NOVA SCHOOL OF SCIENCE & TECHNOLOGY

DEPARTEMENT OF CHEMISTRY

INÊS DE FREITAS DOMINGOS

BSc in Biochemistry

MULTIPLEXED PROTEIN ANALYSIS OF HUMAN SERUM REVEALS NOVEL PATHWAY TARGETS FOR MULTIPLE MYELOMA FOLLOW-UP AND THERAPY MONITORING

INSIGHTS FOR LABEL-FREE QUANTITATIVE PROTEOMICS.

MASTER IN Biochemistry

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À minha família, em especial Mãe e Pai.

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“Be less curious about people and more curious about ideas.”

(Marie Curie).

ABSTRACT

Significant advancements in molecular characterization have revolutionized the management of multiple myeloma (MM), with novel therapies enhancing overall survival. Yet, MM remains incurable, and treatment strategies often hinge on outdated risk-assessment methods, neglecting the efficacy of modern therapies. Addressing this, our research utilized multiplexed protein analysis, employing label-free quantitative proteomics to profile MM patient serum proteomes. This revealed a distinct protein set in MM patients versus healthy controls, highlighting key biological targets pivotal for MM progression. Notably, a compromised defense against protein misfolding was observed, evidenced by reduced Chaperone-mediated Autophagy (CMA) and protein-folding chaperone activity. This predisposes to protein aggregation and amyloid fiber formation, risking organ dysfunction, especially in kidneys. Pathway analysis further indicated downregulated humoral immune response, glomerular filtration, and autophagy, suggesting weakened immunity and renal function. Genomic instability markers, characteristic of many cancers, were also discerned through downregulated cell cycle, DNA repair, and chromosome maintenance pathways.

In clinical biochemistry, we meticulously quantified routine markers, including Albumin, metabolic and inflammatory markers, and β-2 microglobulin (β-2M), a key MM biomarker. Elevated β-2M levels in MM samples not only track MM progression but also signal potential amyloidosis onset. Collectively, our findings underscore serum proteomics' transformative potential in MM surveillance and amyloidosis detection, heralding it as a vital diagnostic instrument.

Keywords: Multiple Myeloma, Pathway enrichment, Amyloidosis, Serum Amyloid A 1, β-2 microglobulin.

RESUMO

Avanços significativos na caracterização molecular revolucionaram o tratamento do mieloma múltiplo (MM), com novas terapias a melhorar a sobrevivência global. No entanto, o MM permanece incurável, e as estratégias de tratamento muitas vezes dependem de métodos de avaliação de risco desatualizados, negligenciando a eficácia das terapias modernas. Neste contexto, a nossa investigação utilizou análise proteómica quantitativa para traçar o perfil dos proteomas séricos de pacientes com MM. Isto revelou um conjunto distinto de proteínas em pacientes com MM em comparação com controlos saudáveis, destacando alvos biológicos chave para a progressão do MM. Notavelmente, observou-se uma defesa comprometida contra o *folding* inadequado de proteínas, evidenciado pela redução da Autofagia Mediada por Chaperona (CMA) e da atividade chaperona de *folding* de proteínas. Isto predispõe à agregação de proteínas e formação de fibras amiloides, comprometendo a função orgânica, especialmente nos rins. A análise de vias indicou ainda uma resposta imune humoral, filtração glomerular e autofagia reduzidas. Marcadores de instabilidade genómica, característicos de muitos cancros, também foram detetados.

Em bioquímica clínica, quantificámos vários marcadores de rotina, incluindo Albumina, marcadores metabólicos e inflamatórios, e β-2 microglobulina (β-2M), um biomarcador chave do MM. Níveis elevados de β-2M nas amostras de MM não só acompanham a progressão do MM, mas também sinalizam o potencial início de amiloidose. Os nossos resultados sublinham o potencial transformador da proteómica sérica na vigilância do MM e deteção de amiloidose.

Palavras-chave: Mieloma Múltiplo, Enriquecimento de vias metabólicas, Amiloidose, Amiloide Sérica A1, β-2 microglobulina.

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GLOSSARY

Cytoscape	Cytoscape is an open source software platform for visualizing molecular interaction networks and biological pathways and integrating these networks with annotations, gene expression profiles and other state data. Although Cytoscape was originally designed for biological re-search, now it is a general platform for complex network analysis and visualization.
MaxQuant	MaxQuant is specialized software used to analyze large sets of mass-spectrometric data, especially high-resolution MS data. It works with various labeling methods and label-free quantification. MaxQuant includes tools to view raw data and results of identification and quantification. For statistical analysis of MaxQuant's output, the free Perseus framework is available.
Perseus	Perseus is a software that helps scientists make sense of protein data. It has tools for analyzing complex information, like spotting patterns and comparing different data sets. It even uses machine learning to group patients and predict outcomes based on protein patterns. Perseus is user-friendly and documents the methods used in research.
SDS-PAGE	SDS-PAGE (Sodium Dodecyl Sulfate Polyacrylamide Gel Electrophoresis) is a laboratory technique that separates proteins based on their size using a gel and an electric field. It helps scientists study and analyze proteins in biological samples.
Sera	In science, to talk about the patient serums, the word serum can be pluralized when used in certain senses. To speak of multiple serum specimens from multiple people (each with a unique population of anti-bodies), physicians sometimes speak of sera (the Latin plural, as op-posed to serums).
UniProt-Swiss Prot Human	SWISS-PROT contains the information about the name and origin of the protein, protein attributes, general information, ontologies, sequence annotation, amino acid sequence, bibliographic references, cross-references with sequence, structure and interaction databases, and entry information.

ACRONYMS

[#]

β2-M - Beta-2 microblobulin

[A]

ARPC1A - Actin-related protein 2/3 complex subunit 1A

ACN – Acetonitrile

APOC1 - Apolipoprotein C-I

APOAI - Apolipoprotein A-I

AAPOAI - Apolipoprotein A-I mutant

ANXA1 - Annexin A1

ANXA6 - Annexin A6

AL - Immunoglobulin Light Chain Amyloidosis

[B]

BM - Bone marrow

BSA - Bovine Serum Albumin

BCA - Bicinchoninic acid assay

[C]

CAA - Chloroacetamide

CRAB - Hypercalcaemia, Renal Dysfunction, Anaemia, Bone Disease

CAT - Catalase

CRM - Charged Residue Mode

CMA - Chaperone Mediated Autophagy

CRP - C Reactive Protein

[D]

DIA - Data Independent Acquisition

DDA - Data Dependent Acquisition

DSS - Durie Salmon Stage

DBL2 - Protooncogene diffuse B-cell lymphoma

DTT - Dithiothreitol

[E]

ESI - Electrospray Ionization

ESI-MS - Electrospray Ionization Mass Spectrometry

EMM - Extramedullary Multiple Myeloma

[F]

FA - Formic Acid

FDR - False Discovery Rate

FISH - Fluorescent *in situ* hybridization

FGA - Fibrinogen a chain

FLC - Free Light Chain(s)

[H]

HRSMM - High-risk Smouldering Multiple Myeloma

Hsp90 - Heat shock protein 90

HGO - Hospital Garcia de Orta

HGFA - Hepatocyte growth factor activator

HLA - Human leukocyte antigen

HPLC - High Performance Liquid Chromatography

HDL - High-density lipoprotein

HS - Healthy Serum

HSA - Human Serum Albumin

Hb - Hemoglobin
HCl - Hydrochloric acid

[I]
IF - Immunofixation
IMWG - International Myeloma Working Group
ISS - International Staging System
IEM - Ion Evaporation Model
IgA - Immunoglobulin A
IgH - Immunoglobulin H
IgG - Immunoglobulin G

[L]
LDL - Low-Density Lipoprotein
LPA - Apolipoprotein(a)
LDH - Lactate dehydrogenase
LC-ESI-HR-MS/MS – Liquid Chromatography - ESI - High Resolution Mass Spectrometry
LFQ - Label-free Quantification
LOD – Limit of Detection
LOQ – Limit of Quantification

[M]
MALDI - Matrix-assisted laser desorption/ionization
MALDI-TOF - Matrix-assisted laser desorption/ionization - Time-of-flight
MGUS - Monoclonal Gammopathy of Undetermined Significance
MM - Multiple Myeloma
MRI - Magnetic Resonance Imaging
MS - Mass Spectrometry
MS/MS - Tandem MS
m/z ratio - mass/charge ratio
mATTR - Mutant Transthyretin
MIF - Macrophage migration inhibitory factor
MMRN1 - Multimerin-1
MPO - Myeloperoxidase
MAPK - Mitogen-activated protein kinase
mDa - Milidalton

[N]
NPM1 - Nucleophosmin
nm - nanometers

[P]
PSME1 - Proteasome activator complex subunit 1
PSME2 - Proteasome activator complex subunit 2
PSME4 - Proteasome activator complex subunit 4
PEDF - Pigment epithelium-derived factor
P - Pellet

[K]
KLKB1 - Plasma kallikrein
kDa - Kilodalton

[R]
R-ISS - Revised-International Staging System
RT - Room Temperature

[S]
SAA - Serum amyloid-A protein
SAA1 - Serum amyloid A-1 protein
SMM - Smoldering Multiple Myeloma

SPE - Serum Protein Eletrophoresis
STIP1 - Stress-induced-phosphoprotein 1
SRM - Single Reaction Monitoring
SN - Supernatant

[T]

TEAB - Triethylammonium bicarbonate buffer
TCEP - Tris(2-carboxyethyl)phosphine
TRR - Transthyretin

[U]

UHR-QqTOF - Ultra-High Resolution – Quadrupole - Time-of-flight

[V]

VBD - Vitamin D-binding protein
VIM - Vimentin
VCAM1 - Vascular cell adhesion protein 1

[W]

W - Tryptophan
WR - Working Reagent
wtATTR - Wild-type Transthyretin

[X]

XIC - Extracted Ion Chromatogram

[Z]

ZAG - Zinc alpha 2-glycoprotein

1

INTRODUCTION

1.1 Multiple Myeloma

Multiple myeloma (MM) is a disorder of plasma cells that originates from the malignant transformation of mature plasma cells, which have been activated by antigens, situated post-germinal centre, and are found in the bone marrow (BM).[1] Multiple myeloma constitutes 1.3% of all malignancies and accounts for 15% of blood cancers, positioning it as the second most prevalent hematologic malignancy, following non-Hodgkin lymphoma.[2]

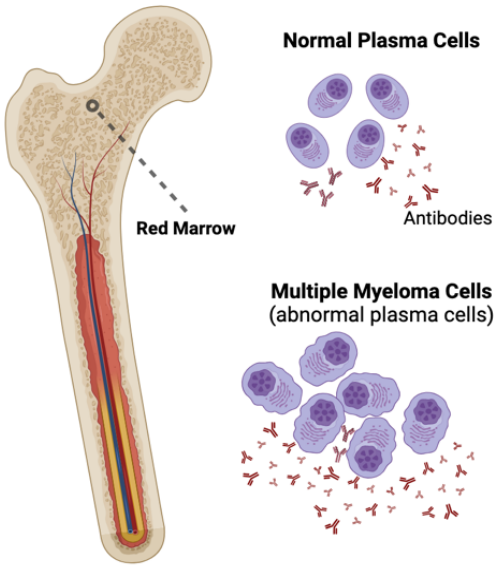

Figure 1 - Multiple Myeloma representation, plasma cells are made in bone marrow. Adapted from: *© 2023 Terese Winslow LLC, U.S. Govt. has certain rights* | Created with BioRender.com (accessed on 23 November 2022)

The primary risk factor for myeloma is age, making it uncommon for individuals under 45 to be diagnosed with the condition. Additionally, men have a higher likelihood of contracting myeloma compared to women, and Black individuals are over twice as susceptible to it than White individuals.[3]

In some rare instances, exposure to X-rays or other forms of ionizing radiation can increase the risk. Being overweight or obese is also associated with an elevated risk of developing this disease.[4]

In Portugal, the incidence of myeloma is relatively low, with approximately 500 to 700 new diagnoses annually. In Western countries, the rate stands at about 3 new cases annually for every 100 000 residents.[4]

1.2 Diagnosis

For a definitive diagnosis of MM, the presence of at least 10% clonal plasma cells in the bone marrow and detectable monoclonal protein in serum or urine is required. The evaluation and diagnosis of this disease involve two main aspects: diagnosis and prognosis.

When addressing diagnosis, various parameters are taken into account, including reviewing the patient's medical history and conducting a physical examination, performing routine tests, such as complete blood count and chemical analysis, bone marrow testing, and utilizing imaging techniques like skeletal surveys and magnetic resonance imaging (MRI) when needed.[5]

The prognosis is determined based on serum albumin, ß2-microglobulin, and lactate dehydrogenase.[6]

1.3 Natural history of the disease

When the body is invaded by bacteria or viruses, a specific type of white blood cell known as plasma cells, which are found in the bone marrow, launch a counterattack. They generate unique proteins called antibodies or immunoglobulins that work to eliminate or disable the harmful microorganisms responsible for the infection. However, like other forms of cancer, this process can sometimes malfunction, causing the bone marrow to produce an excessive amount of plasma cells originating from a single cell that has undergone malignant transformation. Such cells are referred to as clonal cells.[7]

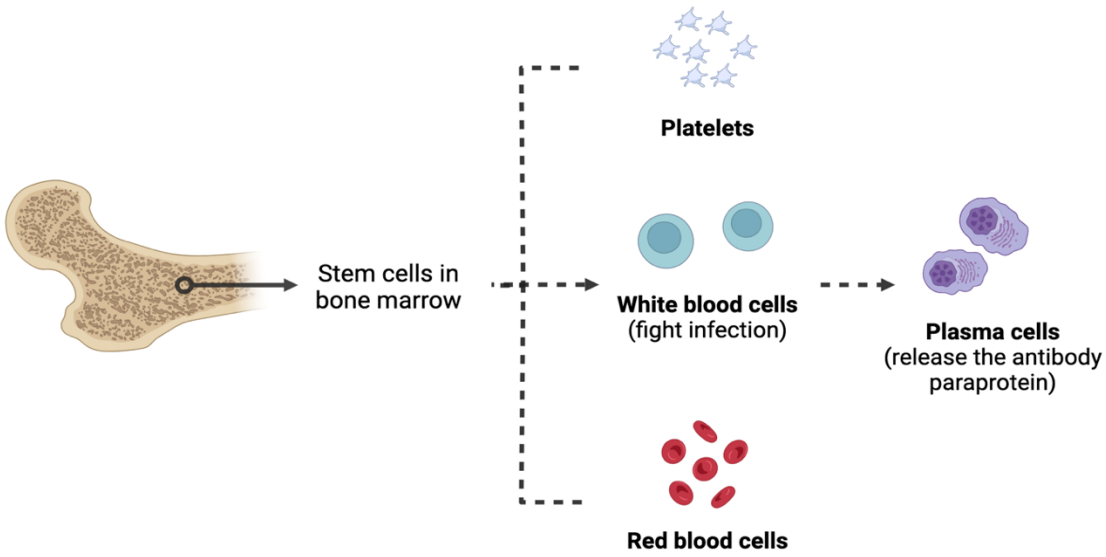

Figure 2 - Stem cells in the bone marrow divisions. Adapted from: Cancer Council (2022)[86] | Created with BioRen-der.com

These clonal cells possess the ability to generate proteins called cytokines, which stimulate the breakdown of bone tissue, leading to the formation of cavities within the bone called lytic lesions. These lesions compromise the strength of the bone and increase the risk of fractures. Given that multiple lytic lesions can develop, this condition is commonly known as multiple myeloma.[1]

Malignant plasma cells predominantly reside in the bone marrow, although they can also be detected in peripheral blood and other extramedullary locations like soft tissues and organs, especially in the later stages of the disease.[1]

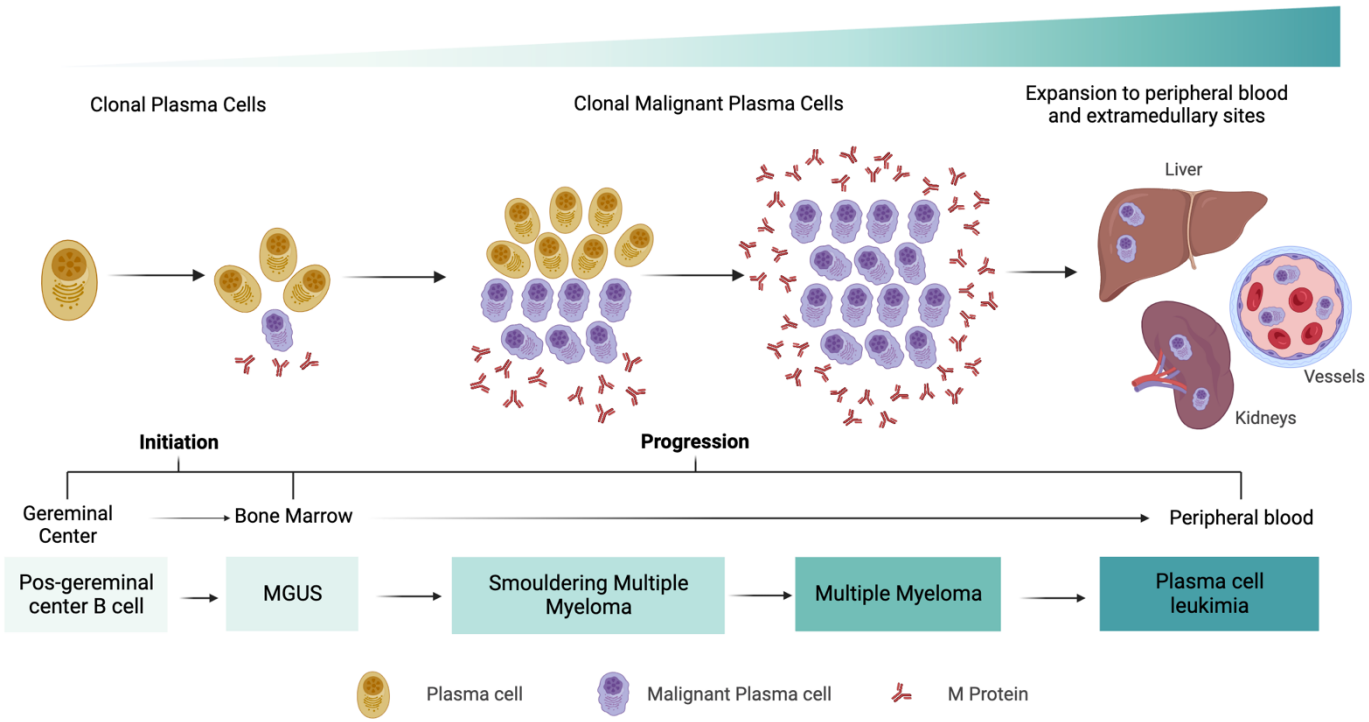

Figure 3 - Monoclonal gammopathies develop in stages. Multiple myeloma is the final stage and it happens after several changes occur in the bone marrow. Before multiple myeloma, there are earlier stages called monoclonal gammopathy of undetermined significance (MGUS) and smoldering multiple myeloma (SMM). Adapted from: Kumar, S., (2017)[1] | Created with BioRender.com (accessed on 23 November 2022)

Monoclonal Gammopathies of Undetermined Significance

Individuals diagnosed with monoclonal gammopathy of undetermined significance (MGUS) exhibit a plasma cell disorder characterized by relatively low levels of M-protein found in the blood and/or urine. The proportion of plasma cells in the bone marrow is less than 10%. Notably, these patients do not display myeloma-related symptoms such as anemia, renal failure, hypercalcemia, or lytic lesions.[8]

Although MGUS patients are not afflicted with cancer, there exists a risk of progressing to myeloma over time. On average, the annual risk of MGUS patients transitioning to myeloma is 1%.[8] However, some MGUS patients carry a higher likelihood of evolving into active myeloma. For instance, those with MGUS who also exhibit an abnormal free light chain ratio have an elevated propensity to advance to active myeloma compared to MGUS patients whose free light chain ratio falls within the normal reference range[9].

Recent studies indicate that MGUS patients might also contend with additional medical conditions or comorbidities that could impact both their quality of life and overall lifespan. In light of these considerations, it is imperative for each MGUS patient to undergo vigilant monitoring by their healthcare provider.[10]

Smouldering Multiple Myeloma

Individuals with smoldering multiple myeloma (SMM) exhibit elevated levels of immunoglobulins, free light chains, and plasma cells in their bloodstream when compared to those with monoclonal gammopathy of undetermined significance (MGUS). The likelihood of progressing to active myeloma is significantly higher in SMM patients compared to MGUS patients. High-risk SMM (HRSMM) can be identified through standard tests used to evaluate active disease status, such as the Freelite test.[9]

Asymptomatic patients whose free light chain ratio is either equal to or exceeds 100, or is equal to or less than 0.01, are now classified as having active myeloma. Likewise, patients with bone marrow plasma cells constituting 60% or more of their marrow are also categorized as having active myeloma. Additionally, individuals with multiple focal lesions detected via Magnetic Resonance Imaging now fall under the International Myeloma Working Group's (IMWG) definition of active myeloma. Patients meeting any one of these three criteria face an 80% or greater likelihood of developing CRAB criteria (organ damage) within a span of two years.[8]

Amyloidosis

Amyloidosis comprises a range of clinical conditions characterized by proteins with a propensity for misfolding that are transported through the bloodstream to vital organs, affecting organs like the heart, kidneys, liver, as well as the peripheral and autonomic nervous systems.[11]

A total of 36 proteins has the potential to induce the extracellular accumulation of amyloid, resulting in damage to cells and organs. These deposits can either form at the site of their origin, leading to localized amyloidosis, as seen in Alzheimer's disease.[12]

In addition, 14 proteins can trigger systemic amyloidosis, with the defective protein being able to accumulate in locations distant from its production site. For instance, proteins like TTR (pre-albumin) are synthesized in the liver, while immunoglobulin light chains are produced in the bone marrow, yet they can deposit in other areas of the body.[13]

There are different types of systemic amyloidosis and they're named according to the type of amyloid protein which is produced. Starts with 'A', followed by one or more letters that identify the particular amyloid protein.[12, 14 15]

Systemic amyloidosis encompasses several prevalent types. These include Immunoglobulin Light Chain (AL) amyloidosis, which is associated with abnormal plasma cell production. Mutant Transthyretin (mATTR) amyloidosis is another form, caused by genetic mutations in the transthyretin protein. Wild-type Transthyretin (wtATTR) amyloidosis occurs due to the natural aging process. Reactive (AA) amyloidosis is triggered by chronic inflammatory conditions. Additionally, Fibrinogen amyloidosis is related to mutations in fibrinogen genes, and Apolipoprotein A-I (AApoAI)

amyloidosis stems from genetic mutations affecting apolipoprotein A-I (APoAI). These various types of systemic amyloidosis each have distinct underlying causes and manifestations.[14]

There are at least 28 different proteins associated with amyloidosis and amyloid diseases.[13] The most common type of amyloidosis which is associated with a poor prognosis if left untreated is AL amyloidosis, which is due to the position of light chains of clonal immunoglobulin produced by plasma cells in the medulla. [16]

1.4 Biomarkers history in Multiple Myeloma

1.4.1 Established Biomarkers in Multiple Myeloma Detection

A. Durie-Salmon Staging System (DSS)

The emergence of biomarkers in the context of multiple myeloma dates back to 1975 when the Durie-Salmon Staging System[17] was introduced. This staging system stratifies multiple myeloma into three stages based on specific clinical parameters, as delineated in Table 1. Nevertheless, a notable limitation of this method lies in its inherent subjectivity in evaluating the extent of bone disease, prompting the development and adoption of the International Staging System (ISS) as an alternative staging system for myeloma.[18]

Table 1 - Durie-Salmon Staging System (DSS) for MM. Adapted from: Durie *et al.* (1975)[17]

Stage	Levels of components in serum
I	• Hb > 10 g/dL • Normal calcium • Skeletal survey: normal or single plasmacytoma or osteoporosis • Serum M protein level < 5 g/dL if IgG | < 3 g/dL if IgA • Urinary light chain excretion < 4 g/24h
II	Neither I or III
III	• Hb < 8,5 g/dL • High calcium > 12 mg/dL • Skeletal survey: three or more lytic bone lesions • Serum M protein > 7 g/dL if IgG | > 5 g/dL if IgA • Urinary light chain excretion > 12 g/24h
Stages I, II and III of DSS can be divided further into A or B based on kidney function as assessed by serum creatinine	
A	Serum creatinine < 2 mg/dL
B	Serum creatinine > 2 mg/dL

B. International Staging System (ISS)

To help in the diagnosis and prognosis, a risk stratification system for this condition has been implemented. The two crucial parameters of this system are the serum levels of β-2 microglobulin and albumin[8] , however, individuals with this condition accompanied by symptoms such as kidney dysfunction due to other factors like diabetes or hypertension may also present elevated levels of β-2 microglobulin or albumin.

This fact can lead to the incorrect classification of individuals as cases of multiple myeloma when, in reality, they may not have this condition. For this reason, it is advisable that this system be used in conjunction with the DSS table for a more precise identification.[19] To address these limitations, revisions have been made to the existing ISS method, as described in Table 2. These updates aim to provide a more accurate and reliable framework for the assessment of multiple myeloma.

Revised ISS (R-ISS)[20], incorporates for improved disease assessment and diagnosis, not only the measurement of β-2 microglobulin and albumin levels but also includes the evaluation of serum lactate dehydrogenase (LDH) and the presence of chromosomal abnormalities.

Table 2 - International Staging System (ISS)[18] and Revised ISS[20] for Multiple Myeloma patients. Adapted from: Greipp P., *et al.* (2005) & Palumbo, A. *et al.* (2015).

Stage	Levels of components in serum
International Staging System	
I	• β2 microglobulin (β2-M) < 3.5 mg/L, albumin ≥ 3.5 g/dL
II	• β2 microglobulin (β2-M) < 3.5 mg/L, albumin ≤ 3.5 g/dL or β2-M 3.5 – 5.5 mg/L, irrespective of serum albumin
III	• β2 microglobulin (β2-M) ≥ 5.5 mg/L
Revised International Staging System	
I	• International Staging System stage I • Normal lactate dehydrogenase (LDH) levels • Standard risk cytogenic markers, detected using fluorescent *in situ* hybridization (FISH)
II	• Stage II: not stage I or III
III	• International Staging System stage III • Either higher than normal LDH levels or high-risk cytogenic markers detected using FISH

C. Plasma cell percentage

Multiple myeloma is characterized by the malignancy of plasma cells within the bone marrow. In healthy individuals, plasma cells typically constitute less than 3% of the bone marrow. However, in MM patients, this percentage can surge from 10% to 100%, depending on the disease's progression.[1]

Bone marrow biopsy, while being a definitive test for MM, is notably invasive and often associated with significant discomfort and pain. During this procedure, bone marrow cells are stained and then analyzed based on their cellular structure. These cells are then counted to determine the proportion of plasma cells present.[20]

D. Chromosomal abnormalities

Multiple myeloma, conventionally regarded as a single disease, is, in reality, an aggregation of several distinct cytogenetically characterized plasma cell malignancies.[21,22] Fluorescent *in situ* hybridization (FISH) examinations performed on bone marrow specimens reveal that approximately 40% of multiple myeloma cases manifest trisomies within the malignant plasma cells, a condition known as hyperdiploid multiple myeloma. In contrast, the majority of other cases exhibit translocation events involving the immunoglobulin heavy chain (IgH) locus situated on chromosome 14q32, referred to as IgH translocated multiple myeloma.[23–26]

A minor subset of patients exhibit the coexistence of trisomies and IgH translocations, that are recognized as primary cytogenetic irregularities that manifest during the inception of MGUS. Moreover, during the progression of multiple myeloma, additional cytogenetic alterations referred to as secondary cytogenetic abnormalities emerge, encompassing gain(1q), del(1p), del(17p), del(13), and secondary translocations involving MYC. Both primary and secondary cytogenetic abnormalities have the potential to impact the course of the disease, therapeutic response, and prognosis.[10,27]

E. Serum proteins electrophoresis (SPE)

One of the ways to detect and monitor MM is by looking for these M proteins in the blood. This is done using a laboratory technique called serum protein electrophoresis (SPE). When a patient's blood serum is subjected to this test, the proteins in the serum separate based on their size and charge. If M proteins are present, they will appear as a distinct peak or "spike" on the electrophoresis graph. This spike is commonly referred to as the ‘M spike’.[28,29]

The type of globulin in the M spike can be categorized as alpha, beta, or gamma, with gamma being the most common in MM. The presence of an M spike is a strong indicator of MM or other

related conditions. Moreover, the size and intensity of this spike can provide valuable information about the progression of the disease. For instance, an increasing M spike might indicate disease progression, while a decreasing or disappearing spike could suggest remission. Monitoring the M spike over time is thus crucial for assessing how well a patient is responding to treatment and whether the disease is in remission or has recurred.

F. Bence-Jones Protein Urine

Two different classes of these proteins have also been identified known as kappa and lambda.[30]

The urinary Bence-Jones protein, displaying an amino acid composition and thermal characteristics closely resembling those of the light chains originating from a circulating IgG monoclonal protein, assumes a central role in the diagnostic and prognostic assessment of this condition.[31]

G. Serum free light chains (FLC)

Normal plasma cells typically produce both heavy chains and light chains, with light chains being generated in greater quantities than heavy chains. The excess of light chains does not become incorporated into immunoglobulins and consequently remains in the circulation as free light chains.[19]

Patients with MM exhibit elevated levels of both kappa and lambda free light chains, which are quantifiable in the bloodstream. Additionally, they present with structural abnormalities that contribute to the development of amyloid deposits within tissues and organs.[15,32] The ratio between kappa and lambda light chains typically deviates from the norm in the majority of patients, serving as a potential tool for monitoring disease progression and treatment efficacy. In fact, a decrease of 30% in the serum free light chain ratio has been observed in survivors, thus establishing it as a sensitive indicator for this disease.[19]

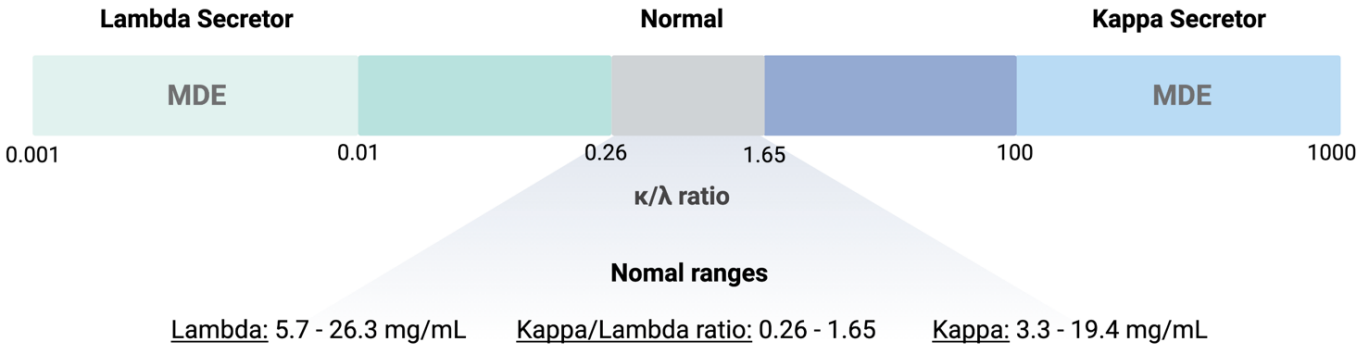

Figure 4 - Free light chains ranges in the serum of healthy individuals and patients. MDE: Myeloma Defining Event. Adapted from: Understanding Freelite ® and Hevylite ® Tests[87], (2018) (accessed in December 2022)

1.4.2Next generation Biomarkers

In the evolving landscape of medical diagnostics, next-generation biomarkers are paving the way for more precise and timely disease detection, prognosis, and therapeutic monitoring of MM. Among these, genomic markers, and proteomic-based markers stand out as promising to improve MM detection and management.

Genomic markers in MM offer insights into the genetic variations and mutations associated with the disease. Transitioning from the genetic landscape, proteomic-based markers focus on the protein expressions in MM cells, offering real-time insights into the disease's state as extensively exemplified in the literature.

1.4.3 Proteomic Biomarkers

In a series of compelling studies, researchers have delved deep into the proteomic landscape of MM to uncover diagnostic and therapeutic insights. Zhang *et al.*[33] pinpointed a distinct expression pattern of several proteins, including serum amyloid A protein and vitamin D-binding protein, in the sera of MM patients (Table 3). Ma, Tian-Ze and colleagues[34] employed a combination of two-dimensional electrophoresis and MALDI-TOF mass spectrometry to identify a myriad of differentially expressed proteins in MM. Dytfeld *et al*.[35] provided a comprehensive analysis of protein alterations in MM patients undergoing bortezomib-based therapy. They highlighted the upregulation of proteins linked to proteosome function and protein folding in refractory patients, while also noting the elevated levels of proteins associated with oxidative stress in non-responsive patients. Furthermore, they identified a unique proteomic signature in the serum of MM patients post-bortezomib therapy, emphasizing the roles of proteins like Apolipoprotein C1 in vital biological processes. Rajpal[36] and his team shed light on the potential of proteins such as Zinca-2-

glycoprotein and vitamin D-binding protein in predicting thalidomide response in MM patients. Their findings underscored the enhanced expression of these proteins in thalidomide-resistant patients, suggesting their potential as markers for MM diagnosis and prognosis.

Finally, Dunphy K.[37] and colleagues conducted a comprehensive proteomic analysis of patients suffering from both MM and Extramedullary Multiple Myeloma (EMM) using plasma proteomics analysis (LFQ). This investigation revealed significant disparities in the abundance of 22 proteins. Notably, among these proteins, vascular cell adhesion molecule 1 (VCAM1), pigment epithelium-derived factor (PEDF), and hepatocyte growth factor activator (HGFA) emerged as promising indicators for the presence of EMM. Impressively, when utilized as a collective panel, these proteins exhibited exceptional accuracy in effectively discerning EMM patients from those afflicted with MM.

Table 3 - Summary of some proteomic based markers studies in Multiple Myeloma.

Proteomic Studies		
Author (s)	**Marker Identified**	**Relevance**
Rajpal et. al. 2011	• Zinc-alfa-2-glycoprotein (ZAG); vitamin D-binding protein (VDB); serum amyloid-A protein (SAA)	Prognostic
Zhang et. al. 2015	• SAA; VDB; Plasma kallikrein (KLKB1); Apolipoprotein A-I (APOA1) and Isoform-1 of multimerin-1 (MMRN1)	Diagnostic
Dytfeld et al. 2016	• Proteasome activator complex subunit 1 (PSME1); PSME2; Heat shock protein 90 (HSP90); Stress-induced-phosphoprotein 1 (STIP1); Nucleophosmin (NPM1); Peroxiredoxins; Catalase (CAT); Myeloperoxidase (MPO); Annexins (ANXA1 and ANXA6); Vimentin (VIM); Macrophage migration inhibitory factor (MIF) and Human leukocyte antigen (HLA) class II histocompatibility antigen	Prognostic
Luczak et. al. 2017	• Apolipoprotein C1 (APOC1), Complement components and Sulphydryl oxidase 1 (QSOX1)	Prognostic
Ze Ma et. al. 2018	• Immunoglobulin heavy constant μ; Protooncogene diffuse B-cell lymphoma (DBL2); 26S protease regulatory subunit4 (PSME4); SAA; Haptoglobin (HP); Actin-related protein 2/3 complex subunit 1A (ARPC1A) and Fibrinogen alpha chain (FGA)	Diagnostic
Dunphy K. et. al. 2023	• Vascular cell adhesion molecule 1 (VCAM1), Pigment epithelium derived factor (PEDF), and Hepatocyte growth factor activator (HGFA)	Prognostic

The previous studies have highlighted the superior capabilities of mass spectrometry-based methods in detecting monoclonal immunoglobulin (M-protein) and other relevant proteins. These methods have been shown to possess a distinct edge over traditional electrophoretic techniques.[38–40]

Notably, they exhibit enhanced analytical sensitivity and specificity compared to serum protein electrophoresis and immunofixation (IF). Beyond mere detection, they also provide intricate details about the proteins, such as insights into light chain glycosylation, which remain elusive to SPEP and IF.[41] As these techniques are still emerging, the medical community is actively exploring their potential impact on patient care and their optimal integration into clinical practice.

1.5 Mass Spectrometry

Mass spectrometry (MS) is a sophisticated analytical method that determines the mass-to-charge ratio (m/z) of ions in the gas phase, enabling the identification and quantification of individual compounds. This technique provides detailed insights into various substances' molecular composition and structure. It can pinpoint the molecules engaged in complex biological processes, define their structure, and observe alterations in their quantity or structure. This provides a deeper understanding of fundamental molecular pathways, rendering it an essential instrument across various scientific disciplines.[42]

Mass spectrometry is a well-established detection method that offers several benefits, such as selectivity sensitivity, and different analytes, such as drugs, metabolites, peptides, and proteins. It can be coupled to various chromatographic techniques, such as liquid chromatography, gas chromatography, or inductively coupled plasma.[43] This technique is widely used in many research fields and industries, including pharmaceutical and food industries, clinical labs, and forensic and environmental testing labs.

1.5.1 MS Equipment

Any mass spectrometer consists of three major elements: sample introduction, data system, and data output as we can see in the figure below. Although several methods exist for introducing ions into the gas phase but only two are relevant in proteomics, MALDI (Matrix Assisted/Laser Desorption Ionization) and ESI (Eletrospray Ionization).

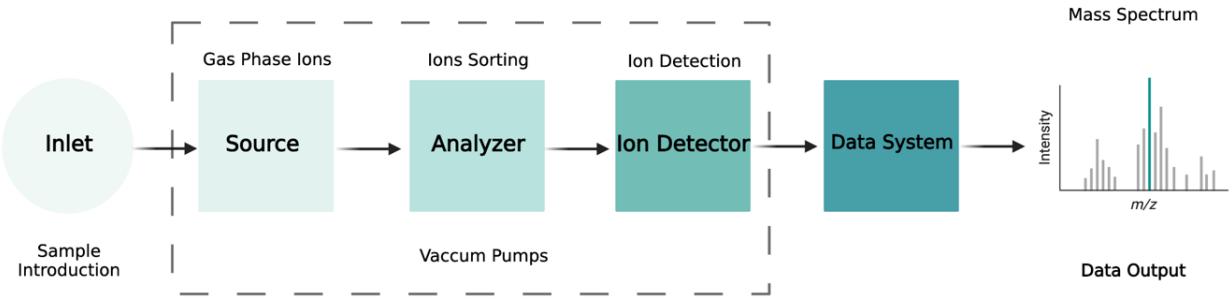

Figure 5 - Mass spectrometry equipment workflow. Created with BioRender.com

The mass analyzer and the detector are always under high vacuum. The ionization may take place either in vacuum or atmospheric pressure. Vacuum at most in MALDI instruments and atmospheric pressure at all ESI and in some MALDI.[44]

1.5.2ESI – Electrospray Ionization

Electrospray ionization (ESI) is a method utilized in mass spectrometry to generate ions. It involves the application of a high voltage to a liquid, resulting in the production of an aerosol.

Electrospray Ionization (ESI) is a method that prevents these molecules from breaking apart when ionized. Unlike other techniques that work at regular air pressure, ESI can create ions with multiple charges, which let us study a broader range of molecule sizes. This enables the detection and analysis of proteins and their associated peptides, which can have magnitudes ranging from kilodaltons (kDa) to millidaltons (mDa).[45]

The Principle of Electrospray Ionization

In ESI, a high voltage is applied to the capillary outlet, creating a strong electric field that causes the liquid flowing out of the capillary to disperse into small charged droplets.

The droplets enter the spray chamber and encounter a counter-current of heated dry gas (such as nitrogen gas). This gas causes the droplets to evaporate, reducing their diameter and increasing the surface charge density. As the droplets approach the Rayleigh limit, the repulsive force between the charges becomes strong enough to counteract the surface tension of the droplet. This leads to the fission of the droplets, resulting in the formation of smaller charged droplets. This allows the analyte to transition into the gas phase as a single or multiple charge species, forming a gas phase ion.[46,47]

The generation mechanism of gas phase ions in ESI can be explained by two models: the ion evaporation model (IEM) proposed by Thomson and Iribarne[48], and the charged residue model

(CRM) advocated by Dole and RIlgen[49]. In both models, the ions of interest are not excited by external energy and do not produce fragments when converting into gas-phase ions.[47]

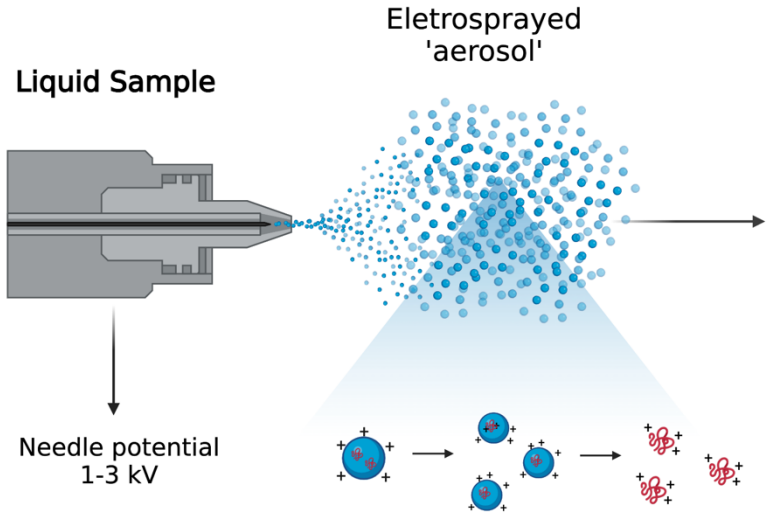

Figure 6 - Electrospray Ionization illustration. Adapted from: Monge E. et. al. (2013)[47] | Created with Biorender.com

1.5.3 Advantages and Disadvantages of ESI

Electrospray ionization (ESI) presents a relatively simple approach to ionizing non-volatile solutions, allowing for sensitive detection in mass spectrometry. This method is not just confined to inorganic substances but also extends to the detection and analysis of organometallic ion complexes and biomacromolecules. One of the notable features of electrospray mass spectrometry is that high molecular weight molecules often possess multiple charges. The distribution of these charge states gives an accurate reflection of their molecular weight, offering both precise molecular mass data and valuable structural insights. ESI provides the flexibility of choosing from various ionization modes, such as positive ion mode and negative ion mode, depending on the analytical needs. Moreover, it seamlessly integrates with different chromatographic methods, combining chromatography's separation strength with ESI mass spectrometry's detection prowess.[45,50]

However, ESI is not without its challenges. The determination of experimental parameters and technical conditions requires a meticulous understanding of the specific issue being addressed. Solvent choices and solution ranges are somewhat restricted. The mass spectrometer's response can differ considerably across ion complexes, complicating accurate quantitative analysis. The spraying process is sensitive to solution parameters, leading to potential ion signal

fluctuations even under the best conditions. Such variability introduces another dimension of complexity to the analytical process. Hence, it's imperative to optimize and control experimental parameters rigorously to mitigate these fluctuations and guarantee consistent and trustworthy outcomes.[45]

1.6 Mass Spectrometry Analysis

Mass spectrometry, while a powerful tool for proteomic analysis, presents challenges when it comes to quantitative measurements. The inherent variability in the response of proteolytic peptides, which possess a wide range of physiochemical properties, can lead to inconsistencies in mass spectrometric readings across different runs. This variability is further compounded by the fact that only a fraction of the total digested peptides in a sample undergo analysis.[51]

To address these challenges and achieve both relative and absolute proteomic quantification, several strategies have been developed:

Metabolic Labelling: This method involves incorporating stable isotopes into proteins during cell growth. The isotopically labelled proteins can then be mixed with unlabelled proteins, digested, and analyzed using mass spectrometry. The relative abundance of proteins can be determined by comparing the intensities of the labelled and unlabelled peptides.

Isotopic and Isobaric Tags: These are chemical tags that can be attached to peptides. Isotopic tags result in peptides with different masses, while isobaric tags produce peptides of the same mass but with different fragmentation patterns. Both types of tags can be used to compare protein levels in different samples.

Selective Reaction Monitoring (SRM): SRM is a targeted mass spectrometry method that allows for the quantification of specific peptides in complex mixtures. It is highly sensitive and can be used to detect low-abundance proteins.

While these methods have significantly improved the quantitative capabilities of mass spectrometry in proteomics, it is essential to choose the appropriate technique based on the specific requirements of the study and the nature of the samples being analyzed. For the specific case of clinical samples, label-free quantitative proteomics has emerged as an alternative tool.

1.6.1 Label-free quantitative proteomics

Label-free quantitation (LFQ) stands out as a preferred approach for extensive sample analyses, such as in clinical screenings or biomarker identification studies. This is attributed to its straightforward experimental design, cost-effectiveness, and its capability to detect a broader spectrum of proteins across a more extensive dynamic range compared to methods that employ labeling.[51]

In label-free quantification, every sample undergoes individual MS analysis under the same acquisition conditions. Proteins from each sample are identified, and their expression levels are determined either by LFQ based on ion counting or LFQ based on the intensity of the MS spectrum features associated with the protein.

Ion Counting LFQ (Spectral Counting Method): This method determines proteins by counting the number of MS/MS spectra identified for a specific protein. The fundamental idea is based on the observation that proteins present in higher quantities produce more peptides, which in turn have a higher likelihood of being analyzed by the mass spectrometer, resulting in an increased spectral count.[52] Although there is a strong correlation between protein abundance and spectral count, utilizing dynamic exclusion to detect low-abundance peptides can negatively impact the accuracy of this quantification method.[51]

Intensity-based LFQ: This method is based on the measurement of a precursor signal intensity from the extracted ion chromatogram (XIC). Consequently, it is crucial to have consistent and reproducible chromatographic separation for accurate peptide identification and quantification. When analyzing a large number of samples, the alignment of retention times becomes a crucial step.[53,54] Additionally, intensity normalization is necessary to decrease bias in signal intensity, especially on large datasets. One of the challenges with this method is the considerable computational capacity required for tasks such as peak identification, noise reduction, retention time alignment, peak intensity calculations, and normalization. [55]

Recent research contrasting ion counting and intensity-based LFQ has shown that intensity-based approaches have a consistent edge over ion counting regarding sensitivity and precision.[56] Based on these insights, our research will utilize label-free quantification, focusing on the measurement of precursor ion signal intensities.

In LFQ, there are two main strategies for data acquisition: Data Independent Acquisition (DIA) and Data Dependent Analysis (DDA).

In Data Independent Acquisition, MS/MS are acquired either by fragmenting all ions that enter the mass spectrometer at a given time (called broadband DIA) or by sequentially isolating and fragmenting ranges of m/z. DIA systematically and repeatedly samples every peptide in a protein digest. This results in a multifaceted array of mixed fragmentation patterns, where individual MS/MS spectra might encompass fragments from several peptides. Given this complexity, conventional search engines like MASCOT or Andromeda are not able to handle these intricate spectra. Instead, researchers turn to spectral libraries, which are compilations of annotated peptide-MS/MS spectrum matches derived from DDA experiments. Notably, established human spectral libraries exist, such as the 2010 Human Plasma Peptide Atlas, and efforts are underway to curate more libraries for various biofluids, including serum, plasma, and urine.[53,54]

Data Dependent Analysis, on the other hand, selects peptide signals exceeding a specific threshold in the first mass analyzer. These peptides are then fragmented, and their MS/MS data is obtained through a second mass analyzer. Since each MS/MS spectrum in DDA contains fragments from only one peptide, identification becomes simpler using search engines and in silico databases. LFQ can then be utilized for quantification in DDA through either ion counting-based or intensity-based LFQ. The peak area of measured peptides often shows a linear correlation with their abundances, allowing for quantification through signal intensity ratios across MS runs.[57]

In DDA, both MS and MS2 spectra are recorded in a single run, with MS2 acquisition being influenced by MS outcomes. A common challenge in DDA is that numerous molecular features might not be identified if they are not selected for fragmentation. Moreover, due to the intensity threshold for precursor selection, certain proteins may have missing values. These issues are less common in DIA. However, as DIA is based on pre-existing spectra libraries, it is limited to detecting peptides that were previously identified by the same technique. The development of these spectral libraries is not only time-consuming but also resource-intensive, making it less feasible for rapid or exploratory studies. Conversely, DDA does not require such libraries, providing greater flexibility in analyzing diverse samples. This versatility, combined with the time and resource constraints associated with library generation, makes DDA the more effective and suitable choice for our study objectives and the nature of our samples.[55]

2

OBJECTIVES AND WORKFLOW

2.1 Objectives

The primary aim of this research was to delve deeply into the molecular intricacies of multiple myeloma (MM) and its management, with specific objectives outlined as follows:

- **Serum Proteome Profiling**: To employ a multiplexed protein analysis technique for a comprehensive profiling of the serum proteome of MM patients using label-free quantitative proteomics.
- **Identification of Differentially Expressed Proteins:** To identify and characterize proteins that are differentially expressed in MM patients compared to healthy controls and to map these proteins onto biological pathways to reveal targets crucial for MM progression.
- **Pathway Enrichment Analysis:** To conduct a pathway enrichment analysis to uncover processes that are dysregulated in MM, and to understand their implications for the patients.
- **Quantification of Clinical Markers:** To precisely quantify routine clinical markers in MM, including Albumin, metabolic parameters, inflammatory markers, and especially β-2 microglobulin (β-2M).
- **Potential of Serum Proteomics:** To underscore the diagnostic potential of serum proteomics as a pioneering tool for MM monitoring and amyloidosis detection.

2.2 Purposed proteomic workflow

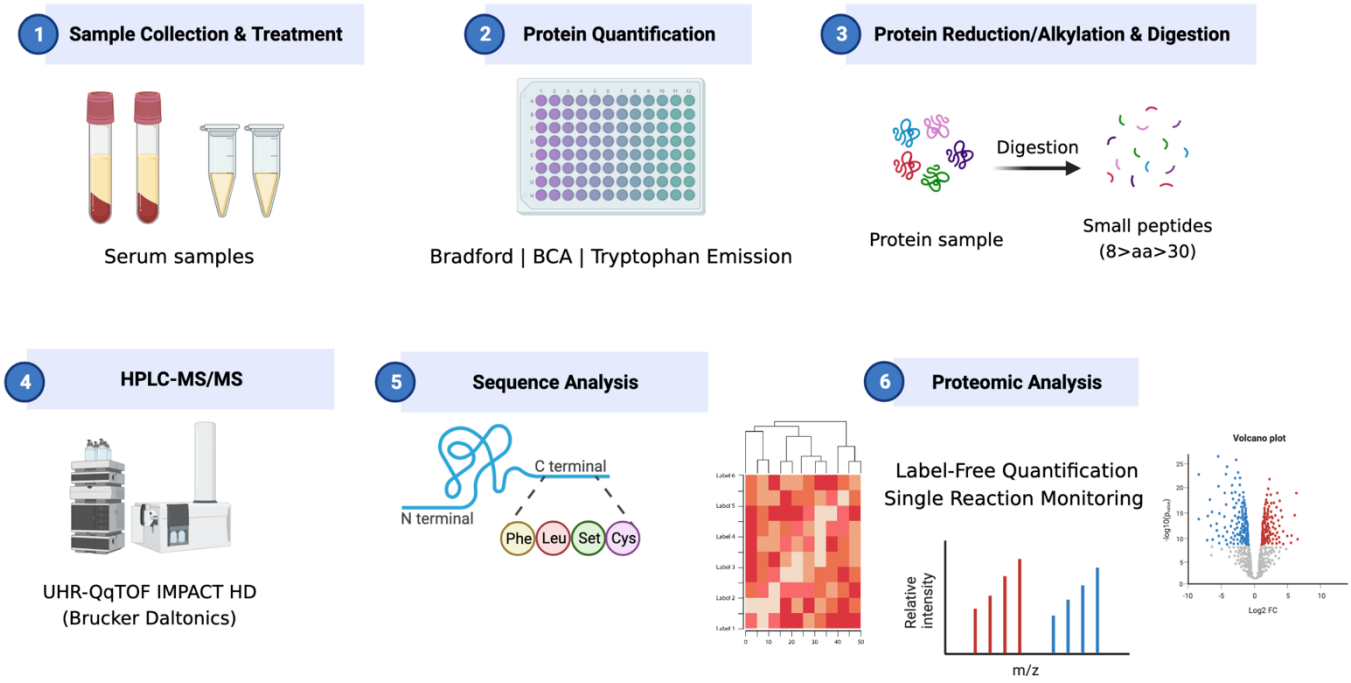

Figure 7 - Proteomic workflow and the main techniques. Created with BioRender.com.

3

EXPERIMENTAL SELECTION

3.1 Sample Collection

The serum samples were facilitated by the Hematology Service of Hospital Garcia de Orta (HGO) in Almada. The study was approved by the Health Ethics Committee of HGO. The selection of patients for this study was made according to the following parameters: all patients with Multiple Myeloma; age range between 18 and 80 years; ability to provide informed consent, and no gender or race restrictions. Exclusion criteria: patients suspected of Human Immunodeficiency Virus (HIV), or other viral infections such as Hepatitis B, C were not enrolled in the study.

3.2 Samples Treatment

Serum samples were collected at the Hospital Garcia de Orta (Almada) in red glass vacutainer tubes without anticoagulants or preserves. The samples were allowed to clot at room

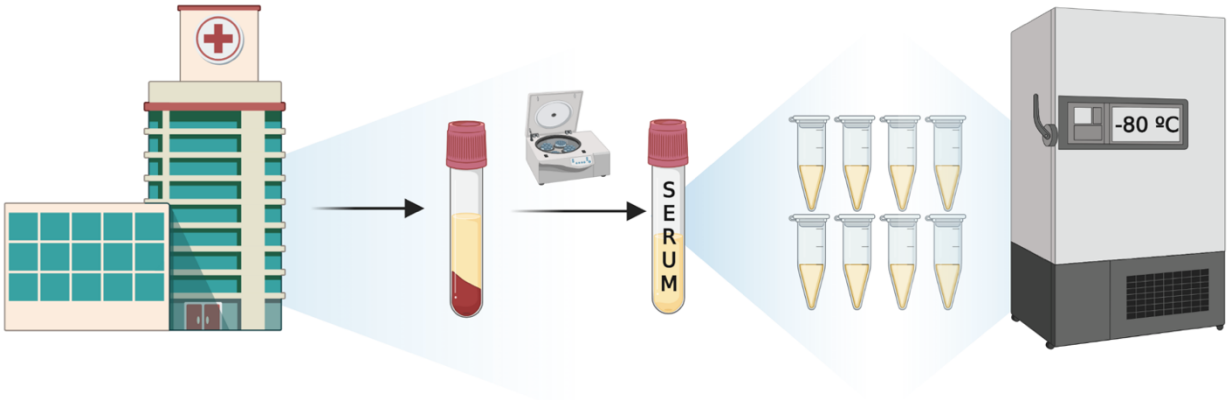

Figure 8 – Serum sample treatment since the collection in the hospital to the laboratory storage. The red tube image is relative e to a glass red vacutainer without anticoagulants or preserves. Created with BioRender.com.

temperature, followed by centrifugation at 2 000 x *g* for 10 minutes at room temperature (RT). After centrifugation, serum was aliquoted and stored at -80 ºC.

3.3 Experimental Study Design

For this work, the study population was differentiated between healthy individuals (HS) and sick patients (MM). Thus, our study population comprises a total of 16 patients, 11 of which are healthy and belong to the control group and 5 are patients diagnosed with this pathology.

From these two cohorts investigated, the group of healthy individuals comprised 54.5% males and 45.5% females, with ages ranging from 53 to 94 years. The mean age for this cohort was 73 ± 13 years. In contrast, the cohort comprising multiple myeloma patients exhibited exclusive male representation, constituting 100% of the participants, with ages spanning from 57 to 79 years. The average age for this particular cohort was 65 ± 11 years. In Appendix D, detailed information about the study population is provided.

The diagram below shows, in a synthetic and simple way, the division of the study population and the following major steps.

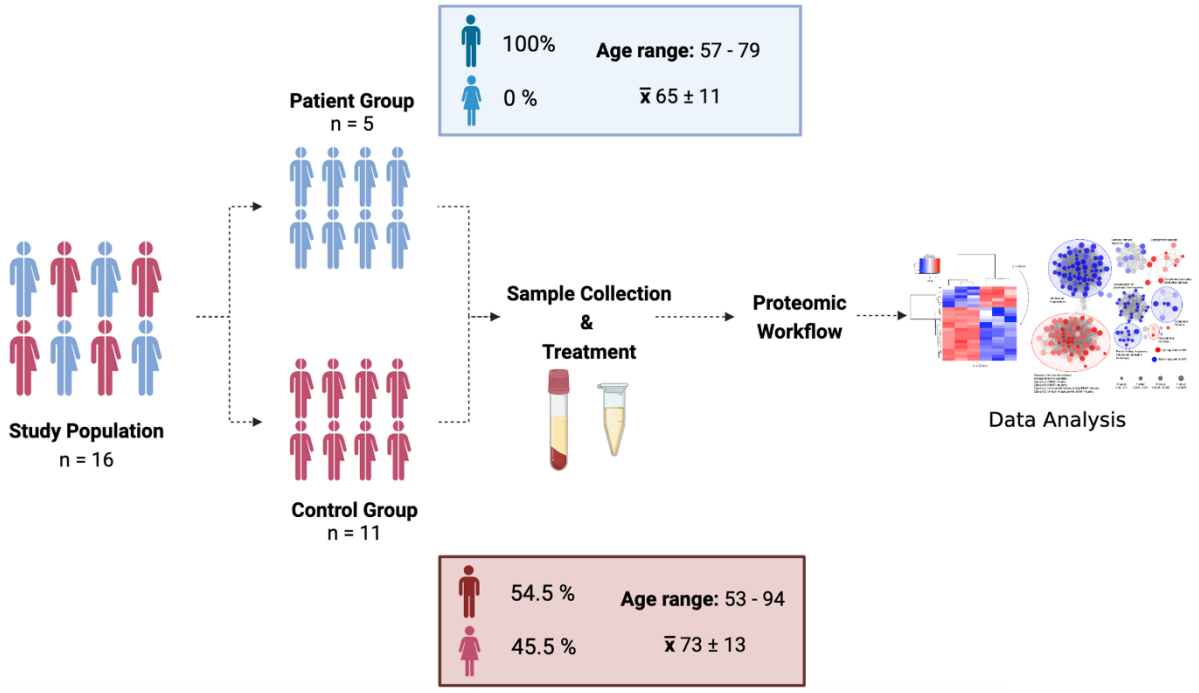

Figure 9 – Experimental study design of study population. Created with BioRender.com.

4

MATERIALS AND METHODS

4.1 Protein Quantification

4.1.1 Bradford Assay

Materials and Reagents: 96-well plate; Clariostar (BMG LABTECH microplate reader); Bradford reagent (Sigma; B6016); Bovine Serum Albumin (BSA) stock solution 200 mg/mL (Sigma; P5369); Milli-Q water.

Procedure

1. Preparation of the BSA working solutions: This solution was prepared by 1:100 diluting the Bovine Serum Albumin (BSA) stock in Milli-Q water (0.5 mL BSA 200 mg/mL to 50 mL). Then, the 2 µg/µL BSA working solution was stored at -20ºC in 400 µL aliquots.

2. Calibration curve preparation:

Table 4 – Dilution scheme used to generate the Bradford assay calibration curve. Cal. Sol. – Calibration solution.

$[BSA]_{Cal.\ sol.}$ (µg/µL)	Vol. MQ-H_2O (µL)	Vol. BSA $_{Working\ sol.}$ (µL)
0	200	0
0.25	175	25
0.5	150	50
1	100	100
1.4	60	140

Five µL of the solutions prepared as described in Table 4 were loaded into a 96-well plate in duplicates, followed by the addition of 250 µL of Bradford Reagent.

3. Preparation of the unknown samples: For samples with unknown protein concentrations, it was necessary to prepare a dilution scheme to ensure that concentrations were within the linear range. To each well being used, five µL of the sample were loaded in duplicate, followed by the addition of 250 µL of Bradford Reagent. Afterwards, samples and standards were incubated at room temperature for 20 minutes. Finally, absorbances at 595 nm were measured using the Clariostar microplate reader.

4.1.2 Bicinchoninic acid assay (BCA)

Materials and Reagents: 96 Well-plate; Clariostar (BMG LABTECH microplate reader); Incubator at 37ºC; Pierce™ BCA Protein Assay Kit (ThermoScientific; 23225); Milli-Q water.

Procedure

1. Preparation of calibration curve

Table 5 - Dilution scheme used to generate the Calibration Curve for BCA assay.

Vial	[BSA] (µg/µL)	Vol. MQ-H_2O (µL)	Vol. BSA $_{Stock\ sol.}$ (µL)
A	2	0	300 (from stock)
B	1.5	125	370 (from stock)
C	1	325	325 (from stock)
D	0.75	175	175 (from vial B)
E	0.5	325	325 (from vial C)
F	0.25	325	325 (from vial E)
G	0.125	400	325 (from vial F)
H	0.05	400	100 (from vial G)
I	0	400	0

2. Preparation of working reagent (WR): To calculate the total volume needed for the working reagent, we followed the formula described in the kit manual[58].

$$Total\ volume\ WR\ required\ =\ (nr.standards\ +\ nr.unknowns)\ x\ (nr.replicates)\ x\ (VWR\ per\ sample)$$

Equation 1

3. Microplate procedure: Pipette 25 µL of each standard and samples, in duplicate, into a microplate well (working range = 0.02 – 2 µg/µL) followed by the addition of 200 µL of the WR. The plate was gently mixed for 30 seconds, covered with aluminium foil, and incubate for 30

minutes at 37 ºC. Finally, absorbances at 562 nm were measured using the Clariostar microplate reader.

4.2 Protein and Peptide Quantification via Tryptophan Emission

Materials and Reagents: 96 Well-plate; Clariostar (BMG LABTECH microplate reader); Tryptophan stock solution 0.0102 µg/µL in 8M Urea/0.1 M Tris-HCl pH 8.0; Urea 8 M Solution/0.1 M Tris-HCl pH 8.0 (appendix A.1).

Procedure

1. Calibration curve preparation: The solutions used for the calibration curve were prepared by a 1:2 serial dilution of the tryptophan (W) stock solution, using 8M Urea/0.1M Tris-HCl pH 8 as solvent, as exemplified in Figure 10.

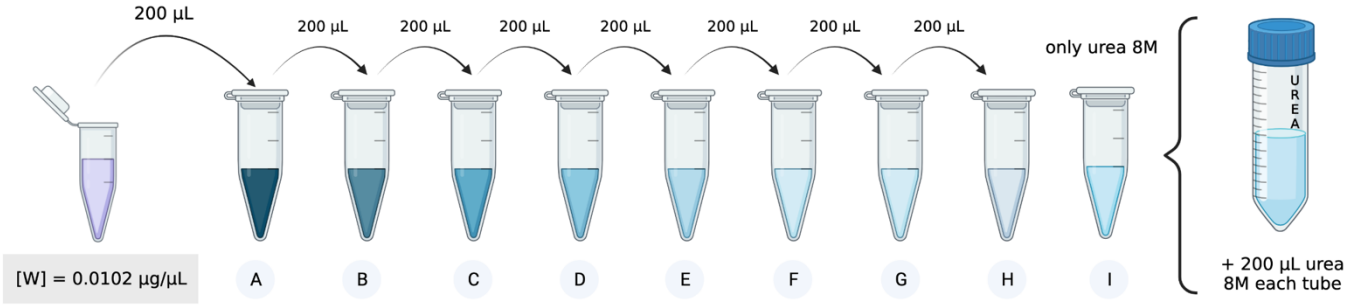

Figure 10 - Scheme of serial dilutions of tryptophan used to generate the calibration curve. Created with BioRender.com

Then using a 96-well plate, 75 µL of the standard solutions were loaded in duplicate.

2. Preparation of the proteome unknown samples: For samples with unknown protein concentrations, it was necessary to prepare a dilution scheme to ensure that concentrations were within the linear range (usually, 1:100 serum dilution fits the quantification linearity range). To each well being used, 5 µL of the sample was loaded in duplicate, followed by the addition of 70 µL 8M Urea/0.1M Tris-HCl pH 8. Finally, the excitation was set to 280 nm and the emission to 350 nm with a 20 nm bandwidth. According to the literature, the tryptophan content in animal tissues, cells and body fluids is 1.17% by weight[59].

3. Preparation of the peptide digests unknown samples: The quantification of peptides was performed after the proteome reduction/alkylation and digestion steps, following the same methods as described for quantifying the total proteome.

4.3 Depletion of abundant proteins in serum

Materials and Reagents: Microtube Centrifuge (MPW-352); Mini incubator 37 ºC (Labnet); 500 mM DTT (appendix A.2); Milli-Q Water.

Procedure

1. Depletion of abundant serum proteins: To 20 µL of the raw serum sample 2.2 µL of 500 mM DTT was added, followed by incubation for 30 minutes at 37 ºC. This procedure was performed in triplicates. After incubation, samples were centrifuged at 20 000 x *g* for 20 minutes. Afterwards, the supernatants were withdrawn to new eppendorfs, and the pellets were gently washed with 10 µL of Milli-Q H_2O. The washing factions were combined with the previous supernatant.
2. Quantifying the protein concentration in the depleted samples: Supernatants (SN) were quantified via Tryptophan Emission as described in 4.2. Quantification of the protein content in the pellet was done using the following formula:

$$\mu g\ of\ Protein\ in\ Pellet\ =\ \mu g\ of\ Protein\ in\ Raw\ Serum\ -\ \mu g\ of\ Protein\ in\ SN$$

Equation 2

4.4 Protein Reduction, Alkylation and Digestion

Materials and Reagents: Reduction/Alkylation solution: 200 mM Chloroacetamide (CAA) solution; 50 mM Tris (2-carboxyethy) phosphine hydrochloride (TCEP), 28 mM TEAB, 58.24 mM TEAB, 0.1 M pH 8.8. (appendix A.4); Milli-Q water; UP50H – Compact Homogenizer (Hielscher); Mini incubator 37 ºC (Labnet). Digestion: Mini incubator 37 ºC, (Labnet); Speedvac Univapo 150 ech; Trypsin/Lys-C Solution: 0.16 µg/µL in 70 mM TEAB, and Trypsin Solution: 0.4 µg/µL in in 70 mM TEAB. Peptide solution: 3% Acetonitrile (ACN), 0,1% Formic Acid (FA). All prepared solutions are available in Appendix A.3.

Procedure

1. Protein reduction/alkylation: The SN samples were diluted as described in Table 6 to obtain 103 ± 8 µg of protein for each sample. Then 5 µL of Reduction/Alkylation solution was added

to each sample, followed by incubation for 30 minutes at 37 ºC. For the case of the pellets, they were solubilised with 150µL of 70 mM TEAB followed by probe sonication for 1 minute (Ultrasonic frequency: 30kHz, Ultrasonic Amplitude: 100%, Cycle time: 0,8 s). Before Reduction/Alkylation of the pellet's proteins, they were diluted as described in Table 6 to obtain 100 ± 3 µg of protein for each sample. Pellet's Reduction/Alkylation step was performed as described for the SN.

Table 6 – Dilution scheme used for reduction and alkylation of SN and Pellet (P) samples.

Sample	Supernatant samples				Pellet samples			
	[Protein] (µg/µL)	V_{SN} (µL)	100 mM TEAB (µL)	V Red./Alk. Solution (µL)	[Protein] (µg/µL)	V_{Pellet} (µL)	70 mM TEAB (µL)	V Red./Alk. Solution (µL)
C10	26	4	16	5	5.1	20	150	5
C15	27	4	16	5	5.4	18	150	5
C25	17.7	6	14	5	5.3	19	150	5
C29	26.9	4	16	5	6.5	15	150	5
C33	28	4	16	5	6.8	15	150	5
C37	31	3	17	5	5.5	18	150	5
C38	24	4	16	5	4.7	20	150	5
C41	23	4	16	5	5.8	17	150	5
C46	24	4	16	5	5.1	20	150	5
C49	33.2	3	17	5	5.7	18	150	5
C57	29	4	16	5	6.0	17	150	5

2. Protein digestion: To the reduced/alkylated samples, 5 µL of 0.16 µg/µL Trypsin/Lysine-C solution prepared in TEAB 70 mM, followed by the addition 5 µL of 0.4 µg/µL of Trypsin in TEAB 70 mM. Samples were then left to digest overnight at 37 ºC and before speedvac dry step, was add 75 µL of 70 mM TEAB to reduce the CAA concentration.

3. After digestion, the samples are dried in the speed vac. Before downstream analysis, peptides were resolubilized in 150 µL of 3% (v/v) ACN in 0.1% (v/v) aqueous FA, followed by 10 minutes of sonication using an ultrasonic bath at 100% ultrasonic amplitude.

4.5 LC-MS/MS Analysis

Materials and Reagents: OPTIMA LC/MS-Grade acetonitrile (Fisher Chemical, A955), OPTIMA LC/MS-Grade water (Fisher Chemical, W6-212); MS-Grade formic acid (Fluka). µPAC™ Trapping column and analytical column (200 cm µPAC™) from PharmaFluidics. UHR-QqTOF IMPACT HD (Bruker).

Procedure

MS analysis was performed using UltiMate 3000 ultra-high performance liquid chromatographer, from Thermo Scientific, coupled to UltraHigh Resolution Quadrupole Time-Of-Flight (UHR-QTOF) IMPACT HD mass spectrometer, from Bruker.

0.5 µL of the sample with a total peptide concentration of 0.6 µg/µL were loaded onto a µPAC™ Trapping column and desalted for 2.7 min with 1% (v/v) Acetonitrile (ACN) in 0.1% aqueous formic acid (FA_{aq}) at a flow rate of 15 µL min^{-1}. Then the peptides were separated using an analytical column (200 cm µPAC™ PharmaFluidics). with a linear gradient at 500 nL min^{-1} (mobile phase A: FA_{aq} 0.1% (v/v); mobile phase B: 99.9% (v/v) ACN and 0.1% (v/v) FA_{aq}) 0–2 min from 3% to 5% of mobile phase B, 5–76 min from 5% to 17% of mobile phase B, 76–104 17% to 25% B, 104–121 25% to 35% B. Chromatographic separation was carried out at 35 ºC. MS acquisition was set to MS (2 Hz) cycles, followed by MS/MS (8–32Hz), cycle time 3.0 seconds, active exclusion, exclude after one spectrum, release after 2 min. The precursor was reconsidered if its current intensity was 3.0 higher than the previous intensity and intensity threshold for fragmentation of 2500 counts.

In brief, protein group LFQ intensities were log2-transformed to reduce the effect of outliers. To overcome the obstacle of missing LFQ values, missing values were imputed before fitting the models.

Log ratios were calculated as the average log2 LFQ intensity values difference between the two digestion methods tested (two-tailed, Student's t-test). A protein was considered statistically significant if its FDR ≤ 0.05 (Permutation Based FDR 0.05 and S0=0).[91]

4.6 Bioinformatics data analysis and functional enrichment

Raw LC–MS/MS data were processed in MaxQuant (V.1.6.10.43) for protein identification and label-free quantification using standard settings[60]. Peptide lists were searched against the human Uniprot FASTA database. A contaminant database generated by the Andromeda search engine[61] was configured with cysteine carbamidomethylation as a fixed modification and N-

terminal acetylation and methionine oxidation as variable modifications. We set the false discovery rate (FDR) to 0.01 for protein and peptide levels with a minimum length of seven amino acids for peptides, and the FDR was determined by searching a reverse database. Enzyme specificity was set as C-terminal to arginine and lysine as expected using trypsin. A maximum of 2 missed cleavages were allowed. Data processing was performed using Perseus (version 1.6.10.50) with default settings[62]. All proteins and peptides matching the reversed database were filtered out [63].

ClueGO v 2.5.10, a plugin of Cytoscape 3.10.1, was used to unveil the most significant pathways. The following analysis parameters were defined for ClueGO: function; two sample lists were loaded, one per cluster; the organism selected was Homo sapiens, and the type of IDs used was Accession ID. Clusters were used to obtain a deep comparison between the different clusters; The Ontologies/Pathways selected were: GO_BiologicalProcess and Reactome_pathways. “All Evidence codes” box was chosen; Regarding network specificity, it was set as “detailed”; The box of “Use GO Term Fusion” and “Show only pathways with p-value ≤ 0.05” was also chosen. GO Tree Interval it was set to Min Level 3 and Max Level 8. Selection criteria for the terms that have associated genes from cluster 1 was set as a minimum of 3 genes per term and a minimum of 4% from all the Genes associated with the term.

5

RESULTS & DISCUSSION

Quantification of the total proteome plays a crucial role in clinical biochemistry laboratories. Specifically in this project, precise, accurate and reproducible measurements of the proteome contents are paramount for reliable label-free quantification of proteins. Also, measuring the total proteome helps assess the quality and integrity of the sample. It provides an indication of whether the sample preparation was successful and whether any biases or contaminations were introduced during the process. Monitoring the total proteome can identify potential variations or technical errors that may affect the reliability of experimental results.

5.1 Total Protein Quantifications

Comparison between Bradford, BCA & Tryptophan Emission Assays

In this work, we compared two common colourimetric methods, Bradford, BCA, and Tryptophan Emission. For this comparison, we used sera from 11 healthy individuals.

For the Bradford and BCA assays, we used BSA to generate a calibration curve, as described in sections 4.1.1, and 4.1.2, respectively. For the W Emission, the calibration curve was generated with L-Tryptophan. The typical calibration curves are depicted in Figure 11.

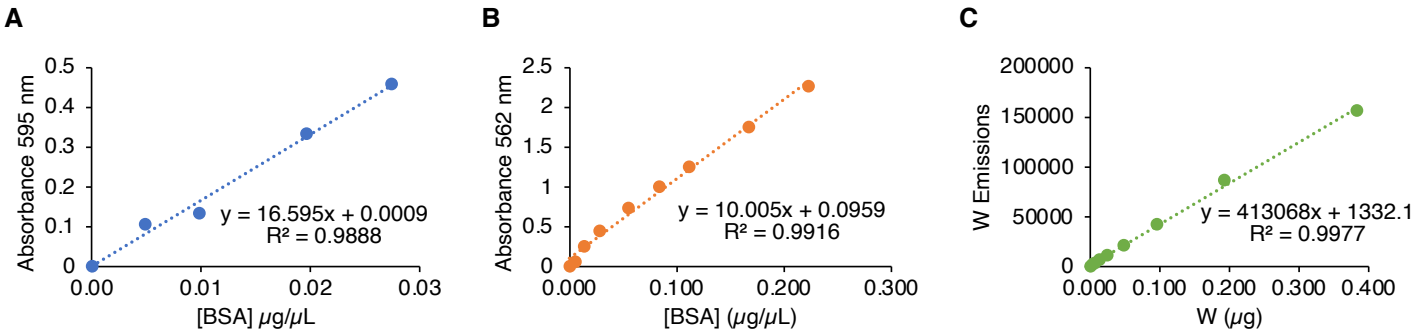

Figure 11 – Calibration curves of three total protein quantification methods. A (in blue) is relative to Bradford Assay, B (orange) is relative to BCA Assay and C (green) is relative to Tryptophan Emission Assay. (More detailed data in appendix B.1)

After the calibration curve was generated, we calculated the limit of quantification (LOQ) and the limit of detection (LOD) for each assay. For the Bradford assay, the detection limit is 0.1 µg/µL, and the quantification limit is 0.3 µg/µL. In contrast, for the BCA meth-od, the LOD is 0.01 µg/µL, and the LOQ is 0.05 µg/µL. Finally, the tryptophan emission assay, with a LOD of 0.001 µg/µL and LOQ of 0.01 µg/µL, proved to be the most sensitive.

Subsequently, a quantification of serum samples was performed, and the results are presented in Table 7.

Table 7 – Quantification of the total proteome in sera samples of healthy individuals (n=11) by Bradford, BCA, and W Emission. Each sample were analyzed in duplicate.

Sample	[Total proteome]$_{Serum}$ (g/L)		
	Bradford Assay	**BCA Assay**	**W Emission**
C10	63 ± 4	66 ± 1	61.5 ± 0.4
C15	61 ± 2	79 ± 4	65 ± 3
C25	65 ± 2	64 ± 2	56 ± 5
C29	69.6 ± 0.3	73 ± 5	73.37 ± 0.03
C33	68 ± 4	79 ± 4	76 ± 5
C37	67.8 ± 0.5	70 ± 5	70 ± 2
C38	61 ± 1	62 ± 4	58 ± 3
C41	57 ± 1	69 ± 5	64 ± 4
C46	64 ± 1	72 ± 3	60 ± 4
C49	69 ± 2	81 ± 3	73 ± 5
C57	70 ± 1	78 ± 1	71 ± 2

The total proteome measurements obtained from the three assays display variations across the samples. When comparing the assays, the BCA assay consistently reports higher values for the total proteome compared to both the Bradford Assay and W Emission assay. This trend is observed in 73% of the samples. In contrast, the W Emission assay demonstrates relatively low standard deviations, indicating higher precision in its measurements than the other two assays.

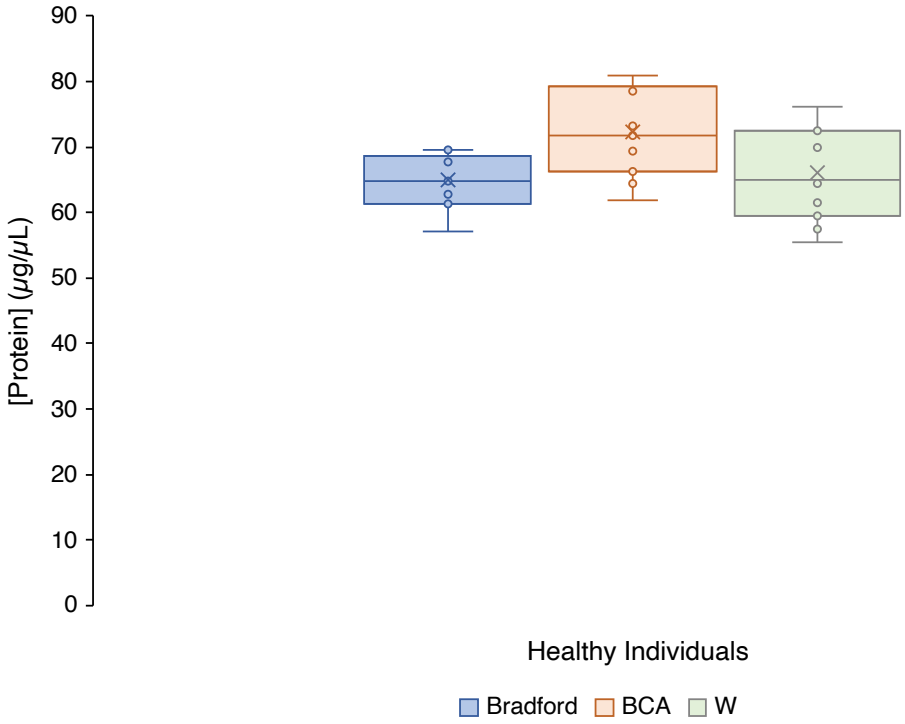

Figure 12 - Box plot of data distribution from three methods comparison in healthy individuals (n=11). In Blue, is the data relative to Bradford Assay, in orange, is the BCA assay, and in green, is the Tryptophan Emission Assay. Each individual was analyzed in duplicate.

It is worth noting that the normal range for serum total protein concentration typically falls within the range of 60–80 g/L.[64] In our study (Figure 12), the Bradford assay indicated a total protein concentration range of 57–70 g/L. This is slightly below the standard range but still offers a close approximation. The BCA assay, on the other hand, spanned a broader range of 62–81 g/L, which encompasses and slightly exceeds the typical range. Meanwhile, the Tryptophan Emission assay showed a range of 56–76 g/L, aligning closely with the standard values. These variations underscore the importance of selecting an appropriate assay for specific applications, considering both accuracy and the context of the study.

Statistical analysis

In clinical proteomics, it is essential to understand that everyone has unique variations in their proteome due to genetic and environmental factors. As a result, each individual's data requires individualized statistical analysis. Initially, we executed a variance comparison test for the three methods, detailed in appendix B.4. The results indicated no significant variance differences among the methods. Subsequently, we conducted a means comparison test, with findings presented in appendix B.3. These results confirm that the average values from the three methods are not statistically different, underscoring the consistency of our methods. The Tryptophan Emission assay, aligning closely with established benchmarks at a range of 56–76 g/L, will serve as our preferred method for future total proteome quantifications.

Total Protein Quantification of Multiple Myeloma Sera

In Tryptophan Emission assay, for MM serum protein quantification we did a Tryptophan calibration curve to do quantification of these patient's proteome. (appendix B.2)

Table 8 - Total proteome quantification of multiple myeloma patient's sera (n=5). Each sample were analyzed in duplicate.

Sample	[Total proteome] $_{Serum}$ (g/L)
MMB	171 ± 2
MMC	97 ± 2
MMF	140 ± 9
AQ01	171 ± 1
JC02	73 ± 3

Elevated total protein levels in MM are indicative of an overproduction of monoclonal proteins or immunoglobulins, a hallmark of the disease stemming from malignant plasma cells. Analyzing the serum samples from MM patients, we observe a notable variation in total protein concentrations. Specifically, patient JC02 exhibited the lowest concentration at 73 g/L, while both patients MMB and AQ01 shared the highest concentration at 171 g/L. This pronounced variability underscores the inherent heterogeneity of MM, suggesting potential differences in disease stages, subtypes, or individual patient responses. Importantly, the consistently low standard deviations across samples attest to the precision of our measurements. Although measuring the total protein content provides an initial overview, it merely provides a preliminary insight of the underlying complexities. To truly understand the intricacies of MM, it is imperative to delve deeper into the individual proteins using proteomics, revealing the specific molecular players and their roles in the disease.

5.2 Depletion of high abundance proteins from serum

Plasma is a complex mixture of proteins, with some being highly abundant and others present in much lower concentrations. For a detailed plasma proteomics analysis, it is essential to implement a depletion strategy to focus on the less abundant, yet potentially more informative proteins. Serum treated with DTT has been observed to be enriched in immunoglobulins[65]. Given that diseases like multiple myeloma are marked by alterations in these proteins, DTT-based depletion emerges as a cost-effective method for such studies, as highlighted by C. Fernández[65] . Adapting the protocol proposed by Fernández *et al*., and with minor adjustments, we effectively distinguished between the high-abundance proteins, which settled as a pellet (P), and the low-abundance proteins that persisted in the supernatant (SN). This separation is pivotal for our research, as our primary interest lies in the proteins found within the less abundant fraction.

Supernatant (SN) & Pellet (P) quantification of healthy sera

The quantification of the supernatant was performed via W emission and the corresponding concentration data was converted into mass (µg). In this way, it is possible to calculate the pellet mass from Equation 2, and the results are shown in Table 9.

Table 9 - Supernatant quantification of healthy sera (n=11). Each sample were analyzed in duplicate.

Sample	Protein in 20 µL of raw sera (µg)	SN Protein (µg)	Pellet Protein (µg)	% Depleted protein
C10	1229.03	466.29	762.74	62
C15	1299.75	484.67	815.08	63
C25	1110.18	317.89	792.28	71
C29	1467.36	484.97	982.38	67
C33	1523.35	504.46	1018.89	67
C37	1397.38	566.13	831.24	59
C38	1150.44	439.25	711.19	62
C41	1288.13	419.76	868.37	67
C46	1191.33	431.15	760.18	64
C49	1451.38	597.93	853.46	59
C57	1415.54	522.53	893.01	63

In our study, we observed that the percentage of depleted proteins averaged 64 ± 4% (Table 9). This aligns with the understanding that the top 10 most abundant serum proteins, including albumin, various immunoglobulins, and others, constitute a significant portion of the total serum protein content, with albumin alone accounting for about 50-60%[66].

Supernatant & Pellet quantification of MM Sera

The process of depleting and quantifying proteins in MM sera was executed following the previously outlined methodology. The quantities of proteins identified in both the supernatant (SN) and pellet (P) fractions post-depletion are detailed in Table 10.

Table 10 - Supernatant quantification of multiple myeloma sera (n=5). Each sample were analyzed in duplicate.

Sample	Protein in 20 μL in raw sera (μg)	SN Protein (μg)	Pellet Protein (μg)	% Depleted protein	Average % Depleted protein (n=3)
MMB	3424	1296	2128	62	59 ± 3
	3424	1369	2056	60	
	3424	1502	1922	56	
MMC	1944	929	1014	52	52 ± 1
	1944	932	1012	52	
	1944	910	1034	53	
MMF	2799	1118	1681	60	60 ± 3
	2799	1036	1763	63	
	2799	1190	1609	57	
AQ01	3428	2107	1321	39	39 ± 3
	3428	2194	1234	36	
	3428	1980	1448	42	
JC02	1468	374	1093	75	75 ± 1
	1468	373	1095	75	
	1468	341	1127	77	

The data outlined in Table 10 indicates an average depletion percentage of 57±12% for MM patients, while the figure for healthy individuals is slightly higher at 60±4%. Although these percentages are similar, the multiple myeloma samples demonstrate a marginally lower average depletion coupled with increased variability. This subtle difference could hint at variations in protein composition and abundance between healthy individuals and those with multiple myeloma. Importantly, it is essential to highlight that the protein concentration in the raw sera of MM patients ranges from 73 to 171 g/L, which is a broader span compared to the 56 to 76 g/L range observed in healthy sera. Furthermore, a student's t-test (data in appendix B.5) confirms that there are no statistically significant differences between the percentage of depleted protein in the two groups.

After this analysis we did reduction, alkylation, and digestion (102±8 µg of protein per sample), peptides were quantified from healthy sera, both from the supernatant and from the pellet, and the raw sera. Quantification was performed via W emission and the results are shown in appendix C.

5.3 Mass Spectrometry Analysis

In our mass spectrometry analysis, we conducted label-free proteomics analysis of liquid biopsies to identify altered protein expression levels in patients with multiple myeloma.

Initially, we observed differences when employing a depletion strategy of the most abundant proteins found in healthy serum samples. Subsequently, we categorized the data into two groups: one for healthy individuals and one for patients. This division possibly allows us to identify deregulated proteins associated with MM and compare our findings with existing literature (section 1.4.3).

To further expand the applicability of our study we investigated the use of the Proteomic Ruler Tool to obtain absolute quantification values for all the quantified proteins for the development of a multiplex MS-based method for clinical biochemistry[67]. The Proteomic Ruler plugin implements computational strategies for absolute protein quantification without spike-in standards.[68]

5.3.1 Differences with and without depletion of most abundant proteins of healthy sera

To visualize the differences in applying this strategy to human serum, we performed a Z-score normalization of the log-2 transformed data followed by a Multiple-sample ANOVA test (Permutation-based FDR, 0.05 FDR, S0=0). The statistically significant proteins were selected, and a Hierarchical cluster was generated using Euclidean Distance for both tree rows and columns as depicted in Figure 13.

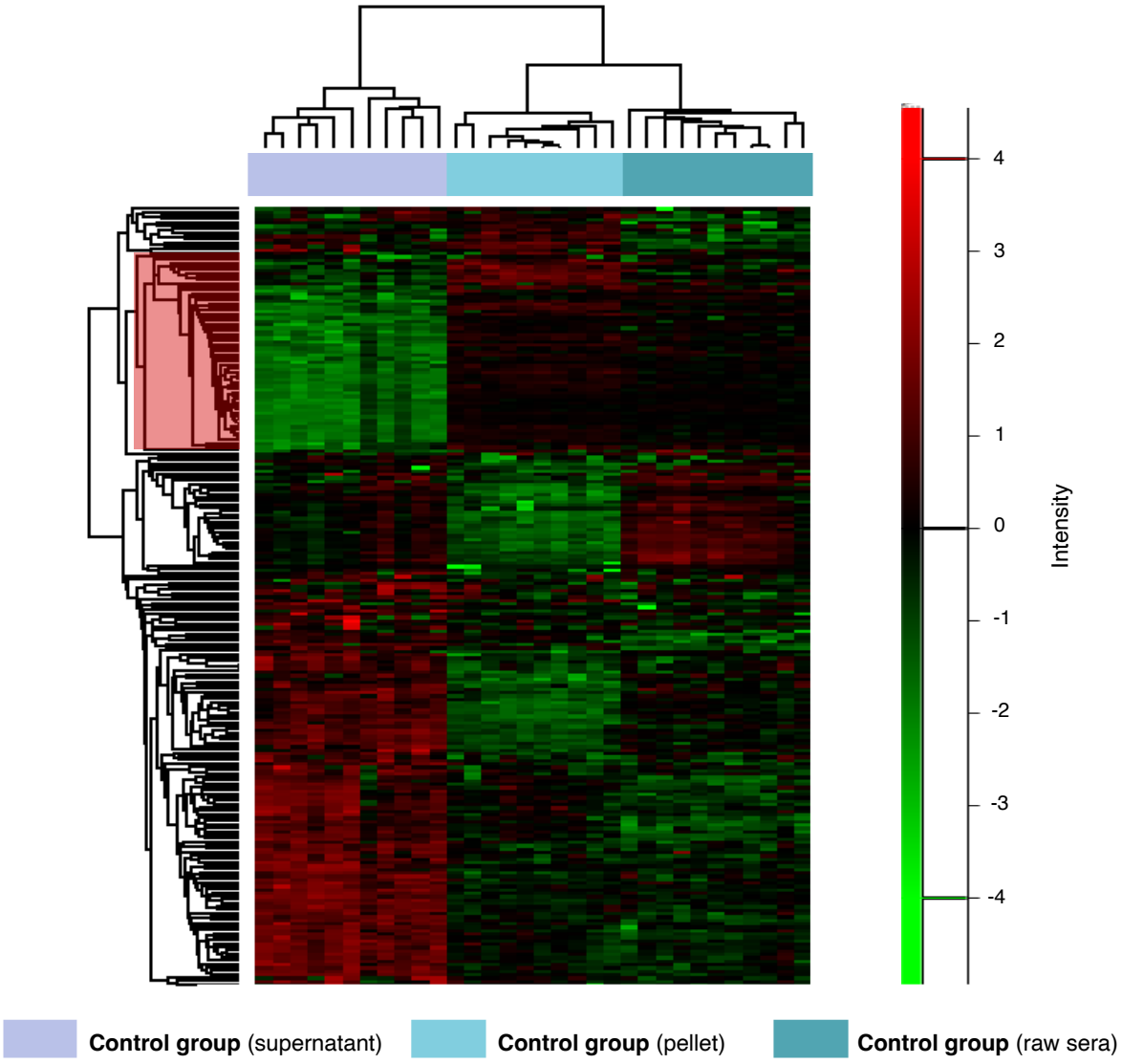

Figure 13 – Comparison of proteome between raw and depleted sera in healthy individuals (n=11). Heatmap was generated using Perseus. Log2-transformed LFQ data was normalized by Z-score, followed by a Multiple-sample ANOVA test (Permutation-based FDR, 0.05 FDR, S0=0).

In the row cluster painted in pail red, corresponding to the proteins enriched in the pellets, it is possible to detect Albumin, serotransferrin, α-1-Antitrypsin, plasminogen, complement-associated proteins, and apolipoproteins which are some of the most abundant proteins present in serum. Analyzing the previous figure, it is evident that there is a pronounced contrast between the supernatant and the pellet, demonstrating that the depletion process is not only efficient but also essential for accessing proteins that were previously 'masked' by more abundant ones.

5.3.2 Comparison between healthy and myeloma individuals

Aiming at identifying a quantitative alteration at the protein level that allows for accurate diagnosis of MM we have conducted a proteomics analysis of serum samples. Our quantitative proteomics approach on depleted sera has rendered the quantification of 264 proteins in the Healthy individuals and 235 proteins in the MM group. We performed a Z-score normalization of the log-2 transformed data followed by a Two-sample test (Student's T test with permutation-based FDR, 0.05 FDR, S0=0). The statistically significant proteins were selected, and a Hierarchical cluster was generated using Euclidean Distance for both tree rows and columns as depicted in Figure 14.

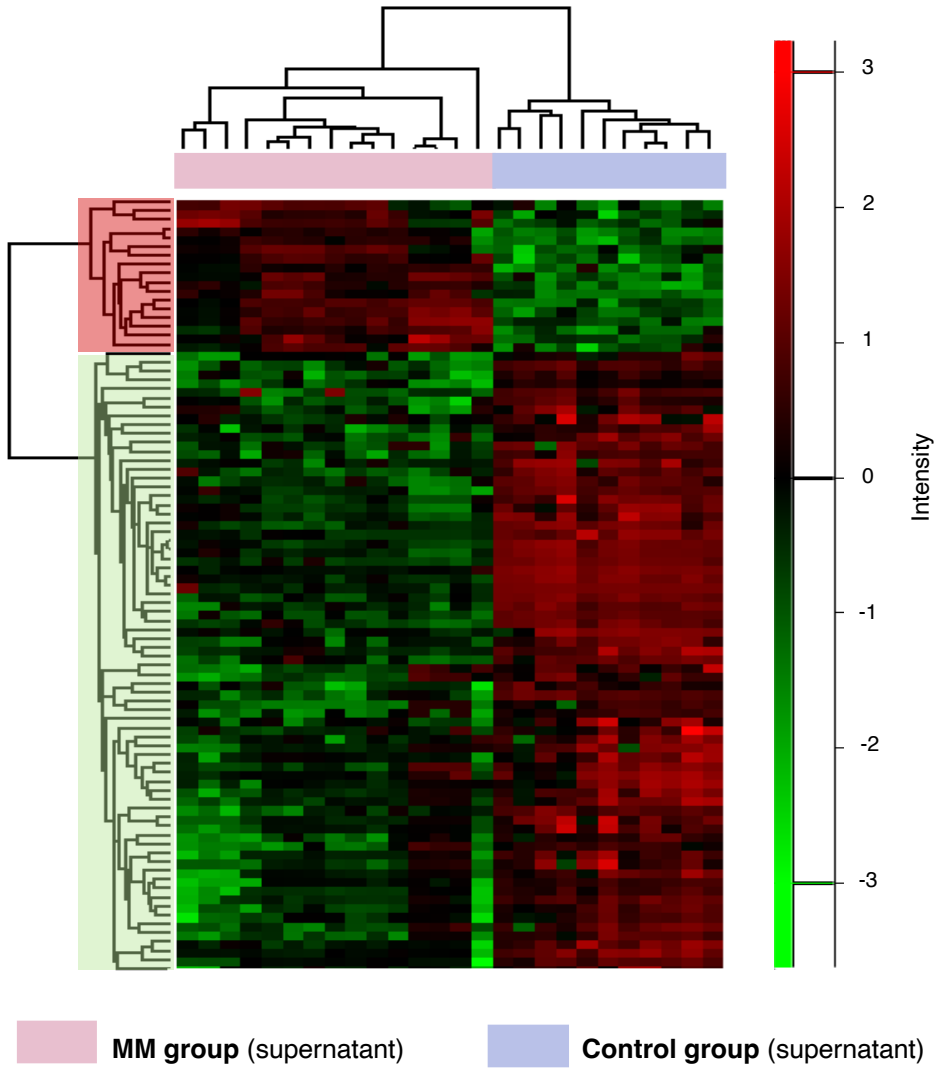

Figure 14 - Comparison of supernatant proteins between healthy individuals (n=11) and patients' group (n=15). Heatmap was generated using Perseus. Log2-transformed LFQ data was normalized by Z-score, followed by Two sample T-test (Permutation-based FDR, 0.05 FDR, S0=0).

A closer look at Figure 14 reveals a pronounced cluster in the MM group (cluster annotated in pail red) corresponding to 17 proteins found up-regulated due to MM compared with the healthy subjects. On the other hand, a second cluster, annotated in green, shows the 70 proteins that are down-regulated due to MM. It is compelling to further investigate these protein sets to discern their identities, their roles within the disease, and their potential influence on diagnosis and prognosis. To this end, we conducted a gene ontology and Reactome pathway analysis using ClueGo plug-in in Cytoscape[69,70] (V 3.10.1) using the statistically significant proteins. The resulting enrichment is displayed in Figure 15.

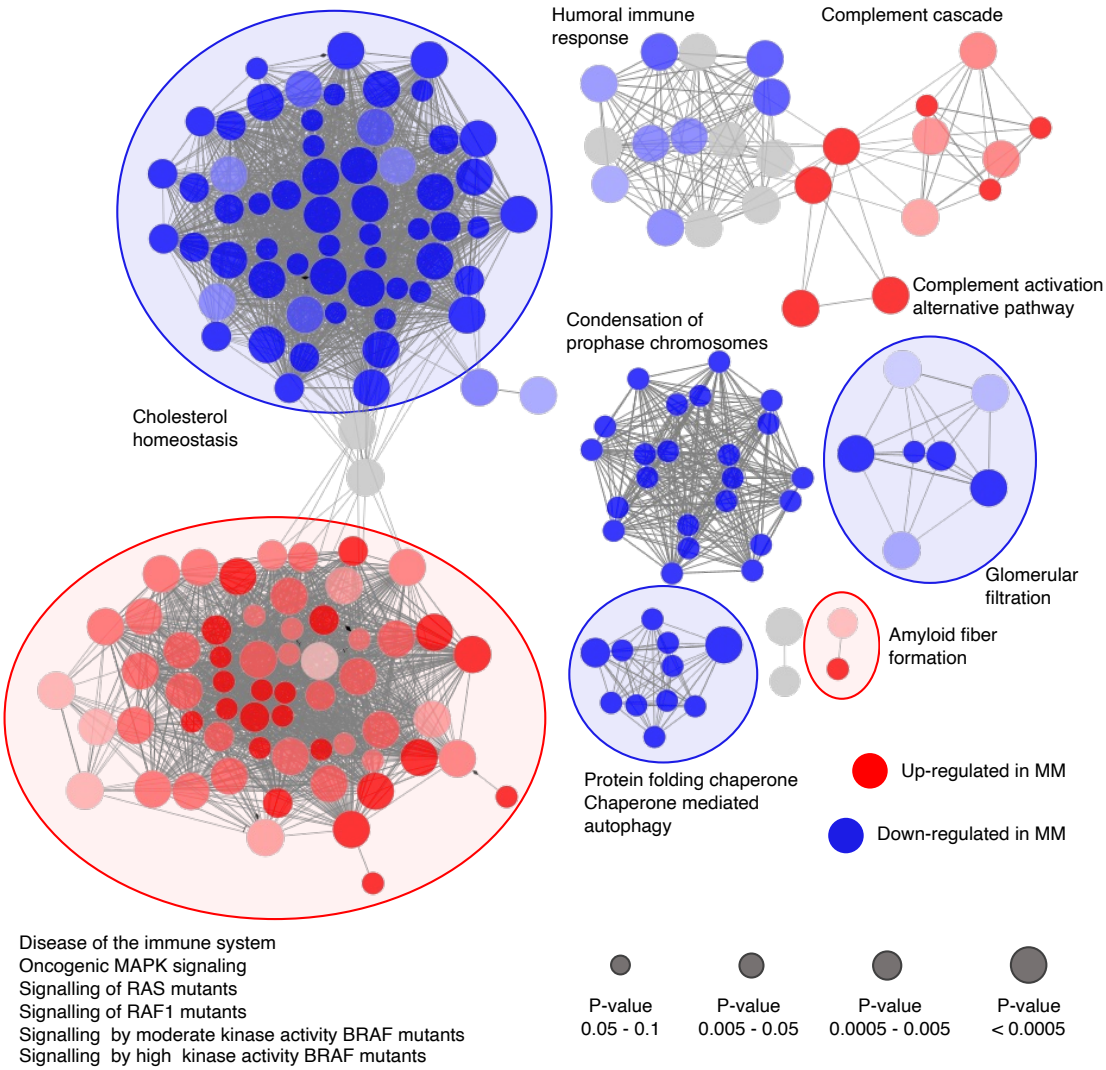

Figure 15 – ClueGO analysis of up- and down-regulated proteins in serum from MM patients (n=5). In red GO/pathway terms specific for upregulated proteins and in blue the GO/pathway terms specific for downregulated proteins. Functionally grouped network with terms as nodes linked based on their kappa score level (≥0.4), where only the label of the most significant term per group is shown. The node size represents the term enrichment significance.

MM is characterized by a monoclonal production of plasma cells, an important part of the immune system. The proliferation of these malignant plasma cells in the bone marrow can lead to several complications such as Bone Lesions, Anemia, Kidney damage and immunodeficiency.[71] As can be seen in Figure 15, Chaperone-mediated Mediated Autophagy (CMA) and protein-folding chaperones are downregulated in MM (p-value $1.1x10^{-3}$ and $2.3x10^{-3}$, respectively; Group p-value Corrected with Bonferroni step down), thus suggesting the body's natural defense mechanisms against protein misfolding and aggregation are compromised. This makes the cellular environment more favorable to protein aggregation.

With the reduced activity of chaperones and CMA, there is less surveillance and clearance of misfolded proteins. This, combined with the overproduction of light chains in MM, can lead to increased amyloid fiber formation (p-value $3.4x10^{-5}$), as indicated in Figure 15 as up-regulated pathway (Red). Consequently, amyloid fibers are not easily degraded and can deposit in various organs, leading to organ dysfunction. The kidneys are especially vulnerable. Amyloid deposits in the kidney can damage the delicate structures responsible for filtration, leading to decreased glomerular filtration and potential kidney failure.[72] This was also observed in our data by a down-regulation of the glomerular filtration pathway in MM patients (p-value $3.7x10^{-11}$).

The proliferation of malignant plasma cells in the bone marrow can suppress the growth and function of normal B cells.[73] This suppression can lead to a decreased production of other essential antibodies, further weakening the humoral immune response (p-value $1.8x10^{-24}$), as observed in Figure 15 with the downregulation of this pathway. In MM patients, the upregulation of the complement cascade (p-value 5.3x10-22), especially the alternative pathway (2.3x10-23), might be a compensatory mechanism. With the downregulation of the humoral immune response, the body might be trying to boost its innate immune defenses by enhancing the complement system's activity. Typically, the classical complement pathway is activated by antibodies bound to antigens. Given the compromised humoral response in MM, there might be fewer antibodies available to initiate the classical pathway, leading the body to rely more on the alternative pathway as observed in our data.

While the complement system plays a protective role, its overactivation can lead to collateral tissue damage.[74] The products of the complement cascade can induce inflammation and damage patient’s tissues, especially if continuously activated. This is particularly concerning for organs like the kidneys, which are already vulnerable due to amyloid deposition in MM.

In Multiple Myeloma (MM), the MAPK pathway's up-regulation (p-value $2.5x10^{-18}$) is a significant factor contributing to disease progression (Figure 15). This pathway, which is crucial for cell growth, differentiation, and survival, is aberrantly activated in MM, leading to increased cell proliferation and reduced apoptosis. Central to this pathway's dysregulation is the Signaling

of RAS mutants. This signaling cascade continuously transmits growth signals from receptors to the cell's nucleus. Additionally, mutations in RAF1 further enhance the MAPK signaling. Another component, BRAF, also shows mutations in MM. Those with moderate kinase activity contribute to cell growth, while high kinase activity mutations suggest a more aggressive disease variant.[75]

In a similar manner, we investigated the proteome enriched in the pellet that results from serum depletion. Our quantitative proteomics approach, of these fractions, has rendered the quantification of 252 protein in the Healthy individuals and 223 proteins in the MM group. We have constructed a heatmap to visualize the statistically significant proteins as described in 5.3.2.

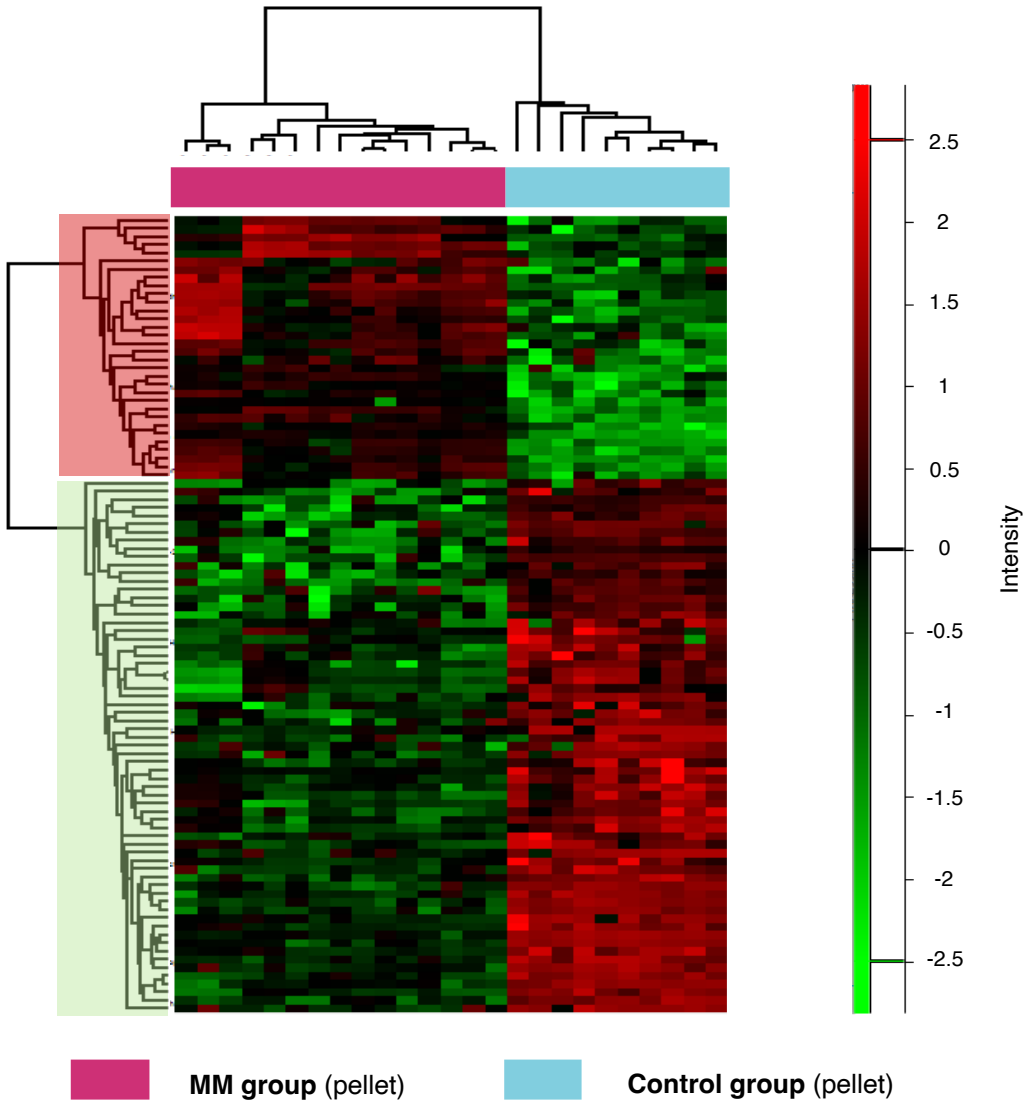

Figure 16 - Comparison of pellet proteins between healthy individuals (n=11) and patients group (n=15). Heatmap was generated using Perseus. Log2-transformed LFQ data was normalized by Z-score, followed by Two sample T-test (Permutation-based FDR, 0.05 FDR, S0=0).

A closer look at Figure 16 reveals a pronounced cluster in the MM group (cluster annotated in pail red) corresponding to 32 proteins that are found up-regulated due to MM in comparison with the healthy subjects. On the other hand, a second cluster, annotated in green, shows the 65 proteins that are down-regulated due to MM. It is compelling to further investigate these protein sets to discern their roles within the organism, and their potential influence on diagnosis and prognosis. To this end, we conducted a gene ontology and Reactome pathway analysis using ClueGo plug-in in Cytoscape (V3.10.1)[69,70] using the statistically significant proteins. The resulting enrichment is displayed in Figure 17.

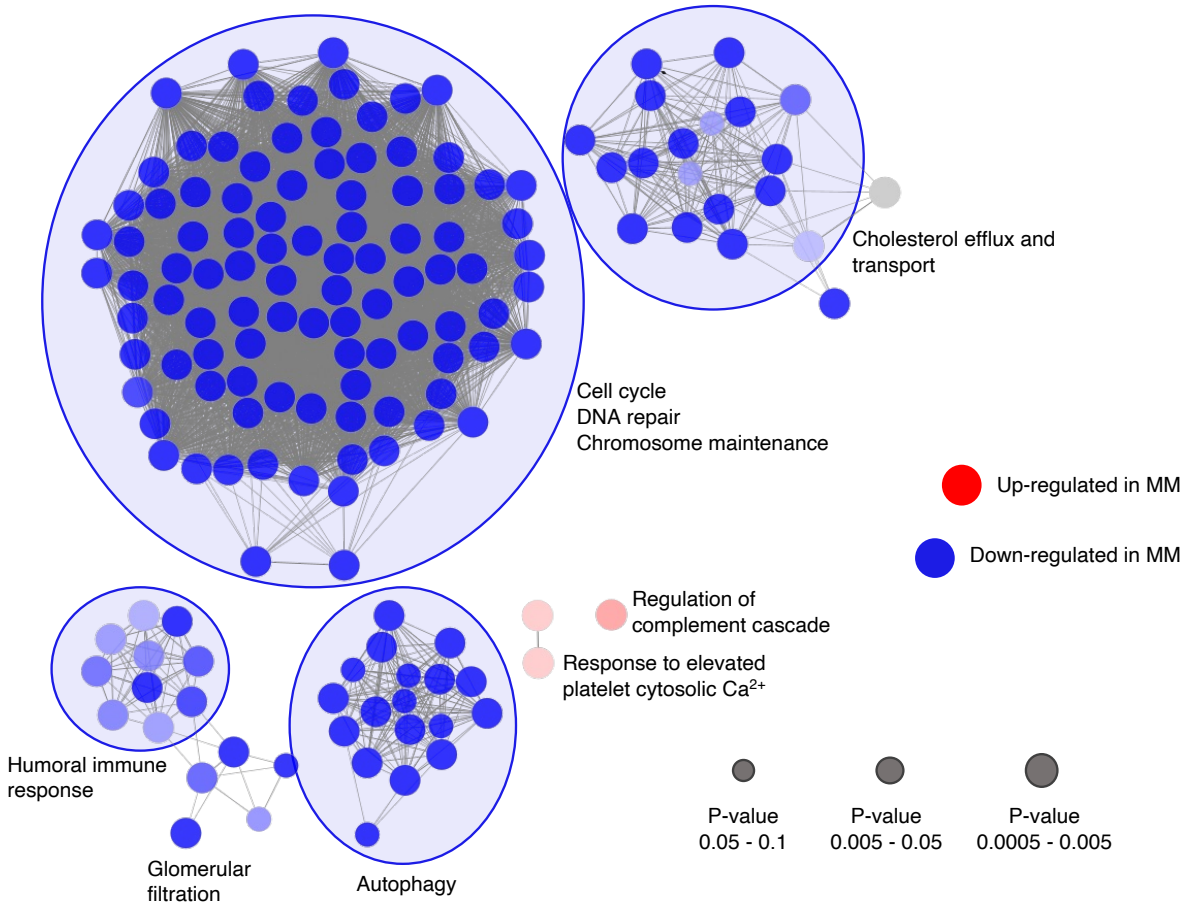

Figure 17 - ClueGO analysis of up- and down-regulated proteins in serum from MM patients (n=5). In red GO/pathway terms specific for upregulated proteins and in blue the GO/pathway terms specific for downregulated proteins. Functionally grouped network with terms as nodes linked based on their kappa score level (≥0.4), where only the label of the most significant term per group is shown. The node size represents the term enrichment significance.

The pathway enrichment depicted in Figure 17 shows an overall downregulation of the processes. Remarkably, as previously observed for the depleted serum, Humoral immune response (p-value 7.8×10^{-17}), glomerular filtration (5.8×10^{-16}) and autophagy (9.1×10^{-5}) are

downregulated in MM thus suggesting immunocompromised response and impaired kidney function. In Figure 17, the downregulation of the Cell cycle, DNA repair, and Chromosome maintenance pathways is evident by the high statistical significance (p-value $1.0x10^{-11}$). This downregulation suggests that the cells may have impaired abilities to repair DNA damage and maintain chromosomal integrity. Such disruptions can lead to genomic instability, which is a hallmark of many cancers. When cells cannot effectively repair DNA, they accumulate mutations and chromosomal abnormalities. Over time, these genetic changes can confer growth advantages to the cells, potentially leading to uncontrolled proliferation and tumor development.[76] In the context of MM, this downregulation might contribute to the disease's progression and the emergence of more aggressive clones.

The upregulation observed in the elevated platelet cytosolic Ca^{2+} (p-value $1.5x10^{-15}$) in the context of this disease can have significant implications, as hypercalcemia, characterized by elevated levels of calcium in the bloodstream, is a frequently encountered complication in individuals with MM.[77] A crucial mechanism contributing to hypercalcemia in MM involves the increase of bone resorption. This process is influenced by myeloma cells, which release factors that employ a stimulatory effect on osteoclasts, specialized cells responsible for the breakdown of bone tissue. Dysregulated calcium signaling, can lead to an increase in the release of calcium from bones and a reduction in calcium excretion by the kidneys, thereby contributing to the development of hypercalcemia.[78]

Furthermore, the perturbation of calcium signaling pathways in multiple myeloma cells may extend its influence on the immune system.[79] Such abnormal calcium signaling could potentially induce immune system dysfunction, indirectly promoting the progression of the disease.
It also underscores the importance of targeting these pathways for potential therapeutic interventions.

Finally, we observe a downregulation in the cholesterol efflux process and transport pathways (p-value $1.6x10^{-9}$). The cholesterol removal process involves remove extra cholesterol from cells, particularly those lining the walls of blood vessels. This process is crucial for preventing the buildup of cholesterol in artery walls, which can lead to the development of atherosclerosis and heart diseases. Cholesterol transportation, on the other hand, refers to the movement of cholesterol molecules through the bloodstream with the help of specialized carriers like low-density lipoprotein (LDL) and high-density lipoprotein (HDL). [80]

In the context of multiple myeloma, the decrease in these critical processes indicates that there are issues in the mechanisms responsible for efficiently removing cholesterol from cells and transporting it to the liver. This alteration can have significant implications for maintaining a healthy cholesterol balance in the body, which, in turn, affects overall health.

5.4 Mass Spectrometry based clinical biochemistry.

Based on the foundational work by Geyer P. *et al.*[67] that delved into the quantitative aspects of the plasma proteome, we have further advanced the field of MS-based clinical biochemistry. We have achieved a significant milestone by utilizing our experimental Label-Free Quantification data and leveraging the Proteome Ruler plug-in's capabilities in Perseus. Our study offers absolute quantification measurements for 238 proteins in serum samples. As a proof-of-concept, we employed this approach on healthy individuals' raw serum samples, aiming to establish a baseline for protein abundance in healthy individuals.

Human serum albumin (HSA) is a predominant protein in serum, making it a suitable reference for quantification studies. In our analysis, HSA concentrations spanned from 689 to 948 µM, a range that is slightly elevated compared to the commonly reported range of 490 to 798 µM[81] for healthy individuals. Several factors could account for this discrepancy. It is possible that variations in sample preparation, storage, or even the intrinsic biological variability among our study subjects might contribute to these differences. While our range is broader, it encompasses the typical accepted values, suggesting that our method provides a comprehensive view of HSA concentrations. Based on the previous promising result, we further selected 14 proteins related to the regulation of metabolic status[67] and obtained concentration data for each of these proteins in all individuals, as depicted in Figure 18.

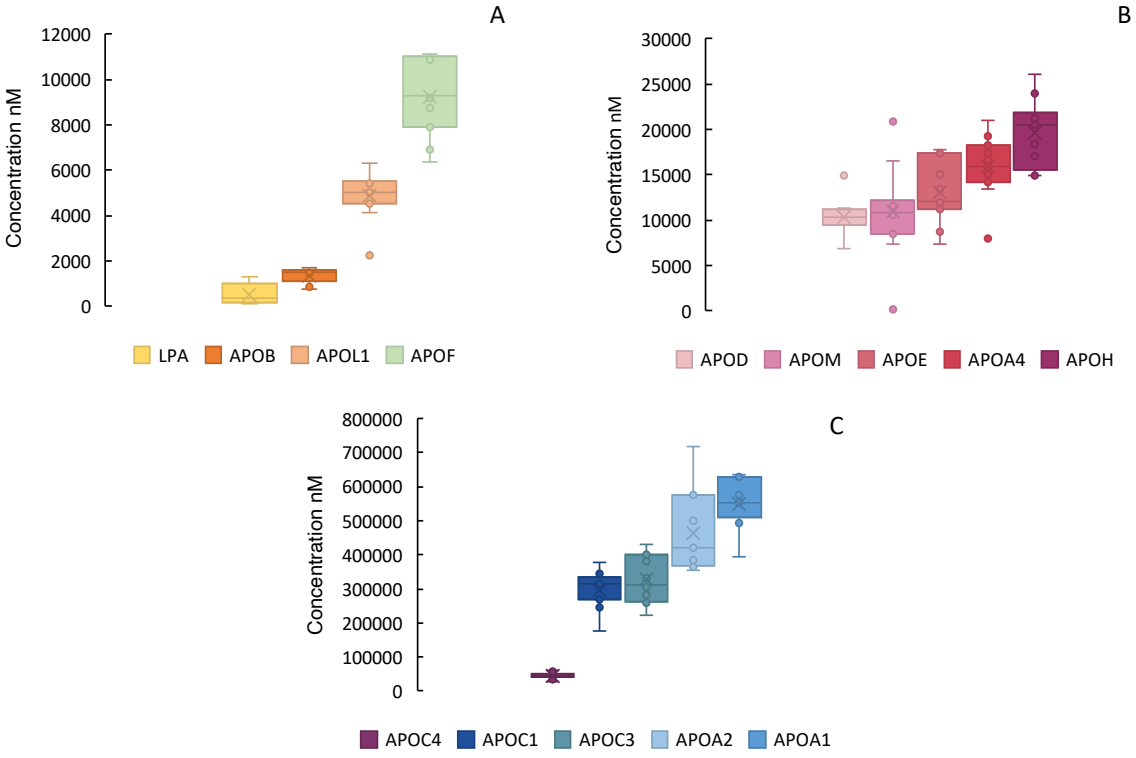

Figure 18 – Boxplot representing the concentration (in nM) of 14 proteins related to the regulation of metabolic status for healthy raw sera (n=11).

Despite the low number of subjects (n=11) used to establish the normal range of these proteins, our results agree with the levels reported in the literature. For instance, the protein LPA has been previously reported to have a concentration range of 170 – 630 nM[82]. In contrast, our MS-based method determined a broader concentration range for LPA, from 96 – 1302 nM. While our lower limit is slightly below the previously reported range, suggesting a lower detection limit, the upper limit significantly exceeds it. This variation could be attributed to the sensitivity and specificity of our MS-based technique, differences in sample preparation, or the inherent variability in the serum proteome among individuals.

In our study, we also quantified proteins that are indicative of inflammatory status, specifically Serum Amyloid A1 protein (SAA1) and C-reactive protein (CRP). These proteins serve as biomarkers for inflammation and can provide insights into an individual's inflammatory state, which is crucial for diagnosing and monitoring various health conditions.

From the cohort of healthy individuals examined in our study, we observed the concentration range for SAA1 to span between 0.5 and 71 µM. This is notably higher than the typical normal value, which is usually less than 0.7 µM.[83]

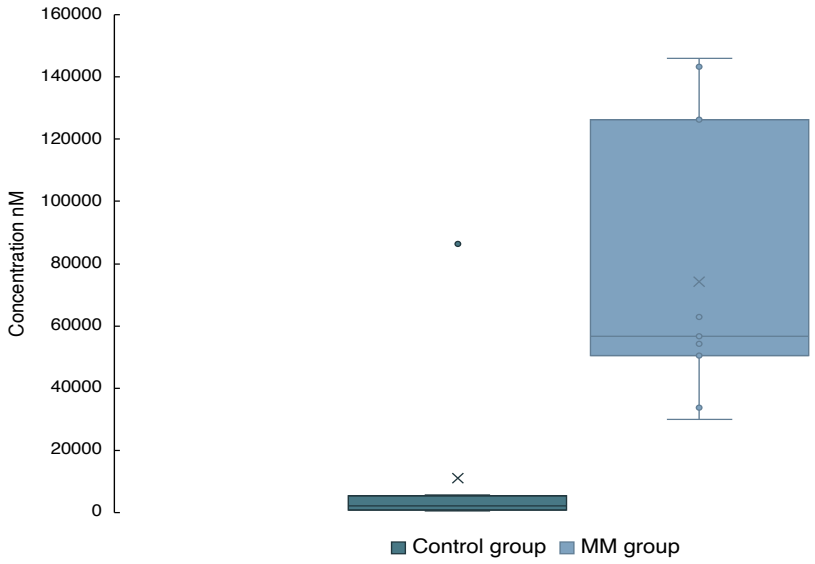

Figure 19 - Boxplot with data distribution of concentration from Control group (n=11) and MM group (n=5), for Serum Amyloid A 1, in nM.

Similarly, for CRP, our observed range was between 117 and 821 nM, which aligns well with the accepted normal value of less than 120 nM[84]. These findings underscore the importance of understanding the baseline levels of these proteins in the general population and their potential elevation in pathological conditions.

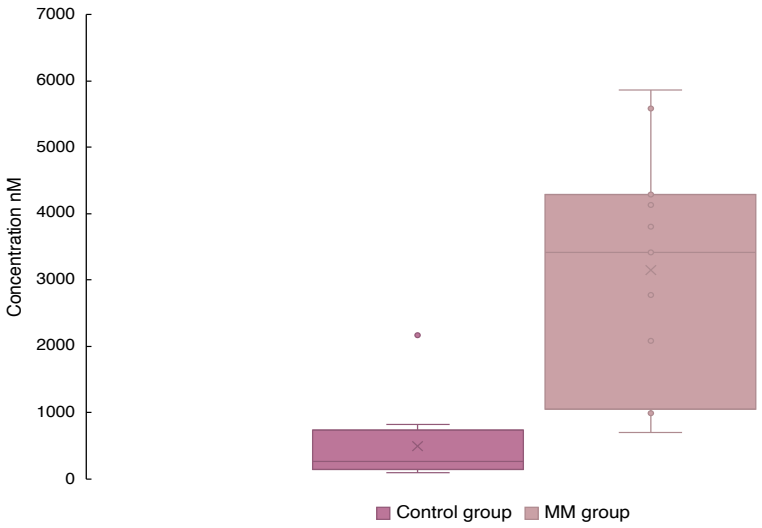

Figure 20 - Boxplot with data distribution of concentration from Control group (n=11) and MM group (n=5), for C Reactive Protein, in nM.

β-2 microglobulin (β-2M) is a crucial biomarker in Multiple Myeloma (MM). Found on the surface of monoclonal plasma cells, β-2M levels offer insights into the severity of MM. Elevated levels of this protein are not just indicative of the disease's progression but also have clinical implications, as high concentrations can lead to amyloidosis, a condition where abnormal proteins accumulate in organs, impairing their function.[85] In our study, a significant level of β-2M was observed in MM-depleted serum, as evidenced by a significant p-value of 1.7×10^{-5} (obtained using a Student's T-test with a False Discovery Rate (FDR) set at 0.05). This finding, illustrated in Figure 21, underscores the potential of β-2M as a diagnostic tool in MM.

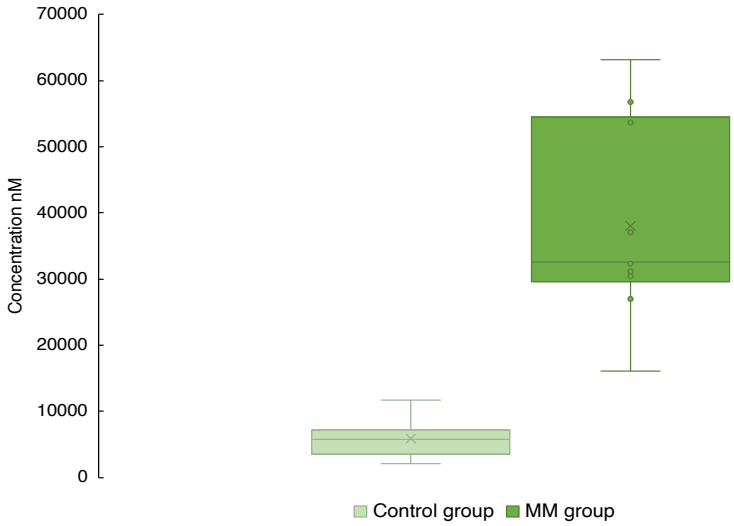

Figure 21 – Boxplot with data distribution of concentration from Control group (n=11) and MM group (n=5), for β-2 Microglobulin, in nM.

Furthermore, the pronounced levels of β-2M underscore its potential as a diagnostic marker for MM and spotlight its utility in the early detection of amyloidosis. The elevated β-2M levels observed in our study suggest a heightened risk of amyloidosis, especially given its known association with amyloid formation. Intriguingly, our findings agree with the upregulation of amyloid fiber formation, as described in the pathway analysis discussed in section 5.3.2. This upregulation suggests an environment conducive to aggregating these abnormal proteins, further emphasizing the role of β-2M as a precursor of such pathological changes. The convergence of our data with established pathways provides a robust foundation for the hypothesis that β-2M can serve as a dual-purpose biomarker as both an indicator of MM progression and a predictor of amyloidosis onset. Moreover, the intricate interplay between β-2M and amyloid fiber formation offers a promising avenue for therapeutic interventions. By targeting and modulating the pathways associated with β-2M and amyloidosis, it might be possible to manage MM more effectively and mitigate the risks associated with amyloid deposition.

6

CONCLUSIONS AND FUTURE PERSPECTIVES

6.1 Conclusions

Throughout this research, we have delved into the critical steps of protein quantification before proteomics analysis, specifically comparing the Bradford, BCA, and Tryptophan Emission assays. The variations observed across these assays emphasise the necessity of recognizing the major advantages of each method in terms of precision and accuracy. Our results indicate that the Tryptophan Emission assay is close to the established benchmarks at a range of 56–76 g/L.

Our investigations into MM sera highlighted the characteristic elevated total protein levels, indicative of the overproduction of monoclonal proteins, a defining feature of MM. It was essential to explore individual proteins through proteomics to gain a more profound understanding of MM, shedding light on the specific molecular entities and their roles in the disease. Following the methodology from C. Fernandez's study, we embarked on a depletion step, crucial for unveiling the less abundant yet potentially more informative proteins. Subsequent mass spectrometry analysis and heatmap comparisons revealed the stark differences between samples, emphasizing the efficiency and necessity of the depletion process.

Our comparative analysis between healthy individuals and MM patients provided insights into the compromised defense mechanisms in MM, particularly the downregulation of Chaperone-mediated Autophagy (CMA) and protein-folding chaperones. This compromised defence against misfolded proteins, coupled with the overproduction of light chains, predisposes the system to protein aggregation, with the potential to damage organs and tissues, especially the kidneys. Furthermore, our research highlighted the potential compensatory mechanisms in MM, such as the upregulation of the complement cascade and the significant role of the MAPK pathway in MM's progression.

Our exploration into the proteome enriched in the pellet from serum depletion revealed potential markers and pathways that could be pivotal in MM's progression. Notably, the dysregulation in calcium signaling and cholesterol metabolism pathways presents potential therapeutic targets.

Building on the foundational work by Geyer P. et al., our research has pushed the boundaries of MS-based clinical biochemistry. Our quantitative approach on healthy individuals' serum samples aimed to establish a baseline for protein abundance, providing insights into proteins like HSA, LPA, SAA1, CRP, and, notably, β-2 microglobulin (β-2M). The elevated levels of β-2M in MM-depleted serum accentuate its diagnostic potential in MM and its role in early amyloidosis detection.

Our findings underscore the transformative potential of proteomics in MM diagnosis and pave the way for future research, especially in understanding the interplay between β-2M and amyloid fiber formation. This research is a stepping stone towards more effective interventions, aiming to manage MM better and reduce the risk of amyloid deposition.

6.2 Future perspectives

As we progress in MM research, the importance of continuous patient follow-up and early detection of complications such as amyloidosis cannot be overstated. The following are some future perspectives in these areas:

- **Enhanced Patient Monitoring:** With the advancements in proteomics and our understanding of MM, there is a pressing need for more frequent and comprehensive patient monitoring. Regular check-ups can help detect disease progression or recurrence early, allowing for timely interventions and improved patient outcomes. Focusing on non-invasive liquid biopsies such as urine analysis, our method can be implemented for patients' follow-up.

- **Amyloidosis Detection**: Given the association between elevated SAA1 and β-2M levels and amyloidosis, our method can be essay implemented in a follow-up strategy. Early detection of amyloidosis can lead to prompt management, preventing organ dysfunction and improving the quality of life for MM patients.

- **Personalized Treatment Plan**s: As we gain a deeper understanding of the molecular intricacies of MM and its associated complications, there is potential for the development of personalized treatment plans. Such plans would consider the unique molecular profile of each patient, ensuring that treatments are tailored to offer maximum efficacy.

7

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A

APPENDIX A | SOLUTION PREPARED IN THE LABORATORY

A.1 Tryptophan Solution

0.1 M Tris-HCl pH 8.0 | It was started by preparing 0.1M Tris-HCl pH 8.0, weighing 12,114 g of Tris base for a beaker, and adding Milli-Q water, leaving in agitation continues to solubilize. After the Tris base solubilizes, place the beaker in a pH meter and add HCl (37%) until the pH reaches 8.0. This solution is transferred to a 100 mL volumetric flask and made up with Milli-Q water. Homogenize and reserve.

Urea 8 M Solution; 0.1 M Tris-HCl pH 8.0 | 240 g of urea was weighed into a beaker and 0.1M Tris-HCl pH 8.0 was added to dissolve the urea. After dissolving, the resulting solution, is transferred to a 500 mL volumetric flask and made up to 0.1M Tris-HCl pH 8.0. Homogenize and reserve.

Tryptophan stock solution 0.0102 µg/µL in 8M Urea; 0.1 M Tris-HCl pH 8.0 | The tryptophan mother solution was initially prepared at a concentration of 10 mg/mL, from which a dilution of 1:1000 was performed, obtaining a concentration of 0.0102 mg/mL.

A.2 Depletion of abundant proteins

500 mM DTT | For a volume of 100 µL, weigh approximately 0.00771 g of DTT for an eppendorf and add 100 µL of H_2O Milli-Q.

A.3 Protein Reduction, Alkylation and Digestion

Alkylation

70 mM Tiethylammonium bicarbonate buffer (TEAB) solution | 28 mL of the 100 mM solution was added to a falcon tube and 12 mL of H_2O Milli-Q was added.

Reduction/Alkylation solution | 200 mM Chloroacetamide (CAA) solution; 50 mM Tris (2-carboxyethy) phosphine hydrochloride (TCEP), 28 mM TEAB, 58.24 mM TEAB, 0.1 M pH 8.8.

200 mM Chloroacetamide (CAA) solution | Weighted 0.004675 g of chloroacetamide and added 250 µL of Mili-Q water.

1.5 M Tris-HCl, pH 8.8 | To a final volume of 1 liter, 181.71 g of Tris-base were weighed into a beaker and added Milli-Q Water q.s. After tris solubilize, HCl (37%) was added to lower pH and finally the solution was transferred to a 1L volumetric flask and made up with Milli-Q water. It was homogenized and stored in a laboratory bottle in the refrigerator at 4°C.

0.5 M Tris (2-carboxyethy) phosphine hydrochloride (TCEP), 95%, 0.5 M in water solution |Alfa Aesar by Thermo Scientific, H51864.

Digestion

Trypsin Vials code:
Trypsin/Lys-C Solution: 0.16 µg/µL in 70 mM TEAB | To a vial of Trypsin (20 µg) + Lyc C, add 125 µL of TEAB 70 mM to a final concentration of 0.16 µg/µL of trypsin.

Trypsin Solution: 0.4 µg/µL in in 70 mM TEAB | To a vial of Trypsin (100 µg), add 250 µL of TEAB 70 mM to a final concentration of 0.4 µg/µL of trypsin.

3% Acetonitrile (ACN), 0,1% Formic Acid (FA) | Previously we prepared a significative volume of ACN in 0.1% Formic Aid (FA) and H_2O in 0.1% Formic acid. Then, to a final volume of 5 mL, add 150 µL of CAN; 0.1%FA and 4850 µL of H_2O; 0.1% FA.

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B

APPENDIX B | RESULTS

B.1 Calibration curves (Bradford, BCA & W Emission)

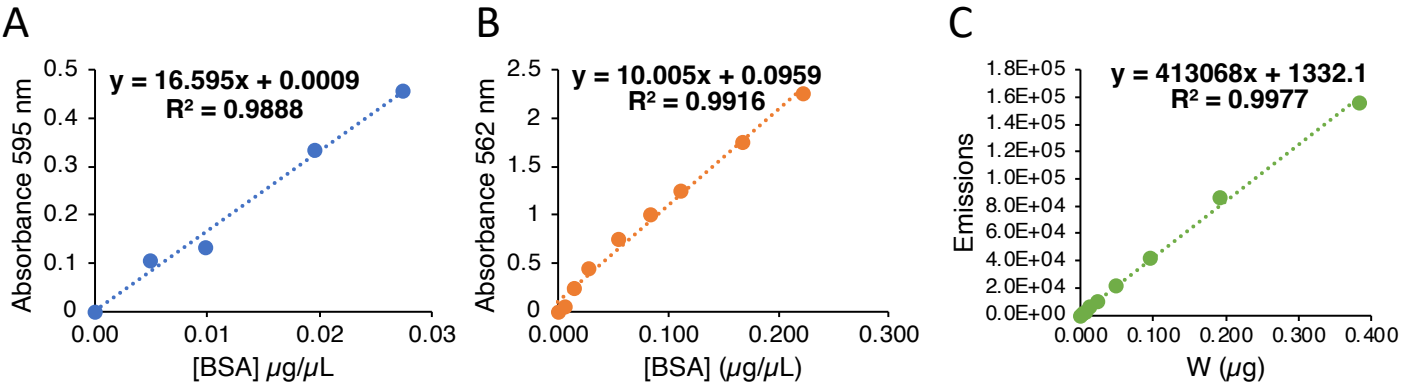

Figure 22 - Calibration Curves generated to compare the 3 methods (Bradford, BCA & Tryptophan Emission).

B.2 Calibration Curves of Tryptophan Emission Assays

All calibration curves presented in the table above were done via Tryptophan Emission Assay.

Table 11 - Slope, intercept of the line and R square of the calibration curves used in tryptophan emission assays.

Calibration Curve	m	b	R^2
(1) Comparison between 3 methods (Thryptophan Emission) & Total protein Quantification of healthy sera	413067.5121	1332.079457	0.9977
(2) Total Protein Quantification of MM sera	436439.1237	1715.030362	0.9984
(3) Protein quantification of SN and Pellet from healthy sera w/ depletion (Half samples)	426579.3977	970.6111111	0.9995
(4) Protein quantification of SN and Pellet from healthy sera w/ depletion (Half samples)	411825.3175	1870.697997	0.9971
(5) Protein quantification of SN and Pellet from MM sera w/ depletion	436439.1237	1715.030362	0.9984
(6) Peptide quantification of SN and Pellet from healthy sera w/ depletion	435187.9145	1141.689922	0.999
(7) Peptide quantification of healthy sera without depletion	427333.1934	1998.344315	0.9977
(8) Peptide quantification of SN and Pellet from MM sera w/depletion	436439.1237	1715.030362	0.9984

B.3 Mean Comparison Statistic Test | Healthy Sera

Table 12 - Mean comparison statistic test between Bradford assay and BCA assay

Sample	Bradford vs BCA		
	F	$F < F_{observed}$	
C 10	8.894757408	True	Não existem diferenças de variâncias
C 15	0.177672899	True	
C 25	0.803418241	True	
C 29	0.005184862	True	
C 33	1.130354589	True	
C 37	0.010966563	True	
C38	0.081016256	True	
C 41	0.078362001	True	
C 46	0.273448137	True	
C 49	0.487320877	True	
C 57	1.138522179	True	
$F_{observed}$ **= F (1,1) =** 647.8			

Table 13 - Mean comparison statistic test between Bradford assay and Tryptophan emission assay

Sample	Bradford vs Tryptophan Emission		
	F	$F < F_{observed}$	
C 10	8.89475741	True	Não existem diferenças de variâncias
C 15	0.1776729	True	
C 25	0.80341824	True	
C 29	0.00518486	True	
C 33	1.13035459	True	
C 37	0.01096656	True	
C38	0.08101626	True	
C 41	0.078362	True	
C 46	0.27344814	True	
C 49	0.48732088	True	
C 57	1.13852218	True	
$F_{observed}$ **= F (1,1) =** 647.8			

Table 14 - Mean comparison statistic test between BCA assay and Tryptophan emission assay

Sample	BCA vs Tryptophan Emission		
	F	**$F < F_{observed}$**	
C 10	10.97820174	True	Não existem diferenças de variâncias
C 15	2.16050745	True	
C 25	0.208322207	True	
C 29	4.77373E-05	True	
C 33	0.450559076	True	
C 37	3.962406049	True	
C38	1.894800657	True	
C 41	2.178737026	True	
C 46	0.443116333	True	
C 49	0.43569611	True	
C 57	0.184736213	True	
$F_{observed}$ = F (1,1) = 647.8			

B.4 Variances Comparison Statistic Test | Healthy Sera

Table 15 - Variance comparison statistic test between Bradford assay and BCA assay

Sample	Bradford vs BCA		
	S^2	t	Statistic difference?
C 10	9.480392901	0.797698144	False
C 15	8.096777309	4.219902299	False
C 25	4.960192242	0.059983877	False
C 29	11.10235781	0.825815662	False
C 33	13.8112098	2.677224283	False
C 37	11.49337635	0.564247725	False
C38	7.986653449	0.140393103	False
C 41	15.29659221	2.866897232	False
C 46	4.843981741	1.859447032	False
C 49	7.813081068	2.885583583	False
C 57	0.968102217	2.060128701	False
Critic value = 4.3			

Table 16 - Variance comparison statistic test between Bradford assay and Tryptophan emission assay

Sample	Bradford vs Tryptophan Emission		
	S^2	t	Statistic difference?
C 10	8.609545102	0.3315	False
C 15	4.403774157	0.8482	False
C 25	15.41256636	2.1423	False
C 29	0.057794528	0.8674	False
C 33	21.71706923	1.9473	False
C 37	2.99381635	0.4825	False
C38	4.497698326	0.8880	False
C 41	7.622231209	1.7135	False
C 46	9.624422688	0.9843	False
C 49	14.61681023	0.9318	False
C 57	2.965909398	0.2649	False
Critic value = 4.3			

Table 17 - Variance comparison statistic test between BCA assay and Tryptophan emission assay

Sample	BCA vs Tryptophan Emission		
	S^2	t	Statistic difference?
C 10	1.045397847	1.12922332	False
C 15	10.05746579	3.3717164	False
C 25	15.95325254	2.08235513	False
C 29	11.04561781	-0.0415784	False
C 33	20.87197303	0.72995752	False
C 37	14.23784155	0.08175047	False
C38	11.28723979	1.02837291	False
C 41	20.69568949	1.1533703	False
C 46	12.38810333	2.84374969	False
C 49	17.30997726	1.9537928	False
C 57	2.903200846	1.79519566	False
Critic value = 4.3			

B.5 Peptide Quantification | Statistic Analysis

To know the reliability of the data obtained and whether and there are statistically significant differences between the control group and the group of patients, we did the t-student test.

The first group (multiple myeloma patients) (n_1), the sample size is 5, the mean ($\bar{x}_1$) is 57 and the standard deviation (s_1) is 12. For the second group (healthy individuals) (n_2), the sample size is 11, the mean ($\bar{x}_2$) is 60 and the standard deviation (s_2) is 4. We use the equation 3 for the t-statistic for two independent samples.

$$t = \frac{\bar{x_1} - \bar{x_2}}{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$$

Equation 3

Calculating the t-statistic for the two means, the value is approximately −1.07. Given the sample sizes and the t-statistic, we can determine the p-value to test the hypothesis that the two means are equal. For a two-tailed test with 14 degrees of freedom, calculated following the equation 4, and our calculated t-statistic, the p-value will indicate the probability of observing a t-statistic as extreme as the one calculated, assuming the null hypothesis (that the two means are equal) is true.

$$df = n_1 + n_2 - 2 = 14$$

Equation 4

The calculated p-value is approximately 0.303 for a significance level of 5%, as the p-value of 0.303 is greater than 0.05, means we fail to reject the null hypothesis that say the two means are equal. Therefore, based on the data collected and the t-test, there isn't sufficient evidence to conclude that the two means (57±12% and 60±4%) are statistically different from each other.

C

APPENDIX C| PEPTIDE QUANTIFICATION

To ensure a consistent amount of peptides are introduced into the LC-MS/MS system for analysis, we employed W emission-based peptide quantification.

Peptide quantification with and without depletion of most abundant proteins of healthy sera

After we did reduction, alkylation, and digestion (102 ± 8 µg of protein per sample), peptides were quantified from healthy sera, both from the supernatant and from the pellet, and the raw sera. Quantification was performed via W emission and the results are shown in Table 18.

Table 18 - Quantification of peptides with and without depletion of most abundant proteins in sera healthy samples (n=11), via tryptophan emission. Each sample were analysed in duplicate (n=2).

Sample	[Peptides] (µg/µL)		
	Healthy sera without depletion	Healthy sera with depletion	
	Raw sera	Supernatant	Pellet
C10	1.9 ± 0.1	0.81 ± 0.04	0.93 ± 0.06
C15	2.0 ± 0.1	0.83 ± 0.02	1.07 ± 0.05
C25	2.7 ± 0.1	0.74 ± 0,03	0.96 ± 0.01
C29	2.1 ± 0.1	0.84 ± 0,01	0.68 ± 0.03
C33	2.0 ± 0.1	0.89 ± 0.05	0.76 ± 0.01
C37	1.49 ± 0.04	0.686 ± 0.001	0.98 ± 0.04
C38	1.78 ± 0.02	0.90 ± 0.06	0.93 ± 0.03
C41	1.77 ± 0.05	0.68 ± 0.01	0.84 ± 0.01
C46	1.61 ± 0.01	0.77 ± 0.03	0.86 ± 0.05
C49	1.70 ± 0.02	0.84 ± 0.02	1.06 ± 0.05
C57	1.64 ± 0.03	0.98 ± 0.05	0.85 ± 0.04

Peptide quantification with depletion of most abundant protein in MM sera

For sera from patients with multiple myeloma, after reduction, alkylation, and digestion (102±8 µg of protein per sample was also digested), peptide quantification was performed, both in the supernatant and the pellet. Quantification was performed via Tryptophan Emission and the results are shown in Table 19.

Table 19 - Quantification of peptides with depletion of most abundant proteins in sera multiple myeloma samples (n=5), via tryptophan emission. Each sample were analysed in duplicate (n=2).

Sample	Peptide (µg/µL)	
	Supernatant	Pellet
MMB	0.57 ± 0.03	0.42 ± 0.02
	0.69 ± 0.03	0.38 ± 0.04
	0.71 ± 0.03	0.39 ± 0.01
MMC	0.622 ± 0.005	0.517 ± 0.024
	0.63 ± 0.01	0.472 ± 0.003
	0.70 ± 0.02	0.683 ± 0.019
MMF	0.70 ± 0.01	0.36 ± 0.01
	0.9 ± 0.1	0.45 ± 0.01
	0.69 ± 0.02	0.4481 ± 0.0001
AQ01	0.58 ± 0.02	0.74 ± 0.01
	0.63 ± 0.01	0.91 ± 0.03
	0.63 ± 0.02	0.94 ± 0.04
JC02	0.881 ±0.004	0.345 ± 0.011
	0.78 ± 0.04	0.375 ± 0.001
	0.72 ± 0.03	0.320 ± 0.009

D

APPENDIX D| STUDY POPULATION

Table 20 - Discrimination of information about the study population.

Healthy Individuals			Multiple Myeloma Patients		
# Patient	**Age**	**Sex**	**# Patient**	**Age**	**Sex**
C10	71	F	**MMB**	57	M
C15	78	M	**MMC**	57	M
C25	94	F	**MMF**	57	M
C29	83	F	**AQ01**	75	M
C33	54	F	**JC02**	79	M
C37	90	M			
C38	78	M			
C41	73	M			
C46	53	F			
C49	67	M			
C57	65	M			

APPENDIX E | PROTEIN QUANTIFICATION (HEALTHY RAW SERA)

id	Gene names	Majority protein IDs	Concentration [nM] C10_raw	Concentration [nM] C15_raw	Concentration [nM] C25_raw	Concentration [nM] C29_raw	Concentration [nM] C33_raw	Concentration [nM] C37_raw	Concentration [nM] C38_raw	Concentration [nM] C41_raw	Concentration [nM] C46_raw	Concentration [nM] C49_raw	Concentration [nM] C57_raw
3	IGLV8-61	A0A075B6I0	6129.82	9467.65	5335.87	3508.81	8096.62	8572.55	6909.23	7093.54	4290.58	4587.42	5681.17
5	IGKV2D-28	A0A075B6P5	1690.16	1160.35	514.103	216.589	382.57	3004.62	1092.34	1374.87	1246.38	1393.52	1185.59
6	IGKV2-24	A0A0C4DH68	1149.47	1701.61	654.921	1229.74	1775.33	1863.59	960.402	504.45	728.725	759.005	839.204
7	IGKV1-27	A0A075B6S5	666.517	1095.19	266.374	204.172	453.23	596.326	385.755	480.054	586.95	400.095	242.287
11	TTR	A0A087WT59	14048.1	17847.3	39263.8	19494.1	15533.3	23558.9	19532.2	35144.8	28359	18599.7	21470.3
15	FCGBP	A0A087WXI2	769.689	641.989	838.451	546.811	704.16	444.027	507.085	604.111	543.717	600.136	557.323
16	CHL1	A0A087X0M8	238.969	249.706	42.9613	180.285	37.8398	56.1205	47.6431	221.063	221.711	195.426	215.528
17	SAA2-SAA4	A0A096LPE2	2660.04	4428.8	2827.62	3539.9	3866.31	2694.37	2799.53	3120.06	11809.2	2527.42	3648.56
18	F5	A0A0A0MRJ7	660.261	553.318	723.488	853.716	1040.77	698.24	730.945	945.157	766.143	596.424	655.031
19	IGHG1	P01857	270923	304361	180752	241866	188524	360441	132456	231839	249422	200568	320399
20	IGHD	A0A0A0MS09	1066.23	141.331	271.574	106.485	439.021	240.577	176.835	102.595	227.689	532.658	434.297
21	IGHV3-49	A0A0A0MS15	233.183	1238.94	712.852	702.723	947.469	2721.78	1129.03	1290.07	913.007	763.003	423.352
22	PRDX1	A0A0A0MSI0	3016.46	4530.77	4551.11	3782.86	7836.23	3801.12	4732.2	4704.98	5246.2	5227.07	5224.56
23	TTN	A0A0A0MTS7	287.444	283.498	265.744	398.385	263.825	379.487	216.698	232.429	257.865	1.68021	213.834
25	IGHV6-1	A0A0B4J1U7	11753.9	11651.8	13330.4	13055.9	12314.7	17709.8	8020.8	13400.8	9878.07	8463.82	11899.1
29	IGHV3-74	A0A0B4J1X5	5725.89	14120.3	11863.4	7068.85	17436.8	11290	13992.7	13141.6	11607.4	13649.8	13005.5
31	IGLL5	A0A0B4J231	6368.31	11180	5852.01	5941.07	6998.33	14313.8	2896.21	8051.1	3946.6	5792.99	3604.65
34	CRTAC1	Q5T4F6	322.731	126.274	63.7987	232.122	63.5019	240.568	150.349	97.7618	98.6998	43.5282	106.655
38	IGHV1-18	A0A0C4DH31	1445.51	181.926	273.205	1503.32	293.91	3332.56	1616.48	1553.06	1881.32	2220.17	2905.62
42	IGHV5-51	A0A0C4DH38	1908.67	1740.01	1635.41	984.971	1169.17	5109.38	1164.39	1313.63	1313.25	1229.65	1064.99
43	IGHV4-61	A0A0C4DH41	259.163	1702.33	155.869	1256.86	922.552	2861.54	508.764	1343.16	489.45	4453.5	407.725
44	IGKV1-6	A0A0C4DH72	258.869	1184.86	246.842	282.241	917.094	433.774	601.511	351.854	1031.21	1243.55	640.12
47		A0A0G2JMB2	5967.76	5001.19	6390.41	4028.16	10974.6	25782.2	5763.73	10055.4	3340.05	16148.5	4220.93
49	IGLV5-45	A0A0G2JSC0	905.107	567.301	2075.08	470.639	1314.6	1450.42	207.049	483.949	255.633	290.57	763.616
51		A0A0J9YY99	5693.5	501.337	770.333	478.624	748.748	447.904	345.353	8970.76	1459.16	663.068	3723.15
52	PROS1	A0A3B3ISJ1	2470.94	2072.93	1883.32	2440.07	1883.74	1718.84	2346.26	1867.6	1501.02	2028.94	2146.38
53	SEPP1	P49908	855.239	969.568	1120.11	1097.81	1415.39	141.447	80.2307	432.35	1552.1	172.811	159.536
55	KRT10	A0A1B0GVI3	405.822	563.76	600.59	550.379	736.966	480.141	1051.99	956.694	1016.03	540.801	543.949
56	IGHG3	A0A286YES1	45650.9	25522.3	32563.3	36150.4	32903.8	73205.8	36206.5	40476.7	50845.5	47878.7	53129.8
57	IGHG2	A0A286YEY4	36033.3	56351.1	12664.6	12907.2	22483.4	108983	26646.1	52082.2	60156.9	29285.9	30414.5
58	IGHG4	A0A286YFJ8	5400.24	6719.77	4252.85	18649	4096.49	22772.4	2083.15	4663.19	16237.9	11580.1	20863.3
60	CFHR2	A0A8V8TQS1	1517.37	1386.42	2158.06	1932.22	1570.2	1456.54	1751.77	2570.01	2013.15	950.196	1031.64
62	C1R	A0A3B3ISR2	1726.22	1341.54	1718.11	1683.37	988.757	2038.66	2341.81	1542.86	1890.99	926.881	1226.24
64	EGF	A0A494C018	828.613	1143.98	1347.8	1421.41	1584.98	1138.77	1444.71	1398.86	1413.71	1501.16	1517.87
65	H2AFV	C9J0D1	31320.6	42334.8	46934.6	38907.7	48425.5	39437	45357.9	41782.7	41751.9	42885.4	49224.2
66	IGHV3-72	A0A4W8ZXM2	19674.3	32339.5	16794.3	17309.9	36457.6	65607.1	17316.6	23168.7	13690.4	24645.2	16882.2
67	H3F3B	K7EMV3	231.291	589.646	847.362	719.582	96259.8	884.552	718.249	432.233	559.824	800.041	443.334
68		A0A6Q8PF87	7297.3	6882.26	3395.74	4396.05	5527.77	8872.02	5860.77	7309.33	3734.88	5548.96	5066.45

69	LMNA	A0A6Q8PFJ0	289.319	332.075	369.172	398.714	774.346	304.263	343.512	476.238	507.651	480.765	550.305
70	SERPING1	A0A7I2V2D2	9643.9	8687.39	11088.8	15514.2	9315.96	8205.96	10537.2	8513.03	11154.3	11868.8	8199.33
72	AGT	A0A7P0T8D1	5278.71	5260.75	10477.4	4113.49	2842.62	8234.15	4860.89	5643.59	5865.99	3409.23	5341.13
73	HSPA5	A0A7P0TAI0	551.673	751.802	817.471	716.296	920.652	656.915	822.256	899.555	742.865	732.635	859.692
74	PDIA3	A0A8I5KRV3	675.394	879.721	1048.16	834.761	2445.15	808.725	1064.07	1041.93	1091.17	1042.85	1100.94
75	PPBP	A0A8I5KW61	30952.2	25088.2	45351	50991.6	41012.9	32535.1	48422.5	36948.6	33550	40041.3	22185.7
76	MYH9	A0A8I5KWT8	103.201	120.285	150.803	115.166	158.937	160.132	153.664	136.938	184.607	164.513	124.949
79	C1QB	A0A8Q3SI33	9636.31	8235.52	10059.6	6852.15	3402	11607.7	4250.88	6160.53	8258.93	7031.86	5960.5
80	C9	A0A8Q3SI95	3425.57	4507.91	5382.89	3702.24	6169.63	2908.36	5155.17	4487.84	3987.17	4919.02	4561.6
82	C5	P01031	1309.93	1528.45	1852.77	1448.12	1230.96	1463.51	1500.9	1600.75	1620.17	1484.34	1472.21
83	C1QC	A0A8Q3SIZ0	16602.6	11546.8	18234.6	9978.86	9068.72	21521.5	9932.28	10396.9	12937	6044.91	7204.07
84	CFD	A0A8Q3WKW0	1682.3	1251.46	1994.84	1322.18	973.439	1439.96	1717.04	1494.06	1199.86	1261.03	1332.47
85	F12	A0A8Q3WL25	1193.06	1271.07	1812.55	1610.22	2236.9	416.79	721.349	440.381	1160.47	1873.55	838.11
86	C8A	A0A8Q3WL79	1447.25	1872.57	1472.23	2324.31	2402.92	1279.83	2693.05	1803.38	2325.42	2767.03	2064.3
88	ANXA2	P07355-2	1583.21	2390.86	2384.57	1942.44	2832.18	1829.28	2527	2210.07	2258.03	2346.81	2218.75
89	IGFBP3	A6XND0	134.464	408.652	947.581	257.965	234.775	604.814	125.921	450.426	70.9707	205.226	151.471
90	APOC3	B0YIW2	401943	381770	418214	429261	222302	257416	304007	282963	332269	311644	260806
91	VIM	B0YJC4	2276.42	4625.38	4503.35	5602.7	7675.58	2984.18	6345.49	6152.58	4415.11	6417.43	3947.5
92	APOL1	B1AH94	5014.45	4615.66	5632.63	4503.72	2271.56	5232.36	4135.67	5440.95	5512.7	5029.14	6320.1
94	UBC	P0CG48	1012.39	1174.35	2368.06	1739.52	52.5253	1249	2117.05	27.6843	47.8783	82.6684	1319.54
95	CFB	B4E1Z4	7336.64	9024.65	7625.72	6972.36	9274.03	6736.27	7374.01	9952.14	7024.66	9325.05	7522.39
96	FGG	C9JEU5	192.4	159.331	141.787	354.144	292.48	122.357	218.209	387.562	144.857	74.3626	228.129
97	APOD	C9JF17	7352.87	11028.6	11244.3	6858.67	14856.8	9414.98	10891.9	10309.2	9619.04	10232.5	11352.7
101		CON__P00761	34461.9	33795	20597.7	26293.1	28239.4	36307	31892.1	28492.9	24217.2	36905.5	26679.9
104		CON__P02768-1	781255	835068	791695	803770	814457	689169	919090	847962	800615	805176	947554
108		CON__P13647	39.9354	241.231	153.843	168.583	241.833	224.398	109.08	255.679	242.173	268.035	73.9598
109		CON__P15636	9400.82	8947.11	6116.68	9595.02	10602	8389.17	10626.2	7140.85	6371.58	10788.4	10158.6
110		CON__P19001	843.13	1117.16	1080.88	972.847	1255.62	875.819	1136.44	1044.27	1033.92	865.535	1253.46
111		CON__P35527	161.502	86.0591	156.36	4.97092	78.0598	22.3578	56.0698	73.4635	31.6843	112.351	8.06942
112		CON__P35908v2	38.5505	28.8918	40.6547	51.4765	35.4282	28.2194	79.1283	60.5213	66.1767	45.0151	36.2386
115		CON__Q32PJ2	7495.22	7898.76	20434.3	3831.93	13759	6088.3	8353.14	11067.4	10228.5	2141.76	7926.73
118	GC	D6RF35	35276.4	31836.8	32913.3	41332	36875.1	34271	39096.2	34340.3	38754.1	34943.7	34425.2
119	COL12A1	D6RGG3	12.2262	27.5375	13.2061	37.371	170.479	124.019	157.662	135.941	146.595	143.494	131.566
120	CA1	E5RH81	919.732	223.149	943.007	407.063	210.923	1362.24	84.4335	610.059	433.826	335.866	742.781
121	PROC	E7END6	535.425	88.8405	350.75	458.676	552.436	497.157	466.419	480.236	155.455	69.9944	202.729
123	CFI	G3XAM2	2598.26	3034.13	2303.06	2114.79	2482.37	2157.26	2580.28	3167.55	2983.05	2473.7	1771.55
125	CFP	P27918	857.195	1214	1151.67	766.292	1230.8	675.859	860.276	978.74	867.172	708.32	878.06
127	CLEC3B	E9PHK0	9300.32	6981.01	5761.1	5103.75	7794.31	7560.76	6854.6	6466.61	7319.92	4835	6483.95
128	HSPA8	P11142	449.919	1279.75	1335.4	679.5	1714.11	1275.13	1530.82	1337.26	1343.7	624.139	1132.57
129	C2	F2Z3N2	608.102	490.484	628.216	503.065	358.193	656.681	753.519	239.28	795.408	830.873	745.272
133	SERPINA10	G3V2W1	919.472	755.867	1001.97	635.727	94.8769	721.048	705.207	918.739	171.186	137.845	58.0148
135	MST1	G3XAK1	57.5289	17.7993	134.609	288.201	95.5366	173.759	33.1646	43.071	404.208	419.356	38.693
136	COMP	G3XAP6	1114.29	384.772	501.75	322.895	605.696	481.702	605.549	571.7	576.225	514.061	644.198
137	KLKB1	H0YAC1	3422.71	2870.66	5223.77	3803.87	4796.79	2719.35	3423.72	3299.88	5659.06	3111.57	3946.93
138	ALDOA	H3BPS8	1392.5	2148.83	2305.71	2497.35	3492.63	1732.09	2312.33	2086.29	2011.89	3136.27	2259.24
139	CETP	H3BRJ9	73.0001	113.842	184.694	84.948	138.081	155.097	93.5154	146.762	380.951	265.934	258.347
143	SHBG	P04278	814.187	575.82	1973.67	387.346	935.329	366.982	452.901	438.889	555.385	482.032	582.163
144	APOC4-APOC.	K7ER74	49174.9	43040.5	39667.1	49023.3	28669.7	34542.8	40284.9	44831.8	56073.2	49046.5	61824.4
145	APOC1	K7ERI9	344830	314070	319184	333384	376686	175376	246294	267767	271446	332034	274887
147	CD5L	O43866	4808.23	2867.37	1969.97	5956.56	7297.85	4124.97	3572.9	2039.74	4953.49	4916.85	7128.45
148	HIST1H2BM	Q99879	13989.9	80565.1	65591.3	63695.8	98501.7	56190.6	86830.6	67434.9	79826.8	84332.9	87431.6
149	FCN3	O75636	828.713	698.17	1307.37	915.519	793.513	1196.4	982.079	867.676	1114.21	840.248	622.576
150	ATRN	O75882-3	440.266	416.65	568.714	438.298	360.276	387.014	356.81	432.938	397.76	243.41	251.626
151	APOM	O95445	8425.55	11571.8	11042	12234.6	7373.65	20820.3	220.675	10628.3	16510	10733	10783.2
153	CP	P00450	9479.96	10680	14276.8	10457.1	11615.7	7077.71	10369.1	8625.23	7355.72	10119.3	9062.04
154	F2	P00734	12299.5	14891.6	14275.1	16188.9	12911.6	12354.3	13164.1	14625	14494.1	12091.5	10566.9
155	HP	P00738	148868	179144	108661	160911	188517	150176	157613	199537	190710	267634	181696
156	HPR	P00739	5648.01	3665.2	2013	7075.29	2678.54	3858.2	4388.39	6599.83	5040.67	6868.94	6487.97
157	F9	P00740	733.778	812.782	997.918	840.214	922.008	868.545	618.454	825.214	818.123	990.467	757.262
158	F10	P00742	1517.88	1353.49	1641.38	1748.22	1013.32	1045.44	2135.33	1816.63	1582.36	1574.48	963.807
159	PLG	P00747	9041.75	7952.43	11140.1	9722.45	8422.3	8139.84	8996.91	9727.35	11112.6	11314.6	7792.92
160	SERPINC1	P01008	6686.42	4013.94	4211.98	6624.38	6068.91	4774.05	8651.11	5037.45	5714.48	5273.79	6451.9
161	SERPINA1	P01009	74767.3	68204.8	132568	107102	108960	51456.6	138241	93929.7	84880	119463	112992
162	SERPINA3	P01011	1277.04	2288.7	3068.75	1728.72	1197.09	892.954	1782.26	1441.45	1642.81	1915.8	762.138
163	A2M	P01023	15098	10363.9	12857.1	10025.6	10909.1	8890.07	10972	12178.9	13007.5	11219.3	11388
164	C3	P01024	9078.52	8306.81	10343	7161.24	5624.95	9866.89	6725.48	10647.1	10939.8	6749.13	7330.71
165	KNG1	P01042-2	28970.7	32842	36417.6	33687.7	34710.7	25032	29418.5	29889.3	31588.1	25188	30340.4
167	IGJ	P01591	16865.7	8385.36	15668.3	20974.9	34268.3	20284.4	20358.6	10604	19331.5	35106.3	13840.4
168		P01594	320.129	184.976	666.77	594.58	778.872	978.176	463.303	438.594	1172.24	431.787	719.62
169		P01599	247.655	2430.91	320.692	1889.51	4114.66	2623.41	402.404	2195.15	565.039	305.064	876.949
170	IGKV1-5	P01602	702.699	2057.22	664.569	669.618	1431.79	125.413	803.541	205.182	249.257	816.602	1166.3
171		P01619	1929.05	2336.24	4497.36	2215.06	3114.58	7417.28	3334.11	635.125	1497.36	1507.26	738.176
172	IGKV3D-7	P01624	2001.71	273.615	662.048	1869.47	674.12	2001.28	1700.94	351.636	602.271	90.5464	925.54
173		P01700	4264.3	3924.97	2677.48	2163.82	3240.27	16285.8	2199.93	3168.32	2357.49	5702.57	2381.32
174		P01701	2328.02	1895.39	932.351	595.771	1600.81	2090.93	1372.01	1797.31	1810.47	3107.49	1773.22
176		P01706	259.81	323.203	1238.89	649.065	548.856	720.712	498.009	294.586	748.513	139.512	811.7
177		P01714	1609.26	458.235	278.022	523.96	297.749	3037.75	250.372	139.982	152.189	223.79	619.788
178		P01715	1062.77	130.83	671.683	445.787	208.152	1930.51	690.339	501.5	337.848	852.918	1348.52
179		P01717	4407.94	4472.49	2943.84	3193.64	2785.45	5798.05	2984.34	3313.35	3371.89	5125.91	2389.14
186		P01780	6728.58	8094.62	3198	7640.25	23880.9	21882.1	2921.67	7425.03	9570.13	5995.74	4912.44
187		P01782	1038.63	792.814	975.157	131.217	652.009	488.183	464.203	1177.12	1050.94	591.893	386.652
189		P01817	198.518	501.884	1208.85	1343.06	335.037	240.273	211.211	416.82	251.063	319.236	692.861
191	IGKC	P01834	470898	463315	256961	441483	591974	568339	391646	453319	394755	493608	426038
192	IGHM	P01871	15158.5	12435.1	13395.1	17595.6	19209.7	15328.6	11725.6	8438.54	21060.5	11901.6	17159.7
193	IGHA1	P01876	183953	124481	62936.3	86639.7	160501	275023	111463	119264	65947.6	167415	52290.5
194	HBD	P02042	1616.51	2410.4	3393.08	1325.45	1935.08	4546.93	190.884	2936.35	1601.66	428.451	1079.86
195	APOA1	P02647	627396	552876	628030	636823	556687	395659	511548	492892	576931	553421	509436
196	APOE	P02649	17476.7	11991.9	17359.7	11176	13375.5	15036.6	17729.1	11287.9	12115.3	7363.47	8770.72
197	APOA2	V9GYM3	385488	368090	354866	499042	363671	386127	588432	426760	419643	718154	577258
198	FGA	P02671-2	5177.57	5864.55	6678.52	6740.66	6876.92	5030.01	6007.8	5528.21	5371.21	6497.64	3543.98
199	FGB	P02675	147.807	263.979	252.769	326.658	217.001	127.09	126.419	149.987	153.198	209.943	102.638
200	CRP	P02741	228.764	408.881	116.584	360.142	405.553	217.385	240.617	212.766	399.774	233.896	185.634
201	APCS	P02743	5015.57	5964.03	4766.72	3336.91	3326.03	9622.9	3087.55	5679.8	6826.93	3239.39	4809.33
202	C1QA	P02745	8516.56	6429.28	5786.94	8869.18	4045.77	5505.51	9917.81	6696.51	6025.52	7999	8339.01
203	APOH	P02749	26090.8	23895	21287.3	16977.7	15534.8	21902.3	14949	20791.5	20463.9	14969.9	18394.6
204	LRG1	P02750	6235.62	5875.87	10221.9	4358.77	4101.65	5272.42	3260.4	3353.75	5749.55	2563.91	3659.76
205	FN1	P02751-14	2157.7	1832.46	2541.96	1192.22	1871.26	1463.02	1519.67	2032.29	1381.29	943.906	1356.6
206	RBP4	Q5VY30	10801.2	7797.97	7244.01	14260.6	7852.16	11413	13621.8	9612.53	8916.25	11813.7	9415.4
207	AMBP	P02760	18362	13436.2	20010.1	18091.3	20047.9	15619.6	16125.4	16083.3	11506.8	15942.5	11216.3
208	ORM1	P02763	73070.2	94229.5	82366.4	69941.5	40961.6	209097	49324.1	63881.6	113429	34439.2	23125.9

209	AHSG	P02765	56813.4	42666.7	62285.9	48340.3	59158.6	35496.5	58113.5	50656.8	36235.9	39478.1	47878
210	TF	P02787	104635	110526	125092	125847	105137	58403.6	113456	113740	116786	81268	111269
211	HPX	P02790	82936.1	86238	127225	86967.5	88460.6	86558.6	88772.1	90041.1	92103.3	84884.2	83597.1
212	C4BPA	P04003	8234.77	7287.4	5105.9	5895.95	5660.79	6436.89	4298.84	6684.87	8790.55	5819.41	9787.06
213	VTN	P04004	9937.65	10913.1	17644	10898.7	9979.04	9867.49	11891.3	11606.9	10290.3	6874.79	7735.06
214	APOB	P04114	1607.14	1456.23	1534.27	782.032	1107.17	1499.54	875.965	1535.76	1630.34	1141.5	1702.66
215	LCAT	P04180	952.255	1034.24	1788.47	671.903	930.244	1208.69	521.285	689.754	1100.36	733.525	867.372
216	HRG	P04196	13781.6	9264.52	21377.8	12606.3	11871.5	12239.8	12732.3	10426.6	9747.95	9006.59	10348.7
217	A1BG	P04217	14050.1	11833.5	18386.2	12243.3	11529	14842.2	10021	9982.36	13412.8	7597.61	6770.05
218	KRT1	P04264	522.442	820.815	722.101	528.349	887.536	676.845	896.925	681.091	685.826	875.59	611.423
219	VWF	P04275	179.125	107.601	75.2502	71.5919	199.106	92.3461	211.631	139.761	140.639	59.2843	177.178
220	IGKV3D-11	P04433	908.286	642.23	627.038	286.867	328.232	578.708	1214	1129.64	1103.19	1138.9	500.962
221	AMY2B	P0DUB6	885.014	1256.62	1379.78	1569.31	2499.56	1117.53	2499.39	1434.66	1388.96	2219.17	1526.87
222	SERPINA5	P05154	745.418	827.633	876.213	742.829	810.782	693.211	825.964	220.709	830.456	848.784	819.02
223	F13B	P05160	548.514	575.056	429.303	444.433	336.965	452.799	425.028	450.94	436.157	499.311	353.902
224	SERPINA7	P05543	172.268	119.545	185.913	59.1784	147.107	219.444	57.4245	172.431	96.8987	109.12	114.035
225	SERPIND1	P05546	5384.09	5133.66	7495.98	4757.26	3288.55	5448.17	3121.25	4810.45	4619.94	5781.84	3937.37
226	BCHE	P06276	580.04	575.048	652.682	345.676	572.73	439.523	1281.56	1403.55	635.998	1227.22	298.927
227	IGKV2D-30	P06310	11182.1	14985	357.451	13671.2	14140	11883.2	7740.14	11949.6	12114.5	13525	9461.35
228	IGKV4-1	P06312	2538.36	106.084	454.271	483.695	514.233	1663.19	199.415	799.161	642.672	837.88	542.456
229	GSN	P06396	7144.49	3412.38	4295.61	4187.34	3647.38	4201.71	6016.67	4724.28	4556.99	4446.58	5498.59
231	APOA4	P06727	18276.4	16627.8	20951.6	15078.8	17449.2	14204.6	15331.4	19294	15878.7	7930.91	13388.7
232	C8B	P07358	1375.64	1579.21	2571.69	2731.45	1810.03	1875.86	3914.92	1879.51	3570.27	2223.17	1992.69
233	C8G	P07360	2551.66	3743.66	6449.53	3018.21	3067.4	3358.6	3952.6	3027.84	3758.11	3286.8	3069.7
234	TUBB	Q5JP53	771.739	1321.8	1108.63	1153.94	2251.69	828.94	1914.39	1331.56	1277.74	1776.9	2044.74
236	HSP90AA1	P07900	807.401	1089.67	360.086	338.418	1143.49	842.186	1170.57	1079.23	35.3016	453.481	1096.17
237	UMOD	X6RBG4	4151.75	8378.16	7803.43	7701.4	9444.38	6615.96	8986.28	8428.68	8847.84	8452.2	9129.17
238	THBS1	P07996	299.796	271.356	344.406	350.316	367.24	226.265	550.354	395.354	252.95	276.609	164.088
239	SERPINA6	P08185	1631.43	1306.31	3020.25	2607.58	815.982	2671.36	1406.67	1364.93	1475.96	1566.04	1628.74
240	HSP90AB1	P08238	370.333	567.801	758.721	563.296	730.707	469.183	596.168	553.178	629.422	619.182	668.422
241	LPA	P08519	1076.87	98.2932	770.323	1302.17	370.906	984.977	310.083	219.381	475.822	96.5477	156.969
242	CD14	P08571	1026.6	1209.91	1557.87	1165.66	1145.31	1043.11	218.214	1138.95	1136.67	1096.3	1010.46
243	CFH	P08603	4882.02	5200.92	5132.97	4282.71	5104.16	3673.08	4987.81	6177.22	4507.03	3519.71	5409.82
244	SERPINF2	P08697	1513.61	1353.39	2981.09	2311.44	2083.46	1698.89	1055.54	1549.2	1179.83	773.593	1057.43
245	C1S	P09871	37081.4	31515.7	52933.6	45814.6	41882.6	30721.9	50448.5	34997.4	44276.5	32387.8	22616.5
246	C4A	P0C0L4	788.565	500.16	616.77	1055.95	421.752	975.402	618.52	1022.68	438.619	444.992	283.793
247	C4B	P0C0L5	4303.23	3881.33	4388.74	4080.93	4394.73	3226.95	4130.34	3943.57	3821.44	3861.57	2118.1
248	SAA1	P0DJI8	1410.45	3521.3	3776.34	498.437	2620.77	566.302	4928.61	1084.55	70782.1	722.757	2619.27
250	IGLC6	P0DOY3	376929	364509	177297	237957	329105	570722	233332	282639	266372	311851	277974
252	HIST1H1E	P10412	10473.6	20101.3	23080.1	19402.3	21027.4	17099.8	20129.1	23686.7	15323.3	20321.1	15848.3
253	opn	Q3LGB0	13656	18931.9	21291.5	17207.5	25966.1	16250.6	21679	16889.6	21585.5	21731.3	22080.3
254	C7	P10643	785.385	791.081	1071.14	644.597	712.814	1584.26	1245.75	1451.69	889.186	843.229	589.708
255	CLU	P10909-4	16748.7	11842.7	22554.6	14617.9	18499.5	15188.1	17571.4	14199.2	15638.6	14306.1	14103.3
256	MBL2	P11226	344.809	803.392	755.769	477.03	437.798	326.906	892.693	101.802	424.64	700.071	1954.46
257	COL6A3	P12111-4	129.805	180.798	188.685	169.678	202.287	168.956	224.333	171.34	209.015	163.341	189.828
258	C6	P13671	1262.84	883.605	1009.54	1612.8	1691.96	1157.82	1574.85	1256.03	1604.14	1512.19	1079.15
259	CPN1	P15169	822.953	639.091	597.763	722.27	1167.99	989.363	748.019	556.313	686.834	767.061	923.885
261	IGFBP2	P18065	147.272	143.872	351.205	175.205	62.4781	103.654	220.316	223.366	101.962	122.939	90.0525
262	LBP	P18428	411.766	436.026	571.359	483.802	75.284	395.84	739.657	125.315	485.143	473.65	72.2189
264	ORM2	P19652	35205.9	42488	28178.5	34492	13207.6	37162.6	24002.7	31854.5	23031.6	16582	20582
265	ITIH2	P19823	8438.31	5688.17	8968.22	8197.76	7204.7	7059.35	9264.15	8347.71	8472.61	7945.02	8485.44
266	ITIH1	P19827	10114	8977.22	12474.9	11180.6	9096.83	9368.75	11025.5	11775.1	12693.3	10824.2	9668.32
267	PZP	P20742	18.4331	101.523	110.083	38.3292	58.027	27.7938	34.5573	48.0929	30.4965	35.238	37.9573
268	C4BPB	P20851	3961.01	3777.79	1479.43	3583.44	4535.19	1839.31	2937.01	4687.51	4661.15	4080.34	4041.53
269	GPX3	P22352	1617.7	2515.33	1643.65	1184.78	1944.56	1175.58	2572.88	1674	1684.25	876.373	1283.29
270	CPN2	P22792	2865.41	3138.38	3154.2	2522.01	3295.05	2402.97	2251.96	2769.25	3029.39	2772.51	3045.92
271	PROZ	P22891	104.318	163.556	309.728	307.172	181.599	284.751	174.092	71.3403	146.132	182.791	70.5793
274	FBLN1	P23142-4	11994.2	4325.95	7728.64	3395.78	11130.1	8967.66	6012.61	15964	6789.28	4109.6	6159.71
275	AZGP1	P25311	438.842	669.976	738.031	717.27	152.759	1035.73	790.726	794.219	584.407	539.727	671.957
276	PON1	P27169	11518.1	10248.2	18102.4	8833.41	10489.4	12796.1	11601.9	13944	13580.3	12883.6	13517.5
277	SERPINA4	P29622	13.7141	54.2634	79.996	125.433	194.04	124.194	30.7855	42.833	123.166	20.9201	124.69
278	CDH5	P33151	392.31	417.851	444.609	272.337	349.247	312.145	334.137	432.408	134.996	423.623	349.782
279	IGFALS	P35858	794.498	940.939	2132.15	665.752	528.301	1521.36	669.167	426.466	1097.9	412.845	613.043
280	SERPINF1	P36955	4410.95	3763.56	5649.12	2540.56	2284.06	4712.41	2857.86	4428.82	3553.94	2185.49	2196.73
281	PTGDS	P41222	4139.18	3650.94	1932.98	359.613	3731.36	2852.32	2212.76	1776.13	3269.89	360.012	3045.21
282	BTD	P43251-4	347.815	587.844	716.217	610.993	619.278	538.654	656.74	792.519	646.427	490.631	687.861
283	AFM	P43652	3540.35	3647.44	7559.47	2814.27	2901.19	4405.58	3684.93	5309.11	4223.63	2890.77	3384.46
284	MASP1	P48740	164.324	28.6042	30.5181	277.269	236.187	191.22	287.12	24.175	148.776	281.828	150.332
285	LUM	P51884	8983.09	6769.8	6764.31	5929.09	6307.32	5017.68	6979.3	6654.3	6539.99	6062.33	4013.53
286	PLTP	P55058-3	35.6346	81.4392	629.914	146.686	171.953	529.947	161.559	96.3655	616.963	155.713	577.064
287	ACTB	P60709	22052.4	32087	25526	29149.6	36708.5	24922.6	30680.9	31430.5	32379.6	33829.6	36680.1
289	B2M	P61769	7000.17	7442.12	9785.45	7304.85	8747.98	7263.15	8423.31	7477.34	6880.06	6331.49	6228.23
291	RPS18	P62269	1422.95	1591	1856.47	1618.81	2117.97	1511.46	497.496	1741.03	1810.73	1742.32	1652.86
293	HIST1H4A	P62805	66676.5	85869.9	71688.2	101560	107171	50966	101721	86543.4	64176.8	71313.5	73116.9
295	HBB	P68871	55894.3	85205.8	75390.7	52582.9	48304.4	158453	52450.8	72432.1	54839.7	23024.4	30068.6
296	HBA1	P69905	71490.9	95687.9	99455.6	66750.3	66847.5	213779	70604.9	94004.2	73054.8	26239.8	36505.9
297	GPLD1	P80108	419.421	620.209	855.587	521.514	439.251	450.728	561.934	518.68	403.322	520.622	528.727
298		P80748	9103.92	330.491	7443.8	592.497	5699.65	18997.8	390.576	676.391	692.312	354.778	448.012
299	HSPG2	P98160	195.038	290.305	292.694	278.304	552.916	259.993	529.71	329.657	536.069	408.87	430.526
300	CFHR1	Q03591	2102.54	3534.8	2225.36	4736.24	4049.78	3886.08	4044.85	4250.22	1268.08	2128.33	1268.03
301	HGFAC	Q04756	556.199	504.265	728.454	619.63	610.714	499.934	586.513	621.155	674.226	512.891	337.425
302	ITIH3	Q06033-2	615.194	429.916	1567.64	618.52	477.491	555.811	1048.32	477.266	834.181	1371.7	643.715
303	LGALS3BP	Q08380	226.814	267.276	294.649	148.959	359.804	310.028	285.004	282.697	252.411	200.134	261.454
304	EFEMP1	Q12805-2	385.992	318.152	446.153	267.835	380.049	416.068	320.519	308.537	110.308	304.37	238.569
305	SPP2	Q13103	552.312	581.841	145.741	404.768	620.992	220.623	395.455	262.457	557.505	144.669	197.996
306	APOF	Q13790	10885.6	9272.63	6927.49	8757.93	11018.6	6348.22	9311.67	7905.37	11070.3	9187.89	11105.3
307	HABP2	Q14520-2	1344.88	813.011	1502.78	1273.58	480.905	1389.37	1063.47	1158.82	1495.02	928.131	643.495
308	ITIH4	Q14624	2992.02	2412.77	4996.94	3443.1	2480.67	3832.37	2592.21	2512.29	3167.21	2439.27	1496.01
310	ADIPOQ	Q15848	942.813	1349.41	643.529	504.549	271.779	639.3	181.773	198.431	183.458	357.247	289.215
311	ECM1	Q16610-4	495.863	330.655	439.351	365.841	369.256	89.1371	391.541	453.152	350.627	301.191	329.372
321	WHAMM	Q8TF30	964.62	894.325	250.193	752.137	1161.52	1169.12	674.077	896.992	490.379	764.109	669.056
322	RYR2	Q92736	205.089	121.502	303.669	88.0171	136.885	252.684	101.741	115.602	183.456	86.3095	148.716
324	PRG4	Q92954-3	371.134	401.97	518.983	251.735	296.06	239.98	239.209	217.813	324.877	277.28	230.628
325	PIK3IP1	Q96FE7-4	15191.9	20154.4	24449.6	18062.7	30197.3	15463.6	22055.7	19276.1	19514.1	20946.5	16929.8
326	CPB2	Q96IY4	1191.41	1378.09	1655.88	1326.62	1021.51	1737.36	1730.02	1247.53	1082.17	1206.03	916.455
327	CNDP1	Q96KN2	839.142	691.035	488.672	1181.56	1043.95	528.222	936.39	917.073	1051.25	808.934	445.175
328	PGLYRP2	Q96PD5	2676.72	2247.9	5924.62	2377.72	1905.64	2916.1	2515.83	2054.62	3239.7	1984.45	1496.59
329	HMCN1	Q96RW7-2	2005.33	1859.62	2340.91	1595.98	1838.67	1936.5	1577.59	2093.45	2059.83	4611.12	11.7382
332	C1RL	Q9NZP8	687.502	558.025	187.896	742.423	717.101	673.096	758.661	821.027	598.893	647.865	658.04
333	FETUB	Q9UGM5	1153.61	778.987	1129.85	568.006	1204.81	644.752	792.379	743.96	611.695	440.478	586.156

APPENDIX F | PROTEIN QUANTIFICATION (HEALTHY DEPLETED SERA)

id	Gene names	Majority protein IDs	Concentration [nM] C10_Depl.	Concentration [nM] C15_Depl.	Concentration [nM] C25_Depl.	Concentration [nM] C29_Depl.	Concentration [nM] C33_Depl.	Concentration [nM] C37_Depl.	Concentration [nM] C38_Depl.	Concentration [nM] C41_Depl.	Concentration [nM] C46_Depl.	Concentration [nM] C49_Depl.	Concentration [nM] C57_Depl.
3	IGLV8-61	A0A075B6I0	11104.2	13712.8	22413.7	10138	60866	4672.58	8533.11	9823.96	5783.27	5674.6	48447.9
5	IGKV2D-28	A0A075B6P5	50173.7	52566.6	34211.6	42236.8	46316.6	48205.4	3693.12	38129.7	25083.4	23252.1	22116.1
6	IGKV2-24	A0A0C4DH68	30950.9	28750.9	9616.78	10784.5	10391.6	29070.8	1490.25	2110.39	5482.73	4300.38	9852.68
7	IGKV1-27	A0A075B6S5	6999.22	3196.77	6814.13	9852.37	7353.55	14780.7	1547.83	2550.33	1482.24	1972.71	4396.96
11	TTR	A0A087WT59	13866.2	18994.7	27583	22316.9	18911.1	12856.8	18789.9	73623.6	35782.7	50809.5	21044.1
15	FCGBP	A0A087WXI2	1005.65	368.6	1228.29	463.477	444.11	365	884.629	1529.79	1266.55	852.007	1172.59
16	CHL1	A0A087X0M8	150.808	117.008	125.261	116.249	174.77	33.9722	150.375	135.644	141.422	82.9721	285.586
17	SAA2-SAA4	A0A096LPE2	6120.69	8571.72	10569.4	17321.7	11318.9	5569.07	9060.52	8343.57	21204	8195.2	5169.57
18	F5	A0A0A0MRJ7	1035.21	686.099	640.077	482.488	319.138	512.733	657.225	394.389	459.626	634.568	753.715
19	IGHG1	P01857	669959	770434	473255	680326	553262	626676	298979	820861	616162	613158	624910
20	IGHD	A0A0A0MS09	3601.52	68.3898	201.515	82.7553	1950.11	839.697	519.762	101.791	313.445	4912.59	2562.7
21	IGHV3-49	A0A0A0MS15	7884.98	11786.8	6856.34	11520.8	12557.2	22962	5766.15	5704.34	5828.4	1855.09	12702.7
22	PRDX1	A0A0A0MSI0	1463.58	1576.56	1478.91	1730.61	2265.76	2702.98	2525.49	2676.55	2310.78	2529.18	3020.05
23	TTN	A0A0A0MTS7	827.517	2716.49	522.294	701.436	645.094	797.488	339.691	549.151	492.286	478.336	423.708
25	IGHV6-1	A0A0B4J1U7	28252.9	14185.8	16034.8	18319.8	30662	17255.4	6213.34	10502.5	11786.6	5369.38	32259.6
29	IGHV3-74	A0A0B4J1X5	49836.3	56823.4	30220.2	46802.8	71374.6	75501.7	12394.9	30088.5	22985	23662.4	20912.2
31	IGLL5	A0A0B4J231	18868	21069.5	14922	20163.7	19604.1	23957.8	11525.2	22812.8	14193.6	18052.4	19386
34	CRTAC1	Q5T4F6	294.708	132.085	237.661	418.232	216.238	162.289	47.3492	67.2572	122.753	40.4505	266.064
38	IGHV1-18	A0A0C4DH31	14964	6285.23	34447.6	38323.9	52008.6	77961.2	31524.4	34475.5	10308.1	49437.9	45449
42	IGHV5-51	A0A0C4DH38	25918.5	25732.3	21451.6	20748.9	23304.9	34269.9	7037.88	7067.51	12506.6	11060.6	15871
43	IGHV4-61	A0A0C4DH41	38358.9	49774.7	34893.1	43038.4	40336.2	55337.5	11759.6	14948.9	17958.4	11836.7	20518.9
44	IGKV1-6	A0A0C4DH72	5706.41	6472.3	4906.46	21355.1	21137.2	7537.1	1777.42	6413.34	6385.65	3066.09	5202.78
47		A0A0G2JMB2	21448.1	20129.6	18374.2	13212.5	34380.7	67508.5	14445.8	30703.2	17641.9	64975.1	21033
49	IGLV5-45	A0A0G2JSC0	5910.99	12986.6	618.475	830.993	1769.1	1838.72	688.84	362.75	937.862	357.043	697.319
51		A0A0J9YY99	23210.6	24587.4	14021.8	17154.9	15587	23462.2	8229.48	32857.3	4424.51	9079.27	40741.2
52	PROS1	A0A3B3ISJ1	2240.99	1648.32	2187.71	2189.33	2014.17	1751.05	2726.16	2374.64	2054.07	1859.25	2401.98
53	SEPP1	P49908	1378.56	1563.94	2386.2	658.302	1492.58	1415.41	1816.23	2579.57	1794.79	1204.53	1134
55	KRT10	A0A1B0GVI3	1462.67	1284.14	1050.45	1457.17	665.713	992.909	361.373	1308.43	2012.36	1200.15	820.812
56	IGHG3	A0A286YES1	54854.5	41165.5	94874.5	92759.7	98846.3	68311.8	64356.1	96075.3	85745.7	96990.7	87531.3
57	IGHG2	A0A286YEY4	152714	192896	58882.5	90825	160142	154301	39480.9	168301	105417	85174.3	95013.3
58	IGHG4	A0A286YFJ8	42282.9	59142.2	27508	107485	24425	38783.9	7448.5	28217.9	49295.6	52082.3	94689.1
60	CFHR2	A0A8V8TQS1	74.4342	131.936	138.089	147.481	215.759	86.9372	687.785	223.715	510.409	95.415	157.704
62	C1R	A0A3B3ISR2	14.0995	12.7702	9.27117	31.1815	20.2535	20.2408	235.275	16.7986	157.766	23.5195	13.5514
64	EGF	A0A494C018	418.898	409.274	495.216	558.976	517.788	567.297	710.1	781.333	735.744	800.143	784.082
65	H2AFV	C9J0D1	24077.9	20029.7	24998.7	22841	23818.3	24179.8	30311.8	30349.8	27635.7	27562.5	24838.4
66	IGHV3-72	A0A4W8ZXM2	110715	153657	82872.4	125606	205667	168904	98230.9	108349	86307.1	136523	154399
67	H3F3B	K7EMV3	23545.1	21437.3	24185.9	25859.5	27457.7	28440.4	1594.1	42833.7	496.939	42626.2	34203.7
68		A0A6Q8PF87	81861.1	42435.3	29673	22049.4	38471.5	31736.2	23596.1	29941.8	15835.8	21142.4	27837.6

69	LMNA	A0A6Q8PFJ0	176.121	167.47	130.275	157.526	171.997	173.534	205.835	294.808	191.433	191.51	194.314
70	SERPING1	A0A7I2V2D2	7408.58	8170.38	9078.5	9004.53	11015.3	8428.95	12519.5	12232.8	12643.5	8749.1	6243.11
72	AGT	A0A7P0T8D1	15066.7	16770.6	19822.3	15559.2	14642.4	14428.8	10655.6	20900.8	16254	13054	18062.6
73	HSPA5	A0A7P0TAI0	341.181	462.455	361.577	471.795	522.056	356.955	660.941	708.52	410.724	711.039	598.462
74	PDIA3	A0A8I5KRV3	493.905	444.067	490.537	443.588	515.637	523.874	869.439	676.95	612.353	649.294	547.461
75	PPBP	A0A8I5KW61	3249.33	2654.55	6571.87	4945.81	4616.46	3055.07	11557.9	2824.81	6545.77	3696.47	2569.97
76	MYH9	A0A8I5KWT8	78.5871	57.4175	58.3443	52.1784	74.786	59.5595	107.894	71.2945	76.7016	99.3852	92.1515
79	C1QB	A0A8Q3SI33	8342.05	3117.84	3600.92	3733.02	4290.66	6778.53	8879.19	4422.35	7288.36	4983.77	5439.4
80	C9	A0A8Q3SI95	38.9844	17.5477	86.282	26.8047	94.5551	69.7138	807.63	42.3109	240.304	24.1184	48.3342
82	C5	P01031	42.4343	24.6036	42.5128	39.8725	26.0169	52.7708	120.063	59.3499	263.806	39.2539	29.3349
83	C1QC	A0A8Q3SIZ0	6881.44	5169.51	5044.29	5411.17	5489.4	6358.38	6208.65	5270.49	7455.23	3684.18	5639.58
84	CFD	A0A8Q3WKW0	118.433	109.878	160.985	215.019	141.365	136.555	454.752	112.495	465.116	129.964	147.769
85	F12	A0A8Q3WL25	42.659	168.115	36.2154	139.438	24.8699	109.616	335.972	34.3781	77.9558	54.8867	41.3357
86	C8A	A0A8Q3WL79	40.4422	90.9118	32.5241	11.5357	16.2381	18.3894	380.913	57.8661	115.734	94.5978	26.0294
88	ANXA2	P07355-2	891.195	233.981	764.434	817.392	910.172	1007.8	964.921	1316.08	884.784	1218.11	1095.42
89	IGFBP3	A6XND0	148.7	115.988	379.365	147.36	55.1239	120.129	431.086	149.154	140.159	198.735	151.575
90	APOC3	B0YIW2	270108	177167	285799	307229	146769	181796	352304	255046	304110	338147	259353
91	VIM	B0YJC4	1537.78	2141.66	1813.71	1519.78	1626.68	2555.41	2574.67	3191.55	2451.59	2874.33	2533.18
92	APOL1	B1AH94	7622.62	6121.15	7852.34	8192.6	5511.04	6062.29	7118.13	9123.71	8109.68	7986.52	6809.75
94	UBC	P0CG48	72.5002	1718.14	1971.6	1981.97	2117.28	95.0111	2417.52	2756.74	46.436	54.5542	48.5986
95	CFB	B4E1Z4	338.329	250.852	448.784	360.631	467.33	411.443	1588.92	602.013	1214.71	622.79	438.5
96	FGG	C9JEU5	181.505	179.619	98.4801	137.493	437.489	60.0483	213.837	144.682	242.161	279.013	272.366
97	APOD	C9JF17	29994.8	28508.3	15530.6	20843.3	23325.6	20797.1	37230.1	18879	19986.7	19562.2	23037.3
101		CON__P00761	78629.8	60836.2	49347	59789.6	59138	75918.9	55772	41645.5	54684.4	35063.9	61231.8
104		CON__P02768-1	24164.7	21908	51449.5	48881.1	28648.2	44254	268660	47766.5	138539	78269.5	42281.9
108		CON__P13647	191.157	143.676	221.407	710.465	136.662	149.95	178.18	96.0183	224.107	204.642	189.206
109		CON__P15636	27696.9	17760.3	13392.3	12078.5	11003	14050.2	15900.1	16161.7	11712.6	18501	16981.3
110		CON__P19001	516.969	294.332	255.833	470.35	359.571	457.213	631.453	701.586	339.007	671.295	384.133
111		CON__P35527	1267.38	767.304	1084.77	582.483	192.462	489.552	264.243	683.825	628.742	1170.61	1098.25
112		CON__P35908v2	474.239	140.81	90.6397	132.001	22.9537	94.8524	19.0493	46.7547	154.678	53.0239	42.5339
115		CON__Q32PJ2	2561.23	9162.91	13111	4930.02	5521.52	2135.51	7691.51	14123	14105.1	1653.76	10167
118	GC	D6RF35	578.634	166.085	629.555	487.264	719.003	994.9	7718.82	670.307	3841.38	618.786	531.923
119	COL12A1	D6RGG3	55.4715	4.67923	65.4328	56.1293	65.0152	7.56069	74.0014	16.2809	73.2957	79.6518	73.4007
120	CA1	E5RH81	1088.04	4438.94	4584.66	3812.01	1182.66	8786.69	724.333	1688.89	1129.86	662.045	724.072
121	PROC	E7END6	155.74	51.124	69.6946	158.729	235.902	88.8708	54.1418	95.0136	90.8477	222.97	85.0956
123	CFI	G3XAM2	41.2909	13.8201	59.4093	49.3275	55.3146	25.9435	467.307	80.2572	367.353	99.0195	62.6277
125	CFP	P27918	203.815	294.595	315.263	175.438	253.293	156.118	416.425	311.142	305.065	308.022	280.2
127	CLEC3B	E9PHK0	9586.13	6417.1	9398.51	10920.7	11304.8	7284.11	12047	14108.4	15387.5	11454.1	13348.7
128	HSPA8	P11142	322.899	489.752	627.286	690.829	711.344	350.85	845.578	1117.66	786.359	1060.56	909.208
129	C2	F2Z3N2	327.108	346.542	543.446	625.484	478.716	395.835	594.569	844.618	1169.36	541.217	667.063
133	SERPINA10	G3V2W1	643.332	542.722	1332.82	900.034	1036.69	1078.94	339.58	1151.98	616.781	1219.69	755.009
135	MST1	G3XAK1	39.0242	57.7742	162.759	43.4805	50.0722	21.9956	87.679	62.2658	146.771	58.3918	155.966
136	COMP	G3XAP6	1211.44	415.647	476.222	554.775	450.412	540.594	509.585	703.541	539.936	573.761	640.665
137	KLKB1	H0YAC1	62.1036	1004.78	183.026	35.7072	89.9011	773.553	503.487	189.319	434.177	358.18	380.135
138	ALDOA	H3BPS8	1197.43	1038.17	761.621	806.277	837.205	921.851	1110.92	1566.56	1351.98	1017.63	897.554
139	CETP	H3BRJ9	4535.24	35.351	9886.33	4778.59	12185.7	4172.99	9067.18	7377.05	5295.92	5009	6304.44
143	SHBG	P04278	391.083	318.193	1485	308.42	824.18	224.99	284.523	282.767	285.115	54.1499	519.653
144	APOC4-APOC.	K7ER74	55874.1	32759.1	63555.5	66810.3	44089.9	32485.6	66072.1	53667.1	67869.8	49912.6	71236
145	APOC1	K7ERI9	343063	329737	544709	656518	529082	239217	563430	316119	369587	650773	422175
147	CD5L	O43866	3742.92	2271.2	2774	6023.01	6277.64	3538.14	6507.99	2701.51	6942.19	5942.74	9590.75
148	HIST1H2BM	Q99879	31532.6	23806.8	26201	24521.5	30911.5	29583	42363.6	43022.4	29994.9	48092.4	37682.1
149	FCN3	O75636	406.515	178.643	624.762	122.126	202.69	573.655	988.233	128.694	494.808	107.4	179.648
150	ATRN	O75882-3	354.383	328.196	319.555	299.07	222.228	284.368	195.497	277.756	343.215	169.749	195.865
151	APOM	O95445	3749.75	3203.34	6646.4	10360.9	7393.47	2821.49	7271.77	17978.2	15870	11186.7	6764.15
153	CP	P00450	12737.4	13402.4	28670.5	15612.8	18516.3	9263.47	17643.3	17806.1	11945.5	17941.9	13873.3
154	F2	P00734	13336.2	13734.6	11823.5	14261.4	9944.23	14083.4	10262.8	9124.65	10982.4	8068.32	9462.05
155	HP	P00738	147551	91874.7	133753	93550.4	93037.1	151512	146380	312355	304685	326925	257849
156	HPR	P00739	4094.55	1931.61	2781.76	7271.41	2107.82	3395.18	6494.08	9965.85	9416.68	8254.66	7659.29
157	F9	P00740	436.482	564.158	789.985	684.258	613.429	267.206	813.79	426.986	665.295	398.082	920.347
158	F10	P00742	718.615	898.605	1198.52	918.234	676.803	601.151	879.268	739.004	848.226	686.082	599.279
159	PLG	P00747	76.8893	66.7529	56.7283	11.5932	33.6691	88.1584	1064.19	15.6684	901.979	47.9882	19.889
160	SERPINC1	P01008	4403.56	1938.96	3994.19	3815.69	5345.93	3463.88	6695.15	4224.34	6594.82	2440.36	3928.75
161	SERPINA1	P01009	118327	138014	234906	164495	224467	101600	286334	123382	106930	161267	190816
162	SERPINA3	P01011	22609.8	24676.5	36153.3	11699.9	25924.4	15106.7	6256.42	3517.65	3545.02	7703.99	3263.08
163	A2M	P01023	28068.7	20787.3	33780.2	21965.3	26550.4	13937.6	19617.2	32055.1	28951.3	25361.9	21612.3
164	C3	P01024	8376.86	5439.99	15323.5	8891.08	9447.84	6379.73	7490.51	5851.54	8188.84	6046.97	9594.42
165	KNG1	P01042-2	3724.14	2695.88	3882.35	3265.31	4214.92	3674.92	11550.1	5056.93	8677.1	4817.16	5843.23
167	IGJ	P01591	29781.2	18784.5	22353.9	30026.2	33110.4	36043.3	28057.9	18885.3	23679.9	63501.2	29264.5
168		P01594	8645.46	9685.95	6644.51	9957.86	8311.59	11126.3	311.882	3559.78	4141.76	1869.34	4378.63
169		P01599	4998.63	15782.5	8601.25	22686.6	20010.3	15174.5	3694.1	8020.7	4330.51	14464.8	15336
170	IGKV1-5	P01602	38403.7	61714.8	38598.1	50272.5	63018.1	46255.8	1599.14	2806.22	17186.8	781.56	30858.7
171		P01619	164361	199686	65058.8	114488	105966	267736	5267.12	5682.35	40714.4	24202	34938.6
172	IGKV3D-7	P01624	63081.7	68949.1	25924.6	51331.9	72394.2	48272	2689.61	3200.07	4880.26	2217.52	21595.8
173		P01700	84309.9	110551	14864.8	21713.2	33664	108862	3874.82	26542	5870.23	4626.34	25512.1
174		P01701	4532.96	52907.7	1331.87	3509.65	19506.8	2952.04	3434.61	240.15	8505.63	227.867	7253.15
176		P01706	1267.57	3955.1	180.981	1227.34	12971	268.306	304.14	11754.9	1444.98	251.066	12180.5
177		P01714	6402.52	9248.93	5173.5	4566.97	7134.72	12683.5	267.11	2005.41	3022.15	1186.75	1754.75
178		P01715	7027.5	2497.62	1569.31	2262.91	2503.32	2344.12	1454.64	1708.75	1671.26	1234.66	1490.41
179		P01717	21285	29105.1	9065.68	22863.5	15936.5	28063.3	14347.8	10532.5	17097.6	21881.4	14972.7
186		P01780	60042.1	59982.6	24007.9	49927.8	86134.4	73995.4	23400.1	41902.3	36683.4	41203.3	37335.9
187		P01782	16979.3	14861.2	3050.3	4813.28	7855.91	16522.2	1948.09	2176.73	3814.8	1877.54	3922.72
189		P01817	1905.28	108522	1343.01	1006.39	1324.59	1519.51	174.06	1038.44	976.597	748.333	469.499
191	IGKC	P01834	1400030	1187120	825429	924611	1144770	1494390	1344880	599965	776037	1063740	1722890
192	IGHM	P01871	45294.9	26317.2	26970.2	60706.7	62423.2	37397.8	27451.3	15578.5	49615.5	33823.7	61514.1
193	IGHA1	P01876	167812	99532.9	66122.7	99534.9	172163	319236	183668	181774	90946.5	253292	83101
194	HBD	P02042	3969.69	5863.49	9356.96	3355.7	3975.66	15956	3355.99	7358.09	4669.02	1209.76	2000.57
195	APOA1	P02647	585545	547260	1098270	977800	780853	428768	841943	581625	803718	786907	718628
196	APOE	P02649	3258.8	1862.37	4415.39	4231.22	2815.73	2864.73	6582.17	2308.42	3689.32	2774.5	2372.58
197	APOA2	V9GYM3	360364	320189	389258	386821	384248	272814	594202	566358	497840	641337	505071
198	FGA	P02671-2	5831.8	5761.13	7815.29	7426.35	7277.77	4898.49	4517.76	6743.63	6455.57	8270.76	4796.89
199	FGB	P02675	102.587	64.5485	67.7066	75.8621	395.517	89.4726	105.605	109.946	207.799	166.203	156.941
200	CRP	P02741	821.665	2165.34	263.143	231.757	142.401	98.459	136.48	386.278	338.541	139.681	733.292
201	APCS	P02743	999.441	878.229	279.563	794.777	165.067	867.328	303.205	71.1915	243.75	135.987	259.297
202	C1QA	P02745	4587.09	2264.05	2974.49	3084.53	2861.65	3967.59	5351.13	3255.09	4814.03	2421.48	3257.4
203	APOH	P02749	21179.8	12087.6	24775.8	23965.3	15536.7	16613.7	29467.7	23858.6	26406.5	13996.5	20514.5
204	LRG1	P02750	9452.13	9487.45	15572.2	10592.7	12956.7	5893.69	9283.42	7667.42	8971.1	6659.08	10398
205	FN1	P02751-14	190.859	113.194	127.227	95.2444	140.592	174.671	343.448	146.071	201.909	127.827	108.028
206	RBP4	Q5VY30	27040.7	22212.6	38144.5	41194.1	28870.9	30961.7	46520.7	40936.1	39305.1	34384.1	32502.3
207	AMBP	P02760	18412.5	11683.1	17481.9	15489.8	15941.4	17980.7	20698.2	22369.3	16509.4	15429.6	12677.5
208	ORM1	P02763	202030	293807	190527	207839	199271	293312	103038	191292	263355	197797	91590.7

209	AHSG	P02765	60942.8	45450.8	98934.8	57535	61592.1	35351.7	78016.9	76376.1	48933.9	55313.1	58235
210	TF	P02787	4109.05	2839.21	4082.18	4528.65	4318.84	7406.69	36814.3	11921.8	25156.6	15505.6	11335.5
211	HPX	P02790	22759.8	16828.7	30004.3	17610.9	19272.4	24870.9	36532	23256.1	36507.7	20052.9	20345
212	C4BPA	P04003	56.439	94.3034	67.2109	81.7048	69.1802	90.9527	1076.9	92.2323	1101.47	98.6197	67.6285
213	VTN	P04004	2522.11	1511.92	3195.47	1731.12	1416.73	2163.75	4354.21	2284.01	3785.97	1614.09	1636.2
214	APOB	P04114	2569.62	1651.5	2737.94	1781.07	1994.62	2065.63	1915.22	1998.45	2376.76	1555.94	2382.21
215	LCAT	P04180	1085.07	917.716	1367.34	1220.62	1111.31	844.109	957.835	1642.08	1848.09	1118.92	1095.53
216	HRG	P04196	24715.2	14000.3	41179.8	20069.3	18545.2	18376.8	21651.6	24038.1	18715.4	17344.3	22211.5
217	A1BG	P04217	24833.8	22893.1	31197.8	29237.7	33615	19449.5	24531.1	25469.8	31439.6	23442.1	24221.1
218	KRT1	P04264	2099.74	1541.59	1702.73	1466.71	844.778	1168.07	614.615	1530.08	1755.62	1850.46	1386.23
219	VWF	P04275	5.5344	11.7814	8.25565	5.93369	8.81693	3.77583	48.9807	5.31503	25.7088	24.2521	26.0326
220	IGKV3D-11	P04433	33500.1	52717.3	19037.5	32279.8	41663.1	39263.8	345.308	9937.78	14570.5	2349.55	19818.5
221	AMY2B	P0DUB6	548.772	473.696	565.431	572.265	646.753	637.252	1097.84	1280.79	1027.62	1302.6	1131.93
222	SERPINA5	P05154	1114.83	1384.81	1420.05	899.648	629.264	1305.84	364.052	618.394	548.755	684.032	133.804
223	F13B	P05160	54.584	76.0507	38.9054	27.9961	43.3768	45.8898	220.007	43.8104	92.8108	56.8445	207.86
224	SERPINA7	P05543	3727.53	4507.96	11863.5	3361.05	6707.47	5137.47	1620.7	824.292	1636.21	270.444	984.741
225	SERPIND1	P05546	11469.1	8868.83	13962.2	11982.4	10942.7	10355.6	8614.83	15358.1	13199.3	12595.5	9465.77
226	BCHE	P06276	2693.2	2154.63	4149.62	2131.34	5351.41	1588.15	1097.03	2913.65	3708.12	558.5	1086
227	IGKV2D-30	P06310	132282	109549	58409.4	82034.7	71209.5	122176	39981	38903.5	75321.7	63938.9	54438
228	IGKV4-1	P06312	47926.5	59233.8	42152.1	49046.3	83618.5	72526.6	2901.48	3583.23	14132.6	1730.57	24806
229	GSN	P06396	6805.66	3631.34	4123.69	4280.59	4541.71	3747.92	5556.19	5645.63	4528.42	3714.69	5519.88
231	APOA4	P06727	11488	11611	18664.4	11836.3	9477.85	11398.9	22099	21782.3	19916.9	5034.66	18557
232	C8B	P07358	70.5657	131.444	83.5693	26.0498	65.7716	92.0185	519.742	62.0028	351.783	85.9113	126.067
233	C8G	P07360	588.206	79.2537	477.379	483.498	413.064	520.338	965.581	248.206	825.475	192.376	204.086
234	TUBB	Q5JP53	515.549	383.149	336.816	424.626	394.936	432.103	617.438	580.464	501.512	582.474	792.965
236	HSP90AA1	P07900	513.081	407.113	423.657	454.311	452.965	498.677	570.062	248.846	516.075	1013.04	517.05
237	UMOD	X6RBG4	3008.91	2605.6	2826.22	3089.5	3324.04	3640.75	4973.49	5034.88	3956.49	5031.89	4006.95
238	THBS1	P07996	27.3067	32.0678	56.3307	42.9869	72.378	38.4319	178.919	81.2349	68.16	40.4896	50.3706
239	SERPINA6	P08185	5942.45	5724.12	18448.5	9378.75	11025.3	5987.28	4058.96	8424.49	10033.2	5280.86	7171.45
240	HSP90AB1	P08238	265.093	240.447	274.272	243.935	256.009	294.773	448.807	356.769	290.092	379.572	315.02
241	LPA	P08519	189.088	13.4754	149.742	421.609	109.851	162.69	80.7098	117.918	176.643	11.6742	62.0231
242	CD14	P08571	115.852	46.4901	166.151	34.9464	29.4052	162.871	68.7568	193.705	219.046	34.8544	66.4318
243	CFH	P08603	166.909	41.7329	122.683	58.1516	121.303	163.215	1129.16	118.077	646.23	135.236	26.2178
244	SERPINF2	P08697	5619.24	5181.84	7845.42	4604.53	5533.21	4194.91	3826.93	4455.05	3508.17	2825.57	3494.25
245	C1S	P09871	489.964	143.282	1714.37	22.1168	473.291	607.637	4727.65	1744.97	1851.25	223.411	39.2263
246	C4A	P0C0L4	1215.89	1550.53	1159.95	1486.17	1422.24	2126.14	409.828	1955.31	886.21	874.457	426.143
247	C4B	P0C0L5	5747.12	4073.63	6152.19	4730.89	4856.79	4158.34	2554.74	3607.1	3510.43	3086.59	1560.28
248	SAA1	P0DJI8	1512.8	5640.23	5366.58	1832.76	2242.42	1267.64	4634.85	611.955	86416.6	480.486	847.175
250	IGLC6	P0DOY3	1226010	1314160	651514	926992	1033470	1272000	738353	817817	869267	747874	1064890
252	HIST1H1E	P10412	6926.21	5992.5	7063.53	6731.57	7286.07	7891.33	11449.5	11966.7	8912.79	8277.14	9530.67
253	opn	Q3LGB0	7521.55	7115.72	7043.09	7518.97	8545.3	8711.66	12258.1	12649	9930.61	13124	11267
254	C7	P10643	15.5303	8.95831	13.7605	19.3896	6.97438	18.0487	224.594	18.0511	109.118	20.1623	123.016
255	CLU	P10909-4	2367.62	1107.82	1864.25	1209.35	1599.39	2446.09	3157.02	1641.49	3016.91	2139.94	1535.16
256	MBL2	P11226	176.982	1487.19	2111.42	1550.72	426.311	203.715	3973.96	490.221	555.063	1050.68	7541.35
257	COL6A3	P12111-4	76.1418	81.2472	69.0425	62.1329	83.3867	91.2926	107.712	104.632	91.9426	107.949	90.737
258	C6	P13671	10.8868	48.518	33.51	65.2302	1.84855	64.8109	95.726	18.5262	59.6599	3.99089	66.2364
259	CPN1	P15169	139.395	114.805	200.789	195.684	260.255	185.076	442.311	335.213	413.85	284.436	438.628
261	IGFBP2	P18065	45.9887	164.369	178.812	257.456	219.208	154.286	389.123	134.19	146.013	147.933	127.723
262	LBP	P18428	236.7	218.119	284.723	256.729	275.483	204.186	845.434	440.104	419.079	279.11	63.1067
264	ORM2	P19652	114846	142020	76746.5	100420	63121.6	77811	99693.9	163065	86647.1	86187.5	76168
265	ITIH2	P19823	9552.04	6547.72	14078.7	11276.5	10662.2	7948.79	13125.8	14171.5	14180.5	9982.09	11536
266	ITIH1	P19827	10154	8731.14	16279.6	13687.3	12258.8	8567.33	16445.8	17275.9	17382.4	13164.1	12990.4
267	PZP	P20742	80.2591	75.5717	1837.14	41.0989	1611.44	285.819	63.4408	101.209	496.465	34.0871	41.0946
268	C4BPB	P20851	596.392	495.197	542.007	588.364	594.035	548.168	1459.68	866.474	1328.64	630.707	1033.48
269	GPX3	P22352	2126.03	4231.99	2417.09	3065.32	4925.72	1779.98	6804.09	3228.7	2888.34	3772.32	3804.79
270	CPN2	P22792	465.343	318.226	368.688	479.285	936.62	720.518	1315.1	1186.02	1244.05	971.956	1380.94
271	PROZ	P22891	78.6564	36.4266	55.2559	140.717	135.365	63.4862	92.8599	123.679	152.141	133.518	90.5704
274	FBLN1	P23142-4	26.3548	76.6235	55.1641	30.7128	701.635	132.325	722.805	43.9626	204.475	854.377	136.578
275	AZGP1	P25311	6488.79	3386.74	1996.4	2288.93	2083.66	4922.99	553.45	2217.8	1882.61	1287.07	1181.27
276	PON1	P27169	17879	12990	31251.8	16178.3	20826.2	15738.4	23492.7	27441.2	21025.9	20312.2	21304.1
277	SERPINA4	P29622	3652.98	3362.27	6180.71	2683.82	4524.57	2481.55	967.958	39.2435	197.778	133.437	437.567
278	CDH5	P33151	440.023	337.638	633.084	202.033	297.114	268.012	630.269	486.48	289.284	282.467	474.008
279	IGFALS	P35858	119.697	26.0271	104.689	58.49	58.663	116.93	139.527	98.5721	165.622	71.0433	289.953
280	SERPINF1	P36955	5149.87	3616.58	7401.23	4724.39	3988.97	5022.16	4493.39	5648.63	4312.83	3360.6	4311.65
281	PTGDS	P41222	1707.42	1126.27	5323.8	1534.72	1932.47	1153.49	2427.63	1974.14	1759.42	2604.89	3143.92
282	BTD	P43251-4	422.42	1635.65	2029.12	1408.69	1766.61	1264.43	1073.91	836.905	1227.55	539.9	1477.88
283	AFM	P43652	189.476	105.425	364.164	81.6263	102.224	307.432	769.445	418.931	780.401	83.5779	125.521
284	MASP1	P48740	236.612	154.907	176.216	137.946	132.766	175.348	256.579	217.094	178.781	216.244	161.622
285	LUM	P51884	3203.64	2039.23	3259.46	3237.3	2111.32	2470.45	5782.79	6221.48	5499.47	2962.43	2825.35
286	PLTP	P55058-3	854.054	581.738	672.861	748.347	562.942	547.97	396.831	533.159	516.301	110.999	109.072
287	ACTB	P60709	10091.4	9015.6	8193.5	9928.83	11030.5	11979.7	16552.3	17608.4	13180.3	15905.6	13190.8
289	B2M	P61769	3405.92	2130.22	11699.4	5740.22	5888.42	3511.22	8869.76	7139.95	5097.03	4956.64	5978.72
291	RPS18	P62269	636.255	694.463	890.243	895.836	631.744	687.819	1139.92	85.9534	1044.6	1089.96	1072.51
293	HIST1H4A	P62805	51926.1	54495.5	60298.6	51294.5	56555.4	50768.6	77758.3	73112.9	56282.2	61529.6	61268.4
295	HBB	P68871	79409.2	101280	174443	92125.4	90630.9	237844	96930.7	158284	87958	39210.3	71433.5
296	HBA1	P69905	97019	120794	211254	100700	109260	244876	111058	205902	117014	64021.1	79984.8
297	GPLD1	P80108	184.438	197.761	245.482	223.885	167.299	203.292	435.077	211.308	297.244	205.974	314.585
298		P80748	71973.9	76401.2	30591.5	60211.8	34535.3	94697	568.065	31873.9	24015.7	30771.7	18595.9
299	HSPG2	P98160	172.14	144.276	152.362	236.488	258.076	272.919	245.582	375.298	276.799	352.818	282.544
300	CFHR1	Q03591	153.762	223.23	92.3178	247.769	133.145	169.572	1602.02	468.732	318.542	181.08	137.597
301	HGFAC	Q04756	205.759	90.0243	68.1875	32.1027	119.594	243.297	183.783	182.833	136.462	42.8591	185.381
302	ITIH3	Q06033-2	179.766	130.899	499.682	135.176	296.135	115.371	457.635	189.964	531.463	361.727	196.719
303	LGALS3BP	Q08380	4309.29	620.676	1912.07	1220.5	1579.11	1063.35	506.85	918.248	928.09	352.109	1043.17
304	EFEMP1	Q12805-2	469.71	221.531	284.91	197.917	207.865	245.12	199.691	273.887	191.693	234.869	154.52
305	SPP2	Q13103	418.981	258.891	304.24	383.365	141.691	328.446	160.541	388.793	489.029	285.975	320.053
306	APOF	Q13790	5610.73	3730.15	5142.2	7794.53	6848.38	3910.59	12411.2	6590.8	9494.96	8967.19	8397.27
307	HABP2	Q14520-2	47.656	40.0313	38.2888	93.7155	60.3394	50.488	198.13	66.7131	291.39	81.1292	35.2897
308	ITIH4	Q14624	11447.2	8934.78	12203.2	9136.79	9346.88	10940.8	3522.37	5582	7523.66	6705.44	3555.7
310	ADIPOQ	Q15848	4033.25	2413.45	1114.47	4091.81	4841.85	2117.22	452.575	1998.59	646.914	1380.16	1850.35
311	ECM1	Q16610-4	82.8936	40.0806	144.116	19.88	165.079	75.7455	164.69	101.608	136.799	20.9284	54.4797
321	WHAMM	Q8TF30	25234.9	24809.4	17250.6	21392.1	27728.6	27257.8	19789.3	10399.9	14261.3	2145.16	27492.3
322	RYR2	Q92736	2072.32	2425.85	98.8747	483.584	490.432	131.073	285.861	345.94	170.645	346.825	481.469
324	PRG4	Q92954-3	70.2643	22.9209	19.3267	27.7289	11.0771	45.3059	161.722	39.7907	56.1534	30.0806	35.6746
325	PIK3IP1	Q96FE7-4	5955.69	8419.28	9495.92	10021.4	10777.2	10167.7	12707.7	17216	12495.2	17412.1	13242.4
326	CPB2	Q96IY4	1736.91	1938.87	2496.07	2119.21	2205.11	2312.94	2686.75	2477.41	2270.22	2634.13	2455.77
327	CNDP1	Q96KN2	1092.74	791.209	606.829	1755.47	1192.84	1465.18	1898.17	1723.24	1305.45	1455.18	1397.14
328	PGLYRP2	Q96PD5	1695.55	1009.03	1878.78	2608.91	979.905	2005.65	3518.29	3224.94	4180.21	2390.38	2851.73
329	HMCN1	Q96RW7-2	5.76626	3.70317	16.7611	9.84478	114.989	2.4644	5.15087	6.95635	3.85254	5.39434	13.4341
332	C1RL	Q9NZP8	439.414	248.184	400.04	376.537	448.629	408.07	463.325	141.052	61.3475	44.3179	373.128
333	FETUB	Q9UGM5	40.6054	97.5913	163.342	129.791	61.4258	77.6927	245.543	150.968	219.783	114.739	148.573

APPENDIX G | PROTEIN QUANTIFICATION (HEALTHY PELLET SERA)

id	Gene names	Majority protein IDs	Concentration [nM] C10_p	Concentration [nM] C15_p	Concentration [nM] C25_p	Concentration [nM] C29_p	Concentration [nM] C33_p	Concentration [nM] C37_p	Concentration [nM] C41_p	Concentration [nM] C46_p	Concentration [nM] C49_p	Concentration [nM] C57_p
3	IGLV8-61	A0A075B6I0	9271.81	11269.2	9282.15	9473.6	11357.6	9857.88	10341.9	980.711	9033.45	17980.1
5	IGKV2D-28	A0A075B6P5	3053.97	2819.94	1808.64	2015.67	3579.88	3043.6	1923.63	1505.12	437.334	1406.01
6	IGKV2-24	A0A0C4DH68	1666.68	997.22	727.685	318.503	3037.86	731.217	277.677	1137.14	248.975	3753.95
7	IGKV1-27	A0A075B6S5	1517.95	1404.27	505.422	559.481	1535.7	3508.96	1918.72	1951.14	1307.98	513.529
11	TTR	A0A087WT59	9782.76	13053.2	17887.8	13648.6	16734.2	18918.2	17657.2	19437.2	14197.2	17435.1
15	FCGBP	A0A087WXI2	361.625	471.3	394.324	324.795	416.953	327.609	346.514	393.983	358.983	342.757
16	CHL1	A0A087X0M8	69.5538	64.9772	40.8519	50.4802	62.8914	62.5081	27.7741	36.7085	50.6053	180.484
17	SAA2-SAA4	A0A096LPE2	3057.34	11381	11824.4	9961.54	5524.22	10470.8	8405.8	15271.2	5473.27	4878.99
18	F5	A0A0A0MRJ7	490.199	744.582	1308.12	836.117	579.902	865.301	1005.13	814.666	766.156	591.172
19	IGHG1	P01857	319101	359341	193160	297590	231358	242962	222095	194936	250348	338286
20	IGHD	A0A0A0MS09	1400.2	164.886	165.753	114.295	414.137	276.356	112.319	148.824	1559.68	1231.66
21	IGHV3-49	A0A0A0MS15	913.645	1909.48	482.065	1658.06	1492.82	2092.57	1443.9	850.898	2672.28	2846.68
22	PRDX1	A0A0A0MSI0	1757.35	1895.72	459.781	2378.43	2363.69	2229.25	2162.87	1818.79	1965.76	2001.76
23	TTN	A0A0A0MTS7	442.331	470.532	322.018	372.331	376.178	410.883	298.439	338.839	301.051	299.544
25	IGHV6-1	A0A0B4J1U7	12898.2	14194.4	14819.4	19414.8	17199	18301.4	19787.7	11687.6	9990.21	21038.1
29	IGHV3-74	A0A0B4J1X5	30898.9	23843.6	14173.4	20435	40919.8	32790.7	22075.7	16197.2	7300.66	11931.8
31	IGLL5	A0A0B4J231	7228.35	8874.81	4911.94	6641.95	7183.8	9779.39	7437.25	4811.78	8698.29	6843.14
34	CRTAC1	Q5T4F6	354.466	215.2	243.927	221.887	102.245	79.894	163.369	124.862	166.718	263.917
38	IGHV1-18	A0A0C4DH31	3075.13	3409.1	5936.17	2797.36	6834.35	277.047	353.622	318.074	4904.19	4199.02
42	IGHV5-51	A0A0C4DH38	2905.78	9352.28	6690.19	3754.67	4831.49	9657.42	6562.74	1750.82	1739.66	5181.09
43	IGHV4-61	A0A0C4DH41	14470.9	14646.8	10105.8	13175.5	13257.7	18947.3	9431.93	9582.19	5231.7	6222.65
44	IGKV1-6	A0A0C4DH72	2571.71	3294.05	2505.52	5277.19	4456.3	3891.27	4645.21	356.537	1339.36	3231.2
47		A0A0G2JMB2	9113.4	11071.6	9627	6810.44	16246.9	35861.1	12957.9	6837.81	13551.4	9407.07
49	IGLV5-45	A0A0G2JSC0	509.75	950.943	818.288	303.365	464.337	619.464	464.78	488.212	429.256	608.173
51		A0A0J9YY99	12816.2	12815.7	9416.82	11811.9	8887.2	8511.4	40476	426.176	5580.28	19605.4
52	PROS1	A0A3B3ISJ1	2353.93	2612.06	2545.1	2602.31	2223.89	2401.22	2353.38	2040.23	2229.19	2876
53	SEPP1	P49908	82.3206	485.454	54.3088	68.6869	385.32	91.4356	157.004	261.65	209.008	74.2872
55	KRT10	A0A1B0GVI3	877.904	687.255	790.359	1081.78	389.407	862.641	447.749	467.219	207.322	744.502
56	IGHG3	A0A286YES1	40712.2	22102.1	44331.4	44175.3	54656.3	31478	33515.7	36441.5	48155.5	59491.8
57	IGHG2	A0A286YEY4	52315.9	78572.7	19028.5	31277.1	55722.8	38960.8	33461	24884.2	33897.8	60752.9
58	IGHG4	A0A286YFJ8	13563.6	14670.3	8071.97	33653.6	6373	11660.4	9554.36	12029.3	14965.2	35058.1
60	CFHR2	A0A8V8TQS1	2037.22	1177.54	2868.87	1967.47	2307.55	1476.45	4098.18	2806.37	2031.47	1643.18
62	C1R	A0A3B3ISR2	4684.59	3209.72	4125.93	4261.7	3385.52	4123.09	4559.57	4702.27	2681.05	3252.74
64	EGF	A0A494C018	379.578	423.779	454.486	591.014	562.569	351.689	562.879	491.404	529.17	514.887
65	H2AFV	C9J0D1	23685.3	23977.7	26609.6	27443	26527.1	25356.6	27404	27158.3	826.217	639.405
66	IGHV3-72	A0A4W8ZXM2	22285.8	34688	12169.6	26443.3	47908.8	42785.7	19352.6	14590.2	27028.9	23524.2
67	H3F3B	K7EMV3	411.464	972.905	1037.19	1127.41	579.887	2192.44	1153.44	313.476	1076.72	1042.4
68		A0A6Q8PF87	12715.8	15808.8	6377.17	11478.5	12102	12652.6	16472.6	7334.66	9898.96	11304.9

69	LMNA	A0A6Q8PFJ0	230.919	28.5617	208.962	46.56	238.269	221.045	219.422	226.356	212.396	109.796
70	SERPING1	A0A7I2V2D2	15613	15313.3	20715	26125.2	22843.4	19205.1	17135	19917.1	14920	13561.9
72	AGT	A0A7P0T8D1	4687.37	5675.05	14844.3	7625.64	5727.91	7230.43	5851.03	6615.8	3152.74	5348.93
73	HSPA5	A0A7P0TAI0	223.912	260.045	321.117	336.902	335.625	306.08	307.876	275.768	236.078	283.073
74	PDIA3	A0A8I5KRV3	436.891	287.162	468.742	586.345	517.762	444.25	518.146	476.359	413.288	470.786
75	PPBP	A0A8I5KW61	24658.5	24534.6	41424.2	49449	32942.8	36351.7	31028.9	32311.9	47786.3	30103.2
76	MYH9	A0A8I5KWT8	53.1231	71.5122	56.1068	72.0321	68.9748	61.5948	63.5065	60.9911	67.1077	51.9172
79	C1QB	A0A8Q3SI33	22600.3	21965.4	24763.8	23566.1	22689.3	29535.4	21521.2	21416.6	13009.7	15514
80	C9	A0A8Q3SI95	6199.6	7725.48	7969.83	5947.24	7973.17	5671.77	6788.56	5958.7	7265.52	8184.4
82	C5	P01031	1798.16	1892.32	2429.97	2025.44	2228.46	2067.1	2228.32	2314.14	2379.65	1798.99
83	C1QC	A0A8Q3SIZ0	19988.5	17629.2	19664.5	18410.3	16834.7	21753.9	18269.8	18219.5	11706.7	16124.8
84	CFD	A0A8Q3WKW0	2965.07	2017.09	2970.2	1915.75	1477.88	3080.86	3375.35	2292.17	1887.2	2890.29
85	F12	A0A8Q3WL25	3942.16	2940.28	4322.76	3819.04	3729.49	1680.88	3400	2205.84	2946.42	3056.15
86	C8A	A0A8Q3WL79	2264.72	4098.7	3160.51	2638.72	5052.48	4245.59	4694.23	6001.76	3377.88	4601.91
88	ANXA2	P07355-2	429.222	405.241	505.363	577.327	599.965	479.24	494.75	517.2	482.298	557.868
89	IGFBP3	A6XND0	763.283	215.863	1197.95	865.18	644.445	115.878	176.87	594.939	107.53	578.576
90	APOC3	B0YIW2	190868	186512	224411	211702	124159	198720	176414	221092	228942	183540
91	VIM	B0YJC4	977.386	1108.82	932.703	1322.99	1339.25	976.373	1296.05	1988.37	1552.42	1381.21
92	APOL1	B1AH94	3280.24	4688.46	5798.08	3760.36	3140.24	4197.34	4496.83	3130.65	3030.46	4408.07
94	UBC	P0CG48	954.329	867.201	850.235	1856.5	1764.89	986.386	789.32	1338.5	93.2748	1670.2
95	CFB	B4E1Z4	6190.05	8007.85	8472.16	6948.87	8859.1	7464.94	9441.78	7389.51	11111.9	7792.57
96	FGG	C9JEU5	226.053	272.41	401.394	371.317	276.938	243.53	244.792	82.8749	236.001	187.415
97	APOD	C9JF17	13251.5	14112.6	8124.82	10667.5	12787.8	10722.5	14236.9	11894.4	13386	12848.6
101		CON__P00761	47041.9	47249.2	41176.9	59624.6	57958.6	41226.4	62816.7	56057.2	52161.7	52654.5
104		CON__P02768-1	806530	770712	755670	767478	772537	740377	889308	831575	791907	848142
108		CON__P13647	158.992	176.5	170.162	96.0593	113.606	183.507	168.347	214.902	171.494	161.899
109		CON__P15636	16168.1	14274.7	11311.1	12755.1	10364.6	8789.53	11560.3	10727.9	9206.32	9837.06
110		CON__P19001	560.42	591.281	619.653	659.852	658.886	618.83	583.363	619.427	578.83	535.886
111		CON__P35527	541.085	426.926	368.087	784.281	522.882	545.943	446.118	124.214	138.185	690.78
112		CON__P35908v2	109.106	50.1101	79.8489	57.6353	27.8154	52.4236	59.8253	33.6465	10.9273	26.7473
115		CON__Q32PJ2	4191.48	10444.9	42.7811	4740.1	390.199	4251.59	11150.2	8631.24	631.621	4807.47
118	GC	D6RF35	40155.8	38428.4	53276.5	55191.6	53846.3	49934.6	46492	55174.8	50645.2	48912.6
119	COL12A1	D6RGG3	14.0086	8.30901	40.3115	101.204	17.4032	46.0765	10.8319	20.8554	91.2228	15.1128
120	CA1	E5RH81	170.366	281.916	480.152	405.306	368.196	438.996	676.683	355.958	736.964	266.033
121	PROC	E7END6	163.238	744.909	465.177	35.5787	98.2529	720.354	125.979	216.383	164.69	517.444
123	CFI	G3XAM2	3978.85	4354.24	4424.11	4156.87	4041.6	4083.56	5690.56	5095.37	4621.99	3602.99
125	CFP	P27918	647.377	652.788	967.201	642.627	1404.1	624.633	867.484	773.832	1152.85	1425.4
127	CLEC3B	E9PHK0	3964.73	3383.9	3376.66	3217.5	4601.95	3561.45	3263.26	4030.38	4205.77	3912.48
128	HSPA8	P11142	272.347	293.144	649.752	411.789	714.548	353.302	363.365	331.321	347.966	736.909
129	C2	F2Z3N2	686.745	611.793	1161.37	934.571	918.609	949.984	627.609	986.737	405.657	696.71
133	SERPINA10	G3V2W1	408.629	371.915	512.924	50.1373	533.012	148.374	174.574	117.483	440.799	372.008
135	MST1	G3XAK1	280.804	299.355	413.253	492.657	311.057	504.187	339.312	574.345	247.211	213.492
136	COMP	G3XAP6	292.12	208.679	187.207	267.241	234.995	224.749	258.437	230.028	234.57	228.033
137	KLKB1	H0YAC1	4355.7	3732.62	6276.93	5097.45	5321.79	4718.02	4610.99	6908.6	6252.7	6058.51
138	ALDOA	H3BPS8	802.219	261.46	834.84	995.29	1014.87	933.564	1002.97	880.134	915.519	931.985
139	CETP	H3BRJ9	150.913	45.5366	2897.25	2469.44	3618.71	126.133	2378.51	3631.44	238.999	2601.44
143	SHBG	P04278	1079.79	393.492	1803.63	539.406	1438.55	305.5	310.726	362.513	379.474	793.938
144	APOC4-APOC2	K7ER74	19257.3	15521.5	24735	19959.1	16075.9	18562.9	18729.5	21606.4	25932.7	26550.2
145	APOC1	K7ERI9	160189	134677	104617	172878	235566	118549	130750	163659	240628	296396
147	CD5L	O43866	5138.59	3782.41	3426.36	8538.75	9434.84	6077.06	2767.9	8085.15	8213.72	10842
148	HIST1H2BM	Q99879	8753.5	944.397	28536.9	9654.46	12045.8	8951.03	10932.6	9866.89	32648.2	11926.4
149	FCN3	O75636	7075.18	6159.35	5408.55	2694.12	3934.91	8424.68	9133.63	9365.95	4505.09	2475.9
150	ATRN	O75882-3	580.336	654.133	679.616	651.679	423.602	566.501	704.711	605.436	246.441	408.26
151	APOM	O95445	13250.9	15049.2	14495.5	23616.8	12217.7	13032.6	20770.6	19366.4	31613.4	18395.7
153	CP	P00450	4042.01	5201.61	9402.83	5677.97	6898.65	4033.01	4119.05	3714.12	4902.03	4863.99
154	F2	P00734	15402.7	17165.1	17077.6	19327.7	12923.9	18049.8	18547.3	23545	13001.1	13887
155	HP	P00738	139610	205090	137867	173956	246010	167902	170228	170308	349535	162150
156	HPR	P00739	6205.88	4050.28	4315.45	7453.74	2711.7	4656.73	6434.76	6206.12	7163.74	5669.08
157	F9	P00740	740.088	1235.38	1398.6	1087.23	818.758	1304.49	1038.59	1072.23	1173.8	833.233
158	F10	P00742	1796.24	1732.48	1399.51	1710.01	1068.22	1426.25	1852.19	1850.32	1475.31	1024.03
159	PLG	P00747	15053.8	13728.2	18576.9	16525.4	13385.5	15657.8	16187.8	19340.5	17676.3	13652.6
160	SERPINC1	P01008	9432.48	8504.43	8617.6	10170.3	13877.7	8126.53	8975.16	9441.13	9760.88	10085.5
161	SERPINA1	P01009	19433.4	28268.1	63975.6	14440.4	29565.3	29067.7	27631	43476.7	43101	36952.8
162	SERPINA3	P01011	2943.56	2477.39	2658.05	1981.19	2249.46	3021.97	2860.91	3474	2225.4	1666.92
163	A2M	P01023	18282.4	13047.4	18237.6	12401.5	16645.2	10290.6	15105.9	16667.9	12219.6	13591.2
164	C3	P01024	21740.2	23222.2	25860	21819.3	16431	19053.2	24541.3	26406.5	14292.4	17907.7
165	KNG1	P01042-2	31414.4	30890.9	43102.1	42036.3	40539.6	32685.1	36545.2	35977.9	35842.1	41614.7
167	IGJ	P01591	21270.1	16494.7	22417.6	30573.3	32756.6	31343.6	15330.4	24794.5	46679.3	27433.9
168		P01594	1536.65	1460.29	315.963	1247.84	1443.83	2197.18	1651.95	1232.18	1557.2	1454.42
169		P01599	2598.46	2964.57	2695.81	3377.53	3423.07	6485.2	5840	2889.18	1722.67	2410.53
170	IGKV1-5	P01602	2192.15	3182.83	1542.9	2657.33	2499.75	2949.85	3031.28	1889.23	1693.35	3072.19
171		P01619	21104.1	67057.2	8416.4	49246.3	28804.8	89895.9	22414.7	45294.1	3309.95	18885
172	IGKV3D-7	P01624	5998.52	5672.46	513.862	5189.22	5318.79	6067.49	5315.93	3910.34	2462.87	3728.9
173		P01700	9062.02	8745.71	4781.98	4998.16	4746.64	8350.44	6209.48	3929.84	5020.18	4773.15
174		P01701	3442.15	2673.26	953.014	2197.25	2873.61	3464.75	2704.57	2352.39	2534.76	3076.27
176		P01706	736.989	1284.87	794.912	896.156	2177.93	1021.75	1379.57	708.372	709.705	1457.19
177		P01714	646.294	1808.65	1610.05	420.921	1150.63	8072.85	961.69	1114.79	418.221	754.746
178		P01715	1845.53	2147.85	348.227	1029.06	2091.89	1950.18	1725.12	1393.56	1933.16	1596.26
179		P01717	5151.49	4946.44	2799.01	5590.37	4478.82	8743.38	3970.22	4165.84	17288.6	3465.98
186		P01780	25851.1	30433.4	10893.8	20362.5	40529.5	32398.1	25973.4	15490.8	14649.6	17828.2
187		P01782	8909.74	4020.6	469.456	421.757	814.684	905.524	1559.53	955.491	566.365	491.167
189		P01817	1159.63	4131.16	813.458	994.007	1652.98	716.759	513.663	303.418	209.375	248.742
191	IGKC	P01834	631938	539477	323654	440779	563236	758816	465688	409560	577141	517301
192	IGHM	P01871	18109.8	10941.7	10528.5	26337.8	25859.8	18011.7	7847.86	23738.9	13485.5	27207
193	IGHA1	P01876	128617	85151.5	48820	57517.5	101574	183734	61340.7	40600.6	123921	31747.8
194	HBD	P02042	704.95	1104.1	1015.69	1070.41	2171.87	1957.14	944.519	785.848	460.926	596.835
195	APOA1	P02647	253841	264872	363190	345059	292304	237510	236153	296124	269447	308091
196	APOE	P02649	18846.7	12322.1	15538.4	14237.5	14386.8	18697.9	14385	16228.6	9628.48	13546.3
197	APOA2	V9GYM3	251847	317864	366778	315280	336324	287546	286469	300057	446356	335341
198	FGA	P02671-2	3173.93	3928.66	3750.68	4501.91	4154.63	3796.73	3806.82	3955.69	4705.3	3635.47
199	FGB	P02675	109.167	86.76	66.9302	107.27	196.35	85.8051	165.556	77.1992	125.899	99.7599
200	CRP	P02741	349.322	710.274	440.144	266.978	150.256	213.836	142.324	619.21	454.726	305.911
201	APCS	P02743	21944.9	22855.3	14683.4	7640	5765.14	10676.7	10537	9392.07	5188.32	6679.52
202	C1QA	P02745	14294	12902.3	15945.4	14785.3	13482.7	14845.3	12409.6	13696	13051.6	12743.6
203	APOH	P02749	35019.3	30606.2	40067	36222.8	29281.1	30675.9	34752.4	23788.2	28070.7	27111
204	LRG1	P02750	3035.8	3954.62	5265.25	3876.24	4494.77	2537.91	2237.69	3688.32	1354.39	3724.62
205	FN1	P02751-14	4303.42	3029.83	3418.11	1953.86	2640.91	2889.46	3597.27	2606.91	1164.54	1593.68
206	RBP4	Q5VY30	19920.8	19313.6	26048.7	25105.1	14009.3	22288.6	17929.7	21089.1	19407.8	12581
207	AMBP	P02760	18273.5	13451.3	22139	17777.5	17338.8	15800.3	16883.3	14263.6	18620.5	13542.9
208	ORM1	P02763	100244	139649	86447.9	98622.6	85320.7	126982	75667.2	124459	47558.6	56760.5

209	AHSG	P02765	31956.1	28848.1	49711.5	32055.5	33264.4	26003.1	30803.1	25124.4	26845.8	28458.3
210	TF	P02787	123257	110230	148195	141844	125586	92853.6	128113	139369	121226	137842
211	HPX	P02790	134360	123167	154583	118087	114193	131640	137954	141144	94751	110934
212	C4BPA	P04003	17404.2	15839.5	15519.9	17380.4	19022.9	14697.4	15913.8	21352.3	17264.5	23042.1
213	VTN	P04004	19832.5	20009.7	31137.2	22209.5	14316	20038	26384	22775.2	12122.1	15111.9
214	APOB	P04114	1551.51	1533.55	1958.96	1106.6	1481.65	1941.61	1655.56	1653.32	1330.17	2124.4
215	LCAT	P04180	737.129	897.202	1135.2	1008.03	1016.39	931.366	944.056	955.692	596.996	871.956
216	HRG	P04196	7804.19	5649.85	14169.6	7096.48	8079.18	7804.55	7115.88	6603.04	5509.52	8511.42
217	A1BG	P04217	9352.75	9886.87	11133.5	10587.9	10237.1	9438.86	9702.73	13255.7	9083.29	8449.48
218	KRT1	P04264	1132.84	1102.18	1133.9	1706.11	635.291	1388.09	911.177	763.212	370.076	1409.34
219	VWF	P04275	265.308	173.238	141.628	109.83	308.825	133.385	174.677	171.209	27.0603	275.869
220	IGKV3D-11	P04433	8954.25	3823.29	1258.8	2896.42	3328.35	10300.2	2982.79	2140.77	1908.98	2331.45
221	AMY2B	P0DUB6	656.853	620.528	654.383	655.371	770.899	503.286	568.613	547.786	508.562	681.507
222	SERPINA5	P05154	107.96	359.966	310.028	372.719	446.291	344.382	324.027	324.697	314.267	333.546
223	F13B	P05160	2068.25	1067.63	1750.62	1850.44	1262.16	881.54	1701.03	1785.52	1828.52	1385.7
224	SERPINA7	P05543	105.55	81.7691	125.825	194.571	119.795	38.6216	62.3253	359.698	60.392	46.4905
225	SERPIND1	P05546	3231.13	4351.85	4595.83	4587.91	3391.26	4451.75	4350.01	4811.6	5220.49	3982.43
226	BCHE	P06276	330.013	390.552	432.548	304.068	623.456	393.307	435.843	421.2	313.597	348.071
227	IGKV2D-30	P06310	8777.1	12373.6	4964.16	21816.3	16536.2	22483.9	15372.2	20228.8	8612.35	10840.4
228	IGKV4-1	P06312	1890.57	2083.55	1644.17	2295.81	8507.74	12960.4	7921.44	1648.82	1907.4	5337.73
229	GSN	P06396	5214.97	3675.57	3339.84	3718.49	3378.86	3539.24	4153.84	3965.85	2586.3	3840.72
231	APOA4	P06727	16777.9	12491.3	16482.2	13391.5	13831.3	14020.5	13946.4	11307.3	5989.01	10770.6
232	C8B	P07358	3967.92	4857.36	6154.66	2485.37	4935.59	3236.56	4526.38	5676.11	8195.85	5235.38
233	C8G	P07360	7621.52	9257.31	9226.39	7870.36	7540.18	7788.62	10863.4	11051	6593.51	9743.89
234	TUBB	Q5JP53	384.294	361.553	389.705	485.144	493.382	421.558	439.04	456.307	441.715	462.818
236	HSP90AA1	P07900	418.93	474.112	590.49	648.472	537.329	536.37	559.456	200.128	250.367	591.856
237	UMOD	X6RBG4	2898.28	2623.86	2189.85	2996.56	2720.01	2605.63	3014.16	3148.4	1573.22	3319.28
238	THBS1	P07996	648.717	834.758	1084.75	1079.05	1014.33	865.442	1430.25	831.233	709.395	400.831
239	SERPINA6	P08185	1907.31	2712.03	6578.49	3389.02	2692.32	2453.17	2976.39	3458.39	1429.2	2133.15
240	HSP90AB1	P08238	292.235	326.721	323.227	275.34	275.014	334.763	352.053	342.177	264.822	256.795
241	LPA	P08519	1550.29	76.5817	1209.6	2968.9	799.183	1728.65	574.281	1510.03	222.99	609.072
242	CD14	P08571	1138.58	800.561	1540.59	1603.51	1344.67	1015.38	977.959	974.791	762.129	1349.54
243	CFH	P08603	8833.23	9396	11065.5	7624.71	9126.63	7458.18	11590.5	10080.3	8710.21	8942.2
244	SERPINF2	P08697	1538.48	1493.9	2083.91	1794.58	1721.29	1753.83	1453.4	1452.23	612.096	1355.67
245	C1S	P09871	46448.7	39224.1	53165.5	45868.6	38592.9	47157.7	38240.3	66476.9	49083.3	53536
246	C4A	P0C0L4	1491.92	2068.2	2508.76	3124.9	2422.44	2166.49	3787.2	2126.76	1879.68	1667.36
247	C4B	P0C0L5	7061.64	6628.98	9205.63	8795.8	8343.61	5957.56	8420.29	8078.47	7176.64	4219.69
248	SAA1	P0DJI8	1009.06	2188.18	1255.2	645.217	1109.08	732.95	369.707	32159.5	599.887	1173.51
250	IGLC6	P0DOY3	471733	536751	233569	321779	446907	573906	297750	283994	484988	372686
252	HIST1H1E	P10412	4867.28	5025.31	4926.83	6458.37	8369.08	4747.22	5797.41	6012.95	5586.42	8103.63
253	opn	Q3LGB0	4517.71	4758.14	5012.96	6921.61	6397.76	5320.3	6069.43	5929.17	6128.77	6671.94
254	C7	P10643	2011.39	2250.89	1995.39	1190.97	2726.97	1668.6	3402.98	2149.58	4096.13	1678.12
255	CLU	P10909-4	24959.5	23294.6	26789.9	24090.2	22513.2	28798	30288.9	33898.2	14628.9	19803.8
256	MBL2	P11226	288.45	165.716	496.021	231.428	277.145	212.064	143.819	445.623	327.116	2473.77
257	COL6A3	P12111-4	63.0502	56.9508	109.012	113.204	74.9236	105.503	77.6505	76.7991	59.5577	71.709
258	C6	P13671	1547.62	1231.06	1809.56	1790.84	2372.94	1635.28	1770.39	2256.32	2610.46	1983.77
259	CPN1	P15169	802.848	786.538	1399.71	1230.67	1732.92	1201.82	651.556	1091.38	956.442	1400.36
261	IGFBP2	P18065	238.299	175.41	149.802	329.775	161.8	175.153	176.156	445.145	172.207	99.1905
262	LBP	P18428	713.959	1099.78	1065.56	1025.24	788.714	708.782	1394.57	1253.72	420.275	406.135
264	ORM2	P19652	62755.2	74922	49992.9	56431.7	35146.3	40233.4	51534.7	31583.5	19402.5	37650
265	ITIH2	P19823	6462.01	5343.84	9776.1	7430.19	7458.9	6443.31	7082.69	7193.29	6284	6655.06
266	ITIH1	P19827	8860.35	8180.73	14681.7	10562	9924.6	8877.68	9846.03	10472.6	8053.72	8157.89
267	PZP	P20742	73.6748	64.5458	1003.43	16.8356	861.684	360.155	32.6244	217.973	31.9206	26.6429
268	C4BPB	P20851	4015.54	4457.81	3859.42	4825.07	4951.17	4249.67	5489.4	5615.98	4229.29	7135.52
269	GPX3	P22352	632.695	1048.51	882.548	1031.9	1125.97	1317.63	1246.77	1300.93	1229.19	1627.11
270	CPN2	P22792	3049.9	3242.69	3167.36	3428.22	3903.75	2896.85	2590.34	3133.17	3109.05	3911.21
271	PROZ	P22891	552.638	702.502	697.526	1203.58	483.066	578.479	476.507	284.381	398.304	815.641
274	FBLN1	P23142-4	17054.8	6742.22	12628	3796.54	19093.5	11729.5	17700.2	15640	8238.8	14816
275	AZGP1	P25311	1106.81	617.007	470.921	439.677	404.733	709.829	450.33	431.049	307.164	387.444
276	PON1	P27169	6256.42	5870.56	12394.1	7095.41	7369.38	8949.77	8408.18	9119.67	6829.89	8574.21
277	SERPINA4	P29622	96.6282	101.682	111.127	57.4037	98.998	105.901	78.6215	88.5479	16.259	16.7058
278	CDH5	P33151	138.257	76.1066	240.106	52.2713	30.5293	181.067	35.8195	142.645	178.969	200.514
279	IGFALS	P35858	1369.3	1306.59	3458.52	2001.96	1300.12	2454.56	969.817	2115.61	824.949	1498.94
280	SERPINF1	P36955	2140.95	2098.4	3957.91	2509.75	1957.99	3164.53	3056.79	2244.09	2328.65	2559.12
281	PTGDS	P41222	2783.7	2906.65	3336.37	368.762	3819.04	214.267	1498.62	435.389	1890.9	2822.98
282	BTD	P43251-4	246.499	390.837	598.005	533.464	359.533	519.448	576.069	538.34	90.0305	77.2847
283	AFM	P43652	7284.3	8460.11	14476.5	6526.7	5979.21	8705.7	12239.3	9898.23	5883.43	6606.9
284	MASP1	P48740	396.272	549.516	591.142	359.136	240.735	491.207	346.075	410.039	256.844	316.08
285	LUM	P51884	5324.17	3580.33	5117.11	3915.66	4631.45	4023.27	3754.58	2884.71	4905.99	2711.36
286	PLTP	P55058-3	707.51	704.801	856.775	1024.22	762.064	693.683	659.134	722.862	207.693	724.962
287	ACTB	P60709	4530.11	4797.99	8513.11	11120.9	11778	5532.95	9858.12	4311.39	9944.2	10529.3
289	B2M	P61769	1606.07	1518.89	2621.88	2416.64	2732.53	1987.45	1992.36	1178.23	1677.74	4712.17
291	RPS18	P62269	673.306	567.915	572.84	935.795	913.71	863.105	875.019	845.208	708.573	829.483
293	HIST1H4A	P62805	39473.8	52304.9	45169	58417.5	53920.2	41669.9	46381.4	43730	56461.4	48965.1
295	HBB	P68871	22342.8	49184.7	46170.3	41730	38567.4	86459.6	31812.9	21808.9	17041.3	20262.3
296	HBA1	P69905	29996.7	69453.8	72288.5	55524.5	57838.4	120031	43108.1	32658.9	25808.6	31392.9
297	GPLD1	P80108	698.748	901.247	1034.74	698.621	526.682	754.813	865.732	672.102	367.337	841.658
298		P80748	24701.8	29410.3	7745.77	13238.6	9059.03	38365	23285.5	7260.81	251.49	10412.9
299	HSPG2	P98160	7.12549	11.6788	12.9686	23.7465	129.95	5.87438	72.9222	7.46265	55.0506	211.704
300	CFHR1	Q03591	4581.38	5006.18	5524.48	7927.62	7045.88	7066.4	7888.7	4288.07	6595.9	3139.55
301	HGFAC	Q04756	409.807	353.963	624.78	603.791	525.282	491.179	519.854	589.146	514.471	476.28
302	ITIH3	Q06033-2	1296.94	831.923	2723.95	1749.43	1788.84	1384.04	1289	2527.13	2660.46	1130.87
303	LGALS3BP	Q08380	601.906	255.891	368.461	300.369	240.631	353.352	422.017	253.406	119.631	310.387
304	EFEMP1	Q12805-2	571.365	418.658	524.284	342.034	357.908	477.11	367.421	255.974	263.551	207.356
305	SPP2	Q13103	772.793	310.275	750.654	707.552	878.172	335.185	356.494	191.629	654.669	632.617
306	APOF	Q13790	3028.93	2675.52	3693.91	4938.08	5522.01	3299.08	3091.97	3751.83	4188.93	5546.77
307	HABP2	Q14520-2	2227.3	1540.88	2579.48	2210.84	1892.24	1807.99	2026.27	2341.43	1954.74	1783.46
308	ITIH4	Q14624	6471.12	5912.46	7423.16	7003.75	4647.33	6875.01	6129.54	8225.61	3101.65	2681.31
310	ADIPOQ	Q15848	864.733	672.133	404.364	991.835	2081.43	682.862	237.333	347.621	411.68	815.663
311	ECM1	Q16610-4	427.245	327.976	522.062	434.736	414.7	296.903	518.754	434.954	363.037	687.93
321	WHAMM	Q8TF30	3023.98	8035.72	1384.92	2029.35	3189.93	3818.89	2390.21	1883.92	11015.9	2295.5
322	RYR2	Q92736	1318.5	1376.45	613.772	2162.59	379.296	2315.04	1973.78	1043.41	1605.61	1104.73
324	PRG4	Q92954-3	296.077	330.266	508.078	237.559	284.749	283.618	288.346	318.349	317.623	250.993
325	PIK3IP1	Q96FE7-4	5676.6	6059.91	5908.09	7945.32	7207.33	5937.02	7423.3	6656.46	5741.93	7303.86
326	CPB2	Q96IY4	1725.38	2060.2	2483.89	1465.22	1460.34	2207.84	1654.84	1596.29	1771.51	1518.22
327	CNDP1	Q96KN2	399.676	331.222	272.565	540.362	434.662	467.695	439.134	462.954	358.059	389.12
328	PGLYRP2	Q96PD5	4027.25	3972.85	7948.14	5470.31	4291.94	4353.55	3937.56	3838.67	3696.48	3098.47
329	HMCN1	Q96RW7-2	3730.84	3415.67	2835.31	2963.99	2269.84	3851.65	4162.4	3599.27	2805.28	2542.08
332	C1RL	Q9NZP8	785.423	701.002	968.367	815.468	1308.19	630.494	898.146	130.648	913.602	155.024
333	FETUB	Q9UGM5	1630.88	1112.57	2541.33	1042.81	1419.82	1230.45	1194.37	987.748	1273.46	1276.96

APPENDIX H | PROTEIN QUANTIFICATION (MM DEPLETED SERA)

id	Gene names	Majority protein IDs	Concentration [nM] AQ01.1_Depl.	Concentration [nM] AQ01.2_Depl.	Concentration [nM] AQ01.3_Depl.	Concentration [nM] JC02.1_Depl.	Concentration [nM] JC02.2_Depl.	Concentration [nM] JC02.3_Depl.	Concentration [nM] MMB1_Depl.	Concentration [nM] MMB2_Depl.	Concentration [nM] MMB3_Depl.	Concentration [nM] MMC1_Depl.	Concentration [nM] MMC2_Depl.	Concentration [nM] MMC3_Depl.	Concentration [nM] MMF1_Depl.	Concentration [nM] MMF13_Depl.	Concentration [nM] MMF2_Depl.
3	IGLV8-61	A0A075B6I0	169.978	183.903	2709.91	2855.79	4175.09	4338.69	329.117	3478.24	3377.66	2238.29	2518.55	5015.15	2365.04	2213.14	2259.1
5	IGKV2D-28	A0A075B6P5	551.196	210.158	136.088	568.633	275.041	375.769	455.788	248.065	2028.29	16942	3641.21	3636.63	2501.59	2770.25	3087.17
6	IGKV2-24	A0A0C4DH68	363.883	218.78	149.079	2330.94	2574.84	2473.22	472.963	934.726	764.853	787.607	976.314	456.938	1019.61	817.202	1255.11
7	IGKV1-27	A0A075B6S5	493.538	477.245	771.277	2651.19	121.174	181.806	195.529	238.646	243.73	242.216	336.03	808.963	147.278	368.045	916.705
11	TTR	A0A087WT59	42175.5	47791	43920.1	20602.8	22134.3	19778.7	88104.1	48554.4	53622.1	40235.4	39083.2	37171.3	38092.3	41182.9	42179.9
15	FCGBP	A0A087WXI2	403.397	486.766	472.078	546.294	548.914	503.062	12.7914	1230.15	655.333	892.693	603.08	508.745	593.805	669.945	644.8
16	CHL1	A0A087X0M8	17.9269	45.0406	15.2166	32.8916	143.073	117.04	52.7473	76.7313	40.9799	103.681	42.1072	81.3763	45.7108	23.9508	6.79462
17	SAA2-SAA4	A0A096LPE2	2584.13	2946.97	1000.81	24901.7	20075.8	25344.1	4622.13	6761.37	5700.79	11258.7	6151.34	9173.06	7589.27	10661.6	8160.96
18	F5	A0A0A0MRJ7	16.747	681.823	725.716	1081.29	884.135	987.488	23.5345	933.951	817.007	861.308	830.469	847.962	659.341	304.938	640.926
19	IGHG1	P01857	3036400	2718280	2995190	315569	320752	333017	1804050	2321630	2270290	1549290	1531920	1543820	1915970	1719930	1714100
20	IGHD	A0A0A0MS09	127.873	73.7424	34.0303	102.252	28.3311	102.271	111.939	62.693	58.5256	24.3214	36.4644	30.719	149.701	151.634	42.3644
21	IGHV3-49	A0A0A0MS15	98.1468	205.475	332.649	3001.47	3185.68	3052.6	188.918	819.117	857.779	259.097	1102.16	860.853	342.922	182.247	375.499
22	PRDX1	A0A0A0MSI0	125.167	181.394	152.962	119.96	111.042	171.364	168.36	124.194	354.701	481.644	878.192	153.406	226.802	191.064	279.937
23	TTN	A0A0A0MTS7	1166.86	808.473	824.231	347.01	447.46	450.005	0.612914	1368.72	1477.34	786.488	147.545	760.875	1044.17	940.007	912.169
25	IGHV6-1	A0A0B4J1U7	103.379	1944.57	436.801	12125.6	409.414	11951	92.2785	306.51	195.242	120.526	2898.58	165.878	200.327	4046.89	4296.25
29	IGHV3-74	A0A0B4J1X5	1206.14	3721.06	3576.36	15695.4	15905	16667.7	7685.67	6217.08	3826.95	6818.14	8795.91	8263.89	6098.04	7918.56	7367.88
31	IGLL5	A0A0B4J231	1896.67	2157.67	1889.86	6145.35	6123.83	6121.36	191.206	5491.76	5640.9	5411.47	5774.72	5746.82	5707.55	6239.66	6176.07
34	CRTAC1	Q5T4F6	129.362	198.685	166.521	562.303	575.04	582.339	66.1898	186.631	209.11	429.252	315.802	314.669	272.726	229.073	333.706
38	IGHV1-18	A0A0C4DH31	157.507	99.2799	147.669	40647.8	38424.6	63852.3	419.167	495.96	277.142	256.593	98.131	7780.78	249.903	6428.45	311.935
42	IGHV5-51	A0A0C4DH38	1075.86	205.305	1194.49	6285.53	8160.49	7884.38	303.129	2813.63	2663.1	6745.32	2323.57	6696.87	2449.3	6362.87	6602.78
43	IGHV4-61	A0A0C4DH41	1754.6	330.427	1598.57	9686.78	10176	10850.4	526.925	2128.98	575.896	3664	4678.79	7514.85	2399.54	3242.2	2996.83
44	IGKV1-6	A0A0C4DH72	166.107	105.403	98.2211	2561.5	4793.59	2827.57	209.527	106.762	86.6643	2657.59	566.527	584.27	475.587	1983.96	222.57
47		A0A0G2JMB2	1755.09	2958.91	2945.54	10978.2	11939.5	11465.2	5302.53	5443.34	4261.54	8421.34	8950.3	8770.81	8040.63	9380.32	8483.2
49	IGLV5-45	A0A0G2JSC0	327.937	128.612	149.076	1014.59	250.474	322.369	148.119	482.82	144.982	232.997	130.218	215.698	211.052	360.005	250.581
51		A0A0J9YY99	7103.57	9921.41	8108.26	5030.43	9725.61	232.786	11218.1	13045.6	11368.5	6616.69	11015.2	11094.2	9856.73	11058.7	7278.03
52	PROS1	A0A3B3ISJ1	1346.19	1389.26	1308.62	3029.31	2959.9	2806	1711.49	1764.67	1822.83	1964.89	2135	2050.04	1801.5	1927.47	2001.12
53	SEPP1	P49908	1274.11	1362.39	1084.26	1187.22	1347.95	1151.56	65.505	1315.17	1393.71	1459.18	1115.09	1048.28	1830.79	1495.69	1529.54
55	KRT10	A0A1B0GVI3	3037.69	3083.42	2814.03	466.188	448.861	467.35	433.67	1612.37	1407.26	1149.98	1102.57	1286.97	13233	12450.5	10987.8
56	IGHG3	A0A286YES1	32569.8	36272.6	38603.7	33046.4	31816.5	34171.5	72513.9	59077.2	53732.2	59300.8	56362.8	59098.8	76392.4	84971.6	86798.2
57	IGHG2	A0A286YEY4	28776.5	35768.7	32264.4	30653.6	28746.7	30610.8	76239.2	63094.4	59601.7	57860.5	56756.8	56675.1	67888.3	62123.7	59445.2
58	IGHG4	A0A286YFJ8	3231.72	15541.2	4374.17	13444.3	12861.7	13570.2	16433	16368.2	17030.9	16732.6	17060.9	16700.8	16623.6	16881.3	16938
60	CFHR2	A0A8V8TQS1	44.7439	36.4432	94.8819	727.326	702.675	698.813	107.587	159.566	91.9755	494.512	1092.52	153.495	313.924	103.487	438.856
62	C1R	A0A3B3ISR2	62.4645	56.7994	26.0945	27.0572	35.5076	7.68376	188.27	14.9809	109.197	46.5769	84.001	20.7066	13.8675	7.25162	267.908
64	EGF	A0A494C018	34.0951	9.29222	33.2952	77.9515	27.2195	37.7813	35.5175	43.1888	12.5962	66.3398	20.0324	42.6924	14.3977	73.3147	14.2568
65	H2AFV	C9J0D1	87.5498	12111.4	64.7859	438.649	34.717	225.152	115.226	251.53	180.777	90.9139	282.762	463.467	126.942	197.98	145.424
66	IGHV3-72	A0A4W8ZXM2	18000.1	20705.3	18357.2	34763.4	33896	33282.6	4039.14	23387.2	24713.9	21688.5	23641.4	21309.6	26374.2	31424.9	30617.1
67	H3F3B	K7EMV3	958.664	656.025	415.916	378.311	478.479	1077.52	743.522	1047.94	1213.43	1059.11	717.929	393.076	1014.54	955.727	88.5446
68		A0A6Q8PF87	2746.4	5652.49	4777.23	14205.3	39815.6	10586.6	85.1902	8994.25	9123.42	10041.2	10390.7	9643.19	8772.53	8429.91	8658.9

69	LMNA	A0A6Q8PFJ0	18.7265	15.78	9.32913	74.7362	77.5401	51.6143	58.8446	32.0814	35.404	19.657	28.977	53.7387	72.1636	80.6964	51.5867
70	SERPING1	A0A7I2V2D2	4506.35	4906.31	4314.64	25146.8	26213.1	25543.9	9186.93	8965.66	8928.15	15863.7	15784.1	15463.7	9529.72	9653.5	9690.84
72	AGT	A0A7P0T8D1	16387.4	18324.2	16213.2	12627.7	11615.1	12089.5	8612.23	19097.9	19109	14365.8	13180.4	12818.6	16064.8	15895	15508.2
73	HSPA5	A0A7P0TAI0	247.044	282.897	272.416	158.642	192.721	150.875	384.622	187.628	212.617	215.477	191.217	242.488	185.637	306.892	288.877
74	PDIA3	A0A8I5KRV3	84.8999	100.803	30.3445	102.512	190.599	228.769	33.7439	110.42	77.3507	56.8505	121.014	90.0069	37.6452	199.515	51.4616
75	PPBP	A0A8I5KW61	483.769	1559.53	1490.54	1379.34	1547.01	1468.87	115.831	831.601	969.146	645.894	2652.19	599.465	238.482	1129.32	171.748
76	MYH9	A0A8I5KWT8	33.4076	9.23518	29.1068	6.59979	18.6071	40.8255	7.83928	18.4349	15.8556	46.4858	17.0916	6.45529	13.7292	20.9351	17.8191
79	C1QB	A0A8Q3SI33	3000.48	3695.96	3057.14	3736.71	2410.59	3047.65	4337.25	3532.29	3605.02	3631.37	3266.83	3281.69	4294.32	5143.51	3795.31
80	C9	A0A8Q3SI95	120.536	141.469	152.054	235.659	197.985	263.464	134.922	32.5805	53.0179	216.317	241.826	255.814	97.0291	48.5099	144.883
82	C5	P01031	58.2418	52.4541	70.9435	85.1972	122.195	92.0194	48.3963	57.6983	52.0864	218.414	279.984	151.939	27.9015	61.3176	39.8338
83	C1QC	A0A8Q3SIZ0	6259.86	6653.28	6383.15	3811.6	3545.89	3660.3	12332.4	5562.65	5940.19	7373.22	7048.55	6925.36	6492.41	7529.27	7564.33
84	CFD	A0A8Q3WKW0	338.951	683.809	375.955	1284.52	1829.65	1135.36	267.822	422.559	600.59	1776.18	1854.54	1095.24	482.558	443.199	592.147
85	F12	A0A8Q3WL25	58.167	41.0461	101.071	34.4977	41.2162	74.5123	55.6068	23.351	186.645	90.6171	54.6271	22.0652	47.1807	61.035	76.9155
86	C8A	A0A8Q3WL79	44.8652	25.5838	62.5997	127.916	20.2581	41.5935	53.6192	32.1403	53.7812	96.0258	33.8708	40.5973	30.9685	119.29	15.7648
88	ANXA2	P07355-2	53.5697	160.33	36.4296	81.706	85.1252	100.373	88.3845	81.1028	60.5321	33.1953	38.071	55.0249	109.306	176.547	34.5612
89	IGFBP3	A6XND0	69.98	50.8713	40.0992	145.382	372.723	151.516	84.9975	80.5796	319.674	284.784	293.085	30.7668	104.381	55.1683	157.19
90	APOC3	B0YIW2	133932	145996	125435	277615	284911	263711	454112	151684	151267	235305	236010	195241	179772	198666	209131
91	VIM	B0YJC4	120.175	218.997	100.215	152.641	100.884	91.5264	54.5535	189.587	134.295	136.536	121.941	166.906	137.928	96.3164	57.829
92	APOL1	B1AH94	1895.26	2443.34	2326.18	7192.44	7197.44	7639.06	5220.89	3354.22	2988.94	4183.38	4183.45	3914.49	3541.28	3741.46	3553.73
94	UBC	P0CG48	584.478	888.891	20.3624	481.978	47.9186	442.757	67.6604	886.792	873.667	664.514	81.1247	65.9953	49.6593	866.957	31.8055
95	CFB	B4E1Z4	233.495	264.078	226.867	833.824	841.55	840.447	199.581	275.047	218.917	1255.85	1289.26	1280.15	305.562	343.8	322.571
96	FGG	C9JEU5	472.22	548.651	555.308	1177.98	848.789	1250.72	101.384	1027.04	1304.13	1071.42	1297.63	1027.45	1091.26	1101.93	629.291
97	APOD	C9JF17	15140.4	18147.8	17011	37345.6	40661.6	40258.4	27636.6	19898.2	22088.9	33311.6	32600.4	31574.4	31756.6	33712.3	32415.9
101		CON__P00761	168914	189936	177339	28999.2	28149.9	31980.2	330937	120071	102421	72765.2	74461.3	77809.4	86898.9	89739.7	91925.3
104		CON__P02768-1	75626.4	75598.7	66682.8	96441.7	91835.3	93046.7	46104.7	57233.6	57911.3	113415	116496	122924	67061.3	62052.7	65131.4
108		CON__P13647	177.792	240.807	216.232	37.9901	83.0858	35.3204	51.9989	88.1451	58.1677	117.664	84.5753	51.6626	2776.86	2823.24	1175.7
109		CON__P15636	48417.6	50576	45000	14820.4	15500.2	15607.2	39533.4	34206.4	31314.2	29774.9	31529.1	30681.1	29764.8	32025.3	32242.6
110		CON__P19001	83.5094	274.727	48.5473	203.775	84.4462	45.6389	109.352	46.263	37.7617	92.7824	104.1	57.4382	78.7295	63.9121	43.0088
111		CON__P35527	1487.13	1698.2	1424.15	82.1893	143.515	115.169	262.405	233.336	168.206	108.657	288.061	260.246	10968.5	11764.7	9864.55
112		CON__P35908v2	576.85	1421.49	1233.89	36.0541	30.835	34.5423	58.8652	536.03	238.064	373.808	160.638	138.167	12547	15774.1	9407.59
115		CON__Q32PJ2	3162.33	4137.57	3680.95	20521.8	20572.5	20587.9	5345.27	6930.8	6996.62	17601.4	15032.3	13604.9	10484.2	11250.9	8440.3
118	GC	D6RF35	1562.82	1927.52	1703.03	1447.9	1487.33	1422.04	654.483	838.005	984.424	1921.88	2026.15	1872.81	982.398	991.238	1046.1
119	COL12A1	D6RGG3	10.8775	35.4756	30.7249	44.138	26.5418	8.67854	8.32716	7.12466	3.03368	7.19608	9.50172	10.0374	13.9663	9.42128	25.233
120	CA1	E5RH81	350.203	487.571	117.504	400.687	390.429	278.874	140.678	439.935	550.764	127.001	747.988	302.278	622.908	704.77	667.264
121	PROC	E7END6	97.6879	100.842	38.0558	51.7149	120.904	23.7055	94.3542	150.027	41.1428	53.1145	68.814	135.795	210.865	141.244	69.4771
123	CFI	G3XAM2	57.2944	51.006	32.1832	53.4549	78.7576	68.5334	78.5511	95.7104	67.4366	165.387	180.85	162.007	62.2102	71.0363	26.0168
125	CFP	P27918	211.69	45.0711	68.957	103.447	140.479	45.3565	263.525	73.1526	209.665	179.171	174.793	172.056	28.4611	149.252	190.648
127	CLEC3B	E9PHK0	3799.58	5406.32	7076.12	12877.4	13250.9	12991.2	3231.18	7349.02	9629.56	9306.41	8752.75	8872.94	9183.66	11049.6	9758.78
128	HSPA8	P11142	19.8674	111.709	45.5065	38.5451	32.5851	27.4934	197.629	75.845	87.6051	88.0598	87.0071	107.81	239.201	38.4942	57.1997
129	C2	F2Z3N2	56.7019	384.628	325.387	1014.25	1000.52	798.859	497.254	602.609	521.903	1013.02	1113.82	1100.93	442.4	544.754	328.498
133	SERPINA10	G3V2W1	664.112	759.34	583.537	815.167	689.868	558.293	1594.63	863.393	827.363	709.055	828.872	708.421	875.27	813.97	808.184
135	MST1	G3XAK1	23.0112	65.1172	50.7644	46.3024	36.1628	53.3368	74.3298	59.4326	64.3274	21.3855	94.6469	64.7087	20.2447	21.3521	32.1319
136	COMP	G3XAP6	139.61	168.07	130.931	386.176	534.114	596.98	527.398	220.67	131.758	239.51	280.169	276.278	219.647	275.69	290.198
137	KLKB1	H0YAC1	43.7727	65.0006	130.899	117.64	189.253	713.694	42.8468	720.397	1527.29	445.705	275.203	1008.35	570.929	301.347	541.428
138	ALDOA	H3BPS8	35.6013	42.2289	221.298	259.003	60.0019	186.321	106.618	127.21	168.226	117.094	214.507	143.935	206.787	191.648	289.026
139	CETP	H3BRJ9	128.012	52.1442	85.6016	10469.2	9384.03	9754.55	127.031	57.4451	262.888	5174.22	5046.46	4716.8	4186.12	4502.52	4561.78
143	SHBG	P04278	55.3037	52.6581	350.335	397.303	602.663	321.548	135.717	133.833	469.905	281.788	433.172	80.2488	95.2621	343.178	453.155
144	APOC4-APOC2	K7ER74	35559.4	36738.2	37824.6	62759.7	52055.5	50606.5	59066.2	43589.6	39654.7	37884.8	40057.6	33211.3	43283.8	39235.5	40235.8
145	APOC1	K7ERI9	198084	158097	144382	441532	441994	455069	64203.7	186710	162859	175893	179580	182313	190125	256105	211479
147	CD5L	O43866	1120.97	1235.5	1292.29	795.687	908.146	802.783	1215.5	1191.48	1302.08	1175.89	979.07	701.434	1211.1	1206.21	1176.09
148	HIST1H2BM	Q99879	11295.7	5305.2	4435.24	1484.47	969.015	1053.73	639.127	3637.41	4939.33	2661.83	2810.63	3851.31	4610.24	7302.23	4439.17
149	FCN3	O75636	164.051	89.2078	597.103	215.347	729.223	182.602	57.3153	100.139	518.23	482.433	435.659	743.32	80.3541	79.7542	53.933
150	ATRN	O75882-3	107.408	135.076	106.913	297.575	316.068	302.448	74.7654	129.878	147.033	243.812	292.124	278.228	160.197	178.433	165.634
151	APOM	O95445	4286.4	5008.29	4611.33	13719.9	11579	15075.8	206.217	7110.05	8059.94	14212.5	11268.6	12436.9	13012.7	15035	13951.2
153	CP	P00450	11082	12428	11134.3	21136.3	21004.1	20447.2	22886.9	14678.2	14274.7	15289.9	15900.7	15774.1	15111	15357.1	15437.8
154	F2	P00734	11635.3	14107.4	11313.2	11548.7	10866.4	11492.3	11167.7	9983.48	12106.6	11935.1	12203.4	10622.7	11647.4	13345.8	14136.2
155	HP	P00738	43791.3	47234.4	42252.8	419513	428394	429169	132819	123817	116329	302018	314887	293478	178242	194163	189470
156	HPR	P00739	941.47	712.932	702.609	8254.98	8184.66	7760.49	83.3844	2474.3	2564.13	4285.76	4156.18	3888.9	3221.61	3312.1	3449.59
157	F9	P00740	274.152	300.368	316.52	1101.01	1213.41	1087.45	893.14	414.449	295.392	709.124	343.016	859.053	436.934	431.733	401.034
158	F10	P00742	440.537	540.003	102.843	1451.12	1534.06	1363.58	1472.62	600.862	652.854	909.28	1045.04	976.659	643.102	797.825	801.596
159	PLG	P00747	130.181	175.295	244.744	403.997	518.725	405.118	90.4979	105.143	167.549	241.425	325.078	237.349	76.0717	61.1678	113.638
160	SERPINC1	P01008	1277.83	2050.43	1879.18	3349.72	3324.41	3223.18	3711.67	2046.78	2302.49	3528.72	3067.77	2747.78	2224.92	2148.57	2348.88
161	SERPINA1	P01009	26834.5	28019.4	26449.7	346838	338712	336607	63218.9	58013.5	58663.6	122363	126807	128730	102017	101256	100203
162	SERPINA3	P01011	485.335	696.727	622.187	28127.7	26638.5	26162.2	864.169	1776.92	1837.38	2495.65	2307.76	2121.68	2429.13	2109.44	2362.19
163	A2M	P01023	28312.4	31861.6	28780.4	29813.4	28742.7	27678	43367	32134.8	31818.4	29609.9	29920.9	30040.1	28732.1	31384.7	31301.4
164	C3	P01024	1617.17	1961.02	1804.96	2047.36	2073.73	2052.23	2162.03	1514.43	1621.51	2593.31	2790.55	2629.49	1676.3	1772.12	1753.97
165	KNG1	P01042-2	2515.08	2671.34	2532.11	5023.51	5211.67	5247.89	2051.03	2737.01	2455.62	4370.46	4355.23	4508.08	2704.96	2854.53	2538.55
167	IGJ	P01591	4915.9	7076.71	6275.31	5885.49	5999.78	5820.52	11739.9	8253.45	8975.55	6298.6	5596.6	4848	7159.99	7117.6	6168.83
168		P01594	220.426	215.672	128.113	3996.38	2089.94	2202.6	349.108	262.409	658.93	157.786	621.805	117.772	352.204	333.058	655.753
169		P01599	396.549	497.117	146.583	1389.29	1470.86	1526.24	392.244	252.576	189.888	1857.71	1722.22	2055.93	1364.27	1500.14	174.814
170	IGKV1-5	P01602	325.548	538.553	741.418	14146.1	3567.94	3512.28	376.118	421.9	1175.4	1158.09	1182.51	1158.78	1311.09	1129.85	1162.03
171		P01619	4488.81	294.161	4637.54	81576	78061.7	82199.6	2882.66	7799.84	8365.87	9608.69	10746.4	7853.89	17314.8	9223.44	26628.3
172	IGKV3D-7	P01624	251.935	1219.34	1071.04	3484.19	3685.42	3628.8	3010.01	977.76	179.581	2493.78	2486.13	2053.69	1685.2	1656.44	1637.93
173		P01700	151.958	1806.46	1619.46	3285.69	3799.28	3158.41	287.125	2258.15	2475.36	4501.11	4598.33	4282.25	3358.33	3269	3804.07
174		P01701	276.664	138.393	381.249	171.906	308.783	278.861	300.283	954.882	143.661	1486.96	1707.73	1890.36	133.529	1157.21	444.497
176		P01706	160.86	134.669	229.543	1587.74	203.175	677.896	431.853	122.449	303.013	192.279	221.538	233.498	349.144	454.827	939.862
177		P01714	136.577	266.346	312.125	793.386	1068.25	766.816	1985.99	691.511	691.117	992.91	683.323	743.819	456.77	422.729	90.4736
178		P01715	546.355	369.569	59.6656	839.614	228.526	574.249	393.553	142.461	565.226	434.475	864.216	881.579	100.111	263.19	522.522
179		P01717	351.315	193.542	135.961	6627.73	6450.49	7245.72	183.068	1957.69	2174.88	2539.89	2797.73	2523.38	2194.22	2132.97	2011.64
186		P01780	522.729	310.172	2641.84	7008.46	13991.2	14627.7	282.883	3150.29	3674.08	3328.38	6544.03	4908.02	3744.84	3944.89	4435.27
187		P01782	181.934	131.806	168.176	374.369	194.656	330.69	378.562	182.455	328.812	780.601	387.644	883.923	369.318	286.298	248.301
189		P01817	155.784	127.856	116.917	779.036	254.396	248.249	279.439	217.518	249.458	246.369	427.902	769.683	277.115	170.593	128.936
191	IGKC	P01834	1124980	1352200	1236810	1070070	1059350	1031990	509130	897124	961145	602070	638372	616969	661313	706501	724548
192	IGHM	P01871	10067.6	12604.5	11722.7	5605.33	5633.01	5792.23	14718.9	9786.89	8425.06	8053.84	8417.55	7564.56	8951.63	9236.64	9790.74
193	IGHA1	P01876	18921.2	21860.2	19433.3	70426.5	69707.9	68954.8	32940.2	37130.7	33988.4	50090.5	52026.6	48300.2	39769.7	40443.6	41554.1
194	HBD	P02042	201.624	93.5525	123.795	2019.14	2278.53	2022.91	202.274	792.39	805.016	858.002	906.788	1169.24	900.08	935.262	919.856
195	APOA1	P02647	324113	358313	325172	976673	988608	996340	669505	435685	426973	594013	619937	626312	611498	626900	644501
196	APOE	P02649	2815.93	3324.25	2954.16	8355.67	8926.73	8807.82	6940.17	4325.25	3869.23	6716.71	7601.31	7369.97	4722.2	4999.68	4863.25
197	APOA2	V9GYM3	193398	260154	242404	530233	489262	505619	416836	316098	371919	339818	329861	285512	310919	324785	333185
198	FGA	P02671-2	5413.23	6623.46	6315.47	21061.6	19211	20278	15286	10810.9	9416.32	11942.3	12907	15079.8	11526.1	12431.4	11547.1
199	FGB	P02675	525.388	951.072	878.39	612.257	743.616	697.549	43.2558	776.183	546.539	1037.63	1031.95	827.078	1119.11	1050.35	1227.16
200	CRP	P02741	80.5572	103.462	123.054	704.716	1052.45	999.682	135.785	3416.4	2779.27	3801.63	5862.02	5588.75	2088.8	4290.86	4132.88
201	APCS	P02743	208.561	64.5076	874.768	432.159	240.899	383.798	131.701	698.973	232.661	182.102	79.0031	133.596	150.523	490.894	83.274
202	C1QA	P02745	2254.78	3494.42	3308.12	2273.64	1941.2	2091.9	143.639	3888.63	4486.55	3243.73	3512.09	3501.81	2808.07	4129.72	2603.38
203	APOH	P02749	9820.9	11312.4	9743.96	49027.4	50278.3	50079.8	24257.4	17820.6	20583.1	30104	32615.4	32824.9	23788.7	25224.7	26935.8
204	LRG1	P02750	8761.13	10814	9704.28	27374.6	27985.9	27487.7	22069.8	16681.8	18722.1	19611.9	20207	18809.8	21519.4	21916.7	22428.1
205	FN1	P02751-14	182.162	200.467	179.333	123.115	113.309	102.36	122.804	131.172	144.644	211.091	212.996	213.935	134.39	112.124	119.651
206	RBP4	Q5VY30	24924.9	30221	28092.7	79961.8	77673.4	75716.1	73466.7	48418.5	49211.4	44958.5	47746.2	48121.6	46156.7	46295.7	50709.1
207	AMBP	P02760	6622.18	8137.07	7057.2	25205.1	28550.4	27499.1	16618.3	11024.4	12162.1	17986.5	19459.5	19420.6	16713.8	16080.4	15953
208	ORM1	P02763	216832	249645	216656	348607	347320	350191	643974	350413	375262	534398	514043	532978	399191	470104	467821

209	AHSG	P02765	27255.3	31909.9	29336.1	71541.4	72020.8	68284.1	79487.1	40615.5	41838	48237.5	52928.9	48556.1	47874.8	51493.5	51569.1
210	TF	P02787	6830.51	7245.88	6539.32	10228.5	10022.1	9541.59	10163.3	6355.63	6046.22	13436	14239.1	13926.6	7422.38	7933.96	7954.9
211	HPX	P02790	13389	14383.5	12517.5	37297.6	38167	37243	10285.2	15821.8	16527.7	31781.5	32874.1	31188.4	18122.2	17360	17540.8
212	C4BPA	P04003	218.509	472.158	403.975	309.329	262.879	331.902	131.262	57.8711	43.4909	331.318	505.818	428.566	31.0788	147.115	170.193
213	VTN	P04004	1180.55	1680.66	1290.74	1091.97	1148.22	1022.73	2345.93	1158.19	1172.73	1466.2	1375.64	1296.07	1044.76	1084.92	1014.14
214	APOB	P04114	1773.27	2088.97	1864.62	1876.07	1985	1952.99	2445.65	1881.88	1918.3	1496.26	1513.91	1462.87	1863.03	1924.96	1999.21
215	LCAT	P04180	633.026	739.876	634.059	1346.05	1459.12	1369.53	1709.03	672.884	689.047	1271.45	1203.36	1237.17	1318.55	1134.38	1211.36
216	HRG	P04196	17638.5	21054.9	18312.4	36675.9	34864.4	35133.4	33276.2	25598.9	27269.2	26346.5	28122.2	26710.2	25722.9	28942.3	30407.8
217	A1BG	P04217	13208.3	16614.2	15478.9	38463	36955.8	35679.2	21474.6	19193.7	20035.8	23710.4	23637.7	23103.3	21928.6	23099.9	24691.5
218	KRT1	P04264	3381.54	4338.75	3726.53	463.402	531.246	433.412	2075.48	1377.95	1345.95	1347.18	1262.59	1205.55	15459.9	15283.2	13413.8
219	VWF	P04275	38.5878	46.1926	80.1519	8.34644	11.5546	20.907	25.8906	67.6712	90.6465	60.182	77.4868	62.933	69.4319	14.3891	62.4044
220	IGKV3D-11	P04433	62.3999	408.26	485.783	12479.8	13647.9	13507.1	643.175	798.296	813.531	1483.61	1579.07	2329.74	1378.01	1160.21	1164.55
221	AMY2B	P0DUB6	208.457	270.071	230.637	27.8576	75.9167	57.1057	432.923	193.696	102.016	201.774	52.9007	103.85	127.548	113.328	148.389
222	SERPINA5	P05154	266.922	335.785	243.9	517.471	585.596	535.686	55.1795	344.211	388.538	248.179	109.27	350.533	343.356	348.083	456.082
223	F13B	P05160	20.3876	124.62	35.2859	69.5827	21.3209	92.9202	105.648	34.8681	60.2757	66.1183	70.4035	72.8828	29.7231	32.0716	25.2185
224	SERPINA7	P05543	233.67	460.207	386.153	5108.79	5286.48	4857.11	539.766	887.962	529.731	389.755	341.124	337.283	324.824	448.211	429.162
225	SERPIND1	P05546	5491.57	6239.09	5693.62	8489.7	8788.24	8676.14	9279.01	6740.45	7304.72	8322.75	9303.99	8392.01	7493.8	8517.31	8114.58
226	BCHE	P06276	532.569	574.562	552.644	1400.86	2471.54	2116.54	1032.61	599.243	620.292	697.111	625.086	637.844	610.871	681.066	693.513
227	IGKV2D-30	P06310	183.896	90.3735	184.546	21731.7	10237.7	20870.7	159.768	6597.54	172.903	14139.2	15222.9	14167.3	13553.7	13892.1	14101.1
228	IGKV4-1	P06312	229.497	626.698	227.783	16239.5	16722.2	16373.6	208.853	151.725	337.263	323.546	1069.08	1158.72	259.763	1190.71	1299.76
229	GSN	P06396	3024.43	3624.27	3581.05	7889.76	7694.67	7390.57	8529.09	5468.7	5955.35	5658.45	5776.91	5913.64	5281.09	6080.14	5831.87
231	APOA4	P06727	5823.88	7090.68	5966.42	23863.7	23290.7	23087.6	10224.8	10281.1	9059.11	17304.9	18145.8	17575	12119.9	12859.7	12208
232	C8B	P07358	31.4014	48.6427	33.2902	25.3832	44.0331	30.7965	29.8702	69.9206	43.0435	174.607	38.1916	74.031	71.7401	62.0136	131.364
233	C8G	P07360	93.7419	61.9797	258.881	150.488	245.798	82.4676	215.953	95.0724	159.355	110.741	614.958	233.094	393.988	322.913	203.042
234	TUBB	Q5JP53	68.115	85.4336	40.3705	107.22	115.087	107.182	48.8886	50.9913	764.158	34.919	32.0056	76.8094	60.7144	44.3866	771.047
236	HSP90AA1	P07900	37.4606	56.8908	110.04	156.625	40.9154	54.2986	94.9135	19.0153	18.8553	225.617	218.506	51.3558	54.0808	107.501	157.555
237	UMOD	X6RBG4	636.301	433.016	451.646	146.947	166.054	146.935	409.029	251.251	233.875	327.572	416.078	419.235	438.407	349.751	418.172
238	THBS1	P07996	23.8143	25.9758	13.625	49.89	22.6713	24.1304	71.804	63.1208	21.6306	57.9485	19.443	33.0882	21.6708	55.4546	30.0023
239	SERPINA6	P08185	6466.84	8489.7	7427.85	7811.98	9004.7	8276.9	10162.1	11487.4	11164.1	10568.3	9872.08	9970.39	8809.11	9770.56	9564.77
240	HSP90AB1	P08238	47.0299	24.7883	19.0872	37.0047	28.0618	31.6447	15.6449	170.48	41.4621	176.514	94.2403	40.9065	95.2013	187.196	64.4657
241	LPA	P08519	26.3737	10.4135	53.6725	16.7384	85.2088	43.3821	56.5932	6.3111	8.60817	63.2295	99.3114	19.9695	7.96531	13.8132	26.793
242	CD14	P08571	35.7253	67.1361	81.7377	201.091	121.798	94.1311	71.4659	103.51	106.514	107.443	100.879	76.5677	48.5577	239.04	58.3709
243	CFH	P08603	83.7865	151.07	170.009	182.484	191.011	116.862	38.7202	65.5318	99.0362	361.219	386.942	363.271	72.011	73.5804	53.7527
244	SERPINF2	P08697	1139.27	1580.14	1594.55	2226.62	2284.32	2174.25	588.538	1474.4	1869.57	1719.66	1457.24	1413.07	1852.78	1935.78	1838.94
245	C1S	P09871	1487.69	418.394	71.0772	89.6984	251.981	287.88	716.841	1404.22	149.168	2355.56	236.108	580.062	1448.49	577.74	629.827
246	C4A	P0C0L4	397.636	550.748	509.421	621.04	667.078	672.003	1343.04	890.794	872.155	780.865	870.009	679.449	788.251	775.145	726.576
247	C4B	P0C0L5	766.104	862.309	838.884	2552.41	2598.64	2681.95	2463.91	1549.14	1550.24	1750.85	1893.64	1849.1	1589.51	1698.82	1728.83
248	SAA1	P0DJI8	383.005	232.253	130.42	126246	146128	143428	496.31	29792.2	33752.8	57077.6	62771.9	54133.2	50426.9	55306	56705.3
250	IGLC6	P0DOY3	126384	157186	138467	633161	609385	611866	307813	341374	365787	476427	498003	476316	417186	443821	443378
252	HIST1H1E	P10412	939.352	76.2737	133.976	404.073	271.451	402.656	117.398	175.866	107.484	208.225	1066.01	209.761	186.756	786.331	984.052
253	opn	Q3LGB0	189.819	461.063	367.577	502.199	615.828	607.228	1635.14	373.747	505.501	436.844	538.724	424.292	346.672	373.798	432.932
254	C7	P10643	23.7107	42.1129	20.6523	35.9815	85.4952	8.78337	131.432	32.6926	16.0854	17.751	54.0352	12.4109	10.614	32.9167	13.6443
255	CLU	P10909-4	2792.34	2922.43	2311.51	4777.43	4723.13	4607.75	3812.07	2397.85	2337.79	4739.93	4790.26	4279.03	3527.61	3640.22	3679.03
256	MBL2	P11226	377.571	416.359	425.435	9587.13	10748	11753.5	2068.63	928.748	1399.97	4904.62	4785.28	3769.27	1804.08	1835.09	2758.03
257	COL6A3	P12111-4	9.58334	5.96826	27.9882	8.83693	12.9164	24.7569	9.39417	36.2426	10.6594	16.9357	16.9418	7.70145	29.5181	13.1268	20.1689
258	C6	P13671	8.89453	9.46703	13.051	54.3362	10.6083	5.87055	18.511	32.7356	20.9231	11.5542	22.4435	7.13242	80.9149	5.11921	69.8054
259	CPN1	P15169	163.595	51.5112	141.24	332.225	319.828	202.805	452.383	160.705	227.33	256.278	247.154	215.272	52.6211	187.554	74.9792
261	IGFBP2	P18065	163.081	194.052	82.2916	979.362	834.668	991.525	52.7297	269.797	246.04	370.639	541.346	522.766	313.768	56.827	422.134
262	LBP	P18428	50.2195	74.5869	32.69	266.193	238.14	317.662	49.9727	20.8995	55.9764	180.534	193.775	36.9075	79.0087	190.359	191.43
264	ORM2	P19652	80771.9	94503.9	86536.5	82947.6	88702.5	92972.8	58266.1	126168	141713	127567	135128	130929	112812	133599	134587
265	ITIH2	P19823	6933.51	8059.93	7360.74	11452.1	11668.4	11161.7	14170.8	8850.36	9465.21	9529.93	9812.6	9629.12	9318.14	9390.43	9745.05
266	ITIH1	P19827	6664.22	7483.45	7033.06	13206.3	13424.7	13215.8	12899.2	9570.32	9257.77	9914.2	10489.4	10247.8	9696.07	10163.2	10581.5
267	PZP	P20742	7.29555	19.2665	34.2609	124.402	306.452	245.676	15.2717	25.9968	38.063	48.2467	69.555	71.3093	36.8785	75.1457	59.3937
268	C4BPB	P20851	458.677	501.769	499.184	1514.89	1784.76	957.328	122.85	462.588	654.192	791.99	794.253	737.023	664.566	735.782	703.724
269	GPX3	P22352	4643.26	5825.97	6026.09	3114.36	3552.26	4103.24	179.818	2065.02	2329.77	5423.42	2248.34	3075.81	6355.1	6739.58	6173.18
270	CPN2	P22792	427.39	426.692	257.827	1278.11	1186.64	1413.44	608.149	467.009	590.869	1198.04	1203.53	1014.23	630.437	588.512	679.181
271	PROZ	P22891	34.0253	109.02	134.295	91.3416	54.4525	68.7155	90.8357	32.9812	43.2804	36.4036	32.4796	74.0197	82.4439	40.54	74.6655
274	FBLN1	P23142-4	23.1483	133.018	802.099	41.3568	225.966	61.1236	1293.25	31.3715	115.22	179.474	44.4462	1089.92	10.3243	86.9273	71.1626
275	AZGP1	P25311	3392.13	4250.25	3743.38	5198.61	4194.09	3579.74	1167.7	12495.1	10494.7	14393.9	15551.9	14348.4	11336.2	11646	10056.4
276	PON1	P27169	11240.8	14304.8	12809.2	13708.1	14232.3	14457.3	15960.4	12017.7	12777.6	10981.8	11028.2	10866.4	14073.8	14852.7	13875.3
277	SERPINA4	P29622	35.3111	37.9253	62.5113	2292.11	2176.39	3342.92	59.928	58.0479	36.5172	65.4541	74.1485	36.5854	14.2602	149.748	20.8344
278	CDH5	P33151	224.45	283.677	248.07	557.092	473.637	853.723	497.141	227.881	307.53	371.522	327.528	340.581	321.895	409.663	369.1
279	IGFALS	P35858	28.2442	190.169	72.5449	76.8474	47.6635	44.302	45.8892	74.1888	18.8144	87.6319	117.482	44.6763	34.487	103.869	71.1237
280	SERPINF1	P36955	1870.45	2037.86	1939.85	6338.78	6685.71	6385.04	3332.63	2936.55	2837.75	3913.89	4174.31	3759.17	3902.26	4242.47	4161.91
281	PTGDS	P41222	469.118	304.015	47.4606	16387.3	16602.5	16045.9	178.792	4701.13	9662.3	8141.55	8708.44	8884.76	378.056	194.514	99.8203
282	BTD	P43251-4	469.438	660.793	600.379	1454.42	1313.63	1342.02	89.1331	738.423	714.366	489.207	896.618	580.993	797.317	1189.01	1108.74
283	AFM	P43652	48.598	102.538	138.194	52.8575	128.412	130.912	24.6594	95.8594	40.3718	149.263	172.649	144.382	28.5046	93.3898	19.6371
284	MASP1	P48740	151.552	167.428	163.934	139.038	114.178	124.627	43.6571	190.094	158.942	233.668	260.431	245.155	179.126	200.866	99.9193
285	LUM	P51884	1263.65	1817.81	1682.91	5229.36	5119.99	4923.3	6570.84	3033.98	2913.03	4040.76	4203.35	4123.09	3262.11	3377.51	3382.06
286	PLTP	P55058-3	397.314	582.241	479.543	631	614.269	601.745	1141.03	630.602	568.622	499.143	622.248	566.171	491.968	459.211	574.646
287	ACTB	P60709	1892.99	1459.42	1586.39	979.648	1094.83	1155.3	1162.66	2047.76	1837.24	859.764	1129.83	1230.28	1615.36	1359.21	1309.09
289	B2M	P61769	6329.43	6365.61	5617.5	63215.3	56742.4	53740.2	495.962	8664.33	16135.7	32381	37058.5	30425.2	32754.1	26987.6	31206.1
291	RPS18	P62269	134.029	71.8104	142.933	204.007	49.734	435.423	122	78.0918	56.634	190.881	283.041	116.671	71.6431	368.748	144.382
293	HIST1H4A	P62805	36531.3	31764.3	26196.7	11818.4	8025.13	9992.64	737.455	31632.1	44818.5	18625.9	18745.4	29693.2	32680.6	26626.7	27535.3
295	HBB	P68871	23388.9	26918.5	23706.8	79175.6	76023.1	74152.1	31592.3	25867.1	25792.5	47600.7	48242.8	49053.1	40318.1	40592.3	41113.6
296	HBA1	P69905	46889.1	33579.4	29308.6	83758.7	83188.7	83052.8	21551.8	49049	37543.6	73543	71643.6	91131.8	58796.7	56158.9	65817.7
297	GPLD1	P80108	90.2279	132.336	147.876	282.04	302.23	304.14	408.513	182.93	186.628	265.014	302.843	270.729	178.756	238.285	220.198
298		P80748	3085.76	3380.85	2982.57	10072	10752.8	21578.4	168.994	6336.5	6777.83	11413.8	21829.2	11061.2	8683.69	9797.12	10077.8
299	HSPG2	P98160	145.076	153.664	189.65	9.98277	13.3949	11.7232	200.815	77.8422	158.906	144.642	17.8849	159.108	160.351	5.86262	165.76
300	CFHR1	Q03591	214.445	248.865	243.088	1002.54	643.992	641.539	62.6955	343.249	278.558	1296.47	997.134	964.54	284.325	330.573	282.768
301	HGFAC	Q04756	17.405	73.3201	17.1922	84.6075	62.9786	75.4549	27.5057	66.8245	69.8064	37.7978	27.7921	49.2006	48.9451	69.8357	37.1458
302	ITIH3	Q06033-2	182.35	206.48	118.536	839.848	853.66	846.169	83.6441	294.791	180.462	988.377	617.872	319.65	297.303	253.22	677.419
303	LGALS3BP	Q08380	1315.31	1733.98	1020	328.151	246.829	456.262	1183.77	1231.47	1151.77	741.367	594.335	478.684	935.24	1266.21	1328.65
304	EFEMP1	Q12805-2	201.081	233.975	236.088	661.624	959.063	1175.29	626.197	263.577	241.265	767.478	475.073	543.689	295.257	285.622	420.704
305	SPP2	Q13103	102.863	243.574	99.7817	55.0645	207.722	154.369	40.9017	264.981	45.4215	90.3308	114.67	245.698	211.939	176.564	99.8011
306	APOF	Q13790	3712.27	2590	2917.56	18804.2	18208.8	16870.6	135.479	8707.61	7924.96	10620.1	10557.1	9490.41	9390.95	9914.89	10497.5
307	HABP2	Q14520-2	65.5241	39.802	35.278	64.4415	74.5506	77.335	148.595	46.847	50.7751	135.996	149.613	117.281	32.475	129.327	71.0997
308	ITIH4	Q14624	6875.43	8269.89	7536.35	9887.15	9786.56	10123.9	11564	9164.19	9353.01	8420.22	8328.83	8129.96	7277.93	7073.96	7635.64
310	ADIPOQ	Q15848	1098.13	1180.27	39.4308	224.31	305.299	688.249	352.115	1919.75	1408.42	4092.43	2869.32	5096.11	4019.92	1555.62	4447.64
311	ECM1	Q16610-4	16.4674	71.9994	38.3772	154.159	100.916	94.1791	57.0542	25.7032	35.9705	80.9792	124.724	37.6945	67.7164	27.3628	101.307
321	WHAMM	Q8TF30	2137.61	7769.19	2263.1	17452.3	18065.4	17260.7	1684.73	1774.74	1826.23	1564.68	1572.39	1551.55	1526.06	1572.3	1609.67
322	RYR2	Q92736	2.5662	8.26291	2.84449	4.17462	24.6283	3.89621	4.92509	8.01641	141.427	151.386	168.302	153.535	146.643	168.52	169.99
324	PRG4	Q92954-3	8.26612	29.6239	23.8635	58.2317	15.4136	73.0058	14.7176	17.5711	24.9254	17.138	14.4778	23.7802	27.276	30.7246	18.9667
325	PIK3IP1	Q96FE7-4	179.765	141.267	303.821	83.1544	163.607	125.764	233.48	137.9	118.507	135.949	910.095	1199.86	168.987	155.091	116.392
326	CPB2	Q96IY4	1065.06	1199.78	1317.63	2018.08	1946.39	1879.51	2634.41	912.885	1342.49	1646.57	1835.73	1779.55	1699.12	1929.26	2012
327	CNDP1	Q96KN2	427.924	451.301	480.747	674.182	640.481	635.593	610.376	608.248	561.461	508.136	485.941	318.828	526.066	494.445	670.143
328	PGLYRP2	Q96PD5	640.275	844.545	672.321	2674.04	2620.58	2589.56	432.632	1278.15	1301.5	2430.3	2585.57	2501.6	1643.57	1660.72	1712.65
329	HMCN1	Q96RW7-2	4.80755	3.45624	3.85079	10.2408	476.63	328.672	15.5594	6.42489	138.214	4.05533	493.93	5.11003	9.91021	3.99512	6.87346
332	C1RL	Q9NZP8	59.1897	46.8333	29.6556	153.769	58.1681	58.9485	26.0672	89.5281	375.642	54.1241	460.561	69.4311	109.368	414.027	103.607
333	FETUB	Q9UGM5	141.725	97.6022	151.591	234.365	85.338	150.183	77.8928	99.3897	67.2568	36.4227	98.2789	174.925	69.1237	81.9466	96.8236

APPENDIX I | PROTEIN QUANTIFICATION (MM PELLET SERA)

id	Gene names	Majority protein IDs	Concentration [nM] AQ01.1_p	Concentration [nM] AQ01.2_p	Concentration [nM] AQ01.3_p	Concentration [nM] JC02.1_p	Concentration [nM] JC02.2_p	Concentration [nM] JC02.3_p	Concentration [nM] MMB1_p	Concentration [nM] MMB2_p	Concentration [nM] MMB3_p	Concentration [nM] MMC1_p	Concentration [nM] MMC2_p	Concentration [nM] MMC3_p	Concentration [nM] MMF1_p	Concentration [nM] MMF2_p	Concentration [nM] MMF3_p
3	IGLV8-61	A0A075B6I0	840.929	208.767	381.634	462.138	4210.51	655.641	347.606	222.059	361.874	400.157	799.674	4386.45	305.14	810.183	524.843
5	IGKV2D-28	A0A075B6P5	448.63	603.351	455.208	444.735	557.158	1108.78	311.363	436.612	493.909	378.542	614.475	861.63	479.993	868.235	1192.56
6	IGKV2-24	A0A0C4DH68	213.126	348.854	307.137	726.706	244.261	177.441	258.75	408.732	211.198	770.264	457.372	222.339	469.027	541.91	160.951
7	IGKV1-27	A0A075B6S5	671.599	599.204	611.365	726.387	673.164	671.15	348.377	463.655	202.553	271.416	828.861	442.199	713.435	404.147	232.523
11	TTR	A0A087WT59	9404.68	9452.45	7471.71	9618.4	10205.5	9770.13	7179.21	7493.31	8322.11	10501.8	10274.6	11247.5	14040.3	13278.3	12679
15	FCGBP	A0A087WXI2	327.742	404.09	315.786	216.311	216.638	242.602	380.032	280.386	386.76	256.263	391.323	320.621	287.991	447.897	422.719
16	CHL1	A0A087X0M8	36.1446	26.6735	49.1176	45.5717	76.1748	39.5978	125.548	36.1498	88.5844	27.3999	98.5268	30.723	56.4002	23.605	50.6469
17	SAA2-SAA4	A0A096LPE2	2143.52	1772.36	1393.99	8502.8	7757.04	8402.75	3605.87	4401.83	3361.71	5868	2541.36	7448.29	5967.99	5876.94	4907.35
18	F5	A0A0A0MRJ7	617.001	527.748	646.176	1593.74	1649.98	1753.63	770.352	590.639	688.548	1343.91	1545.83	1544.56	992.679	1141.58	1542.61
19	IGHG1	P01857	1299890	1378600	1448560	187070	192262	200725	1225790	1193480	1200340	595787	541892	534082	882127	854533	890899
20	IGHD	A0A0A0MS09	89.2776	79.0029	84.2319	112.363	75.5859	180.527	63.3999	60.3369	77.5482	122.199	113.295	136.769	108.529	78.415	93.9669
21	IGHV3-49	A0A0A0MS15	155.548	670.143	648.781	214.322	158.112	109.509	297.654	523.671	403.192	579.63	746.565	289.634	967.546	198.849	1431.11
22	PRDX1	A0A0A0MSI0	410.357	1188.71	69.049	672.729	278.475	297.337	389.734	177.075	125.534	258.007	278.249	374.82	134.13	243.213	438.232
23	TTN	A0A0A0MTS7	0.803339	1077.36	0.998103	288.417	265.618	256.016	0.994953	476.049	376.7	338.556	361.551	329.853	594.493	1.48927	0.982877
25	IGHV6-1	A0A0B4J1U7	4393.71	4882.16	366.816	8613.71	8437.74	8318.12	5863.41	6193.28	6574.21	7836.54	7684.17	7966.17	7545.7	6745.65	6597.99
29	IGHV3-74	A0A0B4J1X5	2475.3	3323.39	2511.02	7011.98	6846.2	8740.77	4267.11	3256.18	4805.03	5393.18	4749	5913.98	4092.25	4786.47	4469.53
31	IGLL5	A0A0B4J231	826.254	799.129	628.957	2644.42	3501.16	3739.48	1599.01	1726.98	2051.18	2000.92	2107.22	1957.85	1888.37	2033.82	2168.97
34	CRTAC1	Q5T4F6	133.498	104.376	109.933	277.396	158.329	281.796	46.9281	31.0044	60.8604	86.2229	78.7357	94.6877	97.6822	54.8348	31.8056
38	IGHV1-18	A0A0C4DH31	370.902	595.44	404.312	3922.97	6039.01	7129.38	1312.66	432.757	193.343	452.124	203.505	1054.19	381.53	220.42	663.83
42	IGHV5-51	A0A0C4DH38	98.0178	819.256	264.353	1855.55	177.801	3232.41	304.524	242.205	1091.66	1060.18	1650.83	435.58	1295.77	1568.65	333.391
43	IGHV4-61	A0A0C4DH41	250.01	955.641	857.78	621.275	388.418	783.279	1197.41	998.817	266.33	866.419	309.536	1193.15	316.466	1633.32	1384.7
44	IGKV1-6	A0A0C4DH72	449.665	547.828	402.757	1435.28	354.236	413.929	622.346	1072.57	264.197	480.409	124.511	557.6	330.169	711.151	486.254
47		A0A0G2JMB2	1489.26	2451.11	2091.32	3106.25	3896.13	3326.06	2641.42	2088.4	2425.63	2873.27	2148.69	2998.67	3570.63	3486.71	3337.63
49	IGLV5-45	A0A0G2JSC0	348.906	290.895	336.993	184.023	267.129	231.232	836.22	584.854	309.327	345.928	468.354	495.325	1465.06	687.616	407.705
51		A0A0J9YY99	2863.68	3123.89	2845.86	374.645	471.38	508.14	442.771	3160.3	3269.06	1373.88	742.922	411.796	2930.48	308.751	317.485
52	PROS1	A0A3B3ISJ1	2091.41	2092.13	1958.49	2841.21	3100.58	3134.83	1986.09	2134.02	2155.85	2722.64	3012.5	2984.31	2744.78	2805.82	2575.73
53	SEPP1	P49908	1079.37	1071.46	1059.18	1246.75	1285.4	1340.88	1025.79	1189.32	1220.42	1287.77	1447.46	1152.78	1309.44	1369.12	91.1766
55	KRT10	A0A1B0GVI3	654.668	722.698	784.955	269.932	268.966	270.711	291.382	554.341	520.912	318.898	408.566	488.357	421.817	414.506	478.203
56	IGHG3	A0A286YES1	22460.6	26266.1	24630	16889.7	15930.6	16625.1	17764.4	17511.8	19318.4	22918.3	23808.1	23587.3	20624.1	18615.9	20007.5
57	IGHG2	A0A286YEY4	12650.2	13185.9	7874.22	18380.1	17261.2	19291	16693.7	19093.1	18302.9	20430.1	22300.2	22174.8	19782.1	20762.8	19181.6
58	IGHG4	A0A286YFJ8	3203.96	1600.16	622.446	4879.37	4946.74	6042.01	5075.8	3018.48	2092.83	3284.28	4338.17	4068.59	4087.79	5896.02	4134.29
60	CFHR2	A0A8V8TQS1	1242.36	1353.62	1804.81	5893.4	5996.53	6257.97	2449.12	2280.38	2810.33	4383.17	4988.39	4837.88	3609.51	2997.59	2659.78
62	C1R	A0A3B3ISR2	776.057	1254.73	1181.47	3921.02	3299.69	3599.17	944.686	1172.47	1259.73	3820.52	3543.63	3973.93	2749.41	2993.64	2531.43
64	EGF	A0A494C018	34.3071	34.5994	53.9656	43.7229	77.9026	20.479	73.7469	18.4777	64.8693	108.454	33.1519	77.5324	105.002	49.6928	41.1993
65	H2AFV	C9J0D1	185.774	310.44	187.714	275.31	309.239	559.977	310.294	216.29	215.013	617.586	636.262	993.201	988.141	924.332	407.866
66	IGHV3-72	A0A4W8ZXM2	4888.98	5019.33	7767.49	10230.9	11015.8	11262.5	5706.15	6148.95	6458.71	4953.93	5215.27	5102.34	5669.53	6069.15	7153.42
67	H3F3B	K7EMV3	210.695	770.05	390.32	928.572	1443.57	245.15	1421.58	1201.58	291.661	1145.56	255.036	560.75	492.435	1396.74	704.789
68		A0A6Q8PF87	3072.39	3013.92	3148.07	5015.4	5219.36	5412.65	4012.38	3940.04	4172.36	2335.09	4149.26	4464.08	4069.47	4719.3	4616.86

69	LMNA	A0A6Q8PFJ0	31.7157	173.199	60.1327	60.2358	58.5593	48.7834	74.1262	51.9298	47.0531	49.634	132.063	31.9937	68.1826	17.1129	168.72
70	SERPING1	A0A7I2V2D2	15770.7	17136.7	14144.3	27572.4	29236.9	28226.5	14560.5	15625	15036.2	22962.8	23427.8	22840.9	19660.3	21547.8	19157.1
72	AGT	A0A7P0T8D1	4763.42	4726.28	4364.55	3400.1	3502.27	3416.47	4376.13	4997.34	5079.03	4698.82	4570.43	4330.8	5322.62	6061.45	5427.56
73	HSPA5	A0A7P0TAI0	217.193	136.702	195.769	86.199	310.236	226.247	76.9993	249.709	30.8226	226.653	120.402	117.632	293.981	162.013	216.674
74	PDIA3	A0A8I5KRV3	72.0449	131.789	73.2041	95.4058	241.952	119.999	86.9715	115.994	81.3463	125.211	66.2596	129.11	122.283	109.414	114.595
75	PPBP	A0A8I5KW61	12614.4	12949.2	12692.1	16575.2	17633.6	18112.4	11981.9	12320.2	12680.2	18216	18875	19001.6	15138	15106.3	15318.7
76	MYH9	A0A8I5KWT8	34.4155	18.5044	16.6634	12.4705	14.7079	33.2713	21.6561	27.0007	8.95549	23.1358	16.2503	39.3836	29.4135	33.3175	11.8507
79	C1QB	A0A8Q3SI33	13541.3	15174.6	11765.6	15713.9	18565.7	17377.5	10343.9	12867.2	13588.4	17734.1	20368.9	20969.2	16710.5	18091.9	13803.3
80	C9	A0A8Q3SI95	7156.13	8680.44	7492.83	15932.8	16170	16067.6	8398.76	9615.39	8936.64	14279.8	15619.8	15616.7	11677.2	13101.3	12190.9
82	C5	P01031	2394.78	2528.95	2286.6	2706.76	2562.51	2630.55	2162.79	2305.9	2281.99	2787.93	3020.8	2966.77	2716.9	2860.43	2585.69
83	C1QC	A0A8Q3SIZ0	14990.3	15840.5	15501.5	19839.3	19794.4	20553	10777.8	12148.2	13052	21479.2	21628.6	22844.4	15540.2	17303.2	16210.8
84	CFD	A0A8Q3WKW0	4675.71	4931.43	3962.94	9231.69	9857.31	8991.71	3184.79	5522.1	5860.02	7891.18	8473.22	8226.59	7019.41	7609.97	7140.1
85	F12	A0A8Q3WL25	2209.17	2399.73	1792.55	4347.17	5025.64	3744.21	1943.41	2747.41	2163.64	3585.21	3756.5	4077.95	2621.72	2679.57	2507.21
86	C8A	A0A8Q3WL79	1323.01	1421.65	1370.05	4034.1	2115.12	5157.23	920.765	1253.78	1221.19	1960.36	3225.58	2746.94	1682.55	1819.59	1785.56
88	ANXA2	P07355-2	45.8587	216.598	131.946	297.483	230.816	166.513	86.9891	313.277	177.977	201.646	203.716	148.258	196.535	90.6856	86.488
89	IGFBP3	A6XND0	490.799	571.729	440.239	535.17	775.126	683.491	506.49	533.284	700.703	653.306	109.65	828.625	251.703	653.885	221.542
90	APOC3	B0YIW2	87364.8	87346.3	85425.1	92713.4	95595.7	98395.5	84375.2	80966.9	76638.2	89431.9	90565	91471.7	88530.1	89435.4	83708.2
91	VIM	B0YJC4	177.358	119.87	110.215	196.142	159.838	38.7789	125.881	191.528	126.827	336.747	109.872	147.853	101.372	144.762	94.7195
92	APOL1	B1AH94	1102.58	1471.63	1435.36	1535.04	1507.47	1489.85	1021.49	1223.27	1128.26	1284.04	1415.69	1407.63	1448.62	1317.91	1329.76
94	UBC	P0CG48	370.974	442.562	348.476	411.238	63.4169	483.234	127.786	657.336	556.005	70.5384	20.305	521.135	583.61	610.103	585.468
95	CFB	B4E1Z4	5007.24	5373.08	4663.71	7586.89	7371.03	7340.8	4964.49	5360.44	5421.96	7247.36	7394.12	7563.23	6729.8	7069.75	6598.49
96	FGG	C9JEU5	654.878	761.152	891.118	241.539	241.819	260.805	385.981	421.968	427.259	561.969	396.721	537.501	422.997	492.388	392.52
97	APOD	C9JF17	6656.58	6587.34	5964.51	6116.49	6393.51	6997.64	6439.78	7631.89	7328.88	6077.04	6197.28	6370.57	7097.15	7428.81	7078.62
101		CON__P00761	41090.4	231.033	71386.7	129.423	29777.2	29247.7	88873.1	97104.1	115370	40037.7	40879.5	39142.5	60386.1	55913.1	70020.3
104		CON__P02768-1	912875	818332	876907	1040900	1046550	985824	942839	868455	891979	976721	959695	940503	875141	863557	876781
108		CON__P13647	199.383	16.5015	172.978	104.133	21.8658	166.587	57.1945	63.0706	61.2323	41.237	86.0524	118.355	202.761	40.697	149.422
109		CON__P15636	20755.6	21194	20174.5	16933.7	15466.4	16271.6	27427.8	26743.4	26241.6	14017.6	14440.4	14531.5	26613.5	26054.7	24341.3
110		CON__P19001	112.38	67.4614	21.1003	144.985	299.868	104.236	123.177	218.586	117.939	44.5188	170.713	125.254	406.899	151.28	42.0306
111		CON__P35527	161.623	201.57	306.663	69.5093	21.1618	53.2064	71.3602	134.532	135.64	69.1936	71.9031	113.41	202.257	67.5619	132.512
112		CON__P35908v2	95.8089	103.974	101.426	13.4293	14.5337	11.8114	27.497	21.46	28.5228	7.36351	35.6296	48.397	8.36099	34.3731	19.6022
115		CON__Q32PJ2	4074.08	5237.9	5014.52	108.944	93.042	7033.82	3310.44	118.966	3773.85	7493.87	5784.61	151.384	5306.98	76.7893	5067.36
118	GC	D6RF35	36469.7	40712	38234.3	62071.3	61871.2	64869.4	35677	39601.8	38835.5	55672.6	61864.7	60619.3	47034	49777.3	47781.9
119	COL12A1	D6RGG3	22.3501	8.41966	5.51234	36.4953	7.07082	17.1587	20.0235	13.3383	13.6599	11.7024	46.8256	26.3887	10.641	15.8851	28.937
120	CA1	E5RH81	178.043	403.6	127.361	78.9126	585.034	151.464	145.003	269.378	452.8	386.224	251.379	285.771	144.724	487.319	219.672
121	PROC	E7END6	490.97	577.686	535.545	703.831	617.387	621.221	126.551	67.3124	231.1	803.787	763.768	713.389	715.735	51.3832	577.746
123	CFI	G3XAM2	3029.9	2705.21	2691.94	4719.92	4686.05	4998.27	2143.77	2916.66	2941.68	4273.68	4822.62	4934.76	3681.51	4011.02	4018.36
125	CFP	P27918	1425.61	1316.81	1307.98	544.492	575.019	582.74	595.829	621.68	563.982	696.81	923.112	1378.37	692.343	728.857	670.944
127	CLEC3B	E9PHK0	3003.44	2675.22	2934.53	2014.62	2311.03	2444.63	3215.22	902.241	2179.52	2793.48	2442.29	2690.58	2691.38	3066.67	2829.26
128	HSPA8	P11142	65.0641	66.2293	62.4976	70.8004	40.7985	221.657	94.8506	54.7682	57.0462	123.513	79.3335	174.206	87.6373	90.6364	85.4908
129	C2	F2Z3N2	465.457	557.159	443.854	687.679	893.462	956.126	409.202	745.784	583.567	599.58	663.516	862.016	681.697	873.312	549.655
133	SERPINA10	G3V2W1	343.823	338.948	53.7414	167.102	95.8816	119.162	326.507	74.6532	92.5247	314.025	286.791	126.767	67.8686	353.578	72.8114
135	MST1	G3XAK1	272.539	319.309	268.433	240.699	246.869	283.316	247.522	279.531	236.574	320.611	353.241	356.852	265.155	291.891	270.571
136	COMP	G3XAP6	131.939	165.977	134.154	200.24	195.504	203.331	176.504	134.539	118.431	50.8442	184.092	169.462	133.35	161.27	184.591
137	KLKB1	H0YAC1	3311.14	2236.46	2872.46	3949.69	3617.36	4739.36	1978.35	2117.39	2491.78	4821.76	4364.48	5772.73	4778.8	3792.92	5081.78
138	ALDOA	H3BPS8	71.8757	267.79	91.2197	154.046	310.847	176.786	121	637.276	121.545	176.27	118.513	166.822	88.1473	360.688	59.3639
139	CETP	H3BRJ9	55.3365	3833.72	139.208	3035.73	69.8462	189.937	233.427	136.984	114.945	212.868	229.086	58.1055	119.208	103.875	80.5476
143	SHBG	P04278	612.372	477.283	408.862	483.596	387.703	504.336	443.335	431.702	576.039	652.115	696.312	583.416	543.212	522.792	589.333
144	APOC4-APOC	K7ER74	13280.8	14902.4	13423.1	8431.09	8016.88	7866.55	9685.21	11387.6	12065.2	10412	9927.97	10576.5	11337.3	11225.8	12487.8
145	APOC1	K7ERI9	80454.2	76646.4	59858.4	62433.8	78391.1	97798.7	105023	108640	127143	88218	86312.7	86560.6	119140	127870	118073
147	CD5L	O43866	1913.8	2212.73	1808.58	640.878	720.406	780.577	1247	1575.49	1549.82	1143.43	1372.54	1514.6	1538	1578.51	1470.03
148	HIST1H2BM	Q99879	1369.21	1478.96	1175.26	2065.11	1289.81	1366.86	2035.13	2321.99	3315.32	2214.42	2461.85	2508.92	3254.08	3455.77	3064.84
149	FCN3	O75636	6351.91	4766.92	4060.04	3568.49	3611.46	3525.11	3885.78	4320.79	3986.63	6386.36	5570.38	6569.93	3298.11	5856.88	5735.8
150	ATRN	O75882-3	310.659	247.883	327.945	346.935	406.302	430.568	228.414	230.061	249.817	295.21	340.97	353.069	309.013	340.994	318.806
151	APOM	O95445	10669.2	13027.3	7497.6	21483.4	20211.4	16227.6	12808.4	17447.4	17966.5	24203.1	22119.5	23986.8	14785	19261.9	18597
153	CP	P00450	3875.36	4156.78	3631.63	3529.33	3565.09	3658.4	3526.01	3696.87	3528.64	3962.23	4047.52	4200.87	3890.81	4064.92	3867.96
154	F2	P00734	12880.2	15463.6	12962.1	12953	13097.5	13412.4	11837.8	13990.4	13904.5	14683.4	14933	15901.2	13857.3	14689	15174.1
155	HP	P00738	162279	134098	165238	321494	313774	339160	166590	163108	164684	233266	236104	229947	206166	207041	196938
156	HPR	P00739	909.414	1078.53	687.043	4227.81	4499.26	4400.94	1733.39	1901.8	1903.54	2782.04	3126.74	3190.01	2818.36	3160.58	2712.14
157	F9	P00740	685.746	958.481	638.628	798.806	970.173	646.913	662.936	1102.74	757.293	1207.85	1015.22	1023.49	822.286	860.71	1048.16
158	F10	P00742	1061.15	1200.51	1069.16	1312.06	1218.32	1278.47	1013.56	1015.71	1104.97	1130.07	1436.91	1427.5	1542.36	1523.85	1432.16
159	PLG	P00747	14252	13785.1	13143.7	7377.58	8523.28	7885.42	9461.6	10737.5	10517.6	10809	11536.8	11981.6	11100.1	11662	10555.6
160	SERPINC1	P01008	8026.66	7746.73	6587.12	11546.1	11824	12237.4	6794.84	7881.75	7393.55	10777	10894.1	11352.4	9577.47	10251.7	9561.69
161	SERPINA1	P01009	7505.26	6267.35	5537.99	12505.4	14991	14509.6	7287.73	6881.74	6145.57	7672.36	7416.87	7412.47	10890.2	11196	11072.3
162	SERPINA3	P01011	598.208	498.011	336.714	1279.56	1420.79	1373.47	478.578	786.714	390.667	809.479	981.03	827.968	1160.73	1134.69	1025.09
163	A2M	P01023	17163.5	17246.6	15799.4	10136.9	10205.9	10049.8	13202.6	13251.4	12948.7	11221.6	11742.4	11891.4	13164.5	13669.3	12832.4
164	C3	P01024	21936.9	22456.1	21279.9	22834.9	23286.2	23565.4	19320.7	20647.3	20405.1	24029.4	25388	25310	22791.4	23676.8	21980.3
165	KNG1	P01042-2	26689.1	28178.3	24283	35451.2	35037.4	36037.1	26472.7	28790.4	26588.1	35419.4	36998.1	36753.3	32289.8	33838.9	33510.5
167	IGJ	P01591	7870.13	8481.56	8658.39	3369.99	4183.86	3157.05	1993.62	5712.76	5705.53	6666.61	5281.1	7287.17	1258.16	5334.01	5224.98
168		P01594	394.715	279.848	494.345	859.293	1137.91	463.466	773.723	302.315	416.659	473.973	1252.4	515.016	649.295	587.974	867.003
169		P01599	428.266	222.765	175.726	813.453	319.203	153.3	488.226	425.112	164.071	645.032	859.142	655.595	304.427	219.242	369.722
170	IGKV1-5	P01602	881.827	417.104	1126.76	175.686	542.395	759.778	604.111	698.741	117.625	1090.46	274.72	438.477	726.359	852.666	789.924
171		P01619	2866.61	988.267	1659.81	4197.72	198.531	200.367	3975.66	5306.37	153.707	493.69	508.294	5207.05	1280.84	6399.1	5816.67
172	IGKV3D-7	P01624	274.839	283.076	1180.34	342.389	219.811	536.304	892.819	395.941	173.587	352.392	586.155	483.453	389.475	533.194	1039.83
173		P01700	1171.65	259.646	1173.49	2464.56	2423.15	2556.44	232.376	843.38	642.262	350.308	2046.25	2178.69	2134.64	2864.21	2066.55
174		P01701	190.709	339.318	357.22	1008.5	1887.03	1432.95	379.442	284.711	1276.43	1499.95	1807.61	1877.01	576.049	430.724	1647.33
176		P01706	343.507	259.484	194.617	836.908	133.828	493.244	397.645	363.291	106.048	640.128	305.059	666.865	592.525	408.535	356.411
177		P01714	273.931	372.735	669.536	197.784	577.687	1097.3	375.611	358.737	183.548	540.054	527.958	415.393	296.994	716.258	825.572
178		P01715	399.239	523.619	320.913	485.199	479.422	698.416	424.396	566.827	803.057	468.249	311.309	1556.36	924.354	1113.61	248.798
179		P01717	925.451	275.32	337.067	472.807	2486.58	2502.64	327.266	1299.16	631.283	541.306	400.912	1764.31	445.155	312.724	286.727
186		P01780	240.552	1522.39	634.091	2480.21	2919.93	2798.23	1681.24	390.924	2031.98	2340.07	2029.24	2101.43	475.04	2087.49	2134.04
187		P01782	715.175	218.604	145.841	250.928	384.578	358.696	199.68	262.583	129.023	276.823	611.621	813.058	194.728	498.98	224.177
189		P01817	280.2	174.683	251.485	615.194	621.783	633.378	382.599	221.022	1209.77	146.894	299.966	574.875	371.859	600.711	742.494
191	IGKC	P01834	709416	692656	666991	246303	244589	233773	578897	601672	574071	323424	323117	326335	477564	471665	461578
192	IGHM	P01871	5261.15	5875.67	5238.38	1460.02	1647.11	1835.26	3259.9	3779.77	3689.39	2693.71	2911.15	2939.46	3349.64	3642.08	3469.56
193	IGHA1	P01876	16880.2	18194.9	15924.8	19799.7	22037.2	21107	15795.3	18439.8	17587	17697	19014.4	18877.1	20394.8	22373	19991.9
194	HBD	P02042	564.557	718.622	686.607	142.782	579.351	337.8	290.029	250.791	699.075	661.63	509.474	383.001	144.275	482.236	490.649
195	APOA1	P02647	158171	144520	156377	146699	147936	149699	143882	149714	149329	145592	137470	128464	154348	144881	143457
196	APOE	P02649	8044.33	7950.65	8040.68	17081	16685.3	17431.9	8727.61	10034	9583.86	13768.3	14797.8	15177.6	12536.3	13627.9	12333.2
197	APOA2	V9GYM3	96116.1	122112	105560	161570	150906	144493	110883	109528	112127	132785	134369	133271	122892	133153	124711
198	FGA	P02671-2	4742.7	4876.86	4786.99	8176.25	7524.18	7861.21	5235.22	4720.23	4690.97	7639.07	6867.11	6891.06	6079.8	6516.4	5630.55
199	FGB	P02675	748.709	799.143	762.117	341.651	318.818	332.742	546.041	578.733	523.134	412.583	279.177	440.098	556.163	578.533	553.43
200	CRP	P02741	51.0661	196.512	173.472	4135.64	3709.67	2244.66	860.302	1369.96	925.179	1253.64	1269.56	2488.06	1133.34	1797.52	1864.37
201	APCS	P02743	22529.4	20063.9	21576.1	17668.9	24796.7	22636.8	24432	22456.2	27802.1	22166.1	22452.8	24230.7	29157.4	31061.1	27543.8
202	C1QA	P02745	8582.11	10041.1	6979.82	11936.4	12243.3	13572	7311.43	7649.08	8325.77	12081.9	13816.9	13958.5	11131.2	12003.9	10486.8
203	APOH	P02749	26719.9	27413.6	23710.7	43633.3	42811.5	41592.9	26030.6	28314.3	28129.6	35141.9	36602.4	37282.9	30407.7	35850.9	33323.2
204	LRG1	P02750	3006.03	3249.7	2882.3	5590.39	5212.15	5295.15	4024.43	3938.07	4229.88	5117.46	5731.44	5681.87	4802	5027.54	4916.17
205	FN1	P02751-14	3667.59	3714.89	3552.26	2078.87	1965.84	2065.44	2578.8	2886.57	2837.7	2736.26	2905.68	2984.08	2946.76	3123.25	3039.77
206	RBP4	Q5VY30	16376.2	17393	14887.5	31848.3	32329.9	32766.3	20791.9	20579.7	20304.2	26526.9	28079.9	27717.4	24162.4	28101.1	25214.2
207	AMBP	P02760	8524.62	7734.65	7403.72	33321.7	31033.5	34141.9	15307	16062	16271	24790.2	26977	28097.3	23176.2	24632.8	22709.2
208	ORM1	P02763	94456.7	93212.9	97572.2	159901	172633	169879	116951	117708	112002	130873	130935	136811	121864	135831	138710

209	AHSG	P02765	21897.5	23538.2	20029.2	24515.3	25792.4	25634.2	22379.6	21398.3	19738.3	23999.8	24597.4	23217	22577.7	21723.1	21769.9
210	TF	P02787	92325.5	91225.8	89566.9	101559	99137.2	99198.6	82592.7	82844.8	83017.1	104692	105064	103855	94819	92177.6	90065.9
211	HPX	P02790	108750	106661	103672	168733	160718	171148	115329	113893	111113	146431	154287	153080	123167	126221	137695
212	C4BPA	P04003	14992.1	15168.9	13346.6	18974.7	20474.2	19433.6	13302.6	15033.5	14778.6	20159.8	21762.5	22122.7	18242.7	20150.1	17509.5
213	VTN	P04004	14250.6	15270.8	14103.6	13006.1	12660.3	14618.5	12660.2	14599.3	15467.3	16588.5	17570.4	17828.3	14710.4	16029.5	15062.3
214	APOB	P04114	469.818	503.445	450.647	256.569	253.517	253.628	385.567	424.313	411.52	334.123	337.935	335.395	365.926	387.514	371.334
215	LCAT	P04180	458.126	564.476	465.48	425.595	425.583	448.83	462.177	437.809	422.714	555.436	631.447	533.041	579.792	528.635	469.119
216	HRG	P04196	8721.29	8505.27	7874.71	8484	8668.79	8765.06	8254.47	8030.59	7763.8	8231.61	8257.85	8180.52	8780.65	8842.52	8129.61
217	A1BG	P04217	5479.07	6183.94	6011.6	6329.62	5960.7	6386.35	6064.11	5946.6	6247.3	6181.05	6632.08	6642.77	6491.61	6626.24	6389.59
218	KRT1	P04264	772.499	741.752	770.8	413.631	395.422	398.186	518.627	704.062	634.22	308.15	457.11	505.305	725.769	645.014	640.826
219	VWF	P04275	1734.24	1620.42	1740.86	215.468	242.488	211.439	797.188	926.879	749.349	756.181	987.595	1043	890.577	938.507	791.082
220	IGKV3D-11	P04433	323.046	1016.37	258.034	1087.51	919.873	666.204	581.047	260.15	608.342	316.304	617.637	477.91	329.803	356.834	616.797
221	AMY2B	P0DUB6	98.0009	56.2391	87.0155	118.883	100.664	70.8467	40.7886	48.0529	52.0579	248.904	87.9898	91.4278	67.4811	30.3613	34.9467
222	SERPINA5	P05154	88.3702	115.961	100.249	131.485	177.237	189.681	178.116	179.608	43.7585	120.656	335.853	152.599	90.2941	120.705	251.177
223	F13B	P05160	1239.38	961.496	1223.39	1741.85	1737.76	1830.33	722.383	1133.97	1136.09	1598.56	1826.32	1900.15	1330.92	1728.78	1516.88
224	SERPINA7	P05543	17.0758	117.141	64.0988	98.2628	36.81	92.7228	21.0809	42.6852	30.363	135.445	117.274	154.315	101.189	19.5597	65.0787
225	SERPIND1	P05546	2364.7	2372.88	2084.94	2721.07	2541.94	2782.73	2374.87	2713.51	2604.71	2491.26	2728.77	2757.91	2961.46	3487.47	3007.95
226	BCHE	P06276	53.8916	236.785	435.423	720.147	247.147	347.518	78.7951	284.9	167.934	221.402	220.098	269.843	377.212	416.201	408.239
227	IGKV2D-30	P06310	666.183	6550.7	563.658	479.654	232.253	8922.12	300.797	370.015	305.768	810.348	1055.32	6986.36	674.869	1152.42	424.754
228	IGKV4-1	P06312	421	315.711	507.918	979.601	1004.56	996.237	673.443	1011.06	297.421	661.557	874.439	696.231	720.911	767.221	485.459
229	GSN	P06396	2855.82	3148	2752.16	4231.47	3944.43	4040.1	2943.53	2922.9	2875.93	4032.58	4153.62	4266.17	3550.96	3990.12	3712.54
231	APOA4	P06727	9369.49	8779.57	9188.62	12039.9	13390.5	13335.4	8252.16	8856.02	8882.84	9307.08	9449.95	9665.39	10659.1	11172.7	10407.7
232	C8B	P07358	2720.05	2378.37	2082.72	4629.49	4517.78	4846.61	1391.19	2317.61	2727.58	4111.25	4590.69	4648.06	3661.45	3642.84	2751.9
233	C8G	P07360	4577.4	5220.83	5250.39	8977.96	8697.61	7974.64	4861.83	5956.18	5704.63	7345.49	8364.72	7969.21	7041.63	6358.56	7126.14
234	TUBB	Q5JP53	95.1373	84.5094	72.5226	101.516	239.155	56.4485	50.5629	240.152	270.392	48.2019	284.853	221.083	141.354	67.4873	81.7376
236	HSP90AA1	P07900	112.05	91.2248	122.539	56.4631	148.148	59.8651	21.5982	123.027	84.8304	72.9929	482.663	120.457	183.651	136.916	46.4059
237	UMOD	X6RBG4	218.785	236.648	244.733	197.88	62.0441	82.2477	287.214	326.042	312.108	87.9996	185.249	213.166	325.45	327.717	293.093
238	THBS1	P07996	204.104	222.961	324.942	441.268	413.807	259.528	162.328	312.827	189.405	335.281	394.989	520.383	350.137	290.795	333.838
239	SERPINA6	P08185	2110.51	2429.98	1994.77	2484.41	2428.64	2777.18	2033.16	2253.39	2019.8	3001.07	3112.34	3289.24	2663.09	3026.04	2686.49
240	HSP90AB1	P08238	78.0677	47.501	36.2287	53.5584	216.584	87.6504	23.4705	93.6704	80.8684	165.906	95.4324	29.4062	42.5793	236.554	43.5852
241	LPA	P08519	268.174	277.139	266.327	720.931	772.185	710.549	289.707	302.952	248.264	647.798	804.443	773.609	439.994	511.062	455.884
242	CD14	P08571	820.357	903.531	685.367	1438.43	1450.77	1333.23	864.95	919.582	882.634	1267.17	1597.62	1411.7	1024.41	1115.51	1136.31
243	CFH	P08603	5659.94	5655.58	5465.6	9060.22	9226.63	9626.2	5531.05	5852.81	5761.52	8158.3	8890.32	9253.87	7488.83	7832.77	7458.06
244	SERPINF2	P08697	895.7	1110	743.161	464.333	443.286	452.274	642.44	719.154	767.68	782.303	710.239	663.369	744.921	747.528	887.044
245	C1S	P09871	24443.7	14347.2	15876.1	47535.5	45624.9	48507.2	20789.3	22819.9	16592.5	45908	45721.8	48654.6	29268.6	34682.1	32646.5
246	C4A	P0C0L4	895.758	1093.46	835.557	4769.4	4585.62	4405.11	1863.95	1797.66	1868.32	3363.69	3525.16	3318.41	2705.12	2976.44	2817.89
247	C4B	P0C0L5	1952.57	2071.39	1764.89	12506.9	12568.4	12564.2	4829.11	5317.43	5155.45	8972.06	9530.78	9764.53	7285.82	7772.83	7261.55
248	SAA1	P0DJI8	382.435	183.324	235.714	21209.6	21564.2	21120.3	5268.51	5254.26	8797.95	9730.68	17075.5	17653.5	13466.6	12920.5	7885.18
250	IGLC6	P0DOY3	58273.7	66223.7	51903.5	756894	772423	787592	359180	362294	340295	580684	574826	581177	501709	525440	513691
252	HIST1H1E	P10412	567.726	195.656	199.612	164.094	256.705	160.511	181.185	123.877	232.259	318.057	146.574	611.764	513.255	230.868	109.102
253	opn	Q3LGB0	44.1145	279.078	263.49	317.685	322.212	363.354	283.533	171.195	80.0599	155.776	149.165	236.398	366.817	116.971	373.022
254	C7	P10643	2246.39	2068.57	3600.09	4171.64	4288.13	4779.56	1638.48	2823.4	2512.68	3663.81	4610.79	4924.17	3780.65	2276.99	2183.06
255	CLU	P10909-4	29541.6	30322.1	26728.5	22937.9	24450.3	24065	27175.4	28011.1	28766	26055.1	27340.7	27318.4	31744.8	32564.6	30865.1
256	MBL2	P11226	134.243	85.261	225.492	635.251	473.54	562.069	353.277	647.737	249.775	581.793	628.567	482.505	160.021	580.426	389.256
257	COL6A3	P12111-4	5.65525	73.683	13.7738	7.13729	14.5766	23.4628	9.75691	37.7124	23.0473	25.3304	47.3865	27.2617	32.1339	9.86057	17.3811
258	C6	P13671	1964.59	1936.53	1855.85	2041.32	2233.38	2190.03	1379.49	1518.76	1344.72	2089.24	2193.97	2790.11	1647.73	2048.96	1478.01
259	CPN1	P15169	1015.58	1126.71	1090.95	1121.07	1039.47	672.296	604.042	813.773	575.635	940.102	1243.56	1260.57	1034.21	734.975	854.652
261	IGFBP2	P18065	158.969	338.997	244.495	1445.09	1558.74	1625.35	393.682	537.145	464.917	861.714	1563.89	955.392	639.379	931.5	683.229
262	LBP	P18428	688.906	719.668	625.031	724.187	701.982	670.582	459.206	469.788	502.665	588.034	729.56	818.168	684.036	764.951	600.926
264	ORM2	P19652	28615.4	27609.7	29883.2	55303.7	59822.7	59424.5	40141.3	39893.1	40507	42444.4	42084.9	42150.7	40799.1	42974.2	40463.9
265	ITIH2	P19823	5931.57	6015.68	5329.1	4020.78	4220.22	4102.81	4484.14	4865.68	4640.81	4643.98	4726.62	4773.98	5194.09	5500.86	5131.97
266	ITIH1	P19827	6977.52	7368.46	6354.96	6552.22	6689.69	6709.27	6268.19	6841.13	6432.65	6657	7089.48	7089.02	7397.75	7992.66	7356.14
267	PZP	P20742	23.0327	26.289	10.7812	36.3818	35.0215	32.5286	29.4175	46.842	18.5014	16.9836	12.6059	24.3659	54.0814	20.9973	17.8528
268	C4BPB	P20851	4600.19	5026.05	3409.84	5000.3	5718.16	4990.8	4061.13	4638.55	5910.59	5612.8	5900.71	6591.8	6440.46	5518.08	6471.46
269	GPX3	P22352	1087	2736.88	760.888	415.098	461.613	490.477	746.911	823.679	815.668	674.987	783.096	815.911	985.246	1027.76	996.313
270	CPN2	P22792	2865.32	3092.54	2798.86	2871.32	2734.75	2840.47	2421.3	2703.25	2592.81	3057.39	3144.72	3179.28	3017.28	3156.81	3182.22
271	PROZ	P22891	175.217	484.239	77.9865	34.6598	156.457	54.2573	280.296	192.406	59.4631	821.734	715.621	813.044	220.378	224.898	172.441
274	FBLN1	P23142-4	14984.7	15682.7	16120.4	13681.2	12395.6	12944.1	8380.48	12474.8	9340.36	13242	19666.2	20263	13766.5	15279	14253.6
275	AZGP1	P25311	512.539	493.93	431.423	5526.53	5273.07	5418.81	2455.45	2780.01	2724.35	2886.72	2470.43	2876.89	3069.85	3214.8	3339.76
276	PON1	P27169	5160.51	5972.72	4710.49	2162.83	2152.75	2136.71	3362.41	3705.64	3435.69	3569.78	3732.26	3605.73	3586.8	3741.14	3560.72
277	SERPINA4	P29622	244.908	129.962	122.405	15.3111	473.364	225.062	180.475	107.952	111.037	115.866	290.136	215.68	60.5038	20.7666	13.8131
278	CDH5	P33151	149.203	176.659	83.8527	26.6401	161.101	188.805	150.662	45.627	31.7472	175.365	197.936	196.863	180.852	52.7538	94.5646
279	IGFALS	P35858	1104.83	1115.11	909.198	945.495	900.478	932.951	818.225	884.617	796.083	1055.07	1385.16	1374.86	1286.31	1180.21	1229.97
280	SERPINF1	P36955	1347.21	1375.8	1270.69	2389.07	2432.6	2523.8	1601.86	1776.81	1790.2	2260.48	2436.65	2461.98	2032.26	2301.14	2111.86
281	PTGDS	P41222	65.5319	243.068	1153.88	2665.57	2100.1	2142.08	3809.17	263.937	234.148	413.266	4463.67	2334.45	453.948	211.821	90.331
282	BTD	P43251-4	313.776	340.669	316.791	257.4	267.21	270.993	53.8748	311.821	153.41	277.211	145.572	313.515	311.181	292.652	293.9
283	AFM	P43652	5345.07	5767.6	4959.32	5345.6	5053.74	4853.43	4284.4	4719.85	5052.83	5761.24	6540.77	6690.43	5352.09	5921.64	5436.22
284	MASP1	P48740	278.011	357.656	283.176	388.08	402.892	405.564	275.235	315.307	284.346	252.737	298.59	390.812	356.437	414.726	436.738
285	LUM	P51884	2982.83	2968.66	3156.12	3588.08	3369.17	3369.58	3087.69	3155.58	2875.68	3259.7	3338.59	3250.22	3750.6	3999.07	3450.62
286	PLTP	P55058-3	823.771	763.691	787.09	691.883	660.36	750.061	633.802	675.417	708.48	673.825	793.192	834.006	808.46	805.953	813.829
287	ACTB	P60709	693.053	1004.84	398.777	894.601	809.453	907.142	1186.95	1464.17	799.72	880.61	780.47	1148.76	823.4	854.189	1223.41
289	B2M	P61769	11265.5	12350.7	8188.47	21499.5	22681.6	22457.2	5096.48	12857	3916.61	18859.9	19158.4	19678.4	20149	20600.5	19720.8
291	RPS18	P62269	572.154	297.732	194.123	226.369	254.329	221.551	156.259	791.378	87.0213	222.083	175.162	183.411	259.646	315.954	504.956
293	HIST1H4A	P62805	8222.16	10755.8	6805.37	7482.62	6680.53	6757.89	13956.4	12360.8	12207.8	8780.83	8396.99	9168.72	10055.9	11855.6	12648.1
295	HBB	P68871	15462.9	15718.2	14633.7	15985.1	17073.6	16773.2	14867.2	16586.9	16032.7	16657.2	16752.3	16651.1	17795.4	17242.9	16356.9
296	HBA1	P69905	25853.6	22003.6	22495.2	21050.1	23587.3	22677	24246.9	22901.3	24032.4	24393.3	24400.8	22849.8	20186.2	21515.1	19478.3
297	GPLD1	P80108	457.59	489.171	418.599	485.728	512.334	520.827	357.588	447.54	433.905	509.731	486.573	543.977	500.516	497.783	500.925
298		P80748	489.448	1152.82	1474.23	5289.67	5447.82	10045.5	2871.34	3036.88	3139.7	3549.04	4010.32	4224.47	3731.66	4100.32	3702.36
299	HSPG2	P98160	4.12659	129.816	3.6237	9.66192	4.44292	4.46555	152.404	163.486	160.589	8.4828	5.10133	160.178	16.2963	2.59826	7.31797
300	CFHR1	Q03591	4920.1	5429.22	4719.56	6779.37	6693.97	7084.82	3982.95	4496.57	4651.21	5691.53	6243.1	6301.16	5976.94	6100.72	5624.15
301	HGFAC	Q04756	445.944	558.02	467.046	328.848	333.935	340.468	376.85	458.207	479.61	475.25	506.612	509.45	489.536	518.887	426.818
302	ITIH3	Q06033-2	2451.19	2457.87	1814.53	2994.61	3161.43	3402.23	2291.14	2828.28	2571.72	3132.12	3270.99	3579.77	3208.02	3317.08	3267.09
303	LGALS3BP	Q08380	197.863	334.117	153.043	113.653	152.789	166.824	253.544	273.796	240.811	133.903	221.02	277.484	243.647	235.145	131.933
304	EFEMP1	Q12805-2	304.429	379.565	333.804	1173.15	675.656	1341.24	458.001	526.054	393.146	786.882	785.987	1026.77	977.105	919.938	499.315
305	SPP2	Q13103	647.646	221.675	677.339	1032.21	771.93	792.48	505.238	562.974	563.931	803.752	812.893	1079.18	118.908	83.3375	494.672
306	APOF	Q13790	4083.82	3929.48	3936.44	4614.22	4301.52	3561.1	3267.58	3728.83	3574.02	4094.41	4473.27	3788.27	4505.97	4040.54	4176.11
307	HABP2	Q14520-2	1209.22	1271.17	1146.57	1487.63	1939.88	1614.14	935.459	1165.54	1101.46	1359.93	1625.42	1713.04	1392.87	1547	1310.12
308	ITIH4	Q14624	5730.24	5853.32	4854.58	6007.21	5637.68	5668.3	6008.49	6108.93	6292.14	4918.1	5268.01	5401.18	6748.7	7228.8	7020.84
310	ADIPOQ	Q15848	151.39	310.143	746.159	267.686	758.217	966.118	559.458	84.6487	254.719	328.97	295.327	866.681	893.917	141.375	145.67
311	ECM1	Q16610-4	311.292	339.774	307.132	375.442	25.2171	422.431	301.656	156.584	111.914	134.976	345.735	425.125	365.01	340.129	347.031
321	WHAMM	Q8TF30	2391.96	2633.41	2487.59	814.647	791.529	744.754	1670.89	1736.26	1664.63	1053.74	979.919	971.01	1341.99	1415.3	1384.3
322	RYR2	Q92736	282.009	260.519	4.21137	1146.16	1182.43	1286.05	309.845	328.495	844.476	383.432	395.007	1105.61	140.717	1125.22	473.708
324	PRG4	Q92954-3	140.321	154.177	134.854	124.779	144.311	144.874	159.889	142.007	174.624	182.898	175.687	193.644	160.136	156.489	157.82
325	PIK3IP1	Q96FE7-4	486.916	432.801	387.452	338.65	306.752	391.301	292.89	338.716	284.661	126.071	418.725	431.039	419.318	342.559	560.743
326	CPB2	Q96IY4	916.39	1049.14	1126.85	1276.21	1239.12	1260.18	1028.95	1234.43	1289.73	1389.78	1435.44	1434.85	1357.71	1407.37	1270.63
327	CNDP1	Q96KN2	315.246	409.903	59.1549	294.16	363.944	377.291	84.196	336.059	103.994	79.7951	101.191	226.153	132.812	34.0487	81.9209
328	PGLYRP2	Q96PD5	2560.23	3175.12	2556.29	3077.7	2809.31	2912.57	2291.25	2542.81	2579.82	2884.78	3299.18	3082.34	2986.37	3262.67	3048.41
329	HMCN1	Q96RW7-2	2245.07	3316.9	3176.7	6619.28	4785.48	5710.98	2642.85	3322.84	2735.16	3631.28	2223.63	3150.43	3168.15	3362.48	6074.92
332	C1RL	Q9NZP8	703.36	727.398	695.24	614.061	664.296	784.776	573.937	665.645	678.929	878.021	701.526	866.708	780.25	755.817	869.859
333	FETUB	Q9UGM5	460.548	605.673	623.396	826.415	958.055	1036.84	386.078	432.429	504.078	671.693	850.584	944.022	481.942	543.183	666.563