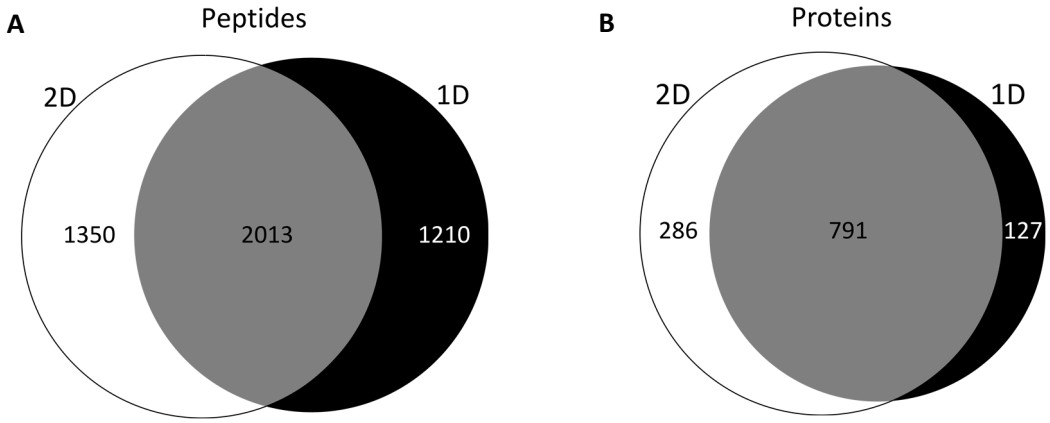

Figure IV.15. Venn diagrams illustrating the number of shared or unique (A) peptides and (B) proteins quantified by SWATH-MS using 1D or 2D IDA libraries. (A) 4573 peptides were quantified, with 2006 being common to both libraries. (B) There are 791 common proteins out of 1204 quantified proteins.

Although the 2D LC-MS/MS analysis is more time consuming (almost two working days) comparing to 1D LC-MS/MS (one hour), it is worth to mention that once the SWATH library is created, it is possible to quantify 17% more proteins in one hour (SWATH acquisition).

IV.2.3. GO analysis

For the biological interpretation of the identified and quantified proteins by both approaches, a GO analysis was performed using the PANTHER tool to visualise proteins according to their cellular component, biological process, and molecular function (section III.8.).

In figure IV.16. it is possible to see that both the identified and quantified proteins by 1D-LC and 2D-LC approaches show similar cellular components, and the majority of the proteins belongs to cell part and organelle (70%), an expected result once no organelle protein extraction procedure was used.

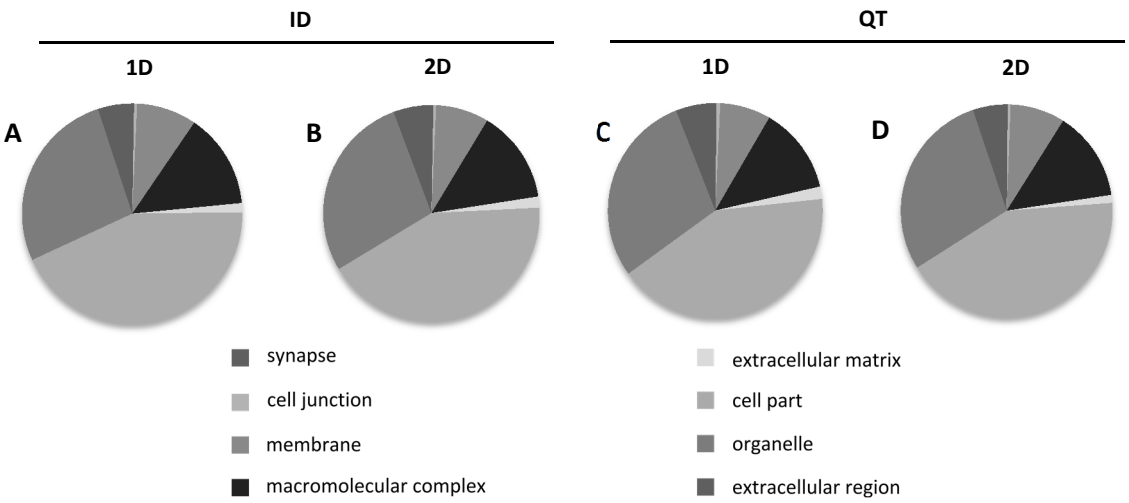

Figure IV.16. Pie charts illustrating the cellular component of the proteins identified by (A) 1D LC-MS/MS and (B) 2D LC-MS/MS, and quantified by SWATH-MS using (C) 1D and (D) 2D libraries.

Regarding the biological processes in which the identified and quantified proteins be part of (Figure IV.17), it is clear that all profiles are quite similar between them, representing proteins involved in very general processes such as cellular component organization, reproduction and localisation. However, more than 50% of the proteins belong to cellular and metabolic processes.

The profiles of the molecular functions of the identified and quantified proteins (Figure IV.18) are also quite similar between them. Such as the biological processes, the represented molecular functions are very general. Among them, catalytic activity and binding are the most represented ones.

Although the two different approaches result in an extremely distinct number of identified proteins, cellular components, biological processes and molecular functions are represented in equal proportions, and the same applies to the quantified proteins. Moreover, the profiles of the quantified proteins are identical to that of the identified proteins, which means that the quantified proteins reflect the GO of the identified proteins.

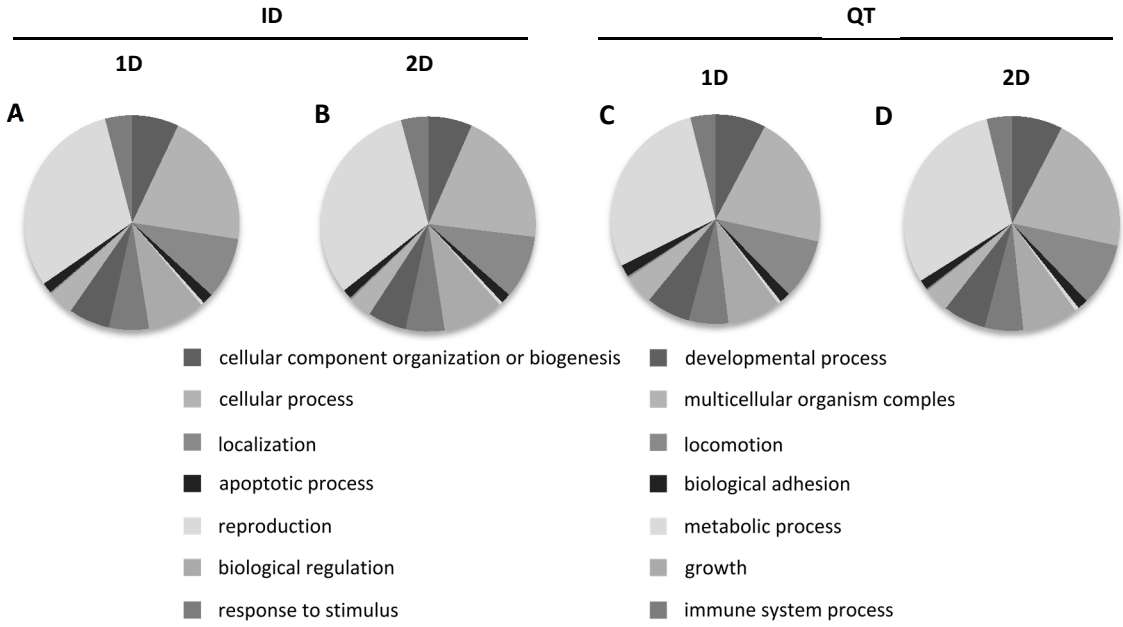

Figure IV.17. Pie charts illustrating the biological process of the proteins identified by (A) 1D LC-MS/MS and (B) 2D LC-MS/MS, and quantified by SWATH-MS using (C) 1D and (D) 2D libraries.

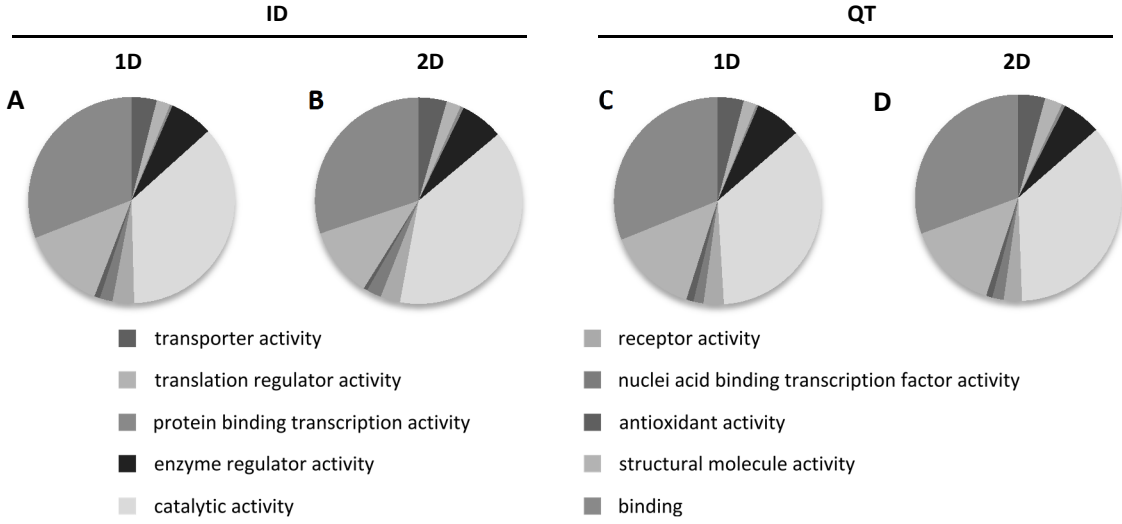

Figure IV.18. Pie charts illustrating the molecular function of the proteins identified by (A) 1D LC-MS/MS and (B) 2D LC-MS/MS, and quantified by SWATH-MS using (C) 1D and (D) 2D libraries.

IV.3. Qualitative analysis

Altogether, this work resulted in the identification of 2071 different proteins (Supplementary Table VII.6.). Previous studies reached a maximum of 1500 identified proteins[41,79–81], except one that achieved 4129 identified proteins[40] however, in this last study 49 different LC-MS/MS analyses were performed.

The GO analysis can be seen in figure IV.19. As found previously, the majority of the proteins belongs to cell part and organelle (69.8%). From those with an "organelle" GO term assigned 60% belong to cytoskeleton (data not shown) and some of these proteins (*e.g.* talin-1, myosin-9, and filamin-A) were the ones identified with the highest number of peptides (more than 100 peptides). Although their function is mainly structural, they have been associated to some pathologies such as cancer[107,108], multiple sclerosis[109], and HIV[110].

Regarding biological processes, 51.4% of the proteins are involved in cellular and metabolic processes, and it is worth to mention that there are studies that point to an energy metabolism dysregulation in SCZ[111,112]. Although only 4.10% of the identified proteins were assigned with an "immune system process" GO term, the analysis of the identified proteins in KEGG database revealed that they are involved in numerous metabolic pathways (Supplementary Figure VII.1. A), namely in "T cell receptor signalling pathway", "B cell receptor signalling pathway", "NK cell mediated cytotoxicity", "leukocyte transendothelial migration", "antigen processing and presentation", "complement and coagulation cascades", and "chemokine signalling pathway" (Supplementary Figures VII.1. B, C, D, E, F, G, and H, respectively). That is, this dataset provide a good coverage of some of the PBMCs metabolic pathways, which means that the approached used provide access to proteins that play important roles in the immune system.

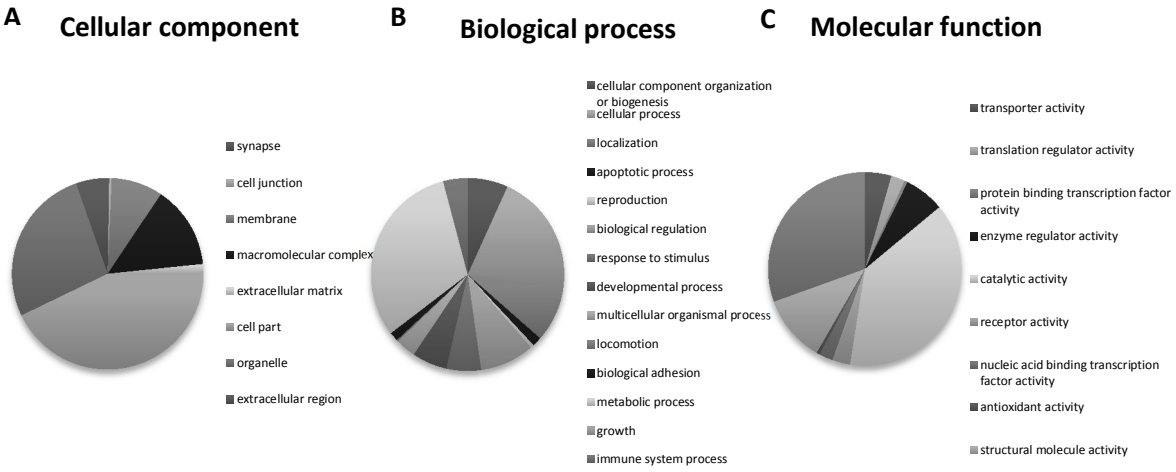

Figure IV.19. Pie charts illustrating the (A) cellular component, (B) biological processes, and (C) molecular functions of all identified proteins.

Similarly to the analysis of the biological processes, the represented molecular functions are quite general. Among them, catalytic activity and binding are the most represented ones (38.5% and 30.5%. respectively).

CD proteins are widely used in the immunophenotyping of PBMCs[97], but they are also used to access activation or proliferation of lymphocytes[113]. Only ten proteins with a CD name assigned were identified, what was already expected since these proteins belong to surface membrane[114] and no protocol of membrane-enrichment was used. Nicotinamide phosphoribosyltransferase, plasminogen activator inhibitor 2, programmed cell death protein 5, and interleukine-1β can also be used to determine PBMCs activation[41] and are included in this dataset too. Various heat shock proteins were identified and it is known that in addition to their role as chaperones, they are also involved in autoimmune diseases[115]. Moreover, there are also some proteins that were previously associated with other human illnesses such as Parkinson's (*e.g.* DJ-1, α-synuclein, and parkin)[116] and Alzheimer's (*e.g.* amyloid β A4)[117] diseases, and SCZ (*e.g.* fructose-bisphosphate aldolase C, β-actin, tropomyosin α-1 chain, and dihydropyrimidinase-related protein 2)[118].

IV.4. SWATH library creation

For the creation of SWATH library, PBMCs samples from six healthy volunteers were pooled together and proteins were identified by 2D LC-MS/MS (section III.5.). This resulted in the identification of 6906 peptides, corresponding to 1102 identified proteins of which 768 (69.7%) were identified with at least two peptides.

In order to verify the reproducibility of the method, the pool of the six biological samples was made and it was analysed three times by SWATH as describe in sections III.3. and III.7. Four hundred and seventeen out of the 1102 identified proteins were quantified. Of these 417 quantified proteins, 358 were quantified with high reproducibility between technical replicates (CV<20%) (Figure IV.20. A and B). Moreover, this method also showed good accuracy with a strong linear correlation (mean r^2 of 0.9922) among the three different replicates (Figure IV.20. C).

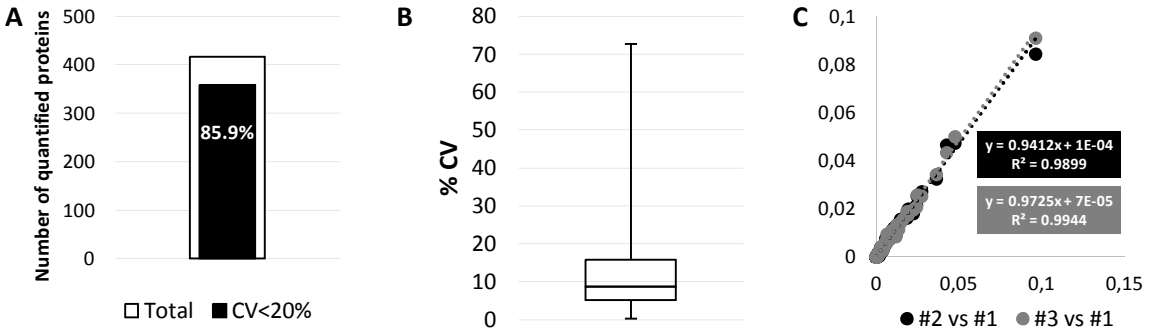

Figure IV.20. Reproducibility analysis of SWATH acquisition method. (A) Total number of quantified proteins among the three technical replicates (white) and those with a CV value below 20% (black). It is presented the percentage of proteins quantified with high reproducibility (CV<20%). (B) Box plot illustrating the range of method reproducibility. (C) Evaluation of the linearity/reproducibility of the method, assessed by plotting the intensity values of the replicates against the intensity value of the first replicate. #1, #2, and #3 = technical replicates.

For SWATH acquisition, the six biological samples were analysed individually (sections III.3 and III.7.). The number of quantified peptides and proteins was similar among the six samples (Figure IV.21.) and it was possible to quantify 922 different proteins. The comparison between the different samples using a Venn diagram (Figure IV.22.) showed that 445 were shared by all samples (Supplementary Table VII.7.), and the number of unique quantified proteins in each sample range between 9 and 27.

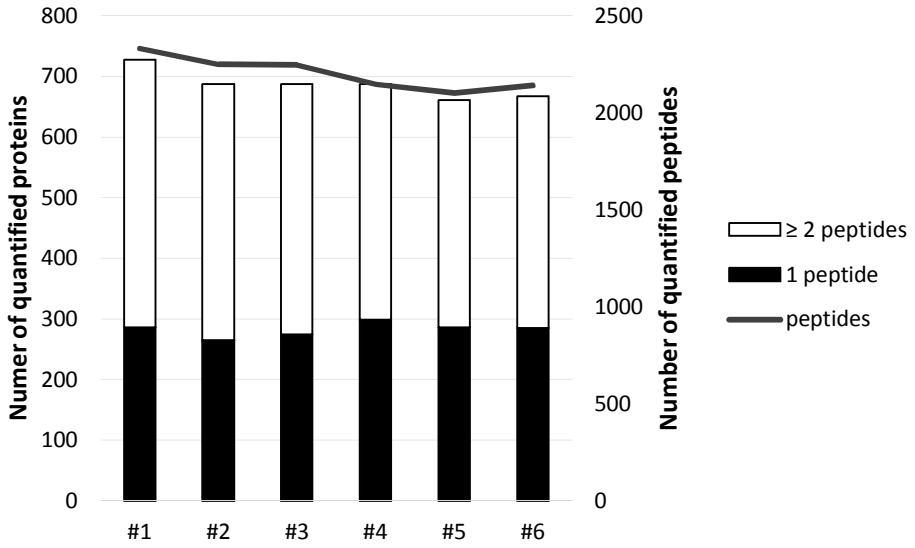

Figure IV.21. Number of peptides and proteins quantified by SWATH-MS. Bar chart of the quantified proteins with at least two peptides (white) and with one peptide (black). The line chart shows the number of quantified peptides. #1, #2, #3, #4, #5, and #6 = biological samples of the six different donors.

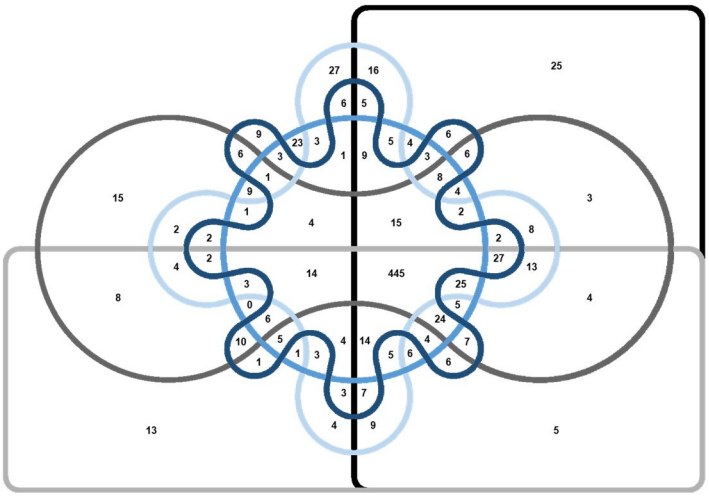

Figure IV.22. Venn diagrams illustrating the number of shared or unique proteins quantified by SWATH-MS. The samples #1, #2, #3, #4, #5, and #6 are represented in black, light grey, dark grey, light blue, blue, and dark blue, respectively.

Considering the quantified proteins common to all samples (445), there are only 85 proteins (19.1%) with a CV value below 20% (Figure IV.23). Although far lower than the CV value obtained among the three technical replicates (85.9%), it is an expected result since among different biological samples (*e.g.* human PBMCs) there is a considerably high variability. However, when considering only female or male samples, the number of quantified proteins with a CV value below 20% is 208 and 191 (Figure IV.23), respectively.

For this reason, a PCA analysis was performed in order to verify if there was any distinction between samples. Figure IV.24. A shows the score values represented in the two first principal components (PC1 and PC2) using Pareto scaling, where 75.7% of sample variance is explained. It is possible to observe the formation of two main groups along the first principal component (PC1), corresponding to female (green) and male (red) samples. The loadings plot (Figure IV.24. B) shows proteins that have the largest contribution along the PC1, and that explain the separation of the two groups. Histone H4 seems to be the main contributor for the separation of males group, whereas females group seems to be distinguished due to talin-1, integrin α-II b, and γ-actin. This confirms that PBMCs proteome of females and males is quite different, calling for the need of considering gender when comparing healthy controls and a disease group. That is, the proportion of females:males should be the same in the two groups (*i.e.* healthy controls and disease), since the observed differences might be due to the gender instead of the disease itself. However, this does not always happens[119,120]; at least one study was found[121] where the two disease groups have more females than males, and the healthy control groups does not even includes females.

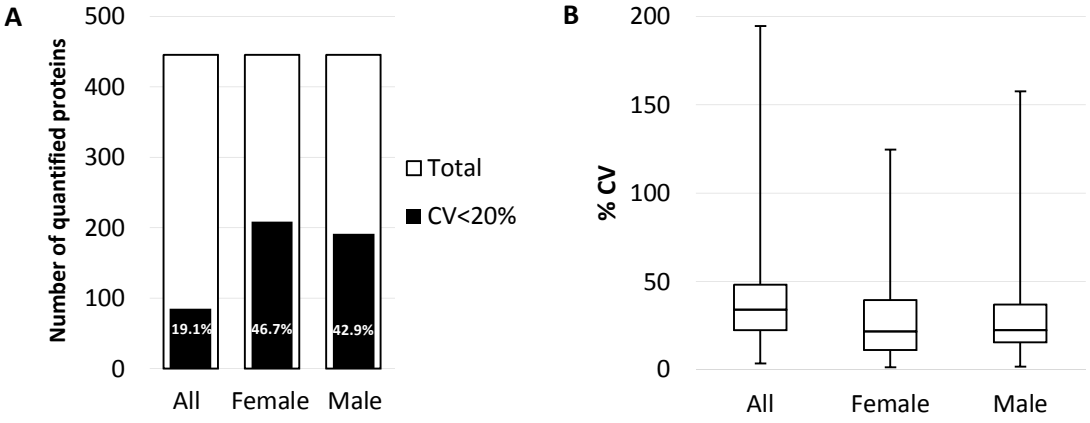

Figure IV.23. Reproducibility analysis of the six biological samples. (A) Number of quantified proteins shared between all samples (white) and those with a CV value below 20% (black) considering all samples, only female samples, and male samples. It is presented the percentage of proteins quantified with high reproducibility (CV<20%). (B) Box plot illustrating the reproducibility range considering all samples, only female samples, and male samples.

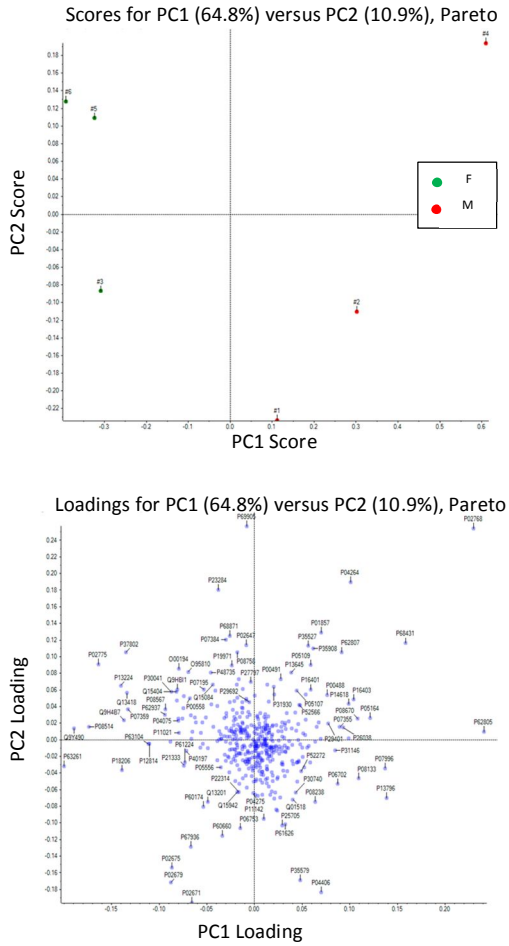

Figure IV.24. PCA analysis of quantified proteins common to the six biological samples with Pareto scaling. (A) Score plot shows two different groups along the PC1, which separation is best explained by the proteins most represented along the PC1 on the loading plot (B).

IV.5. Flow cytometric analysis

Both WB and PBMCs samples from six healthy volunteers (Supplementary Table VII.1.) were analysed by flow cytometry. This analysis aimed to confirm the enrichment in PBMCs after their isolation using the commercially available BD Vacutainer® CPT™, and on the other hand to establish a repertoire of PBMCs subpopulations of healthy individuals so it can be later compared to that of patients with SCZ. Before flow cytometric analysis, cells from PBMCs samples were counted on a COULTER® Ac·T diff2™ (Beckman Coulter) (Supplementary Table VII.8.).

In figure IV.25. it is shown the phenotypic strategy used in the identification of PBMCs subpopulations (the example shown refers to the WB sample of the donor #1) and the results are present in the table IV.1. As expected, the isolation step resulted in an enrichment of all PBMCs subpopulations, corresponding to an increase of more than 100% (Figure IV.26.).

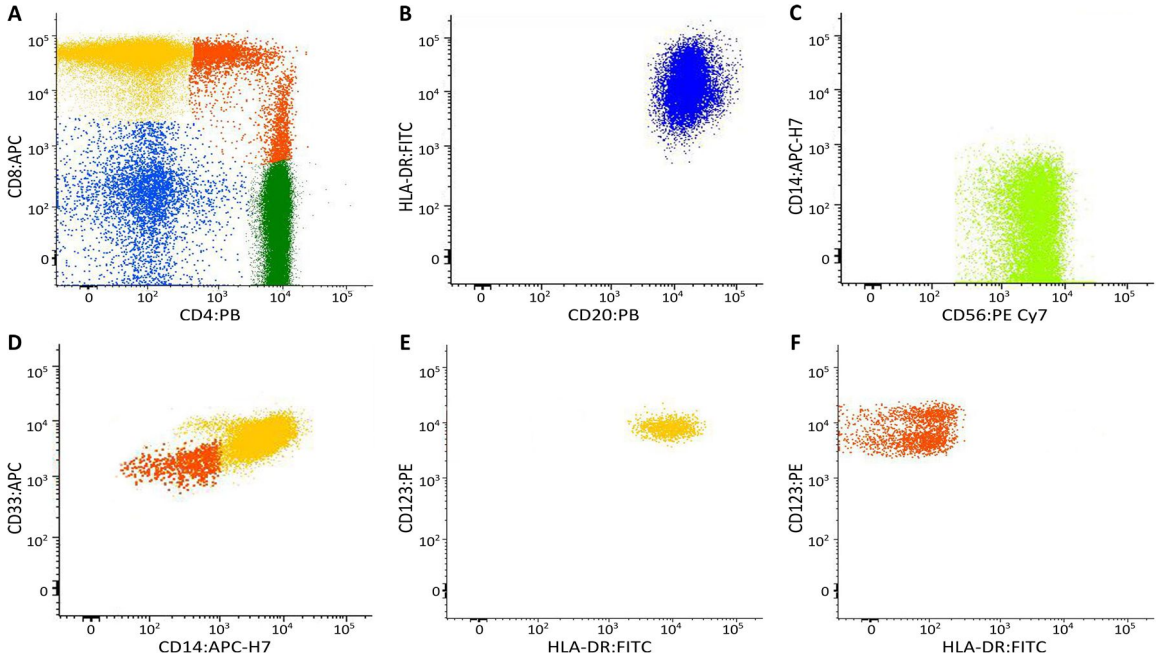

Figure IV.25. Bivariate dot plot histograms illustrating the phenotypic strategy for the identification of the different PBMCs subpopulations in #1 WB sample. (A) T cells subsets. A gate was set on $CD3^+$ and CD4 vs. CD8 expression is shown. $CD4^+$, $CD8^+$, $CD4^+CD8^+$, and γδ T cells are shown in green, yellow, orange, and blue, respectively. (B) B cells. A gate was set on $CD3^-$ and CD20 vs. HLA-DR expression is shown. (C) NK cells. A gate on $CD3^-$ and $CD20^-$ was set and CD56 vs. CD14 expression is shown. (D) Monocytes. A gate was set on $CD3^-$ and CD14 vs. CD33 expression is shown. Classical monocytes are shown in yellow, and non-classical monocytes are shown in orange. (E) Dendritic cells. A gate was set on $CD3^-$, $CD14^-$, and $CD20^-$ and HLA-DR vs. CD123 expression is shown. (F) Basophils. A gate was set on $CD3^-$ and HLA-DR vs. CD123 expression is shown.

Table IV.1. Percentage of PBMCs subpopulations in isolated PBMCs and WB samples determined by flow cytometric analysis.

PBMCs subpopulations	#1		#2		#3		#4		#5		#6	
	PBMCs	WB	PBMCs	WB	PBMCs	WB	PBMCs	WB	PBMCs	WB	PBMCs	WB
T cells	50.20	23.90	61.80	21.30	66.20	27.70	44.00	15.30	65.60	20.90	67.30	23.60
$CD4^+$	51.32	51.10	60.90	58.00	66.00	62.00	62.00	59.00	69.00	69.20	64.10	65.00
$CD8^+$	41.80	41.70	31.90	37.00	24.80	25.26	30.30	31.60	25.20	24.70	30.60	28.00
$CD4^+CD8^+$	2.10	3.40	1.20	2.00	4.40	6.67	3.80	5.90	1.50	1.60	2.70	4.40
γδ	3.06	2.94	3.28	2.60	3.85	3.21	1.73	2.23	3.74	3.00	0.80	1.00
B cells	5.61	2.56	9.43	4.11	8.55	2.85	2.60	1.10	4.57	2.20	8.60	3.30
NK cells	25.00	9.00	11.60	2.60	6.32	2.40	22.67	6.50	15.80	3.90	4.70	1.60
$CD56^{bright}$	1.64	2.20	2.20	1.80	1.87	2.30	1.60	2.20	3.80	3.50	12.30	12.50
Monocytes	18.15	7.60	13.90	5.20	13.90	4.70	23.93	6.90	10.10	3.30	14.90	5.30
NCM	0.79	0.27	0.20	0.12	0.28	0.11	1.52	0.82	0.63	0.22	0.36	0.22
pDC	0.76	0.23	0.30	0.15	0.53	0.21	0.32	0.14	0.40	0.17	0.47	0.15
mDC	0.39	0.14	0.31	0.08	0.70	0.29	0.43	0.19	0.21	0.12	0.50	0.20
Basophils	0.30	0.39	0.29	0.42	0.54	0.76	0.40	0.68	0.19	0.40	0.20	0.40

All results are present in percentage of cells in relation to the total number of cells in each sample, except the percentage of T cells ($CD4^+$, $CD8^+$, $CD4^+CD8^+$, and γδ), and NK cells ($CD56^{bright}$) subsets that is presented in relation to total percentage of T and NK cells, respectively. #1, #2, #3, #4, #5, #6 = biological samples of the six different donors.

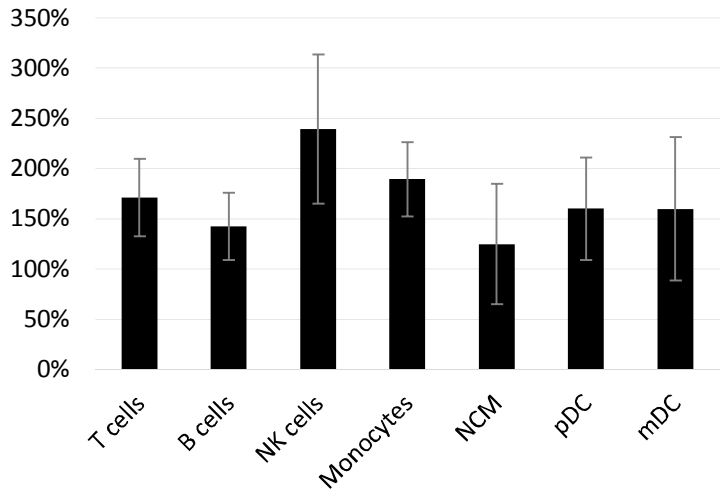

Figure IV.26. Increase of the main PBMCs subpopulations in isolated PBMCs.

V. Conclusions & Future Perspectives

The main goal of this study was to provide a comprehensive proteome characterisation of PBMCs and the creation of a SWATH library. It was also evaluated whether isolated PBMCs could provide access to more immune-relevant proteins than plasma samples do, using the commercially available BD Vacutainer® CPT™ for this purpose. These tubes allow blood collection and PBMCs isolation in a single centrifugation step and therefore are suitable for clinical use. The main PBMCs subpopulations were also analysed by flow cytometry in order to establish a catalogue of some of the PBMCs subpopulations of healthy individuals so it can be later compared to that of patients with diverse pathologies, namely SCZ.

The enrichment test revealed that there are more identified proteins with an "immune system process" GO term assigned in isolated PBMCs than in plasma samples. It was also found that the majority of the quantified "immune" proteins are increased in PBMCs samples.

1D LC-MS/MS was compared to 2D LC-MS/MS in order to choose the approach that perform better in the identification and quantification of PBMCs proteins. 2D LC-MS/MS resulted in an increase of 66.3% in the number of identified proteins and 79.6% in those identified with at least two peptides, comparing to 1D LC-MS/MS approach. It was also observed an increased in protein coverage. Regarding SWATH analysis, using 2D LC-MS/MS library it was possible to quantify 16.9% more proteins.

Altogether, this work allowed the identification of 2071 different proteins, and the qualitative analysis of those proteins revealed that PBMCs proteins are involved in different diseases. Furthermore, it was possible to quantify 992 different proteins in six different samples. Of those, 445 proteins were common to all samples. Although the percentage of quantified proteins with a CV value below 20% was low (19.1%) in the six different samples, technical replicates showed that 85.9% of the quantified proteins have a CV value below 20%. Meaning that SWATH acquisition is a reproducible quantitation method and the higher CV values among biological samples is due to interindividual variation of PBMCs proteome. Flow cytometric data confirm the enrichment of the main PBMCs subpopulations in isolated PBMCs comparing to whole blood samples.

In summary, the results present in this study culminate in a clear conclusion: the comprehensive PBMCs proteome here provide includes proteins related to different diseases, supporting the suggestion that PBMCs are a valuable source of potential biomarker candidates, and can provide an alternative to plasma in future scientific studies. Thus, these findings will be useful to further studies that aim to compare PBMCs proteomes of healthy and diseased individuals.

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VII. Supplementary data

VII.1. PBMCs cryopreservation and culture

In order to assess if PBMCs cryopreservation and its culture influences the amount of protein obtained, cells were cryopreserved during one month and then seeded for two days. PBMCs were isolated and processed as described in III.1.2. but instead of precipitating proteins with methanol, the cell pellet was resuspended in 2 mL of Dulbecco's modified Eagle's medium (DMEM) with Glutamax™ and low glucose supplemented with 10% FBS, Gibco (hereafter DMEM medium). Viable cells were counted in a haemocytometer and then cryopreserved in culture medium with 10% DMSO. After one month of cryopreservation in liquid nitrogen, PBMCs were thawed in a 37˚C water bath and diluted in pre-warmed culture medium. Viable cells were determined using a haemocytometer and PBMCs were seeded at 3.7×10^4 cells/cm^2 in culture medium in 6-well plates (Corning) at 37˚C, 5% CO2/95% air in a humidified incubator (Sheldon Manufacturing, Inc.). After 48 hours of plating, cells were scraped and washed twice with PBS. Proteins were precipitated with methanol and the cell pellet was resuspended in Laemmli Sample Buffer. Protein concentration was determined using the 2-D Quant Kit (section III.1.1.).

Before cryopreservation the number of viable cells was 2.18×10^6 cells and after one month of cryopreservation this number decreased to 1.11×10^6 cells. As PBMCs can be cryopreserved for periods longer than one year without loss of viability[61] this difference in the number of viable cells was not expected. It is recommended to use RPMI-1640 medium in its cryopreservation[122] instead of DMEM which could have led to cell death, although it was found one previous study used DMEM medium in PBMCs culture with no report of cell death[123].

The average of protein obtained without PBMCs cryopreservation and culture was 435 µg per sample, whereas after this procedure the amount of protein per sample was 174 µg. Although in the literature there is no mention of protein content decrease after PBMCs cryopreservation and culture, it was found that the total amount of protein was 2.5 times lower.

VII.2. Tables and figures

Supplementary Table VII.1. Demographic and clinical characteristics of healthy donors.

Samples	Individuals	Gender (F/M)	Age	BMI (kg/m2)	Smokers (Y/N)
ET	#1	M	36	20.83	N
	#2	F	24	24.80	Y
	#3	F	24	24.28	N
	#4	M	22	17.76	Y
SC	#1	M	26	19.62	N
	#2	M	22	17.76	Y
	#3	F	23	20.55	N
	#4	M	36	20.83	N
	#5	F	26	23.03	N
	#6	F	23	24.77	N

BMI = body mass index; ET = samples used in the enrichment test assay; SC = samples used in the SWATH library creation and in the flow cytometric analysis.

Supplementary Table VII.2. Identified proteins with an "immune system" GO term assigned by LC-MS/MS in PBMCs samples. For each protein it is shown its entry name in UniProt database.

Entry name	Protein name
A1BG_HUMAN	Alpha-1B-glycoprotein
A2MG_HUMAN	Alpha-2-macroglobulin
APOH_HUMAN	Beta-2-glycoprotein 1
B2MG_HUMAN	Beta-2-microglobulin
CCL5_HUMAN	C-C motif chemokine 5
CD36_HUMAN	Platelet glycoprotein 4
CD47_HUMAN	Leukocyte surface antigen CD47
CERU_HUMAN	Ceruloplasmin
CFAB_HUMAN	Complement factor B
CO4A_HUMAN	Complement C4-A
CSK_HUMAN	Tyrosine-protein kinase CSK
CSRP1_HUMAN	Cysteine and glycine-rich protein 1
CXCL7_HUMAN	Platelet basic protein
DOPD_HUMAN	D-dopachrome decarboxylase
DUS3_HUMAN	Dual specificity protein phosphatase 3
EF1G_HUMAN	Elongation factor 1-gamma
ENPL_HUMAN	Endoplasmin
F13A_HUMAN	Coagulation factor XIII A chain
FA5_HUMAN	Coagulation factor V
FETUA_HUMAN	Alpha-2-HS-glycoprotein
FHL1_HUMAN	Four and a half LIM domains protein 1
GPVI_HUMAN	Platelet glycoprotein VI
GPX1_HUMAN	Glutathione peroxidase 1

GSTO1_HUMAN	Glutathione S-transferase omega-1
HPT_HUMAN	Haptoglobin
HS90A_HUMAN	Heat shock protein HSP 90-alpha
HS90B_HUMAN	Heat shock protein HSP 90-beta
HSP71_HUMAN	Heat shock 70 kDa protein 1A/1B
HSP7C_HUMAN	Heat shock cognate 71 kDa protein
HSPB1_HUMAN	Heat shock protein beta-1
ILF2_HUMAN	Interleukin enhancer-binding factor 2
ILK_HUMAN	Integrin-linked protein kinase
KSYK_HUMAN	Tyrosine-protein kinase SYK
LOX12_HUMAN	Arachidonate 12-lipoxygenase, 12S-type
LYAM3_HUMAN	P-selectin
MK01_HUMAN	Mitogen-activated protein kinase 1
OTUB1_HUMAN	Ubiquitin thioesterase OTUB1
PECA1_HUMAN	Platelet endothelial cell adhesion molecule
PERM_HUMAN	Myeloperoxidase
PLF4_HUMAN	Platelet factor 4
PP1A_HUMAN	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit
PRDX1_HUMAN	Peroxiredoxin-1
PRDX2_HUMAN	Peroxiredoxin-2
PRDX4_HUMAN	Peroxiredoxin-4
RINI_HUMAN	Ribonuclease inhibitor
S10A4_HUMAN	Protein S100-A4
S10A6_HUMAN	Protein S100-A6
S10A9_HUMAN	Protein S100-A9
S10AB_HUMAN	Protein S100-A11
SLAF5_HUMAN	SLAM family member 5
SRC_HUMAN	Proto-oncogene tyrosine-protein kinase Src
STAT3_HUMAN	Signal transducer and activator of transcription 3
TCTP_HUMAN	Translationally-controlled tumor protein
THAS_HUMAN	Thromboxane-A synthase
THRB_HUMAN	Prothrombin
TRML1_HUMAN	Trem-like transcript 1 protein
XRCC6_HUMAN	X-ray repair cross-complementing protein 6
YES_HUMAN	Tyrosine-protein kinase Yes
ZA2G_HUMAN	Zinc-alpha-2-glycoprotein

Supplementary Table VII.3. Identified proteins with an "immune system" GO term assigned by LC-MS/MS in P+C samples. For each protein it is shown its entry name in UniProt database.

Entry name	Protein name
A1BG_HUMAN	Alpha-1B-glycoprotein
A2MG_HUMAN	Alpha-2-macroglobulin
AMBP_HUMAN	Protein AMBP
APOH_HUMAN	Beta-2-glycoprotein 1
C1R_HUMAN	Complement C1r subcomponent
C1S_HUMAN	Complement C1s subcomponent
C4BPA_HUMAN	C4b-binding protein alpha chain
CERU_HUMAN	Ceruloplasmin
CFAB_HUMAN	Complement factor B
CFAH_HUMAN	Complement factor H
CFAI_HUMAN	Complement factor I
CO2_HUMAN	Complement C2
CO4A_HUMAN	Complement C4-A
CO4B_HUMAN	Complement C4-B
CO5_HUMAN	Complement C5
CO7_HUMAN	Complement component C7
CO8A_HUMAN	Complement component C8 alpha chain
FA12_HUMAN	Coagulation factor XII
FETUA_HUMAN	Alpha-2-HS-glycoprotein
HPT_HUMAN	Haptoglobin
HPTR_HUMAN	Haptoglobin-related protein
LUM_HUMAN	Lumican
PZP_HUMAN	Pregnancy zone protein
THRB_HUMAN	Prothrombin
ZA2G_HUMAN	Zinc-alpha-2-glycoprotein

Supplementary Table VII.4. Identified proteins with an "immune system" GO term assigned by LC-MS/MS in plasma samples. For each protein it is shown its entry name in UniProt database.

Entry name	Protein name
A1BG_HUMAN	Alpha-1B-glycoprotein
A2MG_HUMAN	Alpha-2-macroglobulin
AMBP_HUMAN	Protein AMBP
APOH_HUMAN	Beta-2-glycoprotein 1
C1R_HUMAN	Complement C1r subcomponent
C1S_HUMAN	Complement C1s subcomponent
C4BPA_HUMAN	C4b-binding protein alpha chain
CERU_HUMAN	Ceruloplasmin
CFAB_HUMAN	Complement factor B
CFAH_HUMAN	Complement factor H
CFAI_HUMAN	Complement factor I
CO2_HUMAN	Complement C2
CO4A_HUMAN	Complement C4-A
CO4B_HUMAN	Complement C4-B
CO5_HUMAN	Complement C5
CO6_HUMAN	Complement component C6
CO7_HUMAN	Complement component C7
CO8A_HUMAN	Complement component C8 alpha chain
CO8G_HUMAN	Complement component C8 gamma chain
F13A_HUMAN	Coagulation factor XIII A chain
F13B_HUMAN	Coagulation factor XIII B chain
FETUA_HUMAN	Alpha-2-HS-glycoprotein
GPX3_HUMAN	Glutathione peroxidase 3
HPT_HUMAN	Haptoglobin
HPTR_HUMAN	Haptoglobin-related protein
KV110_HUMAN	Ig kappa chain V-I region HK102 (Fragment)
LBP_HUMAN	Lipopolysaccharide-binding protein
LUM_HUMAN	Lumican
PZP_HUMAN	Pregnancy zone protein
THRB_HUMAN	Prothrombin
ZA2G_HUMAN	Zinc-alpha-2-glycoprotein

Supplementary Table VII.5. Quantified proteins with an "immune system" GO term assigned by SWATH-MS. For each protein it is shown its entry name in UniProt database and its relative intensity in each of the samples.

Entry name	Protein name	PBMCs	P+C	Plasma
A1BG_HUMAN	Alpha-1B-glycoprotein	1.36E-04	5.63E-04	6.27E-04
A2MG_HUMAN	Alpha-2-macroglobulin	2.04E-03	1.33E-02	1.45E-02
AMBP_HUMAN	Protein AMBP	4.70E-05	2.87E-04	3.91E-04
APOH_HUMAN	Beta-2-glycoprotein 1	8.45E-05	5.45E-04	3.36E-04
B2MG_HUMAN	Beta-2-microglobulin	1.80E-04	2.13E-05	1.65E-05
CCL5_HUMAN	C-C motif chemokine 5	3.36E-04	3.28E-06	2.16E-06
CD36_HUMAN	Platelet glycoprotein 4	7.44E-05	1.02E-06	7.95E-07
CERU_HUMAN	Ceruloplasmin	1.48E-04	1.42E-03	1.33E-03
CFAB_HUMAN	Complement factor B	5.81E-05	4.24E-04	9.80E-04
CFAH_HUMAN	Complement factor H	2.27E-05	1.42E-04	9.93E-05
CO4A_HUMAN	Complement C4-A	7.40E-06	1.51E-04	1.19E-04
CSK_HUMAN	Tyrosine-protein kinase CSK	9.41E-05	9.98E-07	1.26E-06
CXCL7_HUMAN	Platelet basic protein	8.80E-03	3.12E-05	5.23E-05
DUS3_HUMAN	Dual specificity protein phosphatase 3	5.41E-05	2.16E-06	2.63E-07
ENPL_HUMAN	Endoplasmin	1.83E-03	8.51E-05	1.07E-04
F13A_HUMAN	Coagulation factor XIII A chain	3.35E-03	6.73E-05	9.39E-05
FA5_HUMAN	Coagulation factor V	6.52E-05	3.24E-06	1.03E-06
FHL1_HUMAN	Four and a half LIM domains protein 1	1.81E-04	6.92E-06	9.14E-07
GPX1_HUMAN	Glutathione peroxidase 1	4.11E-05	6.64E-06	1.44E-05
GSTO1_HUMAN	Glutathione S-transferase omega-1	2.46E-03	4.43E-05	1.07E-05
HPT_HUMAN	Haptoglobin	4.24E-04	2.75E-03	2.08E-03
HS90A_HUMAN	Heat shock protein HSP 90-alpha	1.14E-03	2.20E-05	1.03E-05
HS90B_HUMAN	Heat shock protein HSP 90-beta	1.13E-04	3.26E-06	1.27E-06
HSP71_HUMAN	Heat shock 70 kDa protein 1A	2.53E-04	6.97E-06	9.22E-06
HSP7C_HUMAN	Heat shock cognate 71 kDa protein	2.95E-03	1.97E-04	1.51E-04
HSPB1_HUMAN	Heat shock protein beta-1	1.55E-03	6.69E-05	6.12E-05
ILK_HUMAN	Integrin-linked protein kinase	4.88E-03	1.00E-04	1.20E-04
LYAM3_HUMAN	P-selectin	4.32E-04	2.27E-05	1.88E-05
MK01_HUMAN	Mitogen-activated protein kinase 1	1.38E-04	2.54E-05	1.31E-05
PECA1_HUMAN	Platelet endothelial cell adhesion molecule	2.44E-04	1.38E-05	3.70E-06
PERM_HUMAN	Myeloperoxidase	1.38E-04	1.67E-06	1.80E-06
PLF4_HUMAN	Platelet factor 4	3.92E-03	8.92E-05	9.95E-06
PP1A_HUMAN	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	9.65E-05	8.50E-06	4.69E-07
PRDX1_HUMAN	Peroxiredoxin-1	1.10E-03	1.01E-05	5.62E-06
PRDX2_HUMAN	Peroxiredoxin-2	2.33E-04	1.33E-05	1.05E-05
RINI_HUMAN	Ribonuclease inhibitor	2.09E-04	2.90E-06	1.53E-06
S10A4_HUMAN	Protein S100-A4	7.10E-04	6.77E-05	1.56E-05
S10A9_HUMAN	Protein S100-A9	4.64E-04	1.21E-04	2.38E-05
THAS_HUMAN	Thromboxane-A synthase	3.28E-04	2.87E-06	6.32E-06
THRB_HUMAN	Prothrombin	5.97E-05	2.67E-04	1.66E-04
TRML1_HUMAN	Trem-like transcript 1 protein	3.49E-04	2.80E-05	1.49E-05
ZA2G_HUMAN	Zinc-alpha-2-glycoprotein	4.34E-05	6.93E-05	8.17E-05

Supplementary Table VII.6. All identified proteins during this study. For each protein it is shown its entry name in UniProt database.

Entry name	Protein name	Entry name	Protein name
1433B_HUMAN	14-3-3 protein beta/alpha	MCCB_HUMAN	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial
1433E_HUMAN	14-3-3 protein epsilon	MCTS1_HUMAN	Malignant T-cell-amplified sequence 1
1433F_HUMAN	14-3-3 protein eta	MCU_HUMAN	Calcium uniporter protein, mitochondrial
1433G_HUMAN	14-3-3 protein gamma	MDHC_HUMAN	Malate dehydrogenase, cytoplasmic
1433T_HUMAN	14-3-3 protein theta	MDHM_HUMAN	Malate dehydrogenase, mitochondrial
1433Z_HUMAN	14-3-3 protein zeta/delta	MECP2_HUMAN	Methyl-CpG-binding protein 2
1A01_HUMAN	HLA class I histocompatibility antigen, A-1 alpha chain	MEMO1_HUMAN	Protein MEMO1
1A02_HUMAN	HLA class I histocompatibility antigen, A-2 alpha chain	MESD_HUMAN	LDLR chaperone MESD
1A03_HUMAN	HLA class I histocompatibility antigen, A-3 alpha chain	METK2_HUMAN	S-adenosylmethionine synthase isoform type-2
1B08_HUMAN	HLA class I histocompatibility antigen, B-8 alpha chain	MFN2_HUMAN	Mitofusin-2
1B27_HUMAN	HLA class I histocompatibility antigen, B-27 alpha chain	MGLL_HUMAN	Monoglyceride lipase
1B35_HUMAN	HLA class I histocompatibility antigen, B-35 alpha chain	MGMT_HUMAN	Methylated-DNA--protein-cysteine methyltransferase
1B40_HUMAN	HLA class I histocompatibility antigen, B-40 alpha chain	MGN2_HUMAN	Protein mago nashi homolog 2
1B44_HUMAN	HLA class I histocompatibility antigen, B-44 alpha chain	MGST3_HUMAN	Microsomal glutathione S-transferase 3
1B45_HUMAN	HLA class I histocompatibility antigen, B-45 alpha chain	MIC19_HUMAN	MIC complex subunit MIC19
1B47_HUMAN	HLA class I histocompatibility antigen, B-47 alpha chain	MIC60_HUMAN	MIC complex subunit MIC60
1B81_HUMAN	HLA class I histocompatibility antigen, B-81 alpha chain	MICA1_HUMAN	Protein-methionine sulfoxide oxidase MICAL1
1C03_HUMAN	HLA class I histocompatibility antigen, Cw-3 alpha chain	MICU1_HUMAN	Calcium uptake protein 1, mitochondrial
1C07_HUMAN	HLA class I histocompatibility antigen, Cw-7 alpha chain	MIF_HUMAN	Macrophage migration inhibitory factor
2A5A_HUMAN	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform	MK01_HUMAN	Mitogen-activated protein kinase 1
2AAA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	MK03_HUMAN	Mitogen-activated protein kinase 3
2ABA_HUMAN	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	MK14_HUMAN	Mitogen-activated protein kinase 14
2B1D_HUMAN	HLA class II histocompatibility antigen, DRB1-13 beta chain	ML12A_HUMAN	Myosin regulatory light chain 12A

2B1F_HUMAN	HLA class II histocompatibility antigen, DRB1-15 beta chain	MLEC_HUMAN	Malectin
3BP1_HUMAN	SH3 domain-binding protein 1	MMRN1_HUMAN	Multimerin-1
41_HUMAN	Protein 4.1	MNDA_HUMAN	Myeloid cell nuclear differentiation antigen
4F2_HUMAN	4F2 cell-surface antigen heavy chain	MOB1A_HUMAN	MOB kinase activator 1A
5NT3A_HUMAN	Cytosolic 5'-nucleotidase 3A	MOES_HUMAN	Moesin
6PGD_HUMAN	6-phosphogluconate dehydrogenase, decarboxylating	MOGS_HUMAN	Mannosyl-oligosaccharide glucosidase
6PGL_HUMAN	6-phosphogluconolactonase	MOT4_HUMAN	Monocarboxylate transporter 4
A16A1_HUMAN	Aldehyde dehydrogenase family 16 member A1	MP2K1_HUMAN	Dual specificity mitogen-activated protein kinase kinase 1
A1AT_HUMAN	Alpha-1-antitrypsin	MP2K2_HUMAN	Dual specificity mitogen-activated protein kinase kinase 2
A1BG_HUMAN	Alpha-1B-glycoprotein	MP2K3_HUMAN	Dual specificity mitogen-activated protein kinase kinase 3
A2MG_HUMAN	Alpha-2-macroglobulin	MPCP_HUMAN	Phosphate carrier protein, mitochondrial
A4_HUMAN	Amyloid beta A4 protein	MPI_HUMAN	Mannose-6-phosphate isomerase
AACT_HUMAN	Alpha-1-antichymotrypsin	MPRD_HUMAN	Cation-dependent mannose-6-phosphate receptor
AAKG1_HUMAN	5'-AMP-activated protein kinase subunit gamma-1	MPU1_HUMAN	Mannose-P-dolichol utilization defect 1 protein
AAPK1_HUMAN	5'-AMP-activated protein kinase catalytic subunit alpha-1	MRCKB_HUMAN	Serine/threonine-protein kinase MRCK beta
AATC_HUMAN	Aspartate aminotransferase, cytoplasmic	MRE11_HUMAN	Double-strand break repair protein MRE11A
AATM_HUMAN	Aspartate aminotransferase, mitochondrial	MRVI1_HUMAN	Protein MRVI1
ABCAA_HUMAN	ATP-binding cassette sub-family A member 10	MSRA_HUMAN	Mitochondrial peptide methionine sulfoxide reductase
ABCE1_HUMAN	ATP-binding cassette sub-family E member 1	MTA2_HUMAN	Metastasis-associated protein MTA2
ABCF1_HUMAN	ATP-binding cassette sub-family F member 1	MTAP_HUMAN	S-methyl-5'-thioadenosine phosphorylase
ABCF3_HUMAN	ATP-binding cassette sub-family F member 3	MTCH1_HUMAN	Mitochondrial carrier homolog 1
ABHDA_HUMAN	Mycophenolic acid acyl-glucuronide esterase, mitochondrial	MTCH2_HUMAN	Mitochondrial carrier homolog 2
ABHEB_HUMAN	Alpha/beta hydrolase domain-containing protein 14B	MTHFS_HUMAN	5-formyltetrahydrofolate cyclo-ligase
ABHGA_HUMAN	Abhydrolase domain-containing protein 16A	MTM1_HUMAN	Myotubularin
ABI1_HUMAN	Abl interactor 1	MTMRC_HUMAN	Myotubularin-related protein 12
ABLM1_HUMAN	Actin-binding LIM protein 1	MTNA_HUMAN	Methylthioribose-1-phosphate isomerase
ABLM3_HUMAN	Actin-binding LIM protein 3	MTPN_HUMAN	Myotrophin
ABRAL_HUMAN	Costars family protein ABRACL	MUC19_HUMAN	Mucin-19
ACADM_HUMAN	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	MUCB_HUMAN	Ig mu heavy chain disease protein
ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	MVP_HUMAN	Major vault protein

ACAP1_HUMAN	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 1	MX1_HUMAN	Interferon-induced GTP-binding protein Mx1
ACBP_HUMAN	Acyl-CoA-binding protein	MY18A_HUMAN	Unconventional myosin-XVIIIa
ACDSB_HUMAN	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	MYADM_HUMAN	Myeloid-associated differentiation marker
ACLY_HUMAN	ATP-citrate synthase	MYCT1_HUMAN	Myc target protein 1
ACOC_HUMAN	Cytoplasmic aconitate hydratase	MYG1_HUMAN	UPF0160 protein MYG1, mitochondrial
ACON_HUMAN	Aconitate hydratase, mitochondrial	MYH9_HUMAN	Myosin-9
ACOT9_HUMAN	Acyl-coenzyme A thioesterase 9, mitochondrial	MYL6_HUMAN	Myosin light polypeptide 6
ACOX1_HUMAN	Peroxisomal acyl-coenzyme A oxidase 1	MYL9_HUMAN	Myosin regulatory light polypeptide 9
ACPH_HUMAN	Acylamino-acid-releasing enzyme	MYLK_HUMAN	Myosin light chain kinase, smooth muscle
ACS2L_HUMAN	Acetyl-coenzyme A synthetase 2-like, mitochondrial	MYO1F_HUMAN	Unconventional myosin-If
ACSL1_HUMAN	Long-chain-fatty-acid--CoA ligase 1	MYO1G_HUMAN	Unconventional myosin-Ig
ACSL4_HUMAN	Long-chain-fatty-acid--CoA ligase 4	MYO9B_HUMAN	Unconventional myosin-IXb
ACTB_HUMAN	Actin, cytoplasmic 1	MYPT1_HUMAN	Protein phosphatase 1 regulatory subunit 12A
ACTBL_HUMAN	Beta-actin-like protein 2	NAAA_HUMAN	N-acylethanolamine-hydrolyzing acid amidase
ACTBM_HUMAN	Putative beta-actin-like protein 3	NACAD_HUMAN	NAC-alpha domain-containing protein 1
ACTC_HUMAN	Actin, alpha cardiac muscle 1	NACAM_HUMAN	Nascent polypeptide-associated complex subunit alpha, muscle-specific form
ACTG_HUMAN	Actin, cytoplasmic 2	NAGK_HUMAN	N-acetyl-D-glucosamine kinase
ACTN1_HUMAN	Alpha-actinin-1	NAMPT_HUMAN	Nicotinamide phosphoribosyltransferase
ACTN2_HUMAN	Alpha-actinin-2	NAT10_HUMAN	N-acetyltransferase 10
ACTN4_HUMAN	Alpha-actinin-4	NB5R1_HUMAN	NADH-cytochrome b5 reductase 1
ACTY_HUMAN	Beta-centractin	NB5R3_HUMAN	NADH-cytochrome b5 reductase 3
ACTZ_HUMAN	Alpha-centractin	NBEL2_HUMAN	Neurobeachin-like protein 2
ADA_HUMAN	Adenosine deaminase	NCBP1_HUMAN	Nuclear cap-binding protein subunit 1
ADA10_HUMAN	Disintegrin and metalloproteinase domain-containing protein 10	NCF1_HUMAN	Neutrophil cytosol factor 1
ADAS_HUMAN	Alkyldihydroxyacetonephosphate synthase, peroxisomal	NCF2_HUMAN	Neutrophil cytosol factor 2
ADCY6_HUMAN	Adenylate cyclase type 6	NCK2_HUMAN	Cytoplasmic protein NCK2
ADDA_HUMAN	Alpha-adducin	NCKP1_HUMAN	Nck-associated protein 1
ADDB_HUMAN	Beta-adducin	NCKPL_HUMAN	Nck-associated protein 1-like
ADDG_HUMAN	Gamma-adducin	NCPR_HUMAN	NADPH--cytochrome P450 reductase
ADHX_HUMAN	Alcohol dehydrogenase class-3	NDK3_HUMAN	Nucleoside diphosphate kinase 3
ADK_HUMAN	Adenosine kinase	NDKA_HUMAN	Nucleoside diphosphate kinase A
ADPRH_HUMAN	[Protein ADP-ribosylarginine] hydrolase	NDKB_HUMAN	Nucleoside diphosphate kinase B
ADT2_HUMAN	ADP/ATP translocase 2	NDRG1_HUMAN	Protein NDRG1
ADT3_HUMAN	ADP/ATP translocase 3	NDUA4_HUMAN	Cytochrome c oxidase subunit NDUFA4

AFAM_HUMAN	Afamin	NDUA5_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5
AGFG1_HUMAN	Arf-GAP domain and FG repeat-containing protein 1	NDUA8_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8
AHNK_HUMAN	Neuroblast differentiation-associated protein AHNAK	NDUA9_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial
AHSA1_HUMAN	Activator of 90 kDa heat shock protein ATPase homolog 1	NDUAA_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial
AIFM1_HUMAN	Apoptosis-inducing factor 1, mitochondrial	NDUAB_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11
AIMP1_HUMAN	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	NDUAD_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13
AK1A1_HUMAN	Alcohol dehydrogenase [NADP(+)]	NDUB4_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4
AKT1_HUMAN	RAC-alpha serine/threonine-protein kinase	NDUBA_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10
AL3A2_HUMAN	Fatty aldehyde dehydrogenase	NDUBB_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial
AL5AP_HUMAN	Arachidonate 5-lipoxygenase-activating protein	NDUS1_HUMAN	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial
AL9A1_HUMAN	4-trimethylaminobutyraldehyde dehydrogenase	NDUS2_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial
ALBU_HUMAN	Serum albumin	NDUS3_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial
ALDH2_HUMAN	Aldehyde dehydrogenase, mitochondrial	NDUS5_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5
ALDOA_HUMAN	Fructose-bisphosphate aldolase A	NDUS8_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial
ALDOC_HUMAN	Fructose-bisphosphate aldolase C	NDUV1_HUMAN	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial
ALDR_HUMAN	Aldose reductase	NDUV2_HUMAN	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial
AMBP_HUMAN	Protein AMBP	NEB2_HUMAN	Neurabin-2
AMPB_HUMAN	Aminopeptidase B	NECP2_HUMAN	Adaptin ear-binding coat-associated protein 2
AMPD2_HUMAN	AMP deaminase 2	NEDD8_HUMAN	NEDD8
AMPL_HUMAN	Cytosol aminopeptidase	NEK7_HUMAN	Serine/threonine-protein kinase Nek7
AMPN_HUMAN	Aminopeptidase N	NEMO_HUMAN	NF-kappa-B essential modulator
AN32A_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member A	NEUG_HUMAN	Neurogranin
AN32B_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member B	NEXN_HUMAN	Nexilin
AN32E_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member E	NFKB1_HUMAN	Nuclear factor NF-kappa-B p105 subunit
ANFY1_HUMAN	Rabankyrin-5	NHLC2_HUMAN	NHL repeat-containing protein 2
ANGT_HUMAN	Angiotensinogen	NHRF1_HUMAN	Na(+)/H(+) exchange regulatory cofactor NHE-RF1
ANK1_HUMAN	Ankyrin-1	NIBAN_HUMAN	Protein Niban

ANM1_HUMAN	Protein arginine N-methyltransferase 1	NICA_HUMAN	Nicastrin
ANO6_HUMAN	Anoctamin-6	NID1_HUMAN	Nidogen-1
ANR44_HUMAN	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B	NIPS1_HUMAN	Protein NipSnap homolog 1
ANT3_HUMAN	Antithrombin-III	NIPS2_HUMAN	Protein NipSnap homolog 2
ANX11_HUMAN	Annexin A11	NNRE_HUMAN	NAD(P)H-hydrate epimerase
ANXA1_HUMAN	Annexin A1	NNTM_HUMAN	NAD(P) transhydrogenase, mitochondrial
ANXA2_HUMAN	Annexin A2	NOL4_HUMAN	Nucleolar protein 4
ANXA3_HUMAN	Annexin A3	NONO_HUMAN	Non-POU domain-containing octamer-binding protein
ANXA4_HUMAN	Annexin A4	NOP56_HUMAN	Nucleolar protein 56
ANXA5_HUMAN	Annexin A5	NOP58_HUMAN	Nucleolar protein 58
ANXA6_HUMAN	Annexin A6	NP1L1_HUMAN	Nucleosome assembly protein 1-like 1
ANXA7_HUMAN	Annexin A7	NP1L4_HUMAN	Nucleosome assembly protein 1-like 4
AOFB_HUMAN	Amine oxidase [flavin-containing] B	NPL4_HUMAN	Nuclear protein localization protein 4 homolog
AP1B1_HUMAN	AP-1 complex subunit beta-1	NPM_HUMAN	Nucleophosmin
AP1G1_HUMAN	AP-1 complex subunit gamma-1	NPS3A_HUMAN	Protein NipSnap homolog 3A
AP1M1_HUMAN	AP-1 complex subunit mu-1	NRBP_HUMAN	Nuclear receptor-binding protein
AP1S1_HUMAN	AP-1 complex subunit sigma-1A	NSDHL_HUMAN	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating
AP1S2_HUMAN	AP-1 complex subunit sigma-2	NSF_HUMAN	Vesicle-fusing ATPase
AP2A1_HUMAN	AP-2 complex subunit alpha-1	NSF1C_HUMAN	NSFL1 cofactor p47
AP2B1_HUMAN	AP-2 complex subunit beta	NT5C_HUMAN	5'(3')-deoxyribonucleotidase, cytosolic type
AP2M1_HUMAN	AP-2 complex subunit mu	NTF2_HUMAN	Nuclear transport factor 2
AP2S1_HUMAN	AP-2 complex subunit sigma	NU205_HUMAN	Nuclear pore complex protein Nup205
AP3B1_HUMAN	AP-3 complex subunit beta-1	NUBP2_HUMAN	Cytosolic Fe-S cluster assembly factor NUBP2
AP3D1_HUMAN	AP-3 complex subunit delta-1	NUCB1_HUMAN	Nucleobindin-1
APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase	NUCB2_HUMAN	Nucleobindin-2
API5_HUMAN	Apoptosis inhibitor 5	NUCKS_HUMAN	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1
APMAP_HUMAN	Adipocyte plasma membrane-associated protein	NUCL_HUMAN	Nucleolin
APOA1_HUMAN	Apolipoprotein A-I	NUD16_HUMAN	U8 snoRNA-decapping enzyme
APOA2_HUMAN	Apolipoprotein A-II	NUDC_HUMAN	Nuclear migration protein nudC
APOA4_HUMAN	Apolipoprotein A-IV	NUDT5_HUMAN	ADP-sugar pyrophosphatase
APOB_HUMAN	Apolipoprotein B-100	NUMA1_HUMAN	Nuclear mitotic apparatus protein 1
APOBR_HUMAN	Apolipoprotein B receptor	NUP93_HUMAN	Nuclear pore complex protein Nup93
APOC1_HUMAN	Apolipoprotein C-I	OAS2_HUMAN	2'-5'-oligoadenylate synthase 2
APOC3_HUMAN	Apolipoprotein C-III	ODO1_HUMAN	2-oxoglutarate dehydrogenase, mitochondrial
APOD_HUMAN	Apolipoprotein D	ODO2_HUMAN	Dihydrolipoyllysine-residue succinyltransferase component of

APOE_HUMAN	Apolipoprotein E	ODP2_HUMAN	2-oxoglutarate dehydrogenase complex, mitochondrial Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial
APOH_HUMAN	Beta-2-glycoprotein 1	ODPA_HUMAN	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial
APT_HUMAN	Adenine phosphoribosyltransferase	ODPB_HUMAN	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial
ARAP1_HUMAN	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1	OGFR_HUMAN	Opioid growth factor receptor
ARBK1_HUMAN	Beta-adrenergic receptor kinase 1	OLA1_HUMAN	Obg-like ATPase 1
ARBK2_HUMAN	Beta-adrenergic receptor kinase 2	OPA1_HUMAN	Dynamin-like 120 kDa protein, mitochondrial
ARC1B_HUMAN	Actin-related protein 2/3 complex subunit 1B	OPTN_HUMAN	Optineurin
ARF1_HUMAN	ADP-ribosylation factor 1	OST48_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit
ARF4_HUMAN	ADP-ribosylation factor 4	OSTF1_HUMAN	Osteoclast-stimulating factor 1
ARF6_HUMAN	ADP-ribosylation factor 6	OTU1_HUMAN	Ubiquitin thioesterase OTU1
ARFG2_HUMAN	ADP-ribosylation factor GTPase-activating protein 2	OTUB1_HUMAN	Ubiquitin thioesterase OTUB1
ARH_HUMAN	Low density lipoprotein receptor adapter protein 1	OXR1_HUMAN	Oxidation resistance protein 1
ARHG1_HUMAN	Rho guanine nucleotide exchange factor 1	OXSR1_HUMAN	Serine/threonine-protein kinase R1
ARHG2_HUMAN	Rho guanine nucleotide exchange factor 2	P2RX1_HUMAN	P2X purinoceptor 1
ARHG7_HUMAN	Rho guanine nucleotide exchange factor 7	P3H1_HUMAN	Prolyl 3-hydroxylase 1
ARHL2_HUMAN	Poly(ADP-ribose) glycohydrolase ARH3	PA1B2_HUMAN	Platelet-activating factor acetylhydrolase IB subunit beta
ARK72_HUMAN	Aflatoxin B1 aldehyde reductase member 2	PA24A_HUMAN	Cytosolic phospholipase A2
ARK74_HUMAN	Aflatoxin B1 aldehyde reductase member 4	PA2G4_HUMAN	Proliferation-associated protein 2G4
ARL1_HUMAN	ADP-ribosylation factor-like protein 1	PABP1_HUMAN	Polyadenylate-binding protein 1
ARL8A_HUMAN	ADP-ribosylation factor-like protein 8A	PABP2_HUMAN	Polyadenylate-binding protein 2
ARL8B_HUMAN	ADP-ribosylation factor-like protein 8B	PABP3_HUMAN	Polyadenylate-binding protein 3
ARMX3_HUMAN	Armadillo repeat-containing X-linked protein 3	PACN2_HUMAN	Protein kinase C and casein kinase substrate in neurons protein 2
ARP2_HUMAN	Actin-related protein 2	PACS1_HUMAN	Phosphofurin acidic cluster sorting protein 1
ARP3_HUMAN	Actin-related protein 3	PAI1_HUMAN	Plasminogen activator inhibitor 1
ARP5L_HUMAN	Actin-related protein 2/3 complex subunit 5-like protein	PAI2_HUMAN	Plasminogen activator inhibitor 2
ARPC2_HUMAN	Actin-related protein 2/3 complex subunit 2	PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein

ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3	PAK2_HUMAN	Serine/threonine-protein kinase PAK 2
ARPC4_HUMAN	Actin-related protein 2/3 complex subunit 4	PARK7_HUMAN	Protein DJ-1
ARPC5_HUMAN	Actin-related protein 2/3 complex subunit 5	PARP1_HUMAN	Poly [ADP-ribose] polymerase 1
ARRB1_HUMAN	Beta-arrestin-1	PARP9_HUMAN	Poly [ADP-ribose] polymerase 9
ARRB2_HUMAN	Beta-arrestin-2	PARVB_HUMAN	Beta-parvin
ARSA_HUMAN	Arylsulfatase A	PCAT1_HUMAN	Lysophosphatidylcholine acyltransferase 1
ASAH1_HUMAN	Acid ceramidase	PCBP1_HUMAN	Poly(rC)-binding protein 1
ASAP1_HUMAN	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1	PCBP2_HUMAN	Poly(rC)-binding protein 2
ASAP2_HUMAN	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2	PCKGM_HUMAN	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
ASC_HUMAN	Apoptosis-associated speck-like protein containing a CARD	PCNA_HUMAN	Proliferating cell nuclear antigen
ASML_HUMAN	N-acetylserotonin O-methyltransferase-like protein	PCP_HUMAN	Lysosomal Pro-X carboxypeptidase
ASNA_HUMAN	ATPase ASNA1	PCSK6_HUMAN	Proprotein convertase subtilisin/kexin type 6
AT1A1_HUMAN	Sodium/potassium-transporting ATPase subunit alpha-1	PCY2_HUMAN	Ethanolamine-phosphate cytidylyltransferase
AT1B3_HUMAN	Sodium/potassium-transporting ATPase subunit beta-3	PCYOX_HUMAN	Prenylcysteine oxidase 1
AT2A2_HUMAN	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	PCYXL_HUMAN	Prenylcysteine oxidase-like
AT2A3_HUMAN	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	PDC10_HUMAN	Programmed cell death protein 10
AT5F1_HUMAN	ATP synthase F(0) complex subunit B1, mitochondrial	PDC6I_HUMAN	Programmed cell death 6-interacting protein
AT8A1_HUMAN	Phospholipid-transporting ATPase IA	PDCD4_HUMAN	Programmed cell death protein 4
ATE1_HUMAN	Arginyl-tRNA--protein transferase 1	PDCD5_HUMAN	Programmed cell death protein 5
ATG3_HUMAN	Ubiquitin-like-conjugating enzyme ATG3	PDCD6_HUMAN	Programmed cell death protein 6
ATG7_HUMAN	Ubiquitin-like modifier-activating enzyme ATG7	PDE12_HUMAN	2',5'-phosphodiesterase 12
ATLA3_HUMAN	Atlastin-3	PDE3A_HUMAN	cGMP-inhibited 3',5'-cyclic phosphodiesterase A
ATP5H_HUMAN	ATP synthase subunit d, mitochondrial	PDE5A_HUMAN	cGMP-specific 3',5'-cyclic phosphodiesterase
ATP5I_HUMAN	ATP synthase subunit e, mitochondrial	PDIA1_HUMAN	Protein disulfide-isomerase
ATP5L_HUMAN	ATP synthase subunit g, mitochondrial	PDIA3_HUMAN	Protein disulfide-isomerase A3
ATP6_HUMAN	ATP synthase subunit a	PDIA4_HUMAN	Protein disulfide-isomerase A4
ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial	PDIA5_HUMAN	Protein disulfide-isomerase A5
ATPB_HUMAN	ATP synthase subunit beta, mitochondrial	PDIA6_HUMAN	Protein disulfide-isomerase A6
ATPD_HUMAN	ATP synthase subunit delta, mitochondrial	PDK1_HUMAN	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial

ATPG_HUMAN	ATP synthase subunit gamma, mitochondrial	PDK3_HUMAN	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 3, mitochondrial
ATPK_HUMAN	ATP synthase subunit f, mitochondrial	PDLI1_HUMAN	PDZ and LIM domain protein 1
ATPO_HUMAN	ATP synthase subunit O, mitochondrial	PDLI5_HUMAN	PDZ and LIM domain protein 5
ATX10_HUMAN	Ataxin-10	PDLI7_HUMAN	PDZ and LIM domain protein 7
B2MG_HUMAN	Beta-2-microglobulin	PDPK2_HUMAN	Putative 3-phosphoinositide-dependent protein kinase 2
B3AT_HUMAN	Band 3 anion transport protein	PDS5B_HUMAN	Sister chromatid cohesion protein PDS5 homolog B
BABA1_HUMAN	BRISC and BRCA1-A complex member 1	PDXK_HUMAN	Pyridoxal kinase
BACH_HUMAN	Cytosolic acyl coenzyme A thioester hydrolase	PEA15_HUMAN	Astrocytic phosphoprotein PEA-15
BAF_HUMAN	Barrier-to-autointegration factor	PEAR1_HUMAN	Platelet endothelial aggregation receptor 1
BAG5_HUMAN	BAG family molecular chaperone regulator 5	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1
BAG6_HUMAN	Large proline-rich protein BAG6	PECA1_HUMAN	Platelet endothelial cell adhesion molecule
BAP31_HUMAN	B-cell receptor-associated protein 31	PEDF_HUMAN	Pigment epithelium-derived factor
BASI_HUMAN	Basigin	PEF1_HUMAN	Peflin
BAX_HUMAN	Apoptosis regulator BAX	PEPD_HUMAN	Xaa-Pro dipeptidase
BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3	PERF_HUMAN	Perforin-1
BGLR_HUMAN	Beta-glucuronidase	PERM_HUMAN	Myeloperoxidase
BID_HUMAN	BH3-interacting domain death agonist	PFD2_HUMAN	Prefoldin subunit 2
BIEA_HUMAN	Biliverdin reductase A	PFD4_HUMAN	Prefoldin subunit 4
BIN2_HUMAN	Bridging integrator 2	PFKAL_HUMAN	ATP-dependent 6-phosphofructokinase, liver type
BLMH_HUMAN	Bleomycin hydrolase	PFKAP_HUMAN	ATP-dependent 6-phosphofructokinase, platelet type
BLVRB_HUMAN	Flavin reductase (NADPH)	PGAM1_HUMAN	Phosphoglycerate mutase 1
BRE_HUMAN	BRCA1-A complex subunit BRE	PGES2_HUMAN	Prostaglandin E synthase 2
BRK1_HUMAN	Protein BRICK1	PGH1_HUMAN	Prostaglandin G/H synthase 1
BROX_HUMAN	BRO1 domain-containing protein BROX	PGK1_HUMAN	Phosphoglycerate kinase 1
BRSK2_HUMAN	Serine/threonine-protein kinase BRSK2	PGM1_HUMAN	Phosphoglucomutase-1
BTF3_HUMAN	Transcription factor BTF3	PGM2_HUMAN	Phosphoglucomutase-2
BTK_HUMAN	Tyrosine-protein kinase BTK	PGM2L_HUMAN	Glucose 1,6-bisphosphate synthase
BZW1_HUMAN	Basic leucine zipper and W2 domain-containing protein 1	PGRC1_HUMAN	Membrane-associated progesterone receptor component 1
C1QBP_HUMAN	Complement component 1 Q subcomponent-binding protein, mitochondrial	PGRC2_HUMAN	Membrane-associated progesterone receptor component 2
C1TC_HUMAN	C-1-tetrahydrofolate synthase, cytoplasmic	PHB_HUMAN	Prohibitin
C4BPA_HUMAN	C4b-binding protein alpha chain	PHB2_HUMAN	Prohibitin-2
CA123_HUMAN	UPF0587 protein C1orf123	PI42A_HUMAN	Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha
CA198_HUMAN	Uncharacterized protein C1orf198	PI4KA_HUMAN	Phosphatidylinositol 4-kinase alpha

CAB39_HUMAN	Calcium-binding protein 39	PICAL_HUMAN	Phosphatidylinositol-binding clathrin assembly protein
CACO1_HUMAN	Calcium-binding and coiled-coil domain-containing protein 1	PIMT_HUMAN	Protein-L-isoaspartate(D-aspartate) O-methyltransferase
CAH1_HUMAN	Carbonic anhydrase 1	PIN1_HUMAN	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1
CAH13_HUMAN	Carbonic anhydrase 13	PIPNA_HUMAN	Phosphatidylinositol transfer protein alpha isoform
CAH2_HUMAN	Carbonic anhydrase 2	PITH1_HUMAN	PITH domain-containing protein 1
CALD1_HUMAN	Caldesmon	PKHF2_HUMAN	Pleckstrin homology domain-containing family F member 2
CALM_HUMAN	Calmodulin	PKHO2_HUMAN	Pleckstrin homology domain-containing family O member 2
CALR_HUMAN	Calreticulin	PKN1_HUMAN	Serine/threonine-protein kinase N1
CALU_HUMAN	Calumenin	PLAP_HUMAN	Phospholipase A-2-activating protein
CALX_HUMAN	Calnexin	PLBL1_HUMAN	Phospholipase B-like 1
CAN1_HUMAN	Calpain-1 catalytic subunit	PLCB2_HUMAN	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-2
CAN2_HUMAN	Calpain-2 catalytic subunit	PLCB3_HUMAN	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3
CANB1_HUMAN	Calcineurin subunit B type 1	PLCG2_HUMAN	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2
CAND1_HUMAN	Cullin-associated NEDD8-dissociated protein 1	PLD3_HUMAN	Phospholipase D3
CAP1_HUMAN	Adenylyl cyclase-associated protein 1	PLEC_HUMAN	Plectin
CAP7_HUMAN	Azurocidin	PLEK_HUMAN	Pleckstrin
CAPG_HUMAN	Macrophage-capping protein	PLF4_HUMAN	Platelet factor 4
CAPZB_HUMAN	F-actin-capping protein subunit beta	PLIN3_HUMAN	Perilipin-3
CASP1_HUMAN	Caspase-1	PLMN_HUMAN	Plasminogen
CASP3_HUMAN	Caspase-3	PLP2_HUMAN	Proteolipid protein 2
CASP6_HUMAN	Caspase-6	PLSL_HUMAN	Plastin-2
CASS4_HUMAN	Cas scaffolding protein family member 4	PLST_HUMAN	Plastin-3
CATA_HUMAN	Catalase	PLXB2_HUMAN	Plexin-B2
CATB_HUMAN	Cathepsin B	PML_HUMAN	Protein PML
CATC_HUMAN	Dipeptidyl peptidase 1	PMVK_HUMAN	Phosphomevalonate kinase
CATD_HUMAN	Cathepsin D	PNCB_HUMAN	Nicotinate phosphoribosyltransferase
CATG_HUMAN	Cathepsin G	PNPH_HUMAN	Purine nucleoside phosphorylase
CATS_HUMAN	Cathepsin S	POSTN_HUMAN	Periostin
CATZ_HUMAN	Cathepsin Z	POTEE_HUMAN	POTE ankyrin domain family member E
CAZA1_HUMAN	F-actin-capping protein subunit alpha-1	POTEI_HUMAN	POTE ankyrin domain family member I
CAZA2_HUMAN	F-actin-capping protein subunit alpha-2	PP14A_HUMAN	Protein phosphatase 1 regulatory subunit 14A
CBPN_HUMAN	Carboxypeptidase N catalytic chain	PP1A_HUMAN	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit

CBR1_HUMAN	Carbonyl reductase [NADPH] 1	PP1G_HUMAN	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit
CBX1_HUMAN	Chromobox protein homolog 1	PP1R7_HUMAN	Protein phosphatase 1 regulatory subunit 7
CBX3_HUMAN	Chromobox protein homolog 3	PP2AA_HUMAN	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform
CC50A_HUMAN	Cell cycle control protein 50A	PP2BA_HUMAN	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform
CC90B_HUMAN	Coiled-coil domain-containing protein 90B, mitochondrial	PP2BB_HUMAN	Serine/threonine-protein phosphatase 2B catalytic subunit beta isoform
CCAR2_HUMAN	Cell cycle and apoptosis regulator protein 2	PP6R1_HUMAN	Serine/threonine-protein phosphatase 6 regulatory subunit 1
CCD22_HUMAN	Coiled-coil domain-containing protein 22	PP6R3_HUMAN	Serine/threonine-protein phosphatase 6 regulatory subunit 3
CCD47_HUMAN	Coiled-coil domain-containing protein 47	PPAC_HUMAN	Low molecular weight phosphotyrosine protein phosphatase
CCDC6_HUMAN	Coiled-coil domain-containing protein 6	PPCE_HUMAN	Prolyl endopeptidase
CCL5_HUMAN	C-C motif chemokine 5	PPGB_HUMAN	Lysosomal protective protein
CCS_HUMAN	Copper chaperone for superoxide dismutase	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A
CD109_HUMAN	CD109 antigen	PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B
CD14_HUMAN	Monocyte differentiation antigen CD14	PPID_HUMAN	Peptidyl-prolyl cis-trans isomerase D
CD226_HUMAN	CD226 antigen	PPIF_HUMAN	Peptidyl-prolyl cis-trans isomerase F, mitochondrial
CD2AP_HUMAN	CD2-associated protein	PPIL3_HUMAN	Peptidyl-prolyl cis-trans isomerase-like 3
CD36_HUMAN	Platelet glycoprotein 4	PPIP2_HUMAN	Proline-serine-threonine phosphatase-interacting protein 2
CD3Z_HUMAN	T-cell surface glycoprotein CD3 zeta chain	PPM1A_HUMAN	Protein phosphatase 1A
CD44_HUMAN	CD44 antigen	PPM1B_HUMAN	Protein phosphatase 1B
CD47_HUMAN	Leukocyte surface antigen CD47	PPM1F_HUMAN	Protein phosphatase 1F
CD63_HUMAN	CD63 antigen	PPP5_HUMAN	Serine/threonine-protein phosphatase 5
CD68_HUMAN	Macrosialin	PPP6_HUMAN	Serine/threonine-protein phosphatase 6 catalytic subunit
CD9_HUMAN	CD9 antigen	PPR18_HUMAN	Phostensin
CDC37_HUMAN	Hsp90 co-chaperone Cdc37	PPR21_HUMAN	Protein phosphatase 1 regulatory subunit 21
CDC42_HUMAN	Cell division control protein 42 homolog	PRAF3_HUMAN	PRA1 family protein 3
CDV3_HUMAN	Protein CDV3 homolog	PRDC1_HUMAN	Phosphoribosyltransferase domain-containing protein 1
CE051_HUMAN	UPF0600 protein C5orf51	PRDX1_HUMAN	Peroxiredoxin-1

CECR5_HUMAN	Cat eye syndrome critical region protein 5	PRDX2_HUMAN	Peroxiredoxin-2
CELF2_HUMAN	CUGBP Elav-like family member 2	PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial
CERS2_HUMAN	Ceramide synthase 2	PRDX4_HUMAN	Peroxiredoxin-4
CERU_HUMAN	Ceruloplasmin	PRDX5_HUMAN	Peroxiredoxin-5, mitochondrial
CFAB_HUMAN	Complement factor B	PRDX6_HUMAN	Peroxiredoxin-6
CH10_HUMAN	10 kDa heat shock protein, mitochondrial	PREB_HUMAN	Prolactin regulatory element-binding protein
CH60_HUMAN	60 kDa heat shock protein, mitochondrial	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit
CHID1_HUMAN	Chitinase domain-containing protein 1	PROF1_HUMAN	Profilin-1
CHMP6_HUMAN	Charged multivesicular body protein 6	PROF3_HUMAN	Profilin-3
CI142_HUMAN	Uncharacterized protein C9orf142	PROS_HUMAN	Vitamin K-dependent protein S
CIRBP_HUMAN	Cold-inducible RNA-binding protein	PROSC_HUMAN	Proline synthase co-transcribed bacterial homolog protein
CISD2_HUMAN	CDGSH iron-sulfur domain-containing protein 2	PRP19_HUMAN	Pre-mRNA-processing factor 19
CISY_HUMAN	Citrate synthase, mitochondrial	PRP31_HUMAN	U4/U6 small nuclear ribonucleoprotein Prp31
CJ131_HUMAN	Uncharacterized protein C10orf131	PRP4B_HUMAN	Serine/threonine-protein kinase PRP4 homolog
CK5P3_HUMAN	CDK5 regulatory subunit-associated protein 3	PRP6_HUMAN	Pre-mRNA-processing factor 6
CKAP4_HUMAN	Cytoskeleton-associated protein 4	PRP8_HUMAN	Pre-mRNA-processing-splicing factor 8
CKAP5_HUMAN	Cytoskeleton-associated protein 5	PRPS1_HUMAN	Ribose-phosphate pyrophosphokinase 1
CKLF5_HUMAN	CKLF-like MARVEL transmembrane domain-containing protein 5	PRPS2_HUMAN	Ribose-phosphate pyrophosphokinase 2
CKLF6_HUMAN	CKLF-like MARVEL transmembrane domain-containing protein 6	PRRC1_HUMAN	Protein PRRC1
CLAP1_HUMAN	CLIP-associating protein 1	PRS10_HUMAN	26S protease regulatory subunit 10B
CLC1B_HUMAN	C-type lectin domain family 1 member B	PRS4_HUMAN	26S protease regulatory subunit 4
CLCA_HUMAN	Clathrin light chain A	PRS6A_HUMAN	26S protease regulatory subunit 6A
CLD5_HUMAN	Claudin-5	PRS6B_HUMAN	26S protease regulatory subunit 6B
CLH1_HUMAN	Clathrin heavy chain 1	PRS7_HUMAN	26S protease regulatory subunit 7
CLIC1_HUMAN	Chloride intracellular channel protein 1	PRS8_HUMAN	26S protease regulatory subunit 8
CLIC4_HUMAN	Chloride intracellular channel protein 4	PRSR2_HUMAN	Proline and serine-rich protein 2
CLUS_HUMAN	Clusterin	PRTN3_HUMAN	Myeloblastin
CMC1_HUMAN	Calcium-binding mitochondrial carrier protein Aralar1	PRUNE_HUMAN	Protein prune homolog
CMC2_HUMAN	Calcium-binding mitochondrial carrier protein Aralar2	PSA_HUMAN	Puromycin-sensitive aminopeptidase
CMIP_HUMAN	C-Maf-inducing protein	PSA1_HUMAN	Proteasome subunit alpha type-1
CN166_HUMAN	UPF0568 protein C14orf166	PSA2_HUMAN	Proteasome subunit alpha type-2
CN37_HUMAN	2',3'-cyclic-nucleotide 3'-phosphodiesterase	PSA3_HUMAN	Proteasome subunit alpha type-3
CNDP2_HUMAN	Cytosolic non-specific dipeptidase	PSA4_HUMAN	Proteasome subunit alpha type-4

CNN2_HUMAN	Calponin-2	PSA5_HUMAN	Proteasome subunit alpha type-5
CNPY2_HUMAN	Protein canopy homolog 2	PSA6_HUMAN	Proteasome subunit alpha type-6
CNST_HUMAN	Consortin	PSA7_HUMAN	Proteasome subunit alpha type-7
CO1A1_HUMAN	Collagen alpha-1(I) chain	PSB1_HUMAN	Proteasome subunit beta type-1
CO1A2_HUMAN	Collagen alpha-2(I) chain	PSB10_HUMAN	Proteasome subunit beta type-10
CO3_HUMAN	Complement C3	PSB2_HUMAN	Proteasome subunit beta type-2
CO3A1_HUMAN	Collagen alpha-1(III) chain	PSB3_HUMAN	Proteasome subunit beta type-3
CO4A_HUMAN	Complement C4-A	PSB4_HUMAN	Proteasome subunit beta type-4
CO4B_HUMAN	Complement C4-B	PSB7_HUMAN	Proteasome subunit beta type-7
CO5_HUMAN	Complement C5	PSB8_HUMAN	Proteasome subunit beta type-8
CO6A1_HUMAN	Collagen alpha-1(VI) chain	PSB9_HUMAN	Proteasome subunit beta type-9
CO6A3_HUMAN	Collagen alpha-3(VI) chain	PSD10_HUMAN	26S proteasome non-ATPase regulatory subunit 10
CO9_HUMAN	Complement component C9	PSD11_HUMAN	26S proteasome non-ATPase regulatory subunit 11
COF1_HUMAN	Cofilin-1	PSD12_HUMAN	26S proteasome non-ATPase regulatory subunit 12
COMP_HUMAN	Cartilage oligomeric matrix protein	PSD13_HUMAN	26S proteasome non-ATPase regulatory subunit 13
COMT_HUMAN	Catechol O-methyltransferase	PSDE_HUMAN	26S proteasome non-ATPase regulatory subunit 14
COPA_HUMAN	Coatomer subunit alpha	PSIP1_HUMAN	PC4 and SFRS1-interacting protein
COPB_HUMAN	Coatomer subunit beta	PSMD1_HUMAN	26S proteasome non-ATPase regulatory subunit 1
COPB2_HUMAN	Coatomer subunit beta'	PSMD2_HUMAN	26S proteasome non-ATPase regulatory subunit 2
COPD_HUMAN	Coatomer subunit delta	PSMD3_HUMAN	26S proteasome non-ATPase regulatory subunit 3
COPE_HUMAN	Coatomer subunit epsilon	PSMD5_HUMAN	26S proteasome non-ATPase regulatory subunit 5
COPG1_HUMAN	Coatomer subunit gamma-1	PSMD6_HUMAN	26S proteasome non-ATPase regulatory subunit 6
COPG2_HUMAN	Coatomer subunit gamma-2	PSMD7_HUMAN	26S proteasome non-ATPase regulatory subunit 7
COPZ1_HUMAN	Coatomer subunit zeta-1	PSMD8_HUMAN	26S proteasome non-ATPase regulatory subunit 8
COR1A_HUMAN	Coronin-1A	PSMD9_HUMAN	26S proteasome non-ATPase regulatory subunit 9
COR1B_HUMAN	Coronin-1B	PSME1_HUMAN	Proteasome activator complex subunit 1
COR1C_HUMAN	Coronin-1C	PSME2_HUMAN	Proteasome activator complex subunit 2
CORO7_HUMAN	Coronin-7	PSMF1_HUMAN	Proteasome inhibitor PI31 subunit
COTL1_HUMAN	Coactosin-like protein	PSPC1_HUMAN	Paraspeckle component 1
COX2_HUMAN	Cytochrome c oxidase subunit 2	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1
COX41_HUMAN	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	PTCA_HUMAN	Protein tyrosine phosphatase receptor type C-associated protein
COX5A_HUMAN	Cytochrome c oxidase subunit 5A, mitochondrial	PTMA_HUMAN	Prothymosin alpha
COX5B_HUMAN	Cytochrome c oxidase subunit 5B, mitochondrial	PTN1_HUMAN	Tyrosine-protein phosphatase non-receptor type 1

COX6C_HUMAN	Cytochrome c oxidase subunit 6C	PTN11_HUMAN	Tyrosine-protein phosphatase non-receptor type 11
CP062_HUMAN	UPF0505 protein C16orf62	PTN12_HUMAN	Tyrosine-protein phosphatase non-receptor type 12
CPIN1_HUMAN	Anamorsin	PTN6_HUMAN	Tyrosine-protein phosphatase non-receptor type 6
CPNE1_HUMAN	Copine-1	PTPA_HUMAN	Serine/threonine-protein phosphatase 2A activator
CPNE3_HUMAN	Copine-3	PTPRC_HUMAN	Receptor-type tyrosine-protein phosphatase C
CPNS1_HUMAN	Calpain small subunit 1	PTPRJ_HUMAN	Receptor-type tyrosine-protein phosphatase eta
CPPED_HUMAN	Serine/threonine-protein phosphatase CPPED1	PTPRO_HUMAN	Receptor-type tyrosine-protein phosphatase O
CPSF5_HUMAN	Cleavage and polyadenylation specificity factor subunit 5	PUR2_HUMAN	Trifunctional purine biosynthetic protein adenosine-3
CPSF6_HUMAN	Cleavage and polyadenylation specificity factor subunit 6	PUR4_HUMAN	Phosphoribosylformylglycinamidine synthase
CPT1A_HUMAN	Carnitine O-palmitoyltransferase 1, liver isoform	PUR6_HUMAN	Multifunctional protein ADE2
CREG1_HUMAN	Protein CREG1	PUR8_HUMAN	Adenylosuccinate lyase
CRKL_HUMAN	Crk-like protein	PUR9_HUMAN	Bifunctional purine biosynthesis protein PURH
CRLF3_HUMAN	Cytokine receptor-like factor 3	PURA_HUMAN	Transcriptional activator protein Pur-alpha
CS010_HUMAN	UPF0556 protein C19orf10	PURA2_HUMAN	Adenylosuccinate synthetase isozyme 2
CS066_HUMAN	UPF0515 protein C19orf66	PYGB_HUMAN	Glycogen phosphorylase, brain form
CSCL1_HUMAN	CSC1-like protein 1	PYGL_HUMAN	Glycogen phosphorylase, liver form
CSK_HUMAN	Tyrosine-protein kinase CSK	PYR1_HUMAN	CAD protein
CSK23_HUMAN	Casein kinase II subunit alpha 3	QCR1_HUMAN	Cytochrome b-c1 complex subunit 1, mitochondrial
CSN1_HUMAN	COP9 signalosome complex subunit 1	QCR2_HUMAN	Cytochrome b-c1 complex subunit 2, mitochondrial
CSN2_HUMAN	COP9 signalosome complex subunit 2	QCR7_HUMAN	Cytochrome b-c1 complex subunit 7
CSN4_HUMAN	COP9 signalosome complex subunit 4	QOR_HUMAN	Quinone oxidoreductase
CSN6_HUMAN	COP9 signalosome complex subunit 6	RAB10_HUMAN	Ras-related protein Rab-10
CSN8_HUMAN	COP9 signalosome complex subunit 8	RAB13_HUMAN	Ras-related protein Rab-13
CSRP1_HUMAN	Cysteine and glycine-rich protein 1	RAB14_HUMAN	Ras-related protein Rab-14
CTBP1_HUMAN	C-terminal-binding protein 1	RAB18_HUMAN	Ras-related protein Rab-18
CTL1_HUMAN	Choline transporter-like protein 1	RAB1A_HUMAN	Ras-related protein Rab-1A
CTND1_HUMAN	Catenin delta-1	RAB1B_HUMAN	Ras-related protein Rab-1B
CUL3_HUMAN	Cullin-3	RAB21_HUMAN	Ras-related protein Rab-21
CUL4B_HUMAN	Cullin-4B	RAB2A_HUMAN	Ras-related protein Rab-2A
CUTA_HUMAN	Protein CutA	RAB2B_HUMAN	Ras-related protein Rab-2B
CX6B1_HUMAN	Cytochrome c oxidase subunit 6B1	RAB32_HUMAN	Ras-related protein Rab-32
CX7A2_HUMAN	Cytochrome c oxidase subunit 7A2, mitochondrial	RAB37_HUMAN	Ras-related protein Rab-37
CXCL7_HUMAN	Platelet basic protein	RAB3C_HUMAN	Ras-related protein Rab-3C
CY1_HUMAN	Cytochrome c1, heme protein, mitochondrial	RAB3D_HUMAN	Ras-related protein Rab-3D
CY24A_HUMAN	Cytochrome b-245 light chain	RAB4A_HUMAN	Ras-related protein Rab-4A

CY24B_HUMAN	Cytochrome b-245 heavy chain	RAB4B_HUMAN	Ras-related protein Rab-4B
CYB5B_HUMAN	Cytochrome b5 type B	RAB5A_HUMAN	Ras-related protein Rab-5A
CYBP_HUMAN	Calcyclin-binding protein	RAB5B_HUMAN	Ras-related protein Rab-5B
CYC_HUMAN	Cytochrome c	RAB5C_HUMAN	Ras-related protein Rab-5C
CYFP1_HUMAN	Cytoplasmic FMR1-interacting protein 1	RAB6A_HUMAN	Ras-related protein Rab-6A
CYFP2_HUMAN	Cytoplasmic FMR1-interacting protein 2	RAB6B_HUMAN	Ras-related protein Rab-6B
CYTB_HUMAN	Cystatin-B	RAB6C_HUMAN	Ras-related protein Rab-6C
CYTSB_HUMAN	Cytospin-B	RAB7A_HUMAN	Ras-related protein Rab-7a
DAAM1_HUMAN	Disheveled-associated activator of morphogenesis 1	RAB8A_HUMAN	Ras-related protein Rab-8A
DAB2_HUMAN	Disabled homolog 2	RAB8B_HUMAN	Ras-related protein Rab-8B
DAD1_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	RABL6_HUMAN	Rab-like protein 6
DAPP1_HUMAN	Dual adapter for phosphotyrosine and 3-phosphotyrosine and 3-phosphoinositide	RAC1_HUMAN	Ras-related C3 botulinum toxin substrate 1
DAZP1_HUMAN	DAZ-associated protein 1	RAC2_HUMAN	Ras-related C3 botulinum toxin substrate 2
DBLOH_HUMAN	Diablo homolog, mitochondrial	RAC3_HUMAN	Ras-related C3 botulinum toxin substrate 3
DBNL_HUMAN	Drebrin-like protein	RADI_HUMAN	Radixin
DC1I2_HUMAN	Cytoplasmic dynein 1 intermediate chain 2	RAE1L_HUMAN	mRNA export factor
DCAF7_HUMAN	DDB1- and CUL4-associated factor 7	RALA_HUMAN	Ras-related protein Ral-A
DCD_HUMAN	Dermcidin	RALB_HUMAN	Ras-related protein Ral-B
DCK_HUMAN	Deoxycytidine kinase	RALY_HUMAN	RNA-binding protein Raly
DCPS_HUMAN	m7GpppX diphosphatase	RAN_HUMAN	GTP-binding nuclear protein Ran
DCTN1_HUMAN	Dynactin subunit 1	RANG_HUMAN	Ran-specific GTPase-activating protein
DCTN2_HUMAN	Dynactin subunit 2	RAP1A_HUMAN	Ras-related protein Rap-1A
DCTN3_HUMAN	Dynactin subunit 3	RAP1B_HUMAN	Ras-related protein Rap-1b
DCTN4_HUMAN	Dynactin subunit 4	RAP2B_HUMAN	Ras-related protein Rap-2b
DCUP_HUMAN	Uroporphyrinogen decarboxylase	RASA3_HUMAN	Ras GTPase-activating protein 3
DCXR_HUMAN	L-xylulose reductase	RASH_HUMAN	GTPase HRas
DDAH2_HUMAN	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	RASK_HUMAN	GTPase KRas
DDB1_HUMAN	DNA damage-binding protein 1	RASL3_HUMAN	RAS protein activator like-3
DDRGK_HUMAN	DDRGK domain-containing protein 1	RB11B_HUMAN	Ras-related protein Rab-11B
DDX1_HUMAN	ATP-dependent RNA helicase DDX1	RB27B_HUMAN	Ras-related protein Rab-27B
DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17	RBBP4_HUMAN	Histone-binding protein RBBP4
DDX21_HUMAN	Nucleolar RNA helicase 2	RBBP7_HUMAN	Histone-binding protein RBBP7
DDX3X_HUMAN	ATP-dependent RNA helicase DDX3X	RBM14_HUMAN	RNA-binding protein 14
DDX3Y_HUMAN	ATP-dependent RNA helicase DDX3Y	RBM25_HUMAN	RNA-binding protein 25
DDX5_HUMAN	Probable ATP-dependent RNA helicase DDX5	RBM3_HUMAN	RNA-binding protein 3
DDX6_HUMAN	Probable ATP-dependent RNA helicase DDX6	RBM39_HUMAN	RNA-binding protein 39
DECR_HUMAN	2,4-dienoyl-CoA reductase, mitochondrial	RBMX_HUMAN	RNA-binding motif protein, X chromosome

DEK_HUMAN	Protein DEK	RBP56_HUMAN	TATA-binding protein-associated factor 2N
DEMA_HUMAN	Dematin	RCC2_HUMAN	Protein RCC2
DENR_HUMAN	Density-regulated protein	RCN2_HUMAN	Reticulocalbin-2
DEOC_HUMAN	Deoxyribose-phosphate aldolase	RD23B_HUMAN	UV excision repair protein RAD23 homolog B
DERL1_HUMAN	Derlin-1	RDH11_HUMAN	Retinol dehydrogenase 11
DESP_HUMAN	Desmoplakin	RECQ1_HUMAN	ATP-dependent DNA helicase Q1
DEST_HUMAN	Destrin	REEP5_HUMAN	Receptor expression-enhancing protein 5
DGKA_HUMAN	Diacylglycerol kinase alpha	RENBP_HUMAN	N-acylglucosamine 2-epimerase
DHAK_HUMAN	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	RENT1_HUMAN	Regulator of nonsense transcripts 1
DHB11_HUMAN	Estradiol 17-beta-dehydrogenase 11	RET4_HUMAN	Retinol-binding protein 4
DHB12_HUMAN	Estradiol 17-beta-dehydrogenase 12	RFA1_HUMAN	Replication protein A 70 kDa DNA-binding subunit
DHB4_HUMAN	Peroxisomal multifunctional enzyme type 2	RFA3_HUMAN	Replication protein A 14 kDa subunit
DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial	RFIP3_HUMAN	Rab11 family-interacting protein 3
DHPR_HUMAN	Dihydropteridine reductase	RGCC_HUMAN	Regulator of cell cycle RGCC
DHRS4_HUMAN	Dehydrogenase/reductase SDR family member 4	RGS10_HUMAN	Regulator of G-protein signaling 10
DHRS7_HUMAN	Dehydrogenase/reductase SDR family member 7	RGS18_HUMAN	Regulator of G-protein signaling 18
DHSO_HUMAN	Sorbitol dehydrogenase	RGS6_HUMAN	Regulator of G-protein signaling 6
DHX15_HUMAN	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	RHG01_HUMAN	Rho GTPase-activating protein 1
DHX9_HUMAN	ATP-dependent RNA helicase A	RHG04_HUMAN	Rho GTPase-activating protein 4
DIAP1_HUMAN	Protein diaphanous homolog 1	RHG06_HUMAN	Rho GTPase-activating protein 6
DJB11_HUMAN	DnaJ homolog subfamily B member 11	RHG17_HUMAN	Rho GTPase-activating protein 17
DJC13_HUMAN	DnaJ homolog subfamily C member 13	RHG18_HUMAN	Rho GTPase-activating protein 18
DKC1_HUMAN	H/ACA ribonucleoprotein complex subunit 4	RHG25_HUMAN	Rho GTPase-activating protein 25
DLDH_HUMAN	Dihydrolipoyl dehydrogenase, mitochondrial	RHOA_HUMAN	Transforming protein RhoA
DNJA1_HUMAN	DnaJ homolog subfamily A member 1	RHOC_HUMAN	Rho-related GTP-binding protein RhoC
DNJA2_HUMAN	DnaJ homolog subfamily A member 2	RHOG_HUMAN	Rho-related GTP-binding protein RhoG
DNJB1_HUMAN	DnaJ homolog subfamily B member 1	RIC8A_HUMAN	Synembryn-A
DNJB2_HUMAN	DnaJ homolog subfamily B member 2	RINI_HUMAN	Ribonuclease inhibitor
DNJC3_HUMAN	DnaJ homolog subfamily C member 3	RIPK1_HUMAN	Receptor-interacting serine/threonine-protein kinase 1
DNJC7_HUMAN	DnaJ homolog subfamily C member 7	RISC_HUMAN	Retinoid-inducible serine carboxypeptidase
DNJC9_HUMAN	DnaJ homolog subfamily C member 9	RL10_HUMAN	60S ribosomal protein L10
DNLI3_HUMAN	DNA ligase 3	RL10A_HUMAN	60S ribosomal protein L10a
DNM1L_HUMAN	Dynamin-1-like protein	RL11_HUMAN	60S ribosomal protein L11
DNPH1_HUMAN	2'-deoxynucleoside 5'-phosphate N-hydrolase 1	RL12_HUMAN	60S ribosomal protein L12
DOC10_HUMAN	Dedicator of cytokinesis protein 10	RL13_HUMAN	60S ribosomal protein L13

DOCK2_HUMAN	Dedicator of cytokinesis protein 2	RL13A_HUMAN	60S ribosomal protein L13a
DOCK8_HUMAN	Dedicator of cytokinesis protein 8	RL14_HUMAN	60S ribosomal protein L14
DOK1_HUMAN	Docking protein 1	RL15_HUMAN	60S ribosomal protein L15
DOK2_HUMAN	Docking protein 2	RL17_HUMAN	60S ribosomal protein L17
DOK3_HUMAN	Docking protein 3	RL18_HUMAN	60S ribosomal protein L18
DOPD_HUMAN	D-dopachrome decarboxylase	RL18A_HUMAN	60S ribosomal protein L18a
DP13A_HUMAN	DCC-interacting protein 13-alpha	RL19_HUMAN	60S ribosomal protein L19
DP13B_HUMAN	DCC-interacting protein 13-beta	RL21_HUMAN	60S ribosomal protein L21
DPM1_HUMAN	Dolichol-phosphate mannosyltransferase subunit 1	RL22_HUMAN	60S ribosomal protein L22
DPP2_HUMAN	Dipeptidyl peptidase 2	RL23_HUMAN	60S ribosomal protein L23
DPP3_HUMAN	Dipeptidyl peptidase 3	RL23A_HUMAN	60S ribosomal protein L23a
DPYL2_HUMAN	Dihydropyrimidinase-related protein 2	RL24_HUMAN	60S ribosomal protein L24
DRA_HUMAN	HLA class II histocompatibility antigen, DR alpha chain	RL26L_HUMAN	60S ribosomal protein L26-like 1
DREB_HUMAN	Drebrin	RL27_HUMAN	60S ribosomal protein L27
DRG1_HUMAN	Developmentally-regulated GTP-binding protein 1	RL27A_HUMAN	60S ribosomal protein L27a
DTD1_HUMAN	D-tyrosyl-tRNA(Tyr) deacylase 1	RL28_HUMAN	60S ribosomal protein L28
DUS3_HUMAN	Dual specificity protein phosphatase 3	RL29_HUMAN	60S ribosomal protein L29
DX39A_HUMAN	ATP-dependent RNA helicase DDX39A	RL3_HUMAN	60S ribosomal protein L3
DX39B_HUMAN	Spliceosome RNA helicase DDX39B	RL30_HUMAN	60S ribosomal protein L30
DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1	RL31_HUMAN	60S ribosomal protein L31
DYL2_HUMAN	Dynein light chain 2, cytoplasmic	RL32_HUMAN	60S ribosomal protein L32
DYN1_HUMAN	Dynamin-1	RL34_HUMAN	60S ribosomal protein L34
DYN2_HUMAN	Dynamin-2	RL35_HUMAN	60S ribosomal protein L35
DYN3_HUMAN	Dynamin-3	RL35A_HUMAN	60S ribosomal protein L35a
ECE1_HUMAN	Endothelin-converting enzyme 1	RL36_HUMAN	60S ribosomal protein L36
ECH1_HUMAN	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	RL38_HUMAN	60S ribosomal protein L38
ECHA_HUMAN	Trifunctional enzyme subunit alpha, mitochondrial	RL4_HUMAN	60S ribosomal protein L4
ECHB_HUMAN	Trifunctional enzyme subunit beta, mitochondrial	RL40_HUMAN	Ubiquitin-60S ribosomal protein L40
ECHD1_HUMAN	Ethylmalonyl-CoA decarboxylase	RL5_HUMAN	60S ribosomal protein L5
ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial	RL6_HUMAN	60S ribosomal protein L6
ECI2_HUMAN	Enoyl-CoA delta isomerase 2, mitochondrial	RL7_HUMAN	60S ribosomal protein L7
ECP_HUMAN	Eosinophil cationic protein	RL7A_HUMAN	60S ribosomal protein L7a
EDEM1_HUMAN	ER degradation-enhancing alpha-mannosidase-like protein 1	RL8_HUMAN	60S ribosomal protein L8
EEA1_HUMAN	Early endosome antigen 1	RL9_HUMAN	60S ribosomal protein L9
EF1A3_HUMAN	Putative elongation factor 1-alpha-like 3	RLA0_HUMAN	60S acidic ribosomal protein P0
EF1B_HUMAN	Elongation factor 1-beta	RLA1_HUMAN	60S acidic ribosomal protein P1
EF1D_HUMAN	Elongation factor 1-delta	RLA2_HUMAN	60S acidic ribosomal protein P2
EF1G_HUMAN	Elongation factor 1-gamma	RMXL1_HUMAN	RNA binding motif protein, X-linked-like-1
EF2_HUMAN	Elongation factor 2	RN213_HUMAN	E3 ubiquitin-protein ligase RNF213
EFHD2_HUMAN	EF-hand domain-containing protein D2	RN5A_HUMAN	2-5A-dependent ribonuclease
EFNB1_HUMAN	Ephrin-B1	RNF11_HUMAN	RING finger protein 11
EFTU_HUMAN	Elongation factor Tu, mitochondrial	RNPS1_HUMAN	RNA-binding protein with serine-rich domain 1

EHD1_HUMAN	EH domain-containing protein 1	RNT2_HUMAN	Ribonuclease T2
EHD3_HUMAN	EH domain-containing protein 3	RO52_HUMAN	E3 ubiquitin-protein ligase TRIM21
EHD4_HUMAN	EH domain-containing protein 4	RO60_HUMAN	60 kDa SS-A/Ro ribonucleoprotein
EIF1_HUMAN	Eukaryotic translation initiation factor 1	ROA0_HUMAN	Heterogeneous nuclear ribonucleoprotein A0
EIF3A_HUMAN	Eukaryotic translation initiation factor 3 subunit A	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1
EIF3B_HUMAN	Eukaryotic translation initiation factor 3 subunit B	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1
EIF3C_HUMAN	Eukaryotic translation initiation factor 3 subunit C	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3
EIF3D_HUMAN	Eukaryotic translation initiation factor 3 subunit D	ROAA_HUMAN	Heterogeneous nuclear ribonucleoprotein A/B
EIF3E_HUMAN	Eukaryotic translation initiation factor 3 subunit E	ROCK1_HUMAN	Rho-associated protein kinase 1
EIF3F_HUMAN	Eukaryotic translation initiation factor 3 subunit F	ROCK2_HUMAN	Rho-associated protein kinase 2
EIF3G_HUMAN	Eukaryotic translation initiation factor 3 subunit G	RPB2_HUMAN	DNA-directed RNA polymerase II subunit RPB2
EIF3H_HUMAN	Eukaryotic translation initiation factor 3 subunit H	RPB9_HUMAN	DNA-directed RNA polymerase II subunit RPB9
EIF3I_HUMAN	Eukaryotic translation initiation factor 3 subunit I	RPN1_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1
EIF3J_HUMAN	Eukaryotic translation initiation factor 3 subunit J	RPN2_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2
EIF3K_HUMAN	Eukaryotic translation initiation factor 3 subunit K	RPR1B_HUMAN	Regulation of nuclear pre-mRNA domain-containing protein 1B
EIF3L_HUMAN	Eukaryotic translation initiation factor 3 subunit L	RRAS_HUMAN	Ras-related protein R-Ras
ELAV1_HUMAN	ELAV-like protein 1	RRBP1_HUMAN	Ribosome-binding protein 1
ELMO1_HUMAN	Engulfment and cell motility protein 1	RRF2M_HUMAN	Ribosome-releasing factor 2, mitochondrial
ELNE_HUMAN	Neutrophil elastase	RS10_HUMAN	40S ribosomal protein S10
ELOB_HUMAN	Transcription elongation factor B polypeptide 2	RS11_HUMAN	40S ribosomal protein S11
EM55_HUMAN	55 kDa erythrocyte membrane protein	RS12_HUMAN	40S ribosomal protein S12
EMAL2_HUMAN	Echinoderm microtubule-associated protein-like 2	RS13_HUMAN	40S ribosomal protein S13
EMAL3_HUMAN	Echinoderm microtubule-associated protein-like 3	RS14_HUMAN	40S ribosomal protein S14
EMD_HUMAN	Emerin	RS15A_HUMAN	40S ribosomal protein S15a
EMIL1_HUMAN	EMILIN-1	RS16_HUMAN	40S ribosomal protein S16
EMSA1_HUMAN	ELM2 and SANT domain-containing protein 1	RS17L_HUMAN	40S ribosomal protein S17-like
ENDD1_HUMAN	Endonuclease domain-containing 1 protein	RS18_HUMAN	40S ribosomal protein S18
ENOA_HUMAN	Alpha-enolase	RS19_HUMAN	40S ribosomal protein S19
ENOG_HUMAN	Gamma-enolase	RS2_HUMAN	40S ribosomal protein S2
ENOPH_HUMAN	Enolase-phosphatase E1	RS20_HUMAN	40S ribosomal protein S20
ENPL_HUMAN	Endoplasmin	RS23_HUMAN	40S ribosomal protein S23

ENPP7_HUMAN	Ectonucleotide pyrophosphatase/phosphodiesterase family member 7	RS24_HUMAN	40S ribosomal protein S24
EP15R_HUMAN	Epidermal growth factor receptor substrate 15-like 1	RS25_HUMAN	40S ribosomal protein S25
EPDR1_HUMAN	Mammalian ependymin-related protein 1	RS26_HUMAN	40S ribosomal protein S26
EPN1_HUMAN	Epsin-1	RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a
EPN4_HUMAN	Clathrin interactor 1	RS27L_HUMAN	40S ribosomal protein S27-like
EPS15_HUMAN	Epidermal growth factor receptor substrate 15	RS28_HUMAN	40S ribosomal protein S28
ERAP1_HUMAN	Endoplasmic reticulum aminopeptidase 1	RS3_HUMAN	40S ribosomal protein S3
ERAP2_HUMAN	Endoplasmic reticulum aminopeptidase 2	RS30_HUMAN	40S ribosomal protein S30
ERF1_HUMAN	Eukaryotic peptide chain release factor subunit 1	RS3A_HUMAN	40S ribosomal protein S3a
ERF3A_HUMAN	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	RS4X_HUMAN	40S ribosomal protein S4, X isoform
ERG7_HUMAN	Lanosterol synthase	RS4Y2_HUMAN	40S ribosomal protein S4, Y isoform 2
ERGI1_HUMAN	Endoplasmic reticulum-Golgi intermediate compartment protein 1	RS5_HUMAN	40S ribosomal protein S5
ERLN1_HUMAN	Erlin-1	RS6_HUMAN	40S ribosomal protein S6
ERO1A_HUMAN	ERO1-like protein alpha	RS7_HUMAN	40S ribosomal protein S7
ERP29_HUMAN	Endoplasmic reticulum resident protein 29	RS8_HUMAN	40S ribosomal protein S8
ERP44_HUMAN	Endoplasmic reticulum resident protein 44	RS9_HUMAN	40S ribosomal protein S9
ES1_HUMAN	ES1 protein homolog, mitochondrial	RSMN_HUMAN	Small nuclear ribonucleoprotein-associated protein N
ESAM_HUMAN	Endothelial cell-selective adhesion molecule	RSSA_HUMAN	40S ribosomal protein SA
EST1_HUMAN	Liver carboxylesterase 1	RSU1_HUMAN	Ras suppressor protein 1
ESTD_HUMAN	S-formylglutathione hydrolase	RTCA_HUMAN	RNA 3'-terminal phosphate cyclase
ESYT1_HUMAN	Extended synaptotagmin-1	RTCB_HUMAN	tRNA-splicing ligase RtcB homolog
ESYT2_HUMAN	Extended synaptotagmin-2	RTN1_HUMAN	Reticulon-1
ETFA_HUMAN	Electron transfer flavoprotein subunit alpha, mitochondrial	RTN2_HUMAN	Reticulon-2
ETFB_HUMAN	Electron transfer flavoprotein subunit beta	RTN3_HUMAN	Reticulon-3
ETHE1_HUMAN	Persulfide dioxygenase ETHE1, mitochondrial	RTN4_HUMAN	Reticulon-4
EVL_HUMAN	Ena/VASP-like protein	RU17_HUMAN	U1 small nuclear ribonucleoprotein 70 kDa
EWS_HUMAN	RNA-binding protein EWS	RU2A_HUMAN	U2 small nuclear ribonucleoprotein A'
EXOC2_HUMAN	Exocyst complex component 2	RU2B_HUMAN	U2 small nuclear ribonucleoprotein B''
EZRI_HUMAN	Ezrin	RUFY1_HUMAN	RUN and FYVE domain-containing protein 1
F10A1_HUMAN	Hsc70-interacting protein	RUVB1_HUMAN	RuvB-like 1

F1142_HUMAN	Protein FAM114A2	RUVB2_HUMAN	RuvB-like 2
F120A_HUMAN	Constitutive coactivator of PPAR-gamma-like protein 1	RUXE_HUMAN	Small nuclear ribonucleoprotein E
F13A_HUMAN	Coagulation factor XIII A chain	RUXF_HUMAN	Small nuclear ribonucleoprotein F
F162A_HUMAN	Protein FAM162A	S10A4_HUMAN	Protein S100-A4
F16P1_HUMAN	Fructose-1,6-bisphosphatase 1	S10A6_HUMAN	Protein S100-A6
F1712_HUMAN	Protein FAM171A2	S10A7_HUMAN	Protein S100-A7
F177A_HUMAN	Protein FAM177A1	S10A8_HUMAN	Protein S100-A8
FA10_HUMAN	Coagulation factor X	S10A9_HUMAN	Protein S100-A9
FA49B_HUMAN	Protein FAM49B	S10AA_HUMAN	Protein S100-A10
FA5_HUMAN	Coagulation factor V	S10AB_HUMAN	Protein S100-A11
FA63A_HUMAN	Protein FAM63A	S38A2_HUMAN	Sodium-coupled neutral amino acid transporter 2
FA98B_HUMAN	Protein FAM98B	SAC1_HUMAN	Phosphatidylinositide phosphatase SAC1
FAAA_HUMAN	Fumarylacetoacetase	SAE1_HUMAN	SUMO-activating enzyme subunit 1
FABP5_HUMAN	Fatty acid-binding protein, epidermal	SAFB2_HUMAN	Scaffold attachment factor B2
FACE1_HUMAN	CAAX prenyl protease 1 homolog	SAHH_HUMAN	Adenosylhomocysteinase
FAF1_HUMAN	FAS-associated factor 1	SAHH3_HUMAN	Putative adenosylhomocysteinase 3
FAF2_HUMAN	FAS-associated factor 2	SAMH1_HUMAN	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1
FAK1_HUMAN	Focal adhesion kinase 1	SAP18_HUMAN	Histone deacetylase complex subunit SAP18
FAK2_HUMAN	Protein-tyrosine kinase 2-beta	SAR1A_HUMAN	GTP-binding protein SAR1a
FAS_HUMAN	Fatty acid synthase	SARNP_HUMAN	SAP domain-containing ribonucleoprotein
FBLN1_HUMAN	Fibulin-1	SART3_HUMAN	Squamous cell carcinoma antigen recognized by T-cells 3
FBRL_HUMAN	rRNA 2'-O-methyltransferase fibrillarin	SASH3_HUMAN	SAM and SH3 domain-containing protein 3
FBX7_HUMAN	F-box only protein 7	SC11A_HUMAN	Signal peptidase complex catalytic subunit SEC11A
FCERG_HUMAN	High affinity immunoglobulin epsilon receptor subunit gamma	SC22B_HUMAN	Vesicle-trafficking protein SEC22b
FCG2C_HUMAN	Low affinity immunoglobulin gamma Fc region receptor II-c	SC23A_HUMAN	Protein transport protein Sec23A
FCG3A_HUMAN	Low affinity immunoglobulin gamma Fc region receptor III-A	SC23B_HUMAN	Protein transport protein Sec23B
FCL_HUMAN	GDP-L-fucose synthase	SC24C_HUMAN	Protein transport protein Sec24C
FCN1_HUMAN	Ficolin-1	SC31A_HUMAN	Protein transport protein Sec31A
FEN1_HUMAN	Flap endonuclease 1	SC61B_HUMAN	Protein transport protein Sec61 subunit beta
FETA_HUMAN	Alpha-fetoprotein	SCAFB_HUMAN	Protein SCAF11
FETUA_HUMAN	Alpha-2-HS-glycoprotein	SCAM2_HUMAN	Secretory carrier-associated membrane protein 2
FHL1_HUMAN	Four and a half LIM domains protein 1	SCAM3_HUMAN	Secretory carrier-associated membrane protein 3
FHOD1_HUMAN	FH1/FH2 domain-containing protein 1	SCFD1_HUMAN	Sec1 family domain-containing protein 1
FHR1_HUMAN	Complement factor H-related protein 1	SCMC1_HUMAN	Calcium-binding mitochondrial carrier protein SCaMC-1
FIBA_HUMAN	Fibrinogen alpha chain	SCOT1_HUMAN	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial

FIBB_HUMAN	Fibrinogen beta chain	SCPDL_HUMAN	Saccharopine dehydrogenase-like oxidoreductase
FIBG_HUMAN	Fibrinogen gamma chain	SCRN1_HUMAN	Secernin-1
FINC_HUMAN	Fibronectin	SCYL2_HUMAN	SCY1-like protein 2
FKB15_HUMAN	FK506-binding protein 15	SDHA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial
FKB1A_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP1A	SDHB_HUMAN	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial
FKBP2_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP2	SDOS_HUMAN	Protein syndesmos
FKBP3_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP3	SDPR_HUMAN	Serum deprivation-response protein
FKBP4_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP4	SEC13_HUMAN	Protein SEC13 homolog
FKBP5_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP5	SELH_HUMAN	Selenoprotein H
FLII_HUMAN	Protein flightless-1 homolog	SEP11_HUMAN	Septin-11
FLNA_HUMAN	Filamin-A	SEP15_HUMAN	15 kDa selenoprotein
FLNB_HUMAN	Filamin-B	SEPT1_HUMAN	Septin-1
FLOT1_HUMAN	Flotillin-1	SEPT2_HUMAN	Septin-2
FLOT2_HUMAN	Flotillin-2	SEPT4_HUMAN	Septin-4
FMNL_HUMAN	Formin-like protein 1	SEPT5_HUMAN	Septin-5
FN3K_HUMAN	Fructosamine-3-kinase	SEPT6_HUMAN	Septin-6
FNBP1_HUMAN	Formin-binding protein 1	SEPT7_HUMAN	Septin-7
FPPS_HUMAN	Farnesyl pyrophosphate synthase	SEPT9_HUMAN	Septin-9
FRIH_HUMAN	Ferritin heavy chain	SERA_HUMAN	D-3-phosphoglycerate dehydrogenase
FRIL_HUMAN	Ferritin light chain	SERPH_HUMAN	Serpin H1
FRM4B_HUMAN	FERM domain-containing protein 4B	SET_HUMAN	Protein SET
FUBP1_HUMAN	Far upstream element-binding protein 1	SETD8_HUMAN	N-lysine methyltransferase SETD8
FUBP2_HUMAN	Far upstream element-binding protein 2	SF01_HUMAN	Splicing factor 1
FUBP3_HUMAN	Far upstream element-binding protein 3	SF3A1_HUMAN	Splicing factor 3A subunit 1
FUMH_HUMAN	Fumarate hydratase, mitochondrial	SF3A3_HUMAN	Splicing factor 3A subunit 3
FUS_HUMAN	RNA-binding protein FUS	SF3B1_HUMAN	Splicing factor 3B subunit 1
FYB_HUMAN	FYN-binding protein	SF3B2_HUMAN	Splicing factor 3B subunit 2
FYN_HUMAN	Tyrosine-protein kinase Fyn	SF3B3_HUMAN	Splicing factor 3B subunit 3
G3BP1_HUMAN	Ras GTPase-activating protein-binding protein 1	SF3B4_HUMAN	Splicing factor 3B subunit 4
G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich
G6B_HUMAN	Protein G6b	SFXN1_HUMAN	Sideroflexin-1
G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase	SFXN3_HUMAN	Sideroflexin-3
G6PI_HUMAN	Glucose-6-phosphate isomerase	SH21A_HUMAN	SH2 domain-containing protein 1A
GALK1_HUMAN	Galactokinase	SH3G1_HUMAN	Endophilin-A2
GALM_HUMAN	Aldose 1-epimerase	SH3K1_HUMAN	SH3 domain-containing kinase-binding protein 1

GANAB_HUMAN	Neutral alpha-glucosidase AB	SH3L1_HUMAN	SH3 domain-binding glutamic acid-rich-like protein
GAPR1_HUMAN	Golgi-associated plant pathogenesis-related protein 1	SH3L2_HUMAN	SH3 domain-binding glutamic acid-rich-like protein 2
GAR1_HUMAN	H/ACA ribonucleoprotein complex subunit 1	SH3L3_HUMAN	SH3 domain-binding glutamic acid-rich-like protein 3
GBB1_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	SHBG_HUMAN	Sex hormone-binding globulin
GBB2_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	SHIP1_HUMAN	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1
GBLP_HUMAN	Guanine nucleotide-binding protein subunit beta-2-like 1	SHLB1_HUMAN	Endophilin-B1
GBP1_HUMAN	Interferon-induced guanylate-binding protein 1	SHLB2_HUMAN	Endophilin-B2
GCDH_HUMAN	Glutaryl-CoA dehydrogenase, mitochondrial	SIAS_HUMAN	Sialic acid synthase
GCYA3_HUMAN	Guanylate cyclase soluble subunit alpha-3	SIR2_HUMAN	NAD-dependent protein deacetylase sirtuin-2
GCYB1_HUMAN	Guanylate cyclase soluble subunit beta-1	SKAP1_HUMAN	Src kinase-associated phosphoprotein 1
GDE_HUMAN	Glycogen debranching enzyme	SKAP2_HUMAN	Src kinase-associated phosphoprotein 2
GDIA_HUMAN	Rab GDP dissociation inhibitor alpha	SKP1_HUMAN	S-phase kinase-associated protein 1
GDIB_HUMAN	Rab GDP dissociation inhibitor beta	SLAF5_HUMAN	SLAM family member 5
GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1	SLAI2_HUMAN	SLAIN motif-containing protein 2
GDIR2_HUMAN	Rho GDP-dissociation inhibitor 2	SLFN5_HUMAN	Schlafen family member 5
GDN_HUMAN	Glia-derived nexin	SLK_HUMAN	STE20-like serine/threonine-protein kinase
GDS1_HUMAN	Rap1 GTPase-GDP dissociation stimulator 1	SLMAP_HUMAN	Sarcolemmal membrane-associated protein
GELS_HUMAN	Gelsolin	SLN14_HUMAN	Schlafen family member 14
GET4_HUMAN	Golgi to ER traffic protein 4 homolog	SMAKA_HUMAN	Small membrane A-kinase anchor protein
GFPT1_HUMAN	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	SMAP2_HUMAN	Stromal membrane-associated protein 2
GIMA1_HUMAN	GTPase IMAP family member 1	SMC1A_HUMAN	Structural maintenance of chromosomes protein 1A
GIMA4_HUMAN	GTPase IMAP family member 4	SMC3_HUMAN	Structural maintenance of chromosomes protein 3
GIMA5_HUMAN	GTPase IMAP family member 5	SMD1_HUMAN	Small nuclear ribonucleoprotein Sm D1
GIMA7_HUMAN	GTPase IMAP family member 7	SMD2_HUMAN	Small nuclear ribonucleoprotein Sm D2
GIMA8_HUMAN	GTPase IMAP family member 8	SMD3_HUMAN	Small nuclear ribonucleoprotein Sm D3
GIPC1_HUMAN	PDZ domain-containing protein GIPC1	SMIM1_HUMAN	Small integral membrane protein 1
GIPC3_HUMAN	PDZ domain-containing protein GIPC3	SMRD2_HUMAN	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2
GIT1_HUMAN	ARF GTPase-activating protein GIT1	SNAA_HUMAN	Alpha-soluble NSF attachment protein
GLCM_HUMAN	Glucosylceramidase	SNAG_HUMAN	Gamma-soluble NSF attachment protein

GLGB_HUMAN	1,4-alpha-glucan-branching enzyme	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1
GLO2_HUMAN	Hydroxyacylglutathione hydrolase, mitochondrial	SNP23_HUMAN	Synaptosomal-associated protein 23
GLOD4_HUMAN	Glyoxalase domain-containing protein 4	SNP29_HUMAN	Synaptosomal-associated protein 29
GLPK_HUMAN	Glycerol kinase	SNTB1_HUMAN	Beta-1-syntrophin
GLRX3_HUMAN	Glutaredoxin-3	SNX12_HUMAN	Sorting nexin-12
GLSK_HUMAN	Glutaminase kidney isoform, mitochondrial	SNX2_HUMAN	Sorting nexin-2
GLU2B_HUMAN	Glucosidase 2 subunit beta	SNX3_HUMAN	Sorting nexin-3
GLYC_HUMAN	Serine hydroxymethyltransferase, cytosolic	SNX5_HUMAN	Sorting nexin-5
GLYM_HUMAN	Serine hydroxymethyltransferase, mitochondrial	SNX6_HUMAN	Sorting nexin-6
GLYR1_HUMAN	Putative oxidoreductase GLYR1	SNX9_HUMAN	Sorting nexin-9
GMFG_HUMAN	Glia maturation factor gamma	SODC_HUMAN	Superoxide dismutase [Cu-Zn]
GMPPA_HUMAN	Mannose-1-phosphate guanyltransferase alpha	SODM_HUMAN	Superoxide dismutase [Mn], mitochondrial
GMPPB_HUMAN	Mannose-1-phosphate guanyltransferase beta	SORCN_HUMAN	Sorcin
GMPR1_HUMAN	GMP reductase 1	SP16H_HUMAN	FACT complex subunit SPT16
GNA13_HUMAN	Guanine nucleotide-binding protein subunit alpha-13	SPB10_HUMAN	Serpin B10
GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2	SPB4_HUMAN	Serpin B4
GNAI3_HUMAN	Guanine nucleotide-binding protein G(k) subunit alpha	SPB6_HUMAN	Serpin B6
GNAQ_HUMAN	Guanine nucleotide-binding protein G(q) subunit alpha	SPB8_HUMAN	Serpin B8
GNAS1_HUMAN	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	SPB9_HUMAN	Serpin B9
GNAZ_HUMAN	Guanine nucleotide-binding protein G(z) subunit alpha	SPCS1_HUMAN	Signal peptidase complex subunit 1
GNLY_HUMAN	Granulysin	SPCS2_HUMAN	Signal peptidase complex subunit 2
GOT1B_HUMAN	Vesicle transport protein GOT1B	SPCS3_HUMAN	Signal peptidase complex subunit 3
GP1BA_HUMAN	Platelet glycoprotein Ib alpha chain	SPG20_HUMAN	Spartin
GP1BB_HUMAN	Platelet glycoprotein Ib beta chain	SPHM_HUMAN	N-sulphoglucosamine sulphohydrolase
GPD1L_HUMAN	Glycerol-3-phosphate dehydrogenase 1-like protein	SPN90_HUMAN	NCK-interacting protein with SH3 domain
GPDM_HUMAN	Glycerol-3-phosphate dehydrogenase, mitochondrial	SPRC_HUMAN	SPARC
GPIX_HUMAN	Platelet glycoprotein IX	SPT5H_HUMAN	Transcription elongation factor SPT5
GPV_HUMAN	Platelet glycoprotein V	SPTB1_HUMAN	Spectrin beta chain, erythrocytic
GPVI_HUMAN	Platelet glycoprotein VI	SPTB2_HUMAN	Spectrin beta chain, non-erythrocytic 1
GPX1_HUMAN	Glutathione peroxidase 1	SPTC1_HUMAN	Serine palmitoyltransferase 1
GPX4_HUMAN	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial	SPTN1_HUMAN	Spectrin alpha chain, non-erythrocytic 1
GRAA_HUMAN	Granzyme A	SQRD_HUMAN	Sulfide:quinone oxidoreductase, mitochondrial

GRAH_HUMAN	Granzyme H	SRC_HUMAN	Proto-oncogene tyrosine-protein kinase Src
GRAM_HUMAN	Granzyme M	SRC8_HUMAN	Src substrate cortactin
GRAN_HUMAN	Grancalcin	SRGN_HUMAN	Serglycin
GRAP1_HUMAN	GRIP1-associated protein 1	SRP09_HUMAN	Signal recognition particle 9 kDa protein
GRAP2_HUMAN	GRB2-related adapter protein 2	SRP14_HUMAN	Signal recognition particle 14 kDa protein
GRB2_HUMAN	Growth factor receptor-bound protein 2	SRP54_HUMAN	Signal recognition particle 54 kDa protein
GRHPR_HUMAN	Glyoxylate reductase/hydroxypyruvate reductase	SRPRB_HUMAN	Signal recognition particle receptor subunit beta
GRK6_HUMAN	G protein-coupled receptor kinase 6	SRRT_HUMAN	Serrate RNA effector molecule homolog
GRP2_HUMAN	RAS guanyl-releasing protein 2	SRS10_HUMAN	Serine/arginine-rich splicing factor 10
GRP75_HUMAN	Stress-70 protein, mitochondrial	SRSF1_HUMAN	Serine/arginine-rich splicing factor 1
GRP78_HUMAN	78 kDa glucose-regulated protein	SRSF2_HUMAN	Serine/arginine-rich splicing factor 2
GSDMD_HUMAN	Gasdermin-D	SRSF3_HUMAN	Serine/arginine-rich splicing factor 3
GSHB_HUMAN	Glutathione synthetase	SRSF4_HUMAN	Serine/arginine-rich splicing factor 4
GSHR_HUMAN	Glutathione reductase, mitochondrial	SRSF6_HUMAN	Serine/arginine-rich splicing factor 6
GSTK1_HUMAN	Glutathione S-transferase kappa 1	SRSF7_HUMAN	Serine/arginine-rich splicing factor 7
GSTM2_HUMAN	Glutathione S-transferase Mu 2	SRSF8_HUMAN	Serine/arginine-rich splicing factor 8
GSTM3_HUMAN	Glutathione S-transferase Mu 3	SSBP_HUMAN	Single-stranded DNA-binding protein, mitochondrial
GSTM5_HUMAN	Glutathione S-transferase Mu 5	SSRA_HUMAN	Translocon-associated protein subunit alpha
GSTO1_HUMAN	Glutathione S-transferase omega-1	SSRD_HUMAN	Translocon-associated protein subunit delta
GSTP1_HUMAN	Glutathione S-transferase P	SSRG_HUMAN	Translocon-associated protein subunit gamma
GT251_HUMAN	Procollagen galactosyltransferase 1	SSRP1_HUMAN	FACT complex subunit SSRP1
GTPB2_HUMAN	GTP-binding protein 2	ST134_HUMAN	Putative protein FAM10A4
GTPC1_HUMAN	Putative GTP cyclohydrolase 1 type 2 NIF3L1	ST1A1_HUMAN	Sulfotransferase 1A1
GTR14_HUMAN	Solute carrier family 2, facilitated glucose transporter member 14	ST1A4_HUMAN	Sulfotransferase 1A4
GTR3_HUMAN	Solute carrier family 2, facilitated glucose transporter member 3	STA5A_HUMAN	Signal transducer and activator of transcription 5A
GUAA_HUMAN	GMP synthase [glutamine-hydrolyzing]	STA5B_HUMAN	Signal transducer and activator of transcription 5B
GYS1_HUMAN	Glycogen [starch] synthase, muscle	STAM1_HUMAN	Signal transducing adapter molecule 1
H10_HUMAN	Histone H1.0	STAT1_HUMAN	Signal transducer and activator of transcription 1-alpha/beta

H12_HUMAN	Histone H1.2	STAT3_HUMAN	Signal transducer and activator of transcription 3
H13_HUMAN	Histone H1.3	STAT6_HUMAN	Signal transducer and activator of transcription 6
H14_HUMAN	Histone H1.4	STIM1_HUMAN	Stromal interaction molecule 1
H15_HUMAN	Histone H1.5	STIM2_HUMAN	Stromal interaction molecule 2
H1X_HUMAN	Histone H1x	STING_HUMAN	Stimulator of interferon genes protein
H2A1C_HUMAN	Histone H2A type 1-C	STIP1_HUMAN	Stress-induced-phosphoprotein 1
H2A1J_HUMAN	Histone H2A type 1-J	STK10_HUMAN	Serine/threonine-protein kinase 10
H2A2A_HUMAN	Histone H2A type 2-A	STK24_HUMAN	Serine/threonine-protein kinase 24
H2A2B_HUMAN	Histone H2A type 2-B	STK26_HUMAN	Serine/threonine-protein kinase 26
H2AV_HUMAN	Histone H2A.V	STK38_HUMAN	Serine/threonine-protein kinase 38
H2AY_HUMAN	Core histone macro-H2A.1	STK4_HUMAN	Serine/threonine-protein kinase 4
H2B1C_HUMAN	Histone H2B type 1-C/E/F/G/I	STML2_HUMAN	Stomatin-like protein 2, mitochondrial
H2B1L_HUMAN	Histone H2B type 1-L	STMN1_HUMAN	Stathmin
H2B1M_HUMAN	Histone H2B type 1-M	STOM_HUMAN	Erythrocyte band 7 integral membrane protein
H2B2D_HUMAN	Putative histone H2B type 2-D	STON2_HUMAN	Stonin-2
H2B3B_HUMAN	Histone H2B type 3-B	STRAP_HUMAN	Serine-threonine kinase receptor-associated protein
H31_HUMAN	Histone H3.1	STRN_HUMAN	Striatin
H32_HUMAN	Histone H3.2	STRN4_HUMAN	Striatin-4
H33_HUMAN	Histone H3.3	STT3A_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A
H4_HUMAN	Histone H4	STT3B_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B
HAP28_HUMAN	28 kDa heat- and acid-stable phosphoprotein	STUM_HUMAN	Protein stum homolog
HBA_HUMAN	Hemoglobin subunit alpha	STX11_HUMAN	Syntaxin-11
HBB_HUMAN	Hemoglobin subunit beta	STX12_HUMAN	Syntaxin-12
HBD_HUMAN	Hemoglobin subunit delta	STX4_HUMAN	Syntaxin-4
HBG1_HUMAN	Hemoglobin subunit gamma-1	STX7_HUMAN	Syntaxin-7
HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2	STXB2_HUMAN	Syntaxin-binding protein 2
HCDH_HUMAN	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	STXB3_HUMAN	Syntaxin-binding protein 3
HCFC1_HUMAN	Host cell factor 1	SUCA_HUMAN	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial
HCK_HUMAN	Tyrosine-protein kinase HCK	SUCB1_HUMAN	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial
HCLS1_HUMAN	Hematopoietic lineage cell-specific protein	SUCB2_HUMAN	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial
HDGF_HUMAN	Hepatoma-derived growth factor	SUGT1_HUMAN	Suppressor of G2 allele of SKP1 homolog
HDHD2_HUMAN	Haloacid dehalogenase-like hydrolase domain-containing protein 2	SUMO2_HUMAN	Small ubiquitin-related modifier 2
HEBP1_HUMAN	Heme-binding protein 1	SUMO4_HUMAN	Small ubiquitin-related modifier 4
HEM2_HUMAN	Delta-aminolevulinic acid dehydratase	SUN2_HUMAN	SUN domain-containing protein 2

HEM6_HUMAN	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	SURF4_HUMAN	Surfeit locus protein 4
HEMO_HUMAN	Hemopexin	SYAC_HUMAN	Alanine--tRNA ligase, cytoplasmic
HEP2_HUMAN	Heparin cofactor 2	SYCC_HUMAN	Cysteine--tRNA ligase, cytoplasmic
HEXA_HUMAN	Beta-hexosaminidase subunit alpha	SYDC_HUMAN	Aspartate--tRNA ligase, cytoplasmic
HEXB_HUMAN	Beta-hexosaminidase subunit beta	SYEP_HUMAN	Bifunctional glutamate/proline--tRNA ligase
HG2A_HUMAN	HLA class II histocompatibility antigen gamma chain	SYFA_HUMAN	Phenylalanine--tRNA ligase alpha subunit
HGFA_HUMAN	Hepatocyte growth factor activator	SYFB_HUMAN	Phenylalanine--tRNA ligase beta subunit
HGS_HUMAN	Hepatocyte growth factor-regulated tyrosine kinase substrate	SYG_HUMAN	Glycine--tRNA ligase
HIBCH_HUMAN	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	SYHC_HUMAN	Histidine--tRNA ligase, cytoplasmic
HIKES_HUMAN	Protein Hikeshi	SYIC_HUMAN	Isoleucine--tRNA ligase, cytoplasmic
HINT1_HUMAN	Histidine triad nucleotide-binding protein 1	SYIM_HUMAN	Isoleucine--tRNA ligase, mitochondrial
HINT2_HUMAN	Histidine triad nucleotide-binding protein 2, mitochondrial	SYJ2B_HUMAN	Synaptojanin-2-binding protein
HM13_HUMAN	Minor histocompatibility antigen H13	SYK_HUMAN	Lysine--tRNA ligase
HMGB1_HUMAN	High mobility group protein B1	SYLC_HUMAN	Leucine--tRNA ligase, cytoplasmic
HMGB2_HUMAN	High mobility group protein B2	SYMC_HUMAN	Methionine--tRNA ligase, cytoplasmic
HMGN2_HUMAN	Non-histone chromosomal protein HMG-17	SYNC_HUMAN	Asparagine--tRNA ligase, cytoplasmic
HMHA1_HUMAN	Minor histocompatibility protein HA-1	SYNE3_HUMAN	Nesprin-3
HMOX2_HUMAN	Heme oxygenase 2	SYPL1_HUMAN	Synaptophysin-like protein 1
HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like	SYQ_HUMAN	Glutamine--tRNA ligase
HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H	SYRC_HUMAN	Arginine--tRNA ligase, cytoplasmic
HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2	SYSC_HUMAN	Serine--tRNA ligase, cytoplasmic
HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3	SYTC_HUMAN	Threonine--tRNA ligase, cytoplasmic
HNRL1_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 1	SYTL4_HUMAN	Synaptotagmin-like protein 4
HNRL2_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 2	SYUA_HUMAN	Alpha-synuclein
HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2	SYVC_HUMAN	Valine--tRNA ligase
HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0	SYWC_HUMAN	Tryptophan--tRNA ligase, cytoplasmic
HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F	SYYC_HUMAN	Tyrosine--tRNA ligase, cytoplasmic
HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K	T179B_HUMAN	Transmembrane protein 179B
HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L	T3JAM_HUMAN	TRAF3-interacting JNK-activating modulator
HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M	TACC1_HUMAN	Transforming acidic coiled-coil-containing protein 1

HNRPQ_HUMAN	Heterogeneous nuclear ribonucleoprotein Q	TADBP_HUMAN	TAR DNA-binding protein 43
HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R	TAGL2_HUMAN	Transgelin-2
HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U	TALDO_HUMAN	Transaldolase
HOOK3_HUMAN	Protein Hook homolog 3	TAOK1_HUMAN	Serine/threonine-protein kinase TAO1
HP1B3_HUMAN	Heterochromatin protein 1-binding protein 3	TAOK3_HUMAN	Serine/threonine-protein kinase TAO3
HPCA_HUMAN	Neuron-specific calcium-binding protein hippocalcin	TAP1_HUMAN	Antigen peptide transporter 1
HPCL1_HUMAN	Hippocalcin-like protein 1	TAP2_HUMAN	Antigen peptide transporter 2
HPRT_HUMAN	Hypoxanthine-guanine phosphoribosyltransferase	TB10C_HUMAN	Carabin
HPSE_HUMAN	Heparanase	TBA1A_HUMAN	Tubulin alpha-1A chain
HPT_HUMAN	Haptoglobin	TBA1B_HUMAN	Tubulin alpha-1B chain
HRG_HUMAN	Histidine-rich glycoprotein	TBA1C_HUMAN	Tubulin alpha-1C chain
HS105_HUMAN	Heat shock protein 105 kDa	TBA4A_HUMAN	Tubulin alpha-4A chain
HS90A_HUMAN	Heat shock protein HSP 90-alpha	TBA8_HUMAN	Tubulin alpha-8 chain
HS90B_HUMAN	Heat shock protein HSP 90-beta	TBB1_HUMAN	Tubulin beta-1 chain
HSDL2_HUMAN	Hydroxysteroid dehydrogenase-like protein 2	TBB2A_HUMAN	Tubulin beta-2A chain
HSP71_HUMAN	Heat shock 70 kDa protein 1A/1B	TBB4B_HUMAN	Tubulin beta-4B chain
HSP74_HUMAN	Heat shock 70 kDa protein 4	TBB5_HUMAN	Tubulin beta chain
HSP7C_HUMAN	Heat shock cognate 71 kDa protein	TBB6_HUMAN	Tubulin beta-6 chain
HSPB1_HUMAN	Heat shock protein beta-1	TBC13_HUMAN	TBC1 domain family member 13
HUWE1_HUMAN	E3 ubiquitin-protein ligase HUWE1	TBC15_HUMAN	TBC1 domain family member 15
HV103_HUMAN	Ig heavy chain V-I region V35	TBCA_HUMAN	Tubulin-specific chaperone A
HV303_HUMAN	Ig heavy chain V-III region VH26	TBCB_HUMAN	Tubulin-folding cofactor B
HV305_HUMAN	Ig heavy chain V-III region BRO	TBCD5_HUMAN	TBC1 domain family member 5
HV311_HUMAN	Ig heavy chain V-III region KOL	TBL1X_HUMAN	F-box-like/WD repeat-containing protein TBL1X
HV316_HUMAN	Ig heavy chain V-III region TEI	TBR1_HUMAN	T-box brain protein 1
HXK1_HUMAN	Hexokinase-1	TBRG4_HUMAN	Protein TBRG4
HXK3_HUMAN	Hexokinase-3	TCEA1_HUMAN	Transcription elongation factor A protein 1
HYES_HUMAN	Bifunctional epoxide hydrolase 2	TCP4_HUMAN	Activated RNA polymerase II transcriptional coactivator p15
HYOU1_HUMAN	Hypoxia up-regulated protein 1	TCPA_HUMAN	T-complex protein 1 subunit alpha
IC1_HUMAN	Plasma protease C1 inhibitor	TCPB_HUMAN	T-complex protein 1 subunit beta
ICAL_HUMAN	Calpastatin	TCPD_HUMAN	T-complex protein 1 subunit delta
ICAM2_HUMAN	Intercellular adhesion molecule 2	TCPE_HUMAN	T-complex protein 1 subunit epsilon
ICAM3_HUMAN	Intercellular adhesion molecule 3	TCPG_HUMAN	T-complex protein 1 subunit gamma
IDH3A_HUMAN	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	TCPH_HUMAN	T-complex protein 1 subunit eta
IDH3G_HUMAN	Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	TCPQ_HUMAN	T-complex protein 1 subunit theta
IDHC_HUMAN	Isocitrate dehydrogenase [NADP] cytoplasmic	TCPZ_HUMAN	T-complex protein 1 subunit zeta
IDHP_HUMAN	Isocitrate dehydrogenase [NADP], mitochondrial	TCTP_HUMAN	Translationally-controlled tumor protein

IF16_HUMAN	Gamma-interferon-inducible protein 16	TDRP_HUMAN	Testis development-related protein
IF1AX_HUMAN	Eukaryotic translation initiation factor 1A, X-chromosomal	TEBP_HUMAN	Prostaglandin E synthase 3
IF2A_HUMAN	Eukaryotic translation initiation factor 2 subunit 1	TERA_HUMAN	Transitional endoplasmic reticulum ATPase
IF2B_HUMAN	Eukaryotic translation initiation factor 2 subunit 2	TES_HUMAN	Testin
IF2B2_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 2	TETN_HUMAN	Tetranectin
IF2GL_HUMAN	Putative eukaryotic translation initiation factor 2 subunit 3-like protein	TF65_HUMAN	Transcription factor p65
IF4A1_HUMAN	Eukaryotic initiation factor 4A-I	TFAM_HUMAN	Transcription factor A, mitochondrial
IF4A2_HUMAN	Eukaryotic initiation factor 4A-II	TFG_HUMAN	Protein TFG
IF4A3_HUMAN	Eukaryotic initiation factor 4A-III	TFIP8_HUMAN	Tumor necrosis factor alpha-induced protein 8
IF4B_HUMAN	Eukaryotic translation initiation factor 4B	TGFB1_HUMAN	Transforming growth factor beta-1
IF4E_HUMAN	Eukaryotic translation initiation factor 4E	TGFI1_HUMAN	Transforming growth factor beta-1-induced transcript 1 protein
IF4G1_HUMAN	Eukaryotic translation initiation factor 4 gamma 1	THAS_HUMAN	Thromboxane-A synthase
IF4G2_HUMAN	Eukaryotic translation initiation factor 4 gamma 2	THBG_HUMAN	Thyroxine-binding globulin
IF4G3_HUMAN	Eukaryotic translation initiation factor 4 gamma 3	THIC_HUMAN	Acetyl-CoA acetyltransferase, cytosolic
IF4H_HUMAN	Eukaryotic translation initiation factor 4H	THIK_HUMAN	3-ketoacyl-CoA thiolase, peroxisomal
IF5_HUMAN	Eukaryotic translation initiation factor 5	THIL_HUMAN	Acetyl-CoA acetyltransferase, mitochondrial
IF5A1_HUMAN	Eukaryotic translation initiation factor 5A-1	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial
IF6_HUMAN	Eukaryotic translation initiation factor 6	THIO_HUMAN	Thioredoxin
IFT27_HUMAN	Intraflagellar transport protein 27 homolog	THOC4_HUMAN	THO complex subunit 4
IFT88_HUMAN	Intraflagellar transport protein 88 homolog	THOP1_HUMAN	Thimet oligopeptidase
IGHA1_HUMAN	Ig alpha-1 chain C region	THRB_HUMAN	Prothrombin
IGHA2_HUMAN	Ig alpha-2 chain C region	THTM_HUMAN	3-mercaptopyruvate sulfurtransferase
IGHG1_HUMAN	Ig gamma-1 chain C region	THTR_HUMAN	Thiosulfate sulfurtransferase
IGHG2_HUMAN	Ig gamma-2 chain C region	THUM1_HUMAN	THUMP domain-containing protein 1
IGHM_HUMAN	Ig mu chain C region	TIAR_HUMAN	Nucleolysin TIAR
IGJ_HUMAN	Immunoglobulin J chain	TIF1B_HUMAN	Transcription intermediary factor 1-beta
IGKC_HUMAN	Ig kappa chain C region	TIMP1_HUMAN	Metalloproteinase inhibitor 1
IGLL5_HUMAN	Immunoglobulin lambda-like polypeptide 5	TITIN_HUMAN	Titin

IKKB_HUMAN	Inhibitor of nuclear factor kappa-B kinase subunit beta	TKT_HUMAN	Transketolase
IL16_HUMAN	Pro-interleukin-16	TLN1_HUMAN	Talin-1
IL1B_HUMAN	Interleukin-1 beta	TLN2_HUMAN	Talin-2
ILEU_HUMAN	Leukocyte elastase inhibitor	TM109_HUMAN	Transmembrane protein 109
ILF2_HUMAN	Interleukin enhancer-binding factor 2	TM1L2_HUMAN	TOM1-like protein 2
ILF3_HUMAN	Interleukin enhancer-binding factor 3	TM9S2_HUMAN	Transmembrane 9 superfamily member 2
ILK_HUMAN	Integrin-linked protein kinase	TMED2_HUMAN	Transmembrane emp24 domain-containing protein 2
IMA3_HUMAN	Importin subunit alpha-3	TMED4_HUMAN	Transmembrane emp24 domain-containing protein 4
IMA5_HUMAN	Importin subunit alpha-5	TMED5_HUMAN	Transmembrane emp24 domain-containing protein 5
IMB1_HUMAN	Importin subunit beta-1	TMED9_HUMAN	Transmembrane emp24 domain-containing protein 9
IMDH2_HUMAN	Inosine-5'-monophosphate dehydrogenase 2	TMEDA_HUMAN	Transmembrane emp24 domain-containing protein 10
IMPA1_HUMAN	Inositol monophosphatase 1	TMM33_HUMAN	Transmembrane protein 33
INF2_HUMAN	Inverted formin-2	TMM40_HUMAN	Transmembrane protein 40
INO1_HUMAN	Inositol-3-phosphate synthase 1	TMM43_HUMAN	Transmembrane protein 43
INP4B_HUMAN	Type II inositol 3,4-bisphosphate 4-phosphatase	TMOD3_HUMAN	Tropomodulin-3
IP3KB_HUMAN	Inositol-trisphosphate 3-kinase B	TMX1_HUMAN	Thioredoxin-related transmembrane protein 1
IPO5_HUMAN	Importin-5	TMX3_HUMAN	Protein disulfide-isomerase TMX3
IPO7_HUMAN	Importin-7	TMX4_HUMAN	Thioredoxin-related transmembrane protein 4
IPO9_HUMAN	Importin-9	TNG2_HUMAN	Transport and Golgi organization protein 2 homolog
IPYR_HUMAN	Inorganic pyrophosphatase	TNIK_HUMAN	TRAF2 and NCK-interacting protein kinase
IPYR2_HUMAN	Inorganic pyrophosphatase 2, mitochondrial	TNPO1_HUMAN	Transportin-1
IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1	TNPO2_HUMAN	Transportin-2
IQGA2_HUMAN	Ras GTPase-activating-like protein IQGAP2	TNPO3_HUMAN	Transportin-3
ISOC1_HUMAN	Isochorismatase domain-containing protein 1	TOIP1_HUMAN	Torsin-1A-interacting protein 1
IST1_HUMAN	IST1 homolog	TOLIP_HUMAN	Toll-interacting protein
ITA2_HUMAN	Integrin alpha-2	TOM1_HUMAN	Target of Myb protein 1
ITA2B_HUMAN	Integrin alpha-IIb	TOM70_HUMAN	Mitochondrial import receptor subunit TOM70
ITA6_HUMAN	Integrin alpha-6	TOP1_HUMAN	DNA topoisomerase 1
ITAL_HUMAN	Integrin alpha-L	TOR1A_HUMAN	Torsin-1A
ITAM_HUMAN	Integrin alpha-M	TOR4A_HUMAN	Torsin-4A
ITAX_HUMAN	Integrin alpha-X	TP4A1_HUMAN	Protein tyrosine phosphatase type IVA 1
ITB1_HUMAN	Integrin beta-1	TP8L2_HUMAN	Tumor necrosis factor alpha-induced protein 8-like protein 2
ITB2_HUMAN	Integrin beta-2	TPD54_HUMAN	Tumor protein D54
ITB3_HUMAN	Integrin beta-3	TPIS_HUMAN	Triosephosphate isomerase

ITB5_HUMAN	Integrin beta-5	TPM1_HUMAN	Tropomyosin alpha-1 chain
ITIH1_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H1	TPM2_HUMAN	Tropomyosin beta chain
ITIH2_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H2	TPM3_HUMAN	Tropomyosin alpha-3 chain
ITIH3_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H3	TPM4_HUMAN	Tropomyosin alpha-4 chain
ITIH4_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H4	TPP1_HUMAN	Tripeptidyl-peptidase 1
ITPR1_HUMAN	Inositol 1,4,5-trisphosphate receptor type 1	TPP2_HUMAN	Tripeptidyl-peptidase 2
IVD_HUMAN	Isovaleryl-CoA dehydrogenase, mitochondrial	TPR_HUMAN	Nucleoprotein TPR
JAM1_HUMAN	Junctional adhesion molecule A	TPRKB_HUMAN	EKC/KEOPS complex subunit TPRKB
JAM3_HUMAN	Junctional adhesion molecule C	TPSN_HUMAN	Tapasin
JIP4_HUMAN	C-Jun-amino-terminal kinase-interacting protein 4	TRA2B_HUMAN	Transformer-2 protein homolog beta
K0513_HUMAN	Uncharacterized protein KIAA0513	TRADD_HUMAN	Tumor necrosis factor receptor type 1-associated DEATH domain protein
K1C10_HUMAN	Keratin, type I cytoskeletal 10	TRFE_HUMAN	Serotransferrin
K1C14_HUMAN	Keratin, type I cytoskeletal 14	TRFL_HUMAN	Lactotransferrin
K1C16_HUMAN	Keratin, type I cytoskeletal 16	TRI58_HUMAN	E3 ubiquitin-protein ligase TRIM58
K1C17_HUMAN	Keratin, type I cytoskeletal 17	TRML1_HUMAN	Trem-like transcript 1 protein
K1C9_HUMAN	Keratin, type I cytoskeletal 9	TRNT1_HUMAN	CCA tRNA nucleotidyltransferase 1, mitochondrial
K1H1_HUMAN	Keratin, type I cuticular Ha1	TRPC6_HUMAN	Short transient receptor potential channel 6
K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal	TRUA_HUMAN	tRNA pseudouridine synthase A, mitochondrial
K2C1_HUMAN	Keratin, type II cytoskeletal 1	TRXR1_HUMAN	Thioredoxin reductase 1, cytoplasmic
K2C5_HUMAN	Keratin, type II cytoskeletal 5	TRY1_HUMAN	Trypsin-1
K2C6A_HUMAN	Keratin, type II cytoskeletal 6A	TS101_HUMAN	Tumor susceptibility gene 101 protein
K2C6B_HUMAN	Keratin, type II cytoskeletal 6B	TSN_HUMAN	Translin
KAD1_HUMAN	Adenylate kinase isoenzyme 1	TSN14_HUMAN	Tetraspanin-14
KAD2_HUMAN	Adenylate kinase 2, mitochondrial	TSN33_HUMAN	Tetraspanin-33
KAD3_HUMAN	GTP:AMP phosphotransferase AK3, mitochondrial	TSN9_HUMAN	Tetraspanin-9
KALRN_HUMAN	Kalirin	TSNAX_HUMAN	Translin-associated protein X
KAP0_HUMAN	cAMP-dependent protein kinase type I-alpha regulatory subunit	TSP1_HUMAN	Thrombospondin-1
KAP3_HUMAN	cAMP-dependent protein kinase type II-beta regulatory subunit	TTC1_HUMAN	Tetratricopeptide repeat protein 1
KAPCA_HUMAN	cAMP-dependent protein kinase catalytic subunit alpha	TTHY_HUMAN	Transthyretin
KAPCB_HUMAN	cAMP-dependent protein kinase catalytic subunit beta	TTL12_HUMAN	Tubulin--tyrosine ligase-like protein 12
KCAB2_HUMAN	Voltage-gated potassium channel subunit beta-2	TWF1_HUMAN	Twinfilin-1
KCC1A_HUMAN	Calcium/calmodulin-dependent protein kinase type 1	TWF2_HUMAN	Twinfilin-2

KCC2A_HUMAN	Calcium/calmodulin-dependent protein kinase type II subunit alpha	TXD12_HUMAN	Thioredoxin domain-containing protein 12
KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12	TXD17_HUMAN	Thioredoxin domain-containing protein 17
KCRB_HUMAN	Creatine kinase B-type	TXND5_HUMAN	Thioredoxin domain-containing protein 5
KCY_HUMAN	UMP-CMP kinase	TXNL1_HUMAN	Thioredoxin-like protein 1
KGP1_HUMAN	cGMP-dependent protein kinase 1	TXTP_HUMAN	Tricarboxylate transport protein, mitochondrial
KHDR1_HUMAN	KH domain-containing, RNA-binding, signal transduction-associated protein 1	TYPH_HUMAN	Thymidine phosphorylase
KIF2A_HUMAN	Kinesin-like protein KIF2A	U2AF1_HUMAN	Splicing factor U2AF 35 kDa subunit
KINH_HUMAN	Kinesin-1 heavy chain	U2AF2_HUMAN	Splicing factor U2AF 65 kDa subunit
KLC1_HUMAN	Kinesin light chain 1	U520_HUMAN	U5 small nuclear ribonucleoprotein 200 kDa helicase
KNG1_HUMAN	Kininogen-1	U5S1_HUMAN	116 kDa U5 small nuclear ribonucleoprotein component
KPCA_HUMAN	Protein kinase C alpha type	UB2D3_HUMAN	Ubiquitin-conjugating enzyme E2 D3
KPCB_HUMAN	Protein kinase C beta type	UB2L3_HUMAN	Ubiquitin-conjugating enzyme E2 L3
KPCD_HUMAN	Protein kinase C delta type	UB2V1_HUMAN	Ubiquitin-conjugating enzyme E2 variant 1
KPRA_HUMAN	Phosphoribosyl pyrophosphate synthase-associated protein 1	UB2V2_HUMAN	Ubiquitin-conjugating enzyme E2 variant 2
KPRB_HUMAN	Phosphoribosyl pyrophosphate synthase-associated protein 2	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1
KPYM_HUMAN	Pyruvate kinase PKM	UBA3_HUMAN	NEDD8-activating enzyme E1 catalytic subunit
KRT81_HUMAN	Keratin, type II cuticular Hb1	UBA5_HUMAN	Ubiquitin-like modifier-activating enzyme 5
KS6A3_HUMAN	Ribosomal protein S6 kinase alpha-3	UBA6_HUMAN	Ubiquitin-like modifier-activating enzyme 6
KSYK_HUMAN	Tyrosine-protein kinase SYK	UBA7_HUMAN	Ubiquitin-like modifier-activating enzyme 7
KT3K_HUMAN	Ketosamine-3-kinase	UBC9_HUMAN	SUMO-conjugating enzyme UBC9
KTHY_HUMAN	Thymidylate kinase	UBCP1_HUMAN	Ubiquitin-like domain-containing CTD phosphatase 1
KTN1_HUMAN	Kinectin	UBE2A_HUMAN	Ubiquitin-conjugating enzyme E2 A
KV110_HUMAN	Ig kappa chain V-I region HK102 (Fragment)	UBE2K_HUMAN	Ubiquitin-conjugating enzyme E2 K
KV125_HUMAN	Ig kappa chain V-I region WAT	UBE2N_HUMAN	Ubiquitin-conjugating enzyme E2 N
KV205_HUMAN	Ig kappa chain V-II region GM607 (Fragment)	UBE2O_HUMAN	E2/E3 hybrid ubiquitin-protein ligase UBE2O
KV206_HUMAN	Ig kappa chain V-II region RPMI 6410	UBE3C_HUMAN	Ubiquitin-protein ligase E3C
KV303_HUMAN	Ig kappa chain V-III region NG9 (Fragment)	UBF1_HUMAN	Nucleolar transcription factor 1
KV305_HUMAN	Ig kappa chain V-III region WOL	UBP14_HUMAN	Ubiquitin carboxyl-terminal hydrolase 14
KV309_HUMAN	Ig kappa chain V-III region VG (Fragment)	UBP24_HUMAN	Ubiquitin carboxyl-terminal hydrolase 24
KV313_HUMAN	Ig kappa chain V-III region HIC	UBP2L_HUMAN	Ubiquitin-associated protein 2-like

KV404_HUMAN	Ig kappa chain V-IV region B17	UBP47_HUMAN	Ubiquitin carboxyl-terminal hydrolase 47
LA_HUMAN	Lupus La protein	UBP5_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5
LAC2_HUMAN	Ig lambda-2 chain C regions	UBP7_HUMAN	Ubiquitin carboxyl-terminal hydrolase 7
LAC3_HUMAN	Ig lambda-3 chain C regions	UBQL1_HUMAN	Ubiquilin-1
LACB2_HUMAN	Beta-lactamase-like protein 2	UBR4_HUMAN	E3 ubiquitin-protein ligase UBR4
LACTB_HUMAN	Serine beta-lactamase-like protein LACTB, mitochondrial	UBS3B_HUMAN	Ubiquitin-associated and SH3 domain-containing protein B
LAMP1_HUMAN	Lysosome-associated membrane glycoprotein 1	UBXN6_HUMAN	UBX domain-containing protein 6
LAMP2_HUMAN	Lysosome-associated membrane glycoprotein 2	UCHL5_HUMAN	Ubiquitin carboxyl-terminal hydrolase isozyme L5
LAP2_HUMAN	Protein LAP2	UCRI_HUMAN	Cytochrome b-c1 complex subunit Rieske, mitochondrial
LAP2B_HUMAN	Lamina-associated polypeptide 2, isoforms beta/gamma	UFC1_HUMAN	Ubiquitin-fold modifier-conjugating enzyme 1
LASP1_HUMAN	LIM and SH3 domain protein 1	UFD1_HUMAN	Ubiquitin fusion degradation protein 1 homolog
LAT_HUMAN	Linker for activation of T-cells family member 1	UFL1_HUMAN	E3 UFM1-protein ligase 1
LBR_HUMAN	Lamin-B receptor	UGGG1_HUMAN	UDP-glucose:glycoprotein glucosyltransferase 1
LCP2_HUMAN	Lymphocyte cytosolic protein 2	UGPA_HUMAN	UTP--glucose-1-phosphate uridylyltransferase
LDHA_HUMAN	L-lactate dehydrogenase A chain	ULA1_HUMAN	NEDD8-activating enzyme E1 regulatory subunit
LDHB_HUMAN	L-lactate dehydrogenase B chain	UMPS_HUMAN	Uridine 5'-monophosphate synthase
LEG1_HUMAN	Galectin-1	UN13D_HUMAN	Protein unc-13 homolog D
LEG7_HUMAN	Galectin-7	UN45A_HUMAN	Protein unc-45 homolog A
LEGL_HUMAN	Galectin-related protein	UPAR_HUMAN	Urokinase plasminogen activator surface receptor
LETM1_HUMAN	LETM1 and EF-hand domain-containing protein 1, mitochondrial	UPP1_HUMAN	Uridine phosphorylase 1
LEUK_HUMAN	Leukosialin	URP2_HUMAN	Fermitin family homolog 3
LFG3_HUMAN	Protein lifeguard 3	USMG5_HUMAN	Up-regulated during skeletal muscle growth protein 5
LG3BP_HUMAN	Galectin-3-binding protein	USO1_HUMAN	General vesicular transport factor p115
LGUL_HUMAN	Lactoylglutathione lyase	USP9X_HUMAN	Probable ubiquitin carboxyl-terminal hydrolase FAF-X
LIMA1_HUMAN	LIM domain and actin-binding protein 1	UTRO_HUMAN	Utrophin
LIMS1_HUMAN	LIM and senescent cell antigen-like-containing domain protein 1	VA0D1_HUMAN	V-type proton ATPase subunit d 1
LIS1_HUMAN	Platelet-activating factor acetylhydrolase IB subunit alpha	VAC14_HUMAN	Protein VAC14 homolog
LKHA4_HUMAN	Leukotriene A-4 hydrolase	VAMP3_HUMAN	Vesicle-associated membrane protein 3
LMAN1_HUMAN	Protein ERGIC-53	VAMP7_HUMAN	Vesicle-associated membrane protein 7

LMAN2_HUMAN	Vesicular integral-membrane protein VIP36	VAMP8_HUMAN	Vesicle-associated membrane protein 8
LMNA_HUMAN	Prelamin-A/C	VAPA_HUMAN	Vesicle-associated membrane protein-associated protein A
LMNB1_HUMAN	Lamin-B1	VASP_HUMAN	Vasodilator-stimulated phosphoprotein
LMNB2_HUMAN	Lamin-B2	VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog
LONM_HUMAN	Lon protease homolog, mitochondrial	VATA_HUMAN	V-type proton ATPase catalytic subunit A
LOX12_HUMAN	Arachidonate 12-lipoxygenase, 12S-type	VATB2_HUMAN	V-type proton ATPase subunit B, brain isoform
LOX5_HUMAN	Arachidonate 5-lipoxygenase	VATC1_HUMAN	V-type proton ATPase subunit C 1
LPPRC_HUMAN	Leucine-rich PPR motif-containing protein, mitochondrial	VATE1_HUMAN	V-type proton ATPase subunit E 1
LRBA_HUMAN	Lipopolysaccharide-responsive and beige-like anchor protein	VATH_HUMAN	V-type proton ATPase subunit H
LRC40_HUMAN	Leucine-rich repeat-containing protein 40	VAV_HUMAN	Proto-oncogene vav
LRC47_HUMAN	Leucine-rich repeat-containing protein 47	VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1
LRC59_HUMAN	Leucine-rich repeat-containing protein 59	VDAC2_HUMAN	Voltage-dependent anion-selective channel protein 2
LRRF1_HUMAN	Leucine-rich repeat flightless-interacting protein 1	VDAC3_HUMAN	Voltage-dependent anion-selective channel protein 3
LRRF2_HUMAN	Leucine-rich repeat flightless-interacting protein 2	VIME_HUMAN	Vimentin
LSM1_HUMAN	U6 snRNA-associated Sm-like protein LSm1	VINC_HUMAN	Vinculin
LSM2_HUMAN	U6 snRNA-associated Sm-like protein LSm2	VP13C_HUMAN	Vacuolar protein sorting-associated protein 13C
LSM3_HUMAN	U6 snRNA-associated Sm-like protein LSm3	VP26A_HUMAN	Vacuolar protein sorting-associated protein 26A
LSP1_HUMAN	Lymphocyte-specific protein 1	VPS25_HUMAN	Vacuolar protein-sorting-associated protein 25
LTBP1_HUMAN	Latent-transforming growth factor beta-binding protein 1	VPS29_HUMAN	Vacuolar protein sorting-associated protein 29
LTOR1_HUMAN	Ragulator complex protein LAMTOR1	VPS35_HUMAN	Vacuolar protein sorting-associated protein 35
LTOR2_HUMAN	Ragulator complex protein LAMTOR2	VPS4B_HUMAN	Vacuolar protein sorting-associated protein 4B
LTOR3_HUMAN	Ragulator complex protein LAMTOR3	VPS51_HUMAN	Vacuolar protein sorting-associated protein 51 homolog
LUM_HUMAN	Lumican	VRK1_HUMAN	Serine/threonine-protein kinase VRK1
LV105_HUMAN	Ig lambda chain V-I region NEWM	VTA1_HUMAN	Vacuolar protein sorting-associated protein VTA1 homolog
LXN_HUMAN	Latexin	VTDB_HUMAN	Vitamin D-binding protein
LY66F_HUMAN	Lymphocyte antigen 6 complex locus protein G6f	VTNC_HUMAN	Vitronectin
LYAM3_HUMAN	P-selectin	VWF_HUMAN	von Willebrand factor
LYN_HUMAN	Tyrosine-protein kinase Lyn	WASF2_HUMAN	Wiskott-Aldrich syndrome protein family member 2

LYPA1_HUMAN	Acyl-protein thioesterase 1	WASP_HUMAN	Wiskott-Aldrich syndrome protein
LYPA2_HUMAN	Acyl-protein thioesterase 2	WBP2_HUMAN	WW domain-binding protein 2
LYRIC_HUMAN	Protein LYRIC	WDFY1_HUMAN	WD repeat and FYVE domain-containing protein 1
LYSC_HUMAN	Lysozyme C	WDR1_HUMAN	WD repeat-containing protein 1
M2OM_HUMAN	Mitochondrial 2-oxoglutarate/malate carrier protein	WDR37_HUMAN	WD repeat-containing protein 37
M3K5_HUMAN	Mitogen-activated protein kinase kinase kinase 5	WDR44_HUMAN	WD repeat-containing protein 44
MA2A1_HUMAN	Alpha-mannosidase 2	WIPF1_HUMAN	WAS/WASL-interacting protein family member 1
MACF1_HUMAN	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	XPO1_HUMAN	Exportin-1
MAGD2_HUMAN	Melanoma-associated antigen D2	XPO2_HUMAN	Exportin-2
MAGT1_HUMAN	Magnesium transporter protein 1	XPO7_HUMAN	Exportin-7
MANF_HUMAN	Mesencephalic astrocyte-derived neurotrophic factor	XPOT_HUMAN	Exportin-T
MAOM_HUMAN	NAD-dependent malic enzyme, mitochondrial	XPP1_HUMAN	Xaa-Pro aminopeptidase 1
MAOX_HUMAN	NADP-dependent malic enzyme	XRCC5_HUMAN	X-ray repair cross-complementing protein 5
MAP11_HUMAN	Methionine aminopeptidase 1	XRCC6_HUMAN	X-ray repair cross-complementing protein 6
MAP2_HUMAN	Methionine aminopeptidase 2	YBOX1_HUMAN	Nuclease-sensitive element-binding protein 1
MAP4_HUMAN	Microtubule-associated protein 4	YES_HUMAN	Tyrosine-protein kinase Yes
MARE1_HUMAN	Microtubule-associated protein RP/EB family member 1	ZA2G_HUMAN	Zinc-alpha-2-glycoprotein
MARE2_HUMAN	Microtubule-associated protein RP/EB family member 2	ZAP70_HUMAN	Tyrosine-protein kinase ZAP-70
MAT2B_HUMAN	Methionine adenosyltransferase 2 subunit beta	ZCCHV_HUMAN	Zinc finger CCCH-type antiviral protein 1
MATR3_HUMAN	Matrin-3	ZN185_HUMAN	Zinc finger protein 185
MAVS_HUMAN	Mitochondrial antiviral-signaling protein	ZO2_HUMAN	Tight junction protein ZO-2
MBNL3_HUMAN	Muscleblind-like protein 3	ZYX_HUMAN	Zyxin
MCA3_HUMAN	Eukaryotic translation elongation factor 1 epsilon-1	ZZEF1_HUMAN	Zinc finger ZZ-type and EF-hand domain-containing protein 1
MCAT_HUMAN	Mitochondrial carnitine/acylcarnitine carrier protein		

Supplementary Table VII.7. Common quantified proteins in the six biological samples. For each protein it is shown its entry name in UniProt database.

Entry name	Protein name	Entry name	Protein name
1433B_HUMAN	14-3-3 protein beta/alpha	LYAM3_HUMAN	P-selectin
1433E_HUMAN	14-3-3 protein epsilon	LYRIC_HUMAN	Protein LYRIC
1433F_HUMAN	14-3-3 protein eta	LYSC_HUMAN	Lysozyme C
1433G_HUMAN	14-3-3 protein gamma	MARE2_HUMAN	Microtubule-associated protein RP/EB family member 2
1433T_HUMAN	14-3-3 protein theta	MDHC_HUMAN	Malate dehydrogenase, cytoplasmic
1433Z_HUMAN	14-3-3 protein zeta/delta	MDHM_HUMAN	Malate dehydrogenase, mitochondrial
1A03_HUMAN	HLA class I histocompatibility antigen, A-3 alpha chain	MGLL_HUMAN	Monoglyceride lipase
3BP1_HUMAN	SH3 domain-binding protein 1	ML12A_HUMAN	Myosin regulatory light chain 12A
6PGD_HUMAN	6-phosphogluconate dehydrogenase, decarboxylating	MMRN1_HUMAN	Multimerin-1
6PGL_HUMAN	6-phosphogluconolactonase	MOES_HUMAN	Moesin
A1AT_HUMAN	Alpha-1-antitrypsin	MYH9_HUMAN	Myosin-9
ACON_HUMAN	Aconitate hydratase, mitochondrial	MYL6_HUMAN	Myosin light polypeptide 6
ACTG_HUMAN	Actin, cytoplasmic 2	MYL9_HUMAN	Myosin regulatory light polypeptide 9
ACTN1_HUMAN	Alpha-actinin-1	NB5R3_HUMAN	NADH-cytochrome b5 reductase 3
ACTN4_HUMAN	Alpha-actinin-4	NDKB_HUMAN	Nucleoside diphosphate kinase B
ADT2_HUMAN	ADP/ATP translocase 2	NDUS8_HUMAN	NADH dehydrogenase
AHNK_HUMAN	Neuroblast differentiation-associated protein AHNAK	NHRF1_HUMAN	Na(+)/H(+) exchange regulatory cofactor NHE-RF1
AK1A1_HUMAN	Alcohol dehydrogenase	NP1L1_HUMAN	Nucleosome assembly protein 1-like 1
ALBU_HUMAN	Serum albumin	NPM_HUMAN	Nucleophosmin
ALDOA_HUMAN	Fructose-bisphosphate aldolase A	NTF2_HUMAN	Nuclear transport factor 2
AMPD2_HUMAN	AMP deaminase 2	NUCL_HUMAN	Nucleolin
AMPL_HUMAN	Cytosol aminopeptidase	OSTF1_HUMAN	Osteoclast-stimulating factor 1
AN32A_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member A	PA1B2_HUMAN	Platelet-activating factor acetylhydrolase IB subunit beta
ANX11_HUMAN	Annexin A11	PABP3_HUMAN	Polyadenylate-binding protein 3
ANXA1_HUMAN	Annexin A1	PARK7_HUMAN	Protein deglycase DJ-1
ANXA2_HUMAN	Annexin A2	PARVB_HUMAN	Beta-parvin
ANXA5_HUMAN	Annexin A5	PCBP1_HUMAN	Poly(rC)-binding protein 1
ANXA6_HUMAN	Annexin A6	PCBP2_HUMAN	Poly(rC)-binding protein 2
ANXA7_HUMAN	Annexin A7	PDC6I_HUMAN	Programmed cell death 6-interacting protein
AP2A1_HUMAN	AP-2 complex subunit alpha-1	PDE5A_HUMAN	cGMP-specific 3',5'-cyclic phosphodiesterase
AP2B1_HUMAN	AP-2 complex subunit beta	PDIA1_HUMAN	Protein disulfide-isomerase
APMAP_HUMAN	Adipocyte plasma membrane-associated protein	PDIA3_HUMAN	Protein disulfide-isomerase A3
APOA1_HUMAN	Apolipoprotein A-I	PDIA4_HUMAN	Protein disulfide-isomerase A4
APT_HUMAN	Adenine phosphoribosyltransferase	PDIA6_HUMAN	Protein disulfide-isomerase A6
ARC1B_HUMAN	Actin-related protein 2/3 complex subunit 1B	PDLI1_HUMAN	PDZ and LIM domain protein 1

ARF1_HUMAN	ADP-ribosylation factor 1	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1
ARF4_HUMAN	ADP-ribosylation factor 4	PERM_HUMAN	Myeloperoxidase
ARK72_HUMAN	Aflatoxin B1 aldehyde reductase member 2	PFKAP_HUMAN	ATP-dependent 6-phosphofructokinase, platelet type
ARP2_HUMAN	Actin-related protein 2	PGAM1_HUMAN	Phosphoglycerate mutase 1
ARP3_HUMAN	Actin-related protein 3	PGH1_HUMAN	Prostaglandin G/H synthase 1
ARPC2_HUMAN	Actin-related protein 2/3 complex subunit 2	PGK1_HUMAN	Phosphoglycerate kinase 1
ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3	PGM2_HUMAN	Phosphoglucomutase-2
ARPC4_HUMAN	Actin-related protein 2/3 complex subunit 4	PHB_HUMAN	Prohibitin
ARPC5_HUMAN	Actin-related protein 2/3 complex subunit 5	PHB2_HUMAN	Prohibitin-2
AT2A3_HUMAN	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	PI42A_HUMAN	Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha
ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial	PLEC_HUMAN	Plectin
ATPB_HUMAN	ATP synthase subunit beta, mitochondrial	PLEK_HUMAN	Pleckstrin
ATPO_HUMAN	ATP synthase subunit O, mitochondrial	PLF4_HUMAN	Platelet factor 4
B2MG_HUMAN	Beta-2-microglobulin	PLSL_HUMAN	Plastin-2
BAX_HUMAN	Apoptosis regulator BAX	PNCB_HUMAN	Nicotinate phosphoribosyltransferase
BIN2_HUMAN	Bridging integrator 2	PNPH_HUMAN	Purine nucleoside phosphorylase
C1QBP_HUMAN	Complement component 1 Q subcomponent-binding protein, mitochondrial	PP1A_HUMAN	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit
C1TC_HUMAN	C-1-tetrahydrofolate synthase, cytoplasmic	PP1R7_HUMAN	Protein phosphatase 1 regulatory subunit 7
CAB39_HUMAN	Calcium-binding protein 39	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A
CAH2_HUMAN	Carbonic anhydrase 2	PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B
CALD1_HUMAN	Caldesmon	PRAF3_HUMAN	PRA1 family protein 3
CALR_HUMAN	Calreticulin	PRDX1_HUMAN	Peroxiredoxin-1
CALX_HUMAN	Calnexin	PRDX2_HUMAN	Peroxiredoxin-2
CAN1_HUMAN	Calpain-1 catalytic subunit	PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial
CAN2_HUMAN	Calpain-2 catalytic subunit	PRDX5_HUMAN	Peroxiredoxin-5, mitochondrial
CAND1_HUMAN	Cullin-associated NEDD8-dissociated protein 1	PRDX6_HUMAN	Peroxiredoxin-6
CAP1_HUMAN	Adenylyl cyclase-associated protein 1	PROF1_HUMAN	Profilin-1
CAPG_HUMAN	Macrophage-capping protein	PRTN3_HUMAN	Myeloblastin
CAPZB_HUMAN	F-actin-capping protein subunit beta	PSA_HUMAN	Puromycin-sensitive aminopeptidase
CATA_HUMAN	Catalase	PSA4_HUMAN	Proteasome subunit alpha type-4
CATD_HUMAN	Cathepsin D	PSA6_HUMAN	Proteasome subunit alpha type-6
CAZA1_HUMAN	F-actin-capping protein subunit alpha-1	PSA7_HUMAN	Proteasome subunit alpha type-7

CAZA2_HUMAN	F-actin-capping protein subunit alpha-2	PSB1_HUMAN	Proteasome subunit beta type-1
CCL5_HUMAN	C-C motif chemokine 5	PSB2_HUMAN	Proteasome subunit beta type-2
CD14_HUMAN	Monocyte differentiation antigen CD14	PSB3_HUMAN	Proteasome subunit beta type-3
CD36_HUMAN	Platelet glycoprotein 4	PSB8_HUMAN	Proteasome subunit beta type-8
CD9_HUMAN	CD9 antigen	PSMD1_HUMAN	26S proteasome non-ATPase regulatory subunit 1
CDC42_HUMAN	Cell division control protein 42 homolog	PSMD5_HUMAN	26S proteasome non-ATPase regulatory subunit 5
CH10_HUMAN	10 kDa heat shock protein, mitochondrial	PSME1_HUMAN	Proteasome activator complex subunit 1
CH60_HUMAN	60 kDa heat shock protein, mitochondrial	PSME2_HUMAN	Proteasome activator complex subunit 2
CISY_HUMAN	Citrate synthase, mitochondrial	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1
CLH1_HUMAN	Clathrin heavy chain 1	PTCA_HUMAN	Protein tyrosine phosphatase receptor type C-associated protein
CLIC1_HUMAN	Chloride intracellular channel protein 1	PTN6_HUMAN	Tyrosine-protein phosphatase non-receptor type 6
CNDP2_HUMAN	Cytosolic non-specific dipeptidase	PTPRC_HUMAN	Receptor-type tyrosine-protein phosphatase C
CNN2_HUMAN	Calponin-2	PUR9_HUMAN	Bifunctional purine biosynthesis protein PURH
COF1_HUMAN	Cofilin-1	PYGB_HUMAN	Glycogen phosphorylase, brain form
COPB_HUMAN	Coatomer subunit beta	QCR1_HUMAN	Cytochrome b-c1 complex subunit 1, mitochondrial
COR1A_HUMAN	Coronin-1A	QCR2_HUMAN	Cytochrome b-c1 complex subunit 2, mitochondrial
COR1C_HUMAN	Coronin-1C	RAB14_HUMAN	Ras-related protein Rab-14
COTL1_HUMAN	Coactosin-like protein	RAB1B_HUMAN	Ras-related protein Rab-1B
COX2_HUMAN	Cytochrome c oxidase subunit 2	RAB6B_HUMAN	Ras-related protein Rab-6B
COX41_HUMAN	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	RAB7A_HUMAN	Ras-related protein Rab-7a
CPNS1_HUMAN	Calpain small subunit 1	RALB_HUMAN	Ras-related protein Ral-B
CSK_HUMAN	Tyrosine-protein kinase CSK	RAN_HUMAN	GTP-binding nuclear protein Ran
CXCL7_HUMAN	Platelet basic protein	RAP1B_HUMAN	Ras-related protein Rap-1b
CYC_HUMAN	Cytochrome c	RB11B_HUMAN	Ras-related protein Rab-11B
DBNL_HUMAN	Drebrin-like protein	RB27B_HUMAN	Ras-related protein Rab-27B
DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17	RBBP7_HUMAN	Histone-binding protein RBBP7
DDX3Y_HUMAN	ATP-dependent RNA helicase DDX3Y	RHG01_HUMAN	Rho GTPase-activating protein 1
DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial	RHG18_HUMAN	Rho GTPase-activating protein 18
DHX9_HUMAN	ATP-dependent RNA helicase A	RHOA_HUMAN	Transforming protein RhoA
DIAP1_HUMAN	Protein diaphanous homolog 1	RINI_HUMAN	Ribonuclease inhibitor
DJB11_HUMAN	DnaJ homolog subfamily B member 11	RL11_HUMAN	60S ribosomal protein L11
DNM1L_HUMAN	Dynamin-1-like protein	RL12_HUMAN	60S ribosomal protein L12
DPYL2_HUMAN	Dihydropyrimidinase-related protein 2	RL17_HUMAN	60S ribosomal protein L17
DX39B_HUMAN	Spliceosome RNA helicase DDX39B	RL18_HUMAN	60S ribosomal protein L18
DYN2_HUMAN	Dynamin-2	RL24_HUMAN	60S ribosomal protein L24

EDEM1_HUMAN	ER degradation-enhancing alpha-mannosidase-like protein 1	RL6_HUMAN	60S ribosomal protein L6
EF1A3_HUMAN	Putative elongation factor 1-alpha-like 3	RL7_HUMAN	60S ribosomal protein L7
EF1D_HUMAN	Elongation factor 1-delta	RL8_HUMAN	60S ribosomal protein L8
EF1G_HUMAN	Elongation factor 1-gamma	RLA0_HUMAN	60S acidic ribosomal protein P0
EF2_HUMAN	Elongation factor 2	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1
EFHD2_HUMAN	EF-hand domain-containing protein D2	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1
EHD1_HUMAN	EH domain-containing protein 1	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3
EHD3_HUMAN	EH domain-containing protein 3	RS10_HUMAN	40S ribosomal protein S10
EIF3C_HUMAN	Eukaryotic translation initiation factor 3 subunit C	RS13_HUMAN	40S ribosomal protein S13
ENOA_HUMAN	Alpha-enolase	RS14_HUMAN	40S ribosomal protein S14
ENPL_HUMAN	Endoplasmin	RS15A_HUMAN	40S ribosomal protein S15a
ESYT1_HUMAN	Extended synaptotagmin-1	RS18_HUMAN	40S ribosomal protein S18
ETFB_HUMAN	Electron transfer flavoprotein subunit beta	RS19_HUMAN	40S ribosomal protein S19
EZRI_HUMAN	Ezrin	RS20_HUMAN	40S ribosomal protein S20
F13A_HUMAN	Coagulation factor XIII A chain	RS25_HUMAN	40S ribosomal protein S25
FA49B_HUMAN	Protein FAM49B	RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a
FA5_HUMAN	Coagulation factor V	RS3A_HUMAN	40S ribosomal protein S3a
FCN1_HUMAN	Ficolin-1	RS4X_HUMAN	40S ribosomal protein S4, X isoform
FIBA_HUMAN	Fibrinogen alpha chain	RSSA_HUMAN	40S ribosomal protein SA
FIBB_HUMAN	Fibrinogen beta chain	RSU1_HUMAN	Ras suppressor protein 1
FIBG_HUMAN	Fibrinogen gamma chain	RTN4_HUMAN	Reticulon-4
FKB1A_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP1A	RUXE_HUMAN	Small nuclear ribonucleoprotein E
FLNA_HUMAN	Filamin-A	S10A4_HUMAN	Protein S100-A4
G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase	S10A8_HUMAN	Protein S100-A8
G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase	S10A9_HUMAN	Protein S100-A9
G6PI_HUMAN	Glucose-6-phosphate isomerase	SAMH1_HUMAN	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1
GANAB_HUMAN	Neutral alpha-glucosidase AB	SAR1A_HUMAN	GTP-binding protein SAR1a
GBB1_HUMAN	Guanine nucleotide-binding protein G	SC22B_HUMAN	Vesicle-trafficking protein SEC22b
GBLP_HUMAN	Guanine nucleotide-binding protein subunit beta-2-like 1	SDPR_HUMAN	Serum deprivation-response protein
GBP1_HUMAN	Interferon-induced guanylate-binding protein 1	SEPT6_HUMAN	Septin-6
GDIB_HUMAN	Rab GDP dissociation inhibitor beta	SEPT7_HUMAN	Septin-7
GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1	SEPT9_HUMAN	Septin-9
GDIR2_HUMAN	Rho GDP-dissociation inhibitor 2	SET_HUMAN	Protein SET
GELS_HUMAN	Gelsolin	SH3L2_HUMAN	SH3 domain-binding glutamic acid-rich-like protein 2
GIMA1_HUMAN	GTPase IMAP family member 1	SH3L3_HUMAN	SH3 domain-binding glutamic acid-rich-like protein 3

GMFG_HUMAN	Glia maturation factor gamma	SKAP2_HUMAN	Src kinase-associated phosphoprotein 2
GNAI2_HUMAN	Guanine nucleotide-binding protein G	SMD2_HUMAN	Small nuclear ribonucleoprotein Sm D2
GP1BA_HUMAN	Platelet glycoprotein Ib alpha chain	SMD3_HUMAN	Small nuclear ribonucleoprotein Sm D3
GP1BB_HUMAN	Platelet glycoprotein Ib beta chain	SNP23_HUMAN	Synaptosomal-associated protein 23
GPDM_HUMAN	Glycerol-3-phosphate dehydrogenase, mitochondrial	SODM_HUMAN	Superoxide dismutase
GPIX_HUMAN	Platelet glycoprotein IX	SPB6_HUMAN	Serpin B6
GPV_HUMAN	Platelet glycoprotein V	SPB9_HUMAN	Serpin B9
GPX1_HUMAN	Glutathione peroxidase 1	SPRC_HUMAN	SPARC
GRAN_HUMAN	Grancalcin	SPTB1_HUMAN	Spectrin beta chain, erythrocytic
GRP75_HUMAN	Stress-70 protein, mitochondrial	SQRD_HUMAN	Sulfide:quinone oxidoreductase, mitochondrial
GRP78_HUMAN	78 kDa glucose-regulated protein	SRC_HUMAN	Proto-oncogene tyrosine-protein kinase Src
GSHR_HUMAN	Glutathione reductase, mitochondrial	SRC8_HUMAN	Src substrate cortactin
GSTK1_HUMAN	Glutathione S-transferase kappa 1	SRP14_HUMAN	Signal recognition particle 14 kDa protein
GSTO1_HUMAN	Glutathione S-transferase omega-1	SRSF2_HUMAN	Serine/arginine-rich splicing factor 2
GSTP1_HUMAN	Glutathione S-transferase P	SRSF7_HUMAN	Serine/arginine-rich splicing factor 7
GTR14_HUMAN	Solute carrier family 2, facilitated glucose transporter member 14	ST134_HUMAN	Putative protein FAM10A4
H12_HUMAN	Histone H1.2	ST1A4_HUMAN	Sulfotransferase 1A4
H15_HUMAN	Histone H1.5	STIP1_HUMAN	Stress-induced-phosphoprotein 1
H2A2B_HUMAN	Histone H2A type 2-B	STK4_HUMAN	Serine/threonine-protein kinase 4
H2AV_HUMAN	Histone H2A.V	STOM_HUMAN	Erythrocyte band 7 integral membrane protein
H2AY_HUMAN	Core histone macro-H2A.1	STX7_HUMAN	Syntaxin-7
H2B1C_HUMAN	Histone H2B type 1-C/E/F/G/I	STXB2_HUMAN	Syntaxin-binding protein 2
H2B2D_HUMAN	Putative histone H2B type 2-D	SYHC_HUMAN	Histidine--tRNA ligase, cytoplasmic
H31_HUMAN	Histone H3.1	SYSC_HUMAN	Serine--tRNA ligase, cytoplasmic
H4_HUMAN	Histone H4	SYUA_HUMAN	Alpha-synuclein
HBA_HUMAN	Hemoglobin subunit alpha	TAGL2_HUMAN	Transgelin-2
HBB_HUMAN	Hemoglobin subunit beta	TALDO_HUMAN	Transaldolase
HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2	TBA1A_HUMAN	Tubulin alpha-1A chain
HEM2_HUMAN	Delta-aminolevulinic acid dehydratase	TBA4A_HUMAN	Tubulin alpha-4A chain
HMGB1_HUMAN	High mobility group protein B1	TBA8_HUMAN	Tubulin alpha-8 chain
HMGB2_HUMAN	High mobility group protein B2	TBB1_HUMAN	Tubulin beta-1 chain
HMHA1_HUMAN	Minor histocompatibility protein HA-1	TBB4B_HUMAN	Tubulin beta-4B chain
HNRL2_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 2	TBB5_HUMAN	Tubulin beta chain
HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2	TCP4_HUMAN	Activated RNA polymerase II transcriptional coactivator p15
HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0	TCPA_HUMAN	T-complex protein 1 subunit alpha

HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K	TCPB_HUMAN	T-complex protein 1 subunit beta
HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M	TCPD_HUMAN	T-complex protein 1 subunit delta
HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U	TCPE_HUMAN	T-complex protein 1 subunit epsilon
HP1B3_HUMAN	Heterochromatin protein 1-binding protein 3	TCPG_HUMAN	T-complex protein 1 subunit gamma
HPRT_HUMAN	Hypoxanthine-guanine phosphoribosyltransferase	TCPH_HUMAN	T-complex protein 1 subunit eta
HPT_HUMAN	Haptoglobin	TCPQ_HUMAN	T-complex protein 1 subunit theta
HS90A_HUMAN	Heat shock protein HSP 90-alpha	TCPZ_HUMAN	T-complex protein 1 subunit zeta
HS90B_HUMAN	Heat shock protein HSP 90-beta	TERA_HUMAN	Transitional endoplasmic reticulum ATPase
HSP71_HUMAN	Demerged into P0DMV8 and P0DMV9.	TGFB1_HUMAN	Transforming growth factor beta-1
HSP7C_HUMAN	Heat shock cognate 71 kDa protein	TGFI1_HUMAN	Transforming growth factor beta-1-induced transcript 1 protein
HSPB1_HUMAN	Heat shock protein beta-1	THAS_HUMAN	Thromboxane-A synthase
HXK1_HUMAN	Hexokinase-1	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial
IDHP_HUMAN	Isocitrate dehydrogenase	TIMP1_HUMAN	Metalloproteinase inhibitor 1
IGHG1_HUMAN	Ig gamma-1 chain C region	TKT_HUMAN	Transketolase
IGHG2_HUMAN	Ig gamma-2 chain C region	TLN1_HUMAN	Talin-1
IGKC_HUMAN	Ig kappa chain C region	TM109_HUMAN	Transmembrane protein 109
IL16_HUMAN	Pro-interleukin-16	TMOD3_HUMAN	Tropomodulin-3
ILEU_HUMAN	Leukocyte elastase inhibitor	TPIS_HUMAN	Triosephosphate isomerase
ILF2_HUMAN	Interleukin enhancer-binding factor 2	TPM1_HUMAN	Tropomyosin alpha-1 chain
ILK_HUMAN	Integrin-linked protein kinase	TPM3_HUMAN	Tropomyosin alpha-3 chain
IMA3_HUMAN	Importin subunit alpha-3	TPM4_HUMAN	Tropomyosin alpha-4 chain
IMB1_HUMAN	Importin subunit beta-1	TRFE_HUMAN	Serotransferrin
INF2_HUMAN	Inverted formin-2	TSP1_HUMAN	Thrombospondin-1
IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1	TWF2_HUMAN	Twinfilin-2
ITA2B_HUMAN	Integrin alpha-IIb	TXND5_HUMAN	Thioredoxin domain-containing protein 5
ITA6_HUMAN	Integrin alpha-6	TYPH_HUMAN	Thymidine phosphorylase
ITB1_HUMAN	Integrin beta-1	U2AF2_HUMAN	Splicing factor U2AF 65 kDa subunit
ITB2_HUMAN	Integrin beta-2	UB2V1_HUMAN	Ubiquitin-conjugating enzyme E2 variant 1
ITB3_HUMAN	Integrin beta-3	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1
JAM1_HUMAN	Junctional adhesion molecule A	UBE2N_HUMAN	Ubiquitin-conjugating enzyme E2 N
K1C10_HUMAN	Keratin, type I cytoskeletal 10	UBP5_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5
K1C9_HUMAN	Keratin, type I cytoskeletal 9	UN13D_HUMAN	Protein unc-13 homolog D
K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal	URP2_HUMAN	Fermitin family homolog 3
K2C1_HUMAN	Keratin, type II cytoskeletal 1	USO1_HUMAN	General vesicular transport factor p115

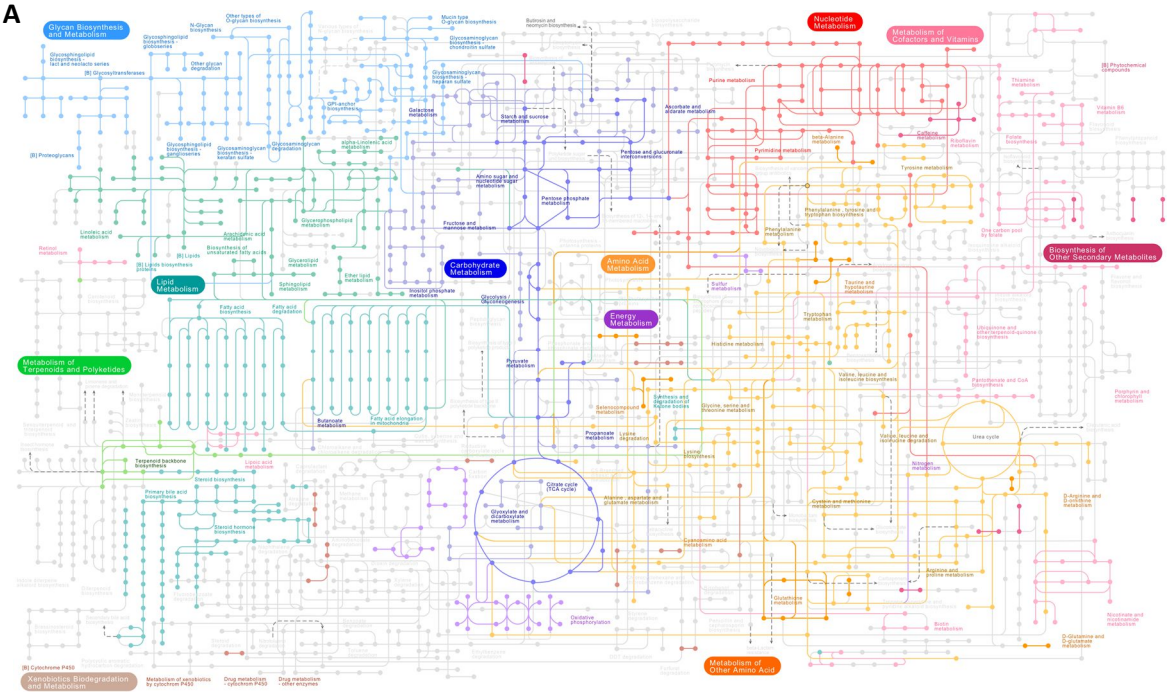
KAD2_HUMAN	Adenylate kinase 2, mitochondrial	VASP_HUMAN	Vasodilator-stimulated phosphoprotein
KAP0_HUMAN	cAMP-dependent protein kinase type I-alpha regulatory subunit	VATA_HUMAN	V-type proton ATPase catalytic subunit A
KCC1A_HUMAN	Calcium/calmodulin-dependent protein kinase type 1	VATE1_HUMAN	V-type proton ATPase subunit E 1
KPYM_HUMAN	Pyruvate kinase PKM	VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1
LAP2B_HUMAN	Lamina-associated polypeptide 2, isoforms beta/gamma	VDAC2_HUMAN	Voltage-dependent anion-selective channel protein 2
LASP1_HUMAN	LIM and SH3 domain protein 1	VDAC3_HUMAN	Voltage-dependent anion-selective channel protein 3
LCP2_HUMAN	Lymphocyte cytosolic protein 2	VIME_HUMAN	Vimentin
LDHA_HUMAN	L-lactate dehydrogenase A chain	VINC_HUMAN	Vinculin
LDHB_HUMAN	L-lactate dehydrogenase B chain	VPS35_HUMAN	Vacuolar protein sorting-associated protein 35
LEG1_HUMAN	Galectin-1	VTNC_HUMAN	Vitronectin
LEGL_HUMAN	Galectin-related protein	VWF_HUMAN	von Willebrand factor
LGUL_HUMAN	Lactoylglutathione lyase	WDR1_HUMAN	WD repeat-containing protein 1
LIMS1_HUMAN	LIM and senescent cell antigen-like-containing domain protein 1	XRCC5_HUMAN	X-ray repair cross-complementing protein 5
LMNB1_HUMAN	Lamin-B1	XRCC6_HUMAN	X-ray repair cross-complementing protein 6
LMNB2_HUMAN	Lamin-B2	ZAP70_HUMAN	Tyrosine-protein kinase ZAP-70
LTBP1_HUMAN	Latent-transforming growth factor beta-binding protein 1	ZYX_HUMAN	Zyxin
LY66F_HUMAN	Lymphocyte antigen 6 complex locus protein G6f		

Supplementary Table VII.8. Cell count of PBMCs samples from six healthy individuals.

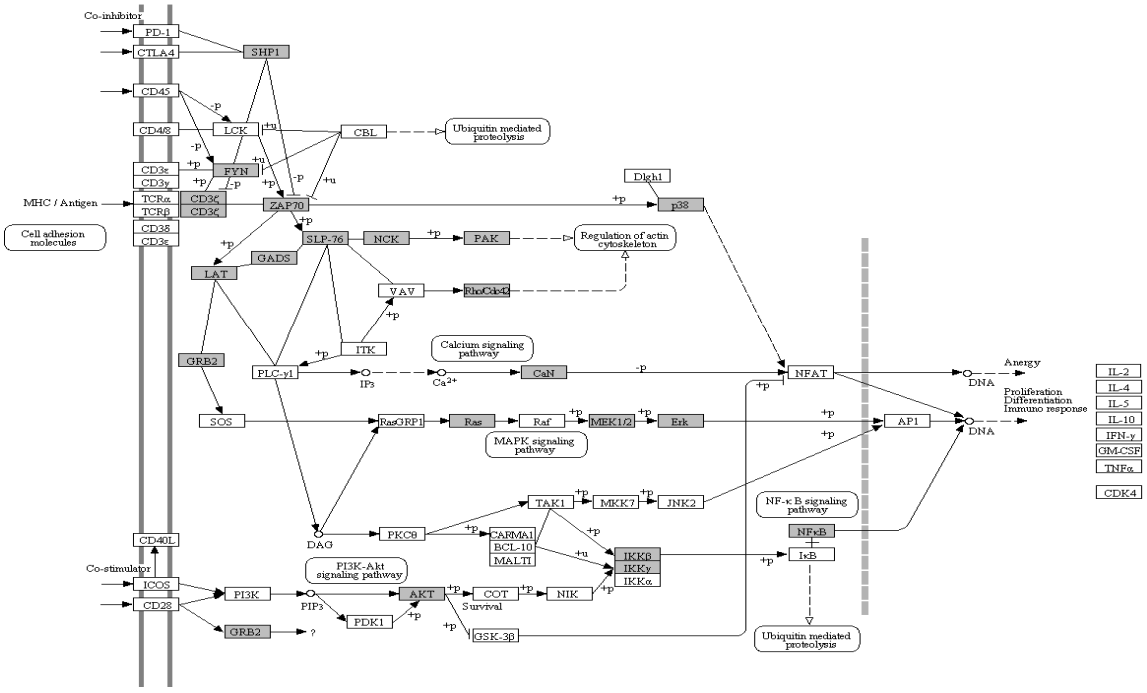
Cells	#1	#2	#3	#4	#5	#6
WBC	8.5	11.9	13.6	8.6	5.8	16.1
RBC	0.01	0.02	0.02	0.01	0.01	0.04

WBC are presented in millions of cells per mL; RBC are presented in millions of cells per µL; RBC = red blood cells; WBC = white blood cells; #1, #2, #3, #4, #5, #6 = biological samples of the six different donors.

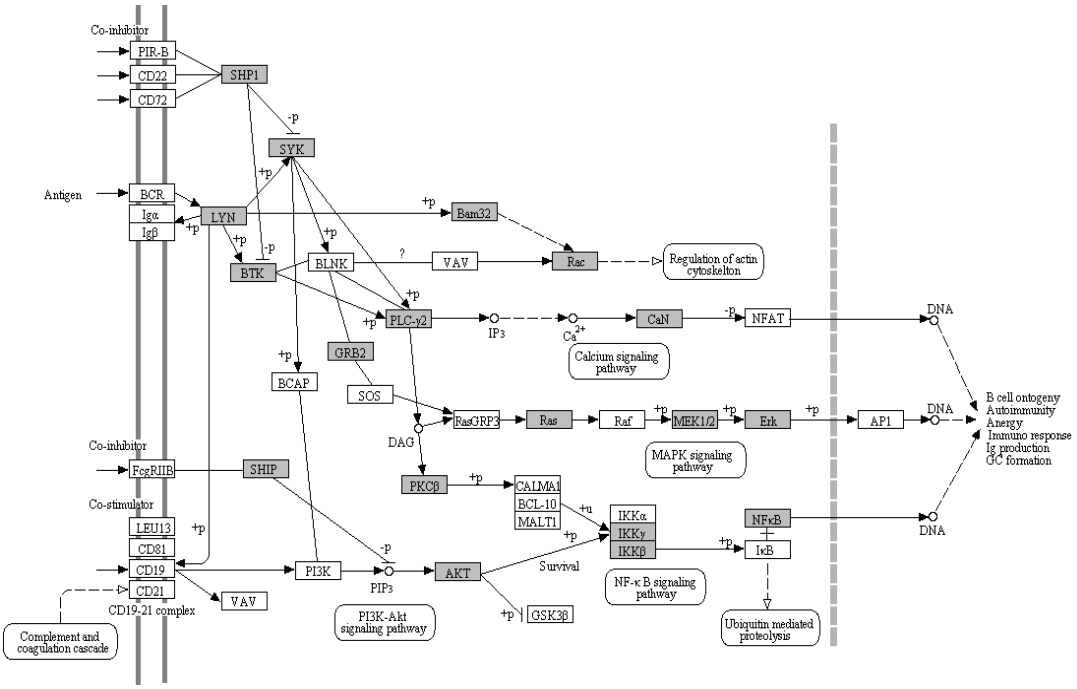
A



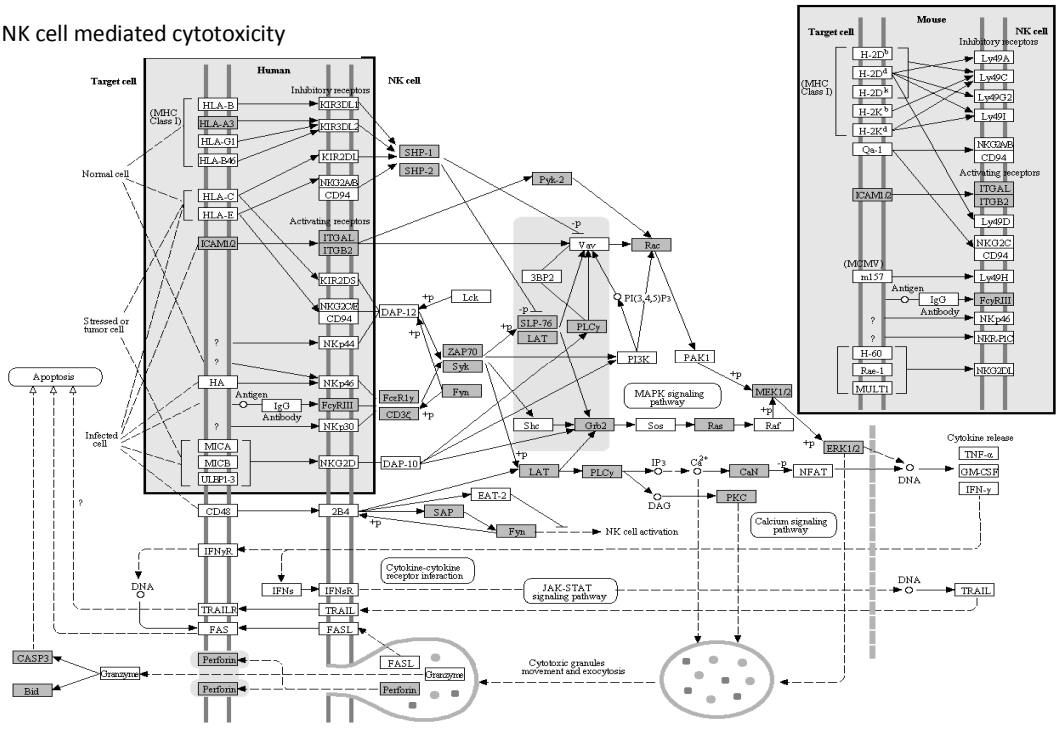
B T cell receptor signaling pathway



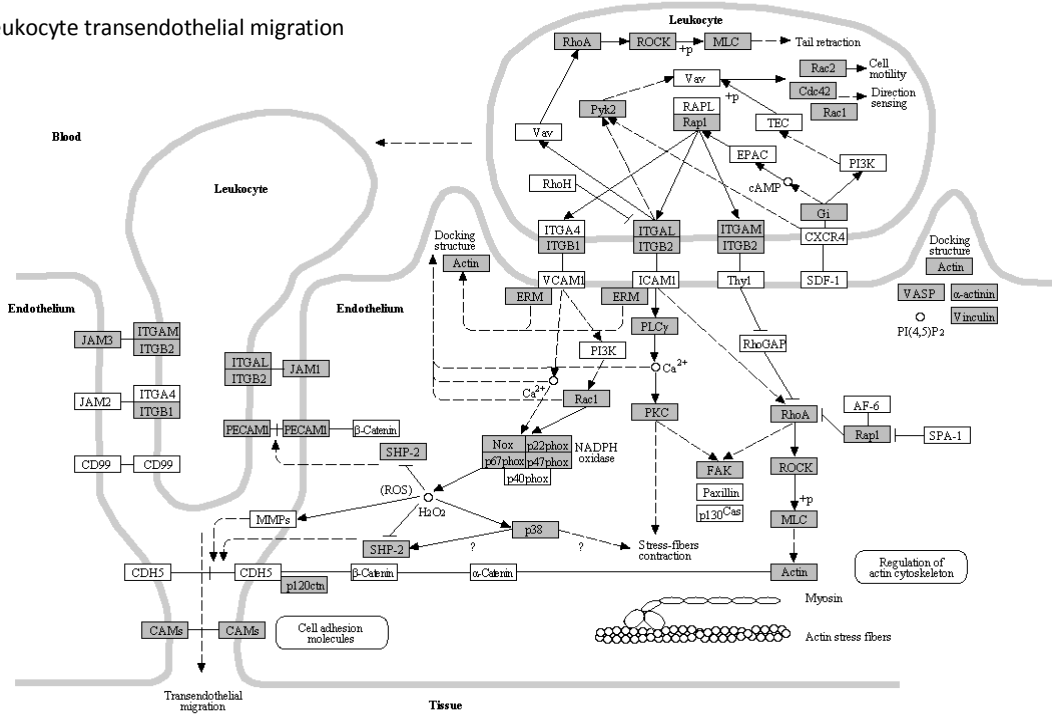
C B cell receptor signaling pathway



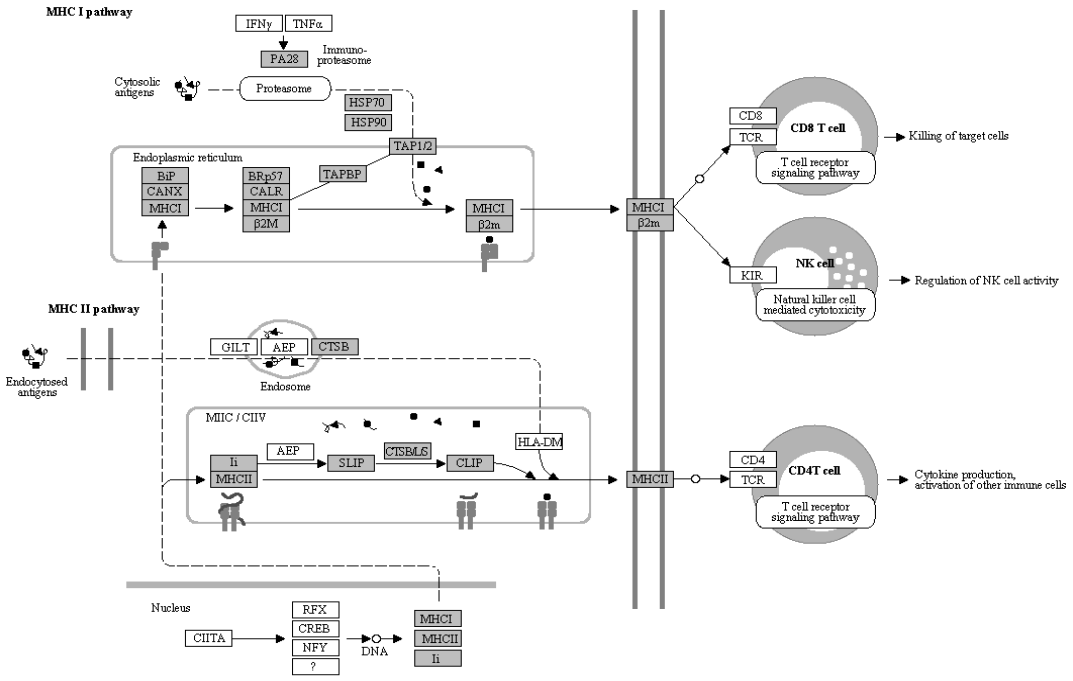
D NK cell mediated cytotoxicity



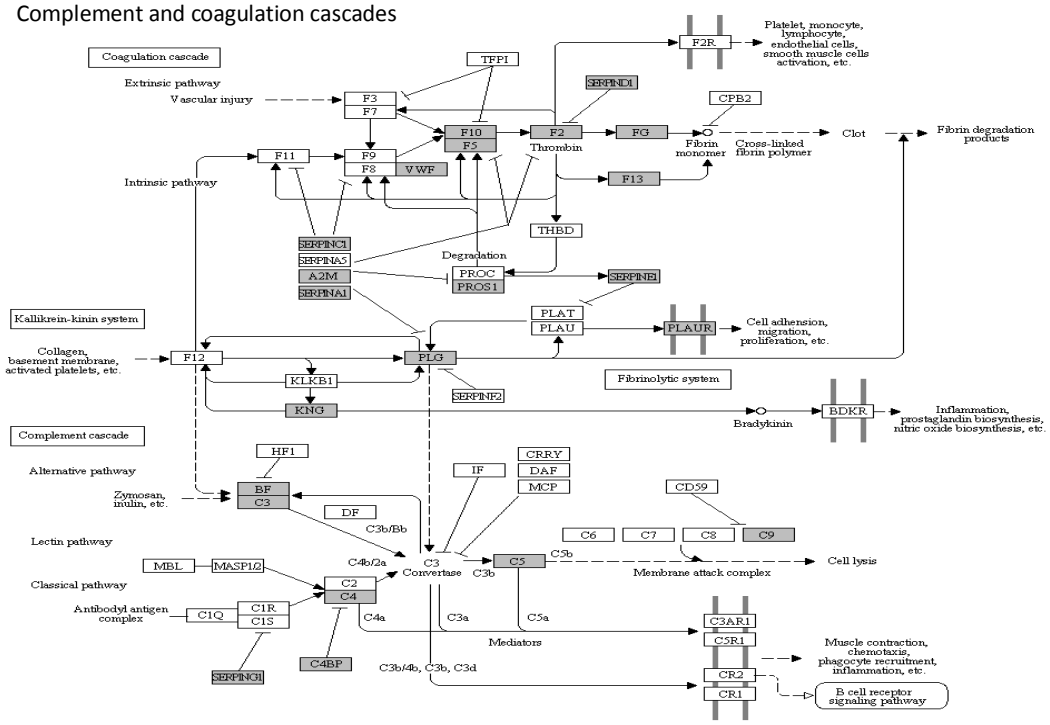
E Leukocyte transendothelial migration



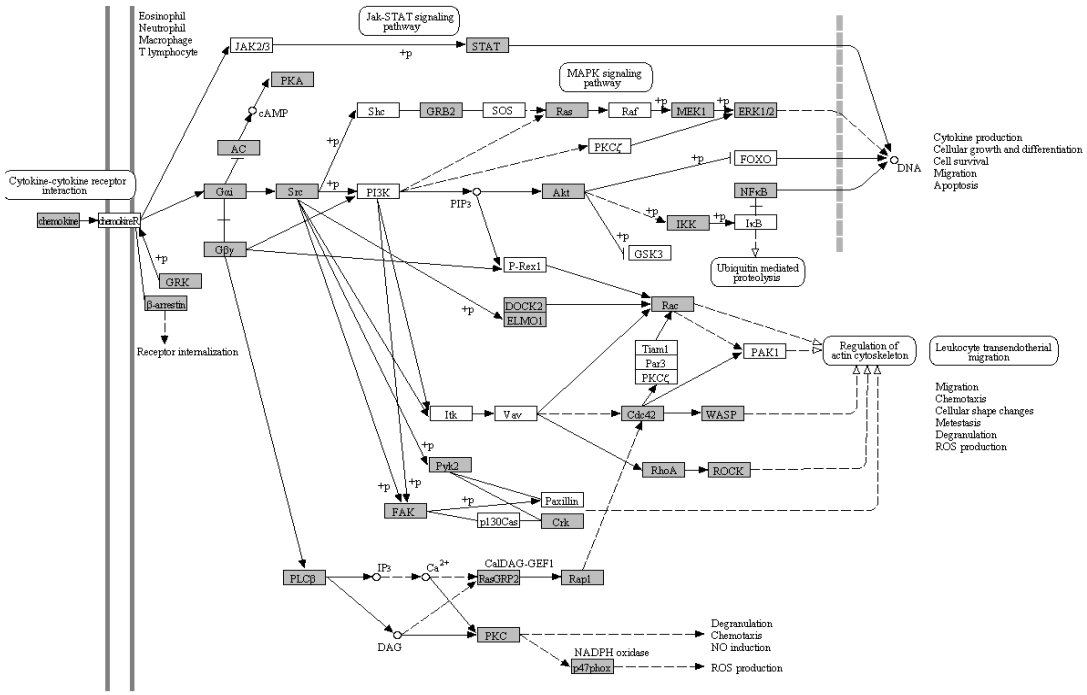
F Antigen processing and presentation



G Complement and coagulation cascades



H Chemokine signaling pathway



Supplementary Figure VII.1. KEGG atlas mapping of metabolic pathways of PBMCs. (A) Global view of all metabolic pathways where PBMCs proteins are involved in (blue). (B), (C), (D), (E), (F), (G), and (H) display diverse immune-system pathways. The identified proteins are highlighted in dark grey boxes.