Short abstinence: Impact on the seminal plasma proteome and accessory sex gland secretions

By Dale Mark Goss

Thesis presented in fulfilment of the requirements for the degree of Master of Science in the Faculty of Medicine and Health Sciences at Stellenbosch University

Supervisor: Professor Stefan S. Du Plessis

Co-supervisor: Professor Gerhard van der Horst

Declaration

By submitting this dissertation, I declare that the entirety of the work contained therein is my own, original work, that I am the sole author thereof, that reproduction and publication thereof by Stellenbosch University will not infringe any third party rights and that I have not previously in its entirety or in part submitted it for obtaining any qualification.

Dale M. Goss March 2018

Abstract

Various studies have sought to determine the typical versus optimal abstinence period after which semen samples should be collected, and many have been found to be contradictory. Several factors influence the semen microenvironment and subsequent sperm basic and functional parameters. In this study we focused on important biomarkers of prostate, seminal vesicle and epididymal secretion. Furthermore, extensive proteomic analysis of seminal plasma was performed for a more comprehensive understanding of the observations. Semen samples were obtained from normozoospermic donors (n = 16) after 4 days and 4 hours of ejaculatory abstinence (EA) and standard semen analysis was performed with the assistance of computer aided sperm analysis (CASA), while the seminal plasma citric acid, neutral alpha-glucosidase and fructose concentrations were measured photometrically with commercially available assay kits. Protein identification was performed using advanced mass spectrometric techniques and pathways were analysed on both Reactome and String databases.

Results of this study displayed significant decreases in semen volume, sperm concentration, total sperm count, and pH after 4 hours of ejaculatory abstinence when compared to 4 days. Furthermore, increases in total sperm motility and progressive motility after short EA periods were observed, accompanied by significant reductions in all epididymal and accessory sex gland biomarker concentrations. However, due to the decreased sperm number, these concentrations translated to a significant increase in citric acid and a decrease in fructose available per spermatozoon, which, along with the effects on semen pH, could more than likely be responsible for increased metabolic function and subsequent increase in the available energy for sperm motility.

Proteomic analysis identified 22 differentially expressed seminal plasma proteins, with 18 proteins upregulated after 4 days of EA and 3 upregulated after 4 hours of EA. Of the proteins differentially expressed, 5 proteins from 4 days of EA and 2 proteins from 4 hours of EA, were identified to be related to sperm function and thus selected for pathway analysis. These proteins were found to be prominent components of cellular processes including metabolism, apoptosis and cell process regulation, which can be linked directly and indirectly to sperm motility parameters. To conclude, the mechanisms by which very short EA improves sperm motility depends on seminal plasma composition thereby affecting metabolic function and protein interactions.

Opsomming

Verskeie studies het probeer om die tipiese versus optimale onthoudingsperiode te bepaal waarna semenmonsters versamel moet word, maar heelwat teenstrydighede is gevind. Verskeie faktore beïnvloed die semen mikro-omgewing en daaropvolgende sperm-basiese en funksionele parameters. In die huidige studie is daar gefokus op belangrike biomerkers in sekresies afkomstig vanaf die prostaat, seminale vesikels en epididimis. Uitgebreide proteomiese analises is ook op die seminale plasma uitgevoer om sodoende 'n meer omvattende begrip vir die waarnemings te verkry. Semenmonsters is bekom vanaf normozoospermiese skenkers (n = 16) na 4 dae en 4 ure van ejakulatoriese onthouding (EO) en ŉ standaard semenanalise is uitgevoer met behulp van rekenaargesteunde spermanalise (RGSA), terwyl die seminale plasma sitroensuur, neutrale alfa-glukosidase en fruktose konsentrasies fotometries bepaal is met kommersieel beskikbare toetsstelle. Proteïenidentifikasie is uitgevoer met behulp van gevorderde massa spektrometriese tegnieke en proteoompad interaksies is geanaliseer op beide Reactome en String databasisse.

Die resultate van hierdie studie toon beduidende afnames in semenvolume, spermkonsentrasie, totale spermtelling en pH aan ná 4 uur van EO in vergelyking met 4 dae. Verder is toenames in totale spermmotiliteit en progressiewe motiliteit na kort EO periodes waargeneem. Dit is vergesel van 'n betekenisvolle vermindering in alle epididimale en bykomende geslagsklierbiomerkerkonsentrasies. Nietemin, as gevolg van die verminderde spermgetal, herlei hierdie konsentrasies egter tot 'n beduidende toename in sitroensuur en 'n afname in fruktose beskikbaar per spermatozoon, wat tesame met die effekte op semen pH waarskynlik verantwoordelik kan wees vir verhoogde metaboliese funksie en daaropvolgende toename in die beskikbare energie vir spermmotiliteit.

Proteomiese analise het 22 differensiaal uitgedrukte seminale plasma proteïene identifiseer, waarvan 18 proteïene opgereguleer was na 4 dae van EO en 3 opgereguleer was na 4 ure van EO. Van die proteïene wat differensiaal uitgedruk was, is 5 proteïene vanaf 4 dae EO en

2 proteïene vanaf 4 ure EO gekoppel aan spermfunksie en gekies vir verdere proteoompad interaksie analise. Daar is bevind dat hierdie proteïne prominente rolspelers is in sellulêre prosesse, insluitende metabolisme, sellulêre motiliteit, apoptose en selprosesregulering. Om mee af te sluit, die meganismes waardeur baie kort EO spermmotiliteit verbeter berus op seminale plasma samestelling met gevolglike effekte op metaboliese funksie en proteïen interaksies.

Acknowledgements

Professor Stefan Du Plessis, Emeritus Professor Gerhard van der Horst and Bashir Ayad, for their academic insight, unwavering support and greatly appreciated optimism.

Dr Marè Vlok, (Central Analytical Facility) and Dr Suzelle Hattingh (Division of Medical Physiology) for their expertise guidance in proteomics.

Division of Medical Physiology, in particular the Stellenbosch University Reproductive Research Group, for all the assistance and many happy memories.

Stellenbosch University for granting me a bursary allowing me to pursue this degree.

Dedication

To my parents Mark and Zelna, and my partner Donna, for your endless support and love, without which I would not have been able to achieve what I have.

Table of Contents

Chapter 1: Introduction

Chapter 2: Literature review

Chapter 3: Materials and methods

Chapter 4: Results

Chapter 5: Discussion

Appendices

List of Tables

Page

List of Figures

Page

Chapter 1

Chapter 2

Chapter 3

Chapter 4

Chapter 5

Chapter 7: Appendices

Abbreviations

µL	Microlitre
µm	Micrometre
µmol	Micromole
1D	One-dimensional
Ac-CoA	Acetyl coenzyme A
ACLY	ATP-citrate synthase
ADP	Adenosine diphosphate
AKT1	V-akt murine thymoma viral oncogene homolog 1
ALH	Amplitude of lateral head displacement
AMP	Adenosine monophosphate
AR	Acrosome reaction
ART	Assisted reproductive techniques
ATP	Adenosine -5'-triphosphate
BCF	Beat-cross frequency
CASA	Computer-aided sperm analysis
CAT	Catalase
CO_2	Carbon dioxide
CoA	Coenzyme A
CRYZ	Crystallin, zeta (quinone reductase)
CYBB	Cytochrome b-245, beta polypeptide
CYP2B2	Cytochrome P450, family 2, subfamily B
Da	Dalton
DECR1	Mitochondrial 2,4-dienoyl-CoA reductase
DMSO	Dimethyl sulfoxide
DNA	Deoxyribonucleic acid
DNase I	Deoxyribonuclease-1
EA	Ejaculatory Abstinence
ERK	Extracellular signal-regulated kinases
FADH2	Flavin adenine dinucleotide, reduced
FDR	False discovery rate
g	Gravity
GSR	Glutathione reductase

GTP	Guanosine-5'-triphosphate
HAM	Hyperactivation motility
HCL	Hydrochloric acid
hPEBP4	Human phosphatidylethanolamine-binding protein 4
HSP	Heat-shock protein
HSPA2	Heat-shock protein A2
kDa	Kilodalton
LC-MS/MS	Liquid chromatography tandem mass spectrometry
LIN	Linearity
M	Molarity
M	Oxidation
MAP2K11	Mitogen-activated protein kinase kinase 1.
MAPK	Mitogen-activated protein kinases
mg	Milligram
min	Minutes
mIU	Milli-international unit
mL	Millilitre
mm	Millimetre
MORC2	MORC family CW-type zinc finger protein 2
MRPL17	Mitochondrial ribosomal protein L17
MRPL23	Mitochondrial ribosomal protein L23
MRPL27	Mitochondrial ribosomal protein L27
MRPL47	Mitochondrial ribosomal protein L46
MRPLA47	Mitochondrial ribosomal protein L47
MS	Mass spectrometry
MST4	Mammalian STE20-like protein kinase 4
mTOR	Mammalian target of rapamycin
N^+	Nitrogen
NADH	Nicotinamide adenine dinucleotide, reduced
NAG	Neutral alpha-glucosidase
NaOH	Sodium hydroxide
NCF1	Neutrophil cytosolic factor 1
NCF2	Neutrophil cytosolic factor 2
nIU	Nano-international unit

nm	Nanometre
NOS3	Nitric oxide synthase 3 (endothelial cell)
NQ	Demamidation
OA	Oxaloacetate
OD	Optical density
PBS	Phosphate-buffered saline
PHPT1	Phosphohistidine phosphatase
Pi	Phosphate ion
PK	Protein kinase
PNP	Para (4)-Nitrophenol
PNPG	Para (4)-Nitrophenyl-alpha-D-glucopyranoside
PNPG7	Para (4)-Nitrophenyl-alpha-D-glucopyranoside
PP	Protein phosphatase
PRKCA	Protein kinase C, alpha
PRKCB	Protein kinase C, beta
PSA	Prostate-specific antigen
PSMA4	Proteasome subunit, alpha type, 4
PSMA5	Proteasome subunit, alpha type, 5
PSMB1	Proteasome subunit, beta type, 1
PSMB3	26S proteasome non-ATPase regulatory subunit 3
PSMB4	Proteasome subunit, beta type, 4
PSMC4	Proteasome 26S subunit, ATPase, 4
PSMC6	Proteasome 26S subunit, ATPase, 6
PSMD12	Proteasome 26S subunit, non-ATPase
PSMD3	Proteasome 26S subunit, non-ATPase, 3
PSMD4	Proteasome 26S subunit, non-ATPase, 4
PSMD6	Proteasome 26S subunit, non-ATPase, 6
PSMD8	26S proteasome non-ATPase regulatory subunit 8
PTEN	Phosphatase and tensin homolog
RICTOR	Rapamycin-insensitive companion of mammalian target of rapamycin
RNA	Ribonucleic acid
ROS	Reactive oxygen species
RPTOR	Regulatory-associated protein of mTOR
SCA®	Sperm-class analyser

SDS-PAGE	Sodium dodecyl sulphate polyacrylamide gel electrophoresis
SE	Standard error
STK11	Serine/threonine kinase 11
STK24	Serine/threonine kinase 24
STK25	Serine/threonine kinase 25
STR	Straightness
STRADA	STE20 - related kinase adaptor alpha
STRADB	STE20 - related kinase adaptor beta
STRADB	STE20-related kinase adaptor beta,
SURRG	Stellenbosch University reproductive research group
T.S.C.	Total sperm count
TBARS	Thiobarbituric acid reactive substrates
TCA	Trichloroacetic
TCEP	Triscarboxyethyl phosphine
Thr	Threonine
TNF	Tumour necrosis factor
UBE2K	Ubiquitin-conjugating enzyme E2 K
VAP	Average path velocity
VCL	Curvilinear velocity
VSL	Straight-line velocity
WHO	World Health Organisation
WOB	Oscillation index
ZAG	Zinc-alpha-2-glycoprotein
ZP	Zona pellucida

Chapter 1

1. Introduction

1.1. Background

The incidence of infertility is approximately 15-20% and is a growing concern in the field of reproductive physiology. Among infertile couples, it is projected that causation lies predominantly with the female in 38% of the cases, and 20% of the cases can be attributed to males. Whereas 27% of observed incidents of infertility among couples have both male and female abnormalities (Boivin *et al.,* 2007). Additionally, no evident cause is identified for the remaining 15%. Male factor infertility is of particular interest as there are many cases which remain unexplained.

Standardized semen analysis, according to the World Health Organization (WHO), remains the initial screening and cornerstone for the evaluation of male sperm quality and patient health (van der Horst & du Plessis, 2017). As stated by the prescribed guidelines of the WHO, subjects must remain abstinent for a minimum period of 48 hours, but no longer than 7 days prior to collecting a sample for a standard semen analysis (WHO, 2010). Various studies have sought to determine the typical versus optimal time after which human semen samples should be collected for favourable sperm functional parameters, as well as use in assisted reproductive techniques (ART), whilst the results are often found to be contradictory. The results from studies performed by Bahadur *et al.* (2016)*,* Alipour *et al.* (2015, 2017) and Ayad *et al.* (2017), challenge the generally accepted guidelines for length of ejaculatory abstinence (EA), since their results show that as little as 40 min, 2 hours and 4 hours of EA yield significantly better sperm samples from a functional perspective. Despite the fact that this study was performed on normozoospermic men, future studies on infertile men could possibly lead to similar findings, thereby advocating shorter abstinence periods as a strategy to improve the outcome of natural conception and ART. Furthermore, ejaculates of both short and long abstinence were collected in quick succession from the same donor, thus eliminating confounding variables.

In the current study we will attempt to further explain the significant results obtained by Ayad *et al*. (2017) by analysing the epididymal and accessory sex gland biomarkers and protein changes in seminal plasma and the possible contribution to sperm function from subjects with 4 hours of EA. Minimizing subject variation by selecting samples from normozoospermic, healthy males between the ages of 19 to 25 may reduce variation in physiological conditions allowing EA to be the primary intervention. The development of highly accurate mass spectrometric techniques, allows for the investigation of a broad array of complex protein and peptide profiles of both plasma and cell components. In this study the proteome of the seminal plasma will be analysed thus providing a potentially more detailed and comprehensive explanation for the functional differences observed between short and long periods of EA. The seminal concentrations of three important molecules, namely: fructose, citric acid and alpha-glucosidase were also measured as markers of epididymal and accessory sex gland function, for a more comprehensive comparison into biochemical differences between samples. Considering the absolute amount of each of these constituents per spermatozoon, may furthermore be considered as a more accurate indicator of their true effect on sperm quality, as semen volume and total sperm count (T.S.C.) must be taken into consideration.

1.2. Motivation for the study

The optimal period of EA in order to maximise the fertilizing capacity of the male factor has been debated for many years. WHO (2010) guidelines state that a minimum of 48 hours, but no longer than 7 days of EA are ideal for standard semen analysis. This may also provide a guideline for the possible improvement of basic semen parameters with couples experiencing difficulties in naturally conceiving, as well as in use in ART. The study by Ayad *et al.* (2017) attempted to explain the differences by means of basic semen analysis as well as functional parameters including acrosome reaction (AR), DNA fragmentation, reactive oxygen species

(ROS eg. superoxide), thiobarbituric acid reactive substrates (TBARS) and antioxidant activity (catalase and superoxide dismutase). There were significant increases in motility parameters and expected basic parameters including volume, pH, total sperm count (T.S.C.) and concentration observed after 4 hours of EA. Ejaculated spermatozoa are differentiated cells and accordingly post-spermatogenesis/post-epididymal, and the main changes/effects are to be exerted by the composition and influence of the seminal plasma (Elzanaty *et al*., 2005; Said *et al.,* 2009). Therefore, seminal plasma, and the composition thereof, has been selected as a biochemically significant medium for the analysis of the effects of abstinence. Additionally, considering how important proteins are to the functioning of all living cells, it was decided that it would be greatly beneficial to further explain these differences in the protein composition of seminal plasma using advanced liquid chromatography tandem mass spectrometry (LC-MS/MS) techniques. Furthermore, none of the studies on very short abstinence have comprehensively analysed the accessory sex gland secretions as part of the seminal plasma as a key attributor to these observations (Alipour *et al.,* 2015; Ayad *et al.,* 2017; Bahadur *et al.,* 2016). In this study, focussing on citric acid, fructose and neutral alpha-glucosidase may help in elucidating possible mechanisms by which very short EA has on sperm quality.

1.3. Preliminary study

Sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) was performed on 2 seminal plasma samples obtained from normozoospermic men having undergone 3 – 4 days of EA, in order to identify a suitable range of protein concentrations for an effective proteomic analysis. Once isolation of seminal plasma was performed using the double wash technique (350g, 15 minutes), increasing volumes of sample were added to each well and allowed to run and separate according to their molecular mass (see Figure 1.1). Refer to materials and methods for full protocol on SDS-PAGE and LC-MS/MS.

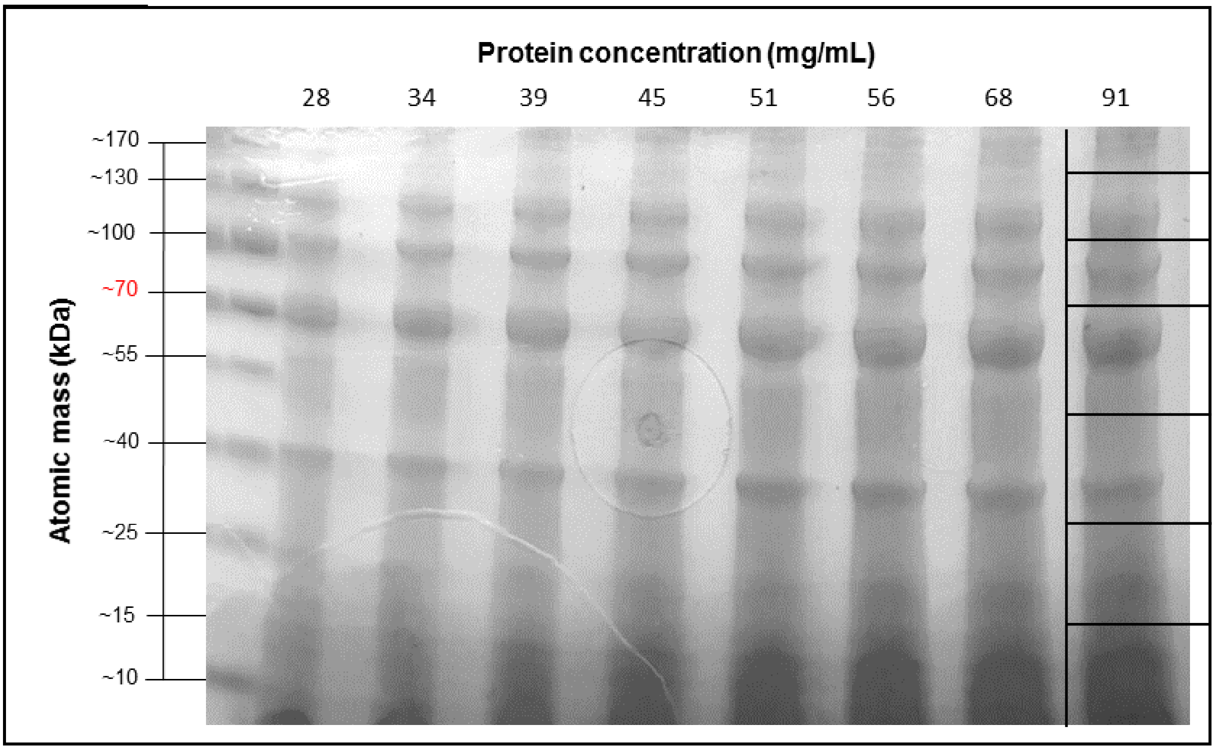


Figure 1.1. SDS-PAGE Gel end product

The SDS-PAGE gel displays separated and stained proteins from the largest molecular weight (Top) to the lowest Molecular weight (Bottom).Bands were excised from the column containing 91mg/mL of protein as indicated by the lines on the figure.

The column containing 91mg/mL of protein was then excised into 7 fractions, which were placed into separate Eppendorf tubes and de-stained. Each fraction was then homogenized and LC-MS/MS was performed resulting in a comprehensive proteome. Over 400 proteins at 1% false discovery rate (FDR), were identified in the seminal plasma which represented a multitude of biochemical and physiological functions. The fractions of proteins where characterized according to biological processes (see Figure 1.2) as well as cellular components. It was noted that a large portion of the proteins identified were intracellular proteins from a multitude of cell portions. Although the cellular function of around 60% of identified proteins was unknown, nearly 45% are involved in celullar processes and 35% are involved in metabolic processes. Furthermore, just less than 10% of the identified proteins are known to be involved in reproduction and reproductive processes.

Another major hurdle when grouping fractions was the issue of high abundance proteins suppressing signals from low abundance proteins. We attempted to reduce the effect of this by grouping specific fractions with similar protein ranges in order to obtain a result which the proteins of interest are represented with the greatest amount of accuracy.

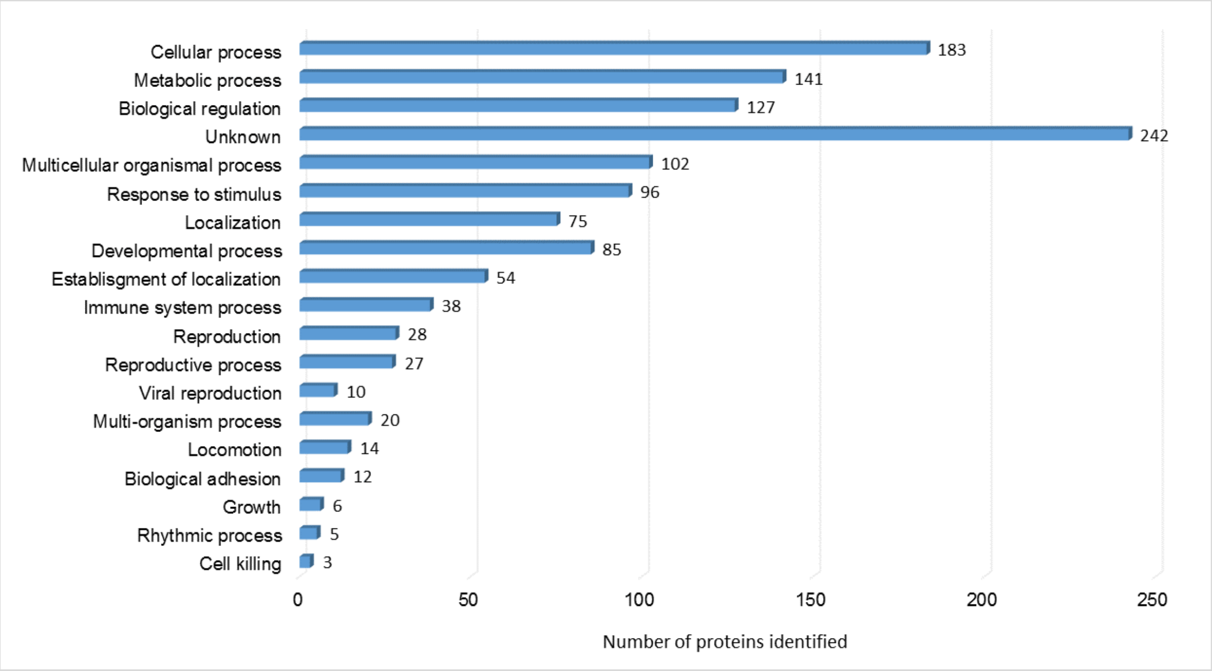


Figure 1.2. Total number of proteins identified in this pilot study by LC-MS/MS using the Uniprot human database related to each stated biological process.

It was concluded that sufficient protein content may be identified in seminal plasma, and that utilizing between 90 and 100 mg/mL of protein per pool of samples, would optimize the protein analysis performed with the available techniques and tools. Furthermore, excising each column into 7 fractions as illustrated in Figure 1.1, would be adequate for the purpose of accurate comparison of expressed proteins between groups.

1.4. Thesis organization

An extensive overview of the current literature relating to abstinence, sperm maturation and the importance of seminal plasma, seminal proteomics and the composition of seminal plasma relating to the secretions from the accessory sex glands will be discussed in chapter 2. Chapter 3 will provide the materials and methods utilized in this study. The results will be presented in chapter 4 and will be discussed according to each objective in chapter 5. Chapter 6 will conclude the study by focusing on the results of each objective and Chapter 7 contains appendices including all proteomic data.

1.5. Setting of the study

The study was performed at the Stellenbosch University Reproductive Research Group (SURRG) laboratory in the Division of Medical Physiology, Faculty of Medicine and Health Sciences, Stellenbosch University, Tygerberg. All proteomic analysis was executed at the Central Analytics Facility, Faculty of Medicine and Health Sciences, Stellenbosch University.

1.6. Aims and objectives

The aim of this study is to provide more comprehensive insight into the biochemical and physiological properties of seminal plasma after a short ejaculatory abstinence period of 4 hours compared to 4 days, in normozoospermic males in order to identify possible mechanisms of variations in sperm functional parameters.

Objective 1: Evaluate the relationship between 4 days and 4 hours of EA by comparing basic semen parameters such as pH and volume, as well as sperm parameters including concentration, total sperm count (T.S.C.), motility and kinematics.

Objective 2: Investigate the role of prominent epididymal and accessory sex gland biomarkers in abstinence and how they relate to sperm functional parameters.

Objective 3: Identify differentially expressed proteins in seminal plasma after 4 days and 4 hours of EA and the subsequently up regulated protein pathways related to sperm functional parameters.

1.7. Conclusion

Male factor infertility has become an increasing concern in the study of human reproduction. Further understanding the effects which storage of sperm in the epididymis have on sperm functional parameters post-ejaculation may open further avenues for low-cost methods of sperm quality improvement, from a functional perspective. Basic and functional semen parameters remain key indicators of sperm fertilizing capacity, thus comparing these parameters to several epididymal and accessory sex gland secretions may aid in the elucidation of EA period and its subsequent role in sperm quality. Furthermore, utilizing modern mechanisms of identifying differentially expressed proteins between these two EA periods as well as the subsequent pathways which are activated or inhibited, might provide additional insight into the physiological mechanisms of very short EA.

Chapter 2

2. Literature review

2.1. Abstinence and fertility

Standardized semen analysis, according to the WHO, remains the cornerstone of sperm quality assessment, yet there are many cases which still require further research in order for the pathophysiology of infertility to be more comprehensively understood. As stated by the prescribed guidelines of the WHO, subjects must abstain for a minimum period of 48 hours, but no longer than seven days prior to collecting a sample for a standard semen analysis. Basic semen parameters such as T.S.C., motility, morphology and concentration are still considered to be the primary predictive factors when it comes to defining the quality of a semen sample, despite variability in sperm production in the same subjects. Approximately 15–20% of human couples are affected by infertility and about a third of these cases of infertility can be attributed to men (Moore & Reijo-Pera, 2000). Sperm motility in particular is believed to be one of the most important parameters when determining the fertilizing ability of ejaculated sperm (Bongso *et al.,* 1989; Donnelly *et al.,* 1989). Furthermore, computer-aided sperm analyses (CASA) has been proven as an accurate and reliable method of motility analysis in clinical and research settings (Hirano *et al.,* 2001; Larsen *et al.,* 2000)

The negative effects of prolonged EA on basic semen parameters such as motility, morphology and viability have been widely reported but the most effective abstinence period is still under debate (Bedford, 1994; Turner, 2008). In the final stage of spermatogenesis, whereby the spermatozoa are subsequently released into the epididymis, they lose the ability of biosynthesis, repair, growth and cell division, and are extremely simple in their metabolic functions (Hammerstedt, 1993). The spermatozoa must then pass through the length of the epididymis where they undergo a series of biochemical and physiological changes which mature the cells before they are ejaculated (Robaire *et al.,* 2006). There are variations in the time in which the spermatozoa spend in the testis, caput, corpus and cauda of the epididymis (Bishop & Walton, 1960). This epididymal transit time has been estimated to be between 2 to 11 days and can be influenced by ejaculatory frequency which affects the rate of passage through the cauda (Amann, 1981; Johnson & Varner, 1988). Prolonged EA could increase exposure of spermatozoa to the damaging effects of ROS in these areas, primarily generated by abnormal spermatozoa and granulocytes (Ayad *et al.,* 2018). This contribution from these spermatozoa to the ejaculate is known to impair semen quality unless regularly ejaculated (Mortimer, 1994). A large recent study which investigated the influence of abstinence on male fertility of over 2000 samples, attributed the decrease in sperm quality after extended periods of EA to ROS-associated DNA damage (Comar *et al*., 2017). It is generally agreed that sperm concentration will increase with increased EA, yet it has been shown to have a negative impact on other sperm parameters such as motility and viability (De Jonge *et al.,* 2004; Magnus *et al.,* 1991; Pellestor *et al.,* 1994). The variation in total and progressive motility of sperm after different periods of EA has previously been attributed to the exposure to varying concentrations of accessory sex gland secretions in the semen microenvironment (Elzanaty *et al.,* 2005).

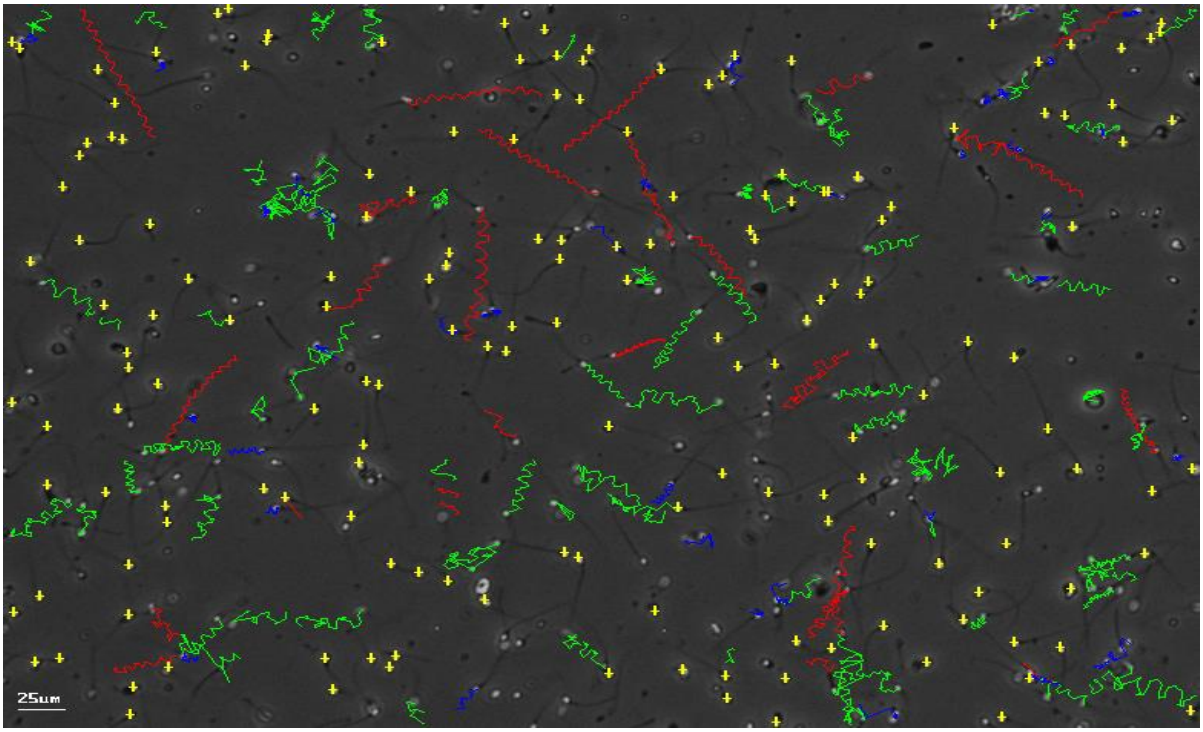
Another question arises regarding whether these ideal abstinence periods apply to normozoospermic men or those with sub-quality sperm samples. Many studies have shown conflicting results attributable to this predicament. One study has shown that as little as one hour of EA could increase volume, concentration and motility of spermatozoa in patients with unacceptable ejaculate quality (Bar-Hava *et al.,* 2000). Another, much larger study found that in oligozoospermic men, morphology and motility were inversely proportional to the length of EA (Levitas *et al.,* 2005). Furthermore, in a clinical study on couples with male factor infertility, increased chances of successful ART were observed with as little as two hours of EA (Alipour *et al.,* 2015). It was presumed that these results were due to the observed increase in sperm motility, but further analysis of biochemical factors in the seminal plasma may help us to elucidate the reasons for these findings. Similarly, a study with an abstinence period of 40 minutes found significantly improved motility parameters in the chosen cohort of oligozoospermic men (Bahadur *et al.,* 2016).

With regard to variations in the sperm quality diagnosis of individuals, it is generally accepted, as shown in early and recent studies on healthy normozoospermic men, sample quality gradually increases with increased abstinence but sharply decreases between 11 and 14 days, yet does not decrease when the EA is shortened (Agarwal *et al.,* 2016; Levitas *et al.,* 2005). Another study performed on both oligozoospermic and normozoospermic donors providing multiple successive samples after an extended EA (up to 10 days) found that motility significantly increased for oligozoospermic donors (Cooper *et al.,* 1993). This reiterates the belief that even though this study will focus on normozoospermic men, the findings may help in providing more insight into a cost effective method to increase the success rate of ART and natural conception in oligozoospermic men.

2.2. Spermatogenesis, sperm capacitation and motility

Spermatogenesis is a complex growth, cell division and maturation process composed of 3 distinct stages occurring within the walls of the seminiferous tubules of the testis. Firstly mitotic proliferation and maturation of stem cell-derived spermatogonia; secondly, two meiotic cleavages form haploid spermatocytes, and finally, spermiogenesis occurs which consists of the maturation of round spermatids into elongated spermatids and subsequent spermatozoa with condensed and elongated genetic material (Stukenborg *et al.,* 2014). Each individual germ cell undergoes intermittent resting phases during cell growth and maturation. Spermatogenesis is highly dependent on optimal conditions in the testis, and has been found to be regulated by several factors including DNA methylation and histone replacement by protamines (Song *et al.,* 2011).

The significance of sperm motility parameters has been extensively studied and found to be positively correlated with sperm fertilizing capacity in several human and animal models (Davis *et al.,* 1991; Hirano *et al.,* 2001; Larsen *et al.,* 2000; Rhemrev *et al.,* 2001; Terriou *et al.,* 1994). The guidelines for assessment of sperm presented by the WHO (2010) identify 4 key variations of motile sperm to be considered as adequate categories of sperm motion namely, rapid progressive motility (type a), slow progressive motility (type b), non-progressive motility (type c) and immotile (see Figure 2.1).



Rapid progressive motility (type a)	**Non-progressive motility (type c)**
Slow progressive motility (type b)	**Immotile**

Figure 2.1. Photomicrograph displaying the various types of progressive motility of spermatozoa assessed using Computer-aided Sperm Analysis (CASA).

Utilizing CASA to determine the intricacies of sperm hyperactivation has been identified as an effective method of determining changes in sperm fertilizing capacity as these parameters are known to be directly related to fertility (Larsen *et al.,* 2000). Generally, the trajectories of spermatozoa are smooth arcs due to the symmetrical waveform of the flagellum (Alavi et al., 2009). The velocity values that are determined are: curvilinear velocity (VCL), straight-line velocity (VSL), and average path velocity (VAP) (see Figure 2.2). The VCL refers to the total distance that the sperm head covers in the observation period, and is always the highest of the 3 velocity values. The VSL is determined from the straight-line distance between the first and last points of the trajectory, and provides the net space gain in the observation period. This is always the lowest of the 3 velocity values for any spermatozoon. The VAP is the distance the spermatozoon has travelled in the average direction of movement during the observation period. Furthermore, due the fact that trajectory shape influences velocity values, these values must be compared (Mortimer, 1994). This is performed by considering the ratios of these velocities, they are as follows: linearity (LIN = (VSL/VCL) x 100), straightness (STR = (VSL/VAP) x 100) and oscillation index (WOB = (VAP/VCL) x 100).

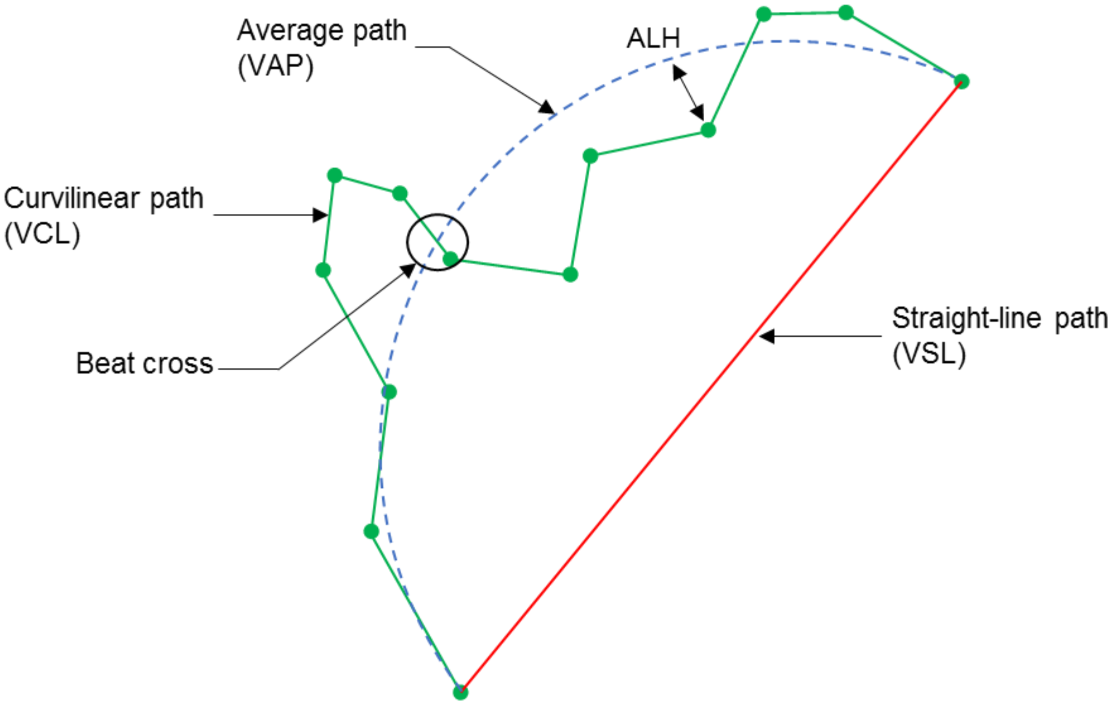


Figure 2.2. Diagram illustrating the typical trajectory of progressively motile sperm and the various parameters which are assessed using the SCA®

Once stored spermatozoa are ejaculated, the main physiological changes which occur are attributed by influencing factors in seminal plasma released by the epididymis, accessory sex glands and other tissues (Elzanaty et al., 2005; Said et al., 2009). Ejaculated spermatozoa, primarily bathing in cauda epididymal fluid are exposed to most, if not all secretions from the accessory sex glands *in vitro*. *In vivo*, however, not all sperm are necessarily exposed to the majority of the secretions from these glands, since sperm fractions are delivered in differential order and are exposed to seminal plasma with different concentrations of constituents, including metabolites, peptides and proteins (Rodríguez-Martínez *et al.,* 2011). Apart from differential order of sex gland secretion, once ejaculated, sperm must move out of the seminal plasma and travel through the cervix within minutes. As soon as sperm are moving out of the ejaculate and passing the cervical mucus, they are rapidly but passively transported in the uterus (oxytocin) and then enter fallopian tubes where they undergo several biochemical changes, collectively called capacitation (Gadella & Visconti 2006).

Sperm capacitation and motility are closely related. Sperm undergo several changes as they travel through the male and female reproductive system and these changes involve molecules integrating into the sperm plasma membrane during epididymal maturation (Ickowicz *et al.,* 2012). The removal or alteration of these molecules prepares the sperm toward successful binding to the egg and subsequent fertilization (Ickowicz *et al.,* 2012).

The process of capacitation can be divided into two prominent signalling events: fast and slow. These events take place during the passage of sperm from the epididymis to the female reproductive tract. The fast events include activation of the vigorous and asymmetric movement of the flagella and these happen as soon as the sperm leave the epididymis (Visconti, 2009). The slow events include changes in the pattern of movement (hyperactivation) and subsequent metabolic changes involved (Visconti, 2009). Eventually, all these changes will lead to the capacitation of the sperm and as a final point, the following events occur: hyperactivation, the ability to carry out the acrosome reaction (AR) induced by biological agonists, zona pellucida (ZP), or progesterone; exhibition of chemotactic behaviour and the ability to fertilize an oocyte.

2.3. Important seminal plasma components

Seminal plasma is made up of secretions from several sources i.e. the accessory sex glands namely the seminal vesicles (65%–75%), prostate (25%–30%), bulbourethral glands (1%); the testicular Sertoli cells (2-5%); and the epididymis (~`1%). These contributions create a nutrient and mineral rich fluid containing a multitude of signalling molecules vital to sperm function and vitality (Mann & Mann, 1982). The importance of these accessory glands is highlighted whenever they lose their functionality, resulting from underlying pathophysiological conditions leading to an unfavourable seminal plasma environment which has a subsequent deleterious impact on fertilizing capacity (Lewis, 2007). The seminal plasma microenvironment is important as the spermatozoon is the only cell that performs its functions outside the body of the organism it originates from (Baccetti, 1984). In addition to acting as a medium transporting spermatozoa to the oocyte, seminal plasma fulfils three pivotal roles in ensuring that fertilization occurs (Poiani, 2006):

- It contributes to the process of sperm capacitation (Khan *et al.,* 1992).
- It influences sperm competition through allospermicidal properties and modification of spermatozoa velocity parameters (Charlesworth & Charlesworth, 1999; Fichtner *et al.,* 1996).
- It influences the process of fertilisation through facilitating sperm motility, controlling pH, providing nutrients for sperm, the AR and sperm immune defence in the female reproductive tract (Arienti *et al.,* 1999; Bencic *et al.,* 2000; Birkhead *et al.,* 1993; Buckett & Lewis-Jones, 2002; Camiña *et al.,* 2002; O'Mahony *et al.,* 2000; Vitali *et al.,* 1995; Wallach *et al.,* 1987;).
- Sperm competition or sperm selection totally under estimated

A large portion of men who are undergoing infertility treatment are oligozoospermic, and this has diminished the effectiveness of using sperm as a diagnostic source in the clinical setting, especially if the semen sample will be further used in ART. Utilizing seminal plasma as a medium for research into possible methods of diagnosis along with improvement of the male factor seems only fitting as it contains contributions from various glands and tissues that have been consistently demonstrated to have observable effects on sperm characteristics.

The prostate gland is a heterogeneous, multilobulated gland, consisting of four morphologically different zones (Lu *et al*., 2007). The gland is anatomically located between the urogenital diaphragm and the neck of the bladder, and completely envelops both ejaculatory ducts and the urethra (Pienta & Esper, 1993). It is a prominent accessory sex gland and its main function is to produce and release large amounts (up to 180 mM) of ionized derivatives of citric acid in the form of citrate into prostatic fluid as well as several hydrolytic enzymes (Kavanagh, 1994). Furthermore, the following compounds are also secreted: zinc, prostate-specific antigen (PSA), spermine, cholesterol, magnesium, phospholipids, muraminidase, fibrinolysin fibrinogenase and acid phosphatase (Ganong, 1981). Accordingly, the amount of citric acid in semen provides an accurate measure of prostate gland secretion (Moellering & Gruber, 1966; WHO, 2010). These secretions make up approximately 25% of the seminal plasma volume and it has been speculated that citric acid may play a role in maintaining the osmotic equilibrium of semen as well as playing a role in sperm energy metabolism (Medrano *et al.,* 2006). Reductions in citric acid concentration in the seminal plasma, may cause a minor increase in pH which has been found to increase sperm motility (Zhou *et al.,* 2015). Prostate specific antigen is a glycoprotein enzyme capable of liquefying the seminal coagulum thereby allowing sperm to swim freely (Balk *et al.,* 2003). Zinc released by the prostate aids in sperm DNA stabilization and low levels of seminal zinc are correlated with low fertility rates (Canale *et al.,* 1986).

The seminal vesicles are a pair of membranous sacs situated between the rectum and the posterior surface of the bladder (Wilson *et al*., 1997). Their secretions make up approximately

65% of the seminal plasma volume. There are a multitude of compounds released by the secretory cells found in the epithelial lining of the seminal vesicles, including a variety of proteins, prostaglandins, fibrinogen, ascorbic acid, flavins, phosphorycholine (Hafex, 1977; Harvey, 1948; WHO, 2010). Fructose is produced primarily by the seminal vesicles with a small contribution from the ampulla of the vas deferens (WHO, 2010), and is essential to the function of sperm, as well as being a major source of glycolyzable energy necessary for sperm motility (Mann, 1946; Schoenfeld *et al.,* 1979). Fructose levels in semen are regularly measured in laboratories to diagnose retrograde ejaculation as well as obstructive and non-obstructive azoospermia (Lu *et al.,* 2007). Seminal vesicle secretion is also proportional to the amount of seminal fructose measured in the ejaculate and it may serve as a marker for seminal vesicule function (Gonzales, 2001; WHO, 2010). Extended periods of sperm storage cause seminal fructose levels to progressively decrease and lactic acid build-up to occur (Mann 1946). Although sperm primarily utilize fructose as their energy source, the enzymatic machinery at their disposal allow for equally efficient metabolism of glucose and mannose substrates (Mann, 1946). The spermatozoon is highly specialized for motility, capacitation, hyperactivation and acrosome reaction which are all highly dependent on the energy state of the cell. This state is determined by the ratio between AMP and ATP. In a patient with a low ejaculate volume, the absence of fructose indicates ejaculatory duct obstruction, seminal vesicle dysfunction or hypoplasia (Aumüller & Riva, 1992). The lower reference limit for fructose is 13 µmol per ejaculate (Cooper *et al.,* 1990).

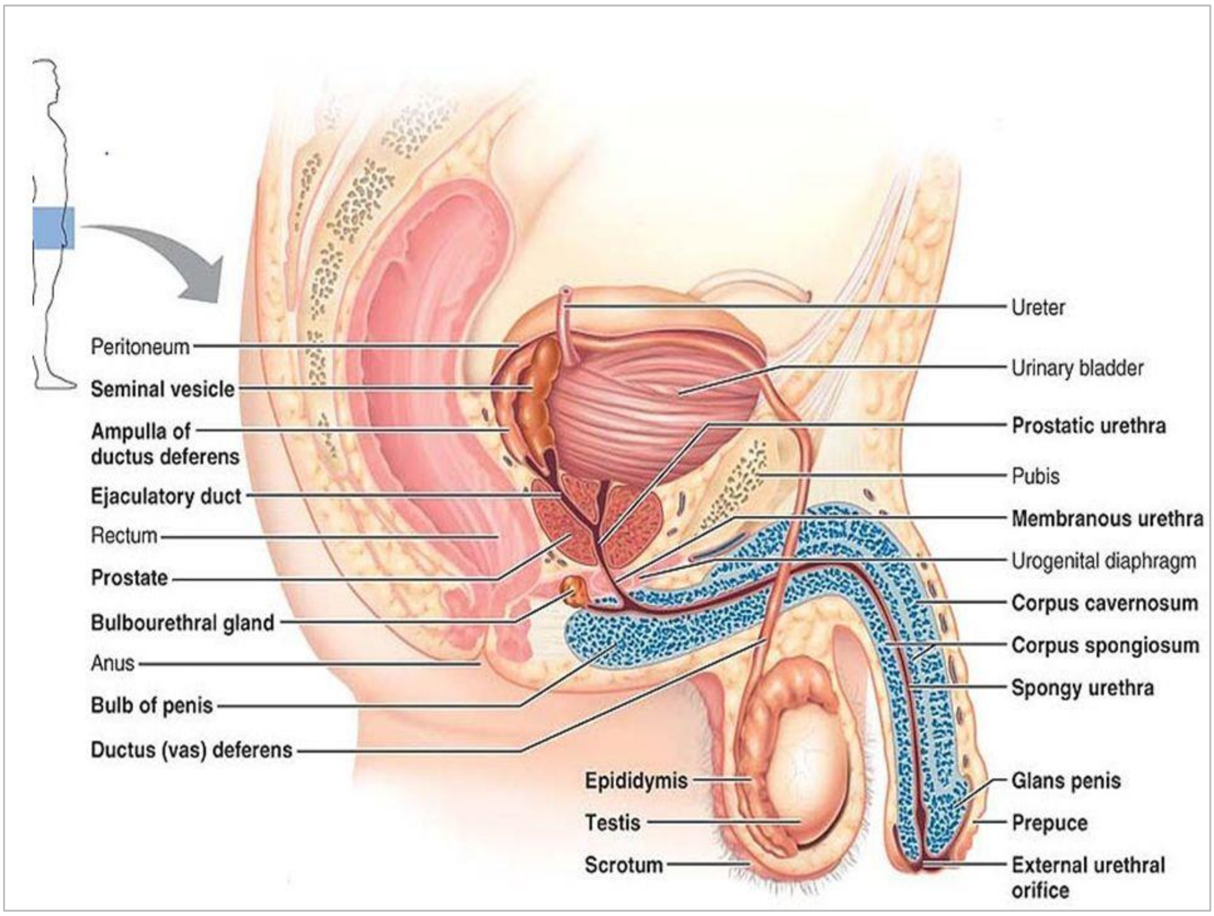


Figure 2.4. Lateral view of the male reproductive system and accessory sex glands (Forbes, 2015).

The epididymis is a narrow, tightly-coiled tube connecting the posterior part of the testicles to the vas deferens. It is anatomically divided into three main zones: the caput, corpus and cauda. As mentioned previously, the epididymis plays a crucial role in the maturation of spermatozoa and their acquisition of progressive motility and fertilizing capacity. It does this by storing and providing passage for immature and immotile spermatozoa to be released through the vas deferens and eventually allowing for capacitation post ejaculation (Cooper, 1996; Haidl & Schill, 1997). A simple photometric measurement of its activity is conventionally useful in assessment of epididymal secretion and function (Mahmoud *et al.,* 1998). Seminal neutral alpha-glucosidase (NAG) levels have been observed to be significantly correlated with semen volume and pH (Said *et al.,* 2009). In addition, strong positive correlations between

NAG activity and motility development have also been observed (Loko *et al.,* 1997; Viljoen *et al.,* 1990).

Studies analysing an array of epididymal markers such as NAG, carnitine and glycerolphosphocholine have been found to be significantly reduced in sub-fertile patients (Zöpfgen *et al.,* 2000). As the length of EA increases, as does the concentration of NAG (Elzanaty *et al.,* 2005). This however does not necessarily relate to an increase in the enzyme's activity and requires further investigation. The levels of seminal alpha-glucosidase may also be useful in the differentiation of causes of various cases of azoospermia (Lu *et al.,* 2006; Mahmoud *et al.,* 1998).

The percentage change in the concentrations of the selected epididymal and accessory sex gland biomarkers, have been widely utilized as clinical reflections of the global changes in the volume of secretions from each component (WHO, 2010). Many studies have attempted to formulate a specific ratio, which causes variations in these secretions, but there are multitude of variables to consider effecting secretion volumes (Elzanaty *et al.,* 2005; Wong *et al.,* 2001; Zöpfgen *et al.,* 2000).

A useful approach to further evaluate the effects which varying concentrations of molecules in the semen have on individual sperm, would be to analyse concentrations on a micro scale. Considering the total amount of a specific molecule in the ejaculate, and dividing that value by the T.S.C., would provide a more representative view of the actual availability of important biomolecules to individual sperm.

2.4. Proteomics

The broad definition of proteomics can be stated as "The collection of all the proteins expressed from the genome in all isoforms, polymorphisms and post-translational modifications" (Graham *et al.,* 2005). In human seminal plasma, approximately 10% of the proteins are of testicular or epididymal origin, while the rest originate from accessory sex glands and other parts of the body (Batruch *et al.,* 2011). Studies have shown that epididymal proteins play a key role in sperm quality and that proteins directly associated with testicular function may be found in seminal plasma (Intasqui *et al.,* 2013; Milardi *et al.,* 2012; Pilch & Mann, 2006; Wang *et al.,* 2009).

Due to the wide variation of seminal plasma protein functions and origin, seminal proteins have the potential for diagnosis and monitoring of pathways and interactions affecting male fertility, such as non-obstructive azoospermia, obstructive azoospermia, asthenozoospermia, varicocele and vasectomy (Batruch *et al.,* 2011; Drabovich *et al.,* 2011; Heshmat *et al.,* 2008; Intasqui *et al.,* 2013; Wang *et al.,* 2009; Zylbersztejn *et al.,* 2013). Within the rapidly evolving field of proteomics, the establishment of extensive databases of a large number of proteins specific to the spermatozoa and seminal plasma can allow for research into male fertility, extending to scenarios such as diagnostics and subsequent treatment modalities (Oliva *et al.,* 2009).

Among the main physiological features necessary for sperm to perform their function, they possess vital components which must be considered when assessing protein function and origin. Firstly, the presence of active mitochondria and glycolysis, which are important for sustaining motility and important for sperm transit through the female reproductive tract to the oocyte (Ferramosca *et al.,* 2012). Secondly, an intact and functional acrosome structure which is essential for sperm penetration of the zona pellucida (Hsu *et al.,* 1999). Finally, sperm DNA integrity of sufficient quality for the production of a viable embryo void of genomic imperfections and negative mutations, ideally leading to the development of a healthy baby (Shamsi *et al.,* 2008).

Furthermore, apart from reflecting abnormalities such as, acrosome damage, DNA fragmentation and reduction in sperm mitochondrial activity, the seminal plasma proteome directly reflects status of important components of spermatogenesis including Sertoli cell secretions, as well as agonists/antagonists of epididymal maturation status in normozoospermic men (Intasqui *et al.,* 2016).

Experimentally, seminal plasma proteins have displayed the ability to regulate sperm function, which is substantiated by both human and bovine studies whereby the addition of seminal plasma from an ejaculate with highly motile sperm, to sperm with low motility, may improve functional sperm parameters (Milardi *et al.,* 2012; Henault & Killian, 1996; Brackett *et al.,* 1996; Barbonetti *et al.,* 2013). Furthermore, it was also found that proteins from damaged and abnormal sperm may also present throughout the male reproductive tract and were thus secreted in seminal plasma (Henault & Killian, 1996).

The average protein concentration of human seminal plasma ranges from 35 to 55 mg/mL, making it an extremely rich source for protein analysis. Specialized methods for proteomic analysis of seminal plasma have been developed and a multitude of high-abundance seminal proteins have been identified using one-dimensional gel electrophoresis as well as mass spectrometry (MS) (Du Plessis *et al.,* 2011). Nonetheless, seminal plasma shares a feature with many other body fluids, that it is characterized by a highly dynamic range of proteins, making low-abundance components difficult to analyse. Strategic selection of separated fractions of the seminal plasma samples may help in preventing large abundance proteins from overshadowing the detection of low abundance proteins in MS analysis.

Thousands of distinct proteins have been identified in human seminal plasma, where approximately 25% are secretory. Interestingly, the physiological roles of seminal plasma proteins among mammals are highly conserved (Rodríguez-Martínez *et al.,* 2011). Research which has focused on the sperm-specific protein profile has constructed an extensive list of cellular maintenance proteins, which contribute to crucial metabolic pathways such as glycolysis and oxidative phosphorylation (Johnston *et al.,* 2005). This has linked seminal plasma proteins to several vital processes preceding fertilization including capacitation, establishment of the oviductal sperm reservoir, modulation of the uterine immune response, and sperm transport in the female genital tract, as well as in gamete interaction and fusion (Calvete *et al.,* 1994). The most abundant proteins found in seminal plasma are the gel-forming adhesion proteins: fibronectin, semenogelin I, semenogelin II and laminin (Lilja *et al.,* 1987). Lactoferrin, known for displaying antimicrobial properties, is also highly expressed. From a preliminary proteomic analysis on seminal plasma from normozoospermic donors, prostatic acid phosphatase and prostate-specific antigen were detected in large amounts compared to the rest of the spectrum. Prostate specific antigen is a protease released into seminal plasma which targets gel forming proteins (Lilja, 1985), whereas prostatic acid phosphatase has been found to have a role in the development of cancer in prostate cells (Muniyan *et al.,* 2013).

Similarly to other bodily fluids, serum albumin is found in relatively high amounts in seminal plasma. It functions as a transport protein and cholesterol sink which is removed from the sperm membrane during capacitation (Pilch & Mann, 2006). Two other proteins of interest are alpha-1-antitrypsin and zinc-alpha-2-glycoprotein (ZAG), which have been found to be involved in sperm maturation and forward motility (Ding *et al.,* 2007). A study performed by Martinez-Heridia *et al.* (2006) on the sperm proteome found that transcription factors were present at the time of the analysis which may insinuate that mature sperm are able to synthesize and secrete proteins themselves.

An extremely important property of proteins is protein phosphorylation. This form of post-translational modification has the ability to regulate many cellular processes via signal transduction pathways. These pathways are generally reversibly controlled by protein phosphorylation and require both protein kinases (phosphorylation) and protein phosphatases (dephosphorylation). Target proteins are phosphorylated at specific sites by one or more protein kinases, and these phosphates are then removed by specific phosphatases (see Figure 2.5).

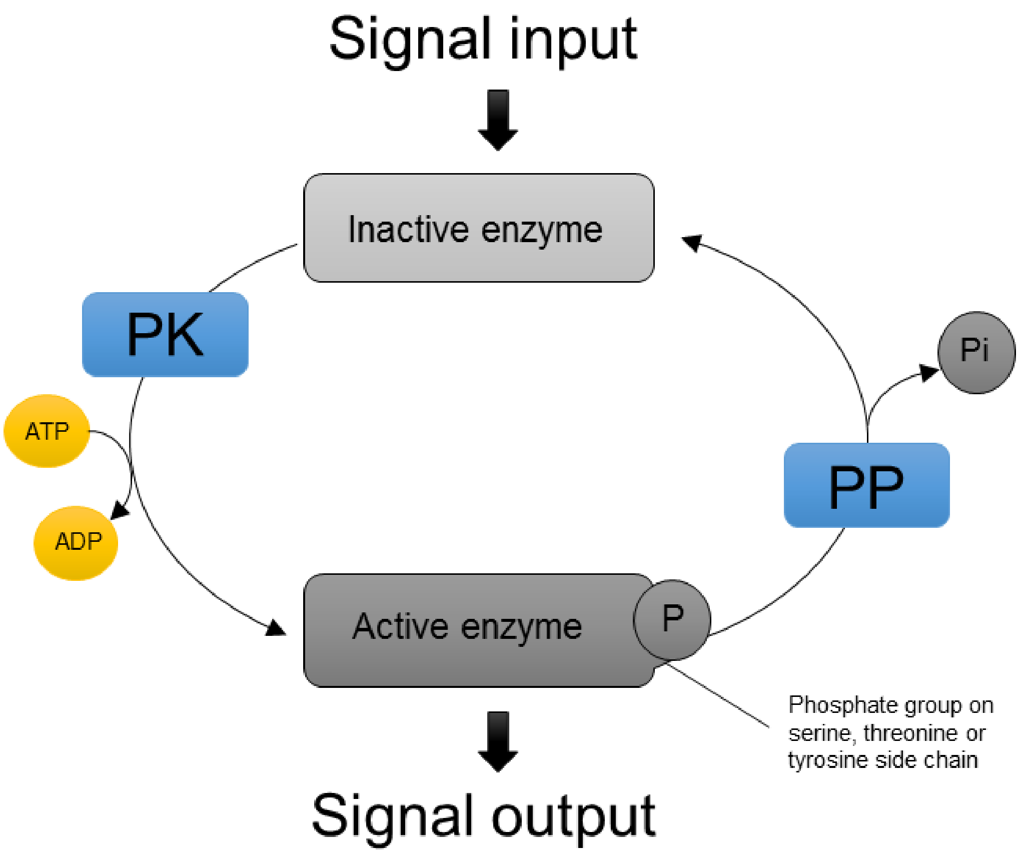


Figure 2.5. Diagrammatic representation of the mechanism for propagation of a cellular signal via phosphorylation of proteins.

An inactive enzyme is activated by the transfer of a phosphate group from a nucleoside triphosphate (usually ATP) to either a serine, threonine or tyrosine side chain of the enzyme. This transfer is facilitated by specialized protein kinases (PK) (Burnett & Kennedy, 1954). Reversing the activation and reverting the enzyme to its inactive state is achieved by protein phosphatases (PP) which dephosphorylate the enzyme (Fischer & Krebs, 1955).

Many signalling pathways have been comprehensively investigated in somatic cells. However, limited information is available on their characterization in spermatozoa, furthermore, there have been no comprehensive proteomic analysis to elucidate the mechanisms of very short EA in the improvement of semen/sperm quality.

Chapter 3

3. Materials and methods

3.1. Ethical clearance

The volunteer donors were informed and ensured anonymity by signing a detailed SURRG consent form, guaranteeing that the sample donated was to be used solely for research purposes and disposed of accordingly following experimental use. Ethical clearance for the use of semen samples was granted by the Stellenbosch University Health Research Ethics Committee (Ethics Reference: S15/02/045A).

3.2. Basic semen analysis

3.2.1. Volunteers

Freshly ejaculated semen samples were collected from healthy donors with scheduled abstinence durations and between the ages of 20 and 25. Information about donor identification and age, date of semen collection, time of semen collection, abstinence duration, sample volume, pH, appearance, colour, odour, liquefaction, viscosity and agglutination were reported. Standard parameters of each sampled were also analyzed including motility, morphology and viability. With regards to sample size, a study performed by Yamakawa *et al.* (2007) on the proteomic profiles of 10 donors was able to identify significant protein differences between these men. Accordingly, it was decided that the current study was to be performed on a slightly larger cohort of 16 normozoospermic donors.

3.2.2. Semen sample collection

All samples were collected according to the WHO guidelines (2010). The first sample from each donor was collected after an EA period of exactly 4 days. The second sample was collected from the same donor exactly 4 hours subsequent to the first collection. Semen was collected by means of masturbation into a labelled sterile wide mouth plastic container in a separate room close to the SURRG laboratory. The sample was placed in an incubator (37°C, 5% CO_2, 30 minutes) within 10 minutes of collection and allowed to fully liquefy before further processing.

3.2.3. Motility

The sperm concentration and motility/kinematic parameters were determined using CASA and the Sperm Class Analyser (SCA) version 5.4, (Microptic, S.L, Barcelona, Spain). The settings of the analyzer were as follows: optics, Ph+; contrast, 435; brightness, 100; objective, 10x; and 50 images (one second); temperature, 37ºC. The components of the SCA® consist of the following: Basler A312fc digital colour camera (Microptic, S.L., Barcelona, Spain), Nikon Eclipse 50i Microscope (IMP, Cape Town, South Africa) and a temperature-regulated microscope stage (Wirsam Scientific, Cape Town, South Africa). To assess the motility, 2µl of semen was pipetted into a single chamber of a four-chamber disposable Leja slide (depth 20µm; length 21mm) (Leja, Nieuw-Vennep, Netherlands). The motility status of at least 1000 motile spermatozoa per sample was examined under photo-microscopic capture in at least 5 randomly selected representative fields (10x objectives). The following motility parameters were analysed: Type A, Type B, Type C, Type D as well as a number of kinematic parameters including VCL, VSL, VAP, LIN, STR, WOB, ALH and BCF.

3.2.4. Viability

Sperm viability was assessed by means of a dye exclusion staining technique (WHO, 2010), which is based on the microscopic visualization of dye that has passed through the compromised plasma membrane, using the Eosin-Nigrosin stain (Sigma-Aldrich, MO, USA). A mixture of 10 µl of 5×10^6 spermatozoa/ml, 20 µl Eosin and 30 µl Nigrosin was smeared across the length of a microscope slide and allowed to air dry at room temperature. The slide was then mounted with a coverslip using DPX as a mounting medium (Sigma-Aldrich, MO, USA). Thereafter, 100 spermatozoa were counted in duplicate from each sample using the SCA counter module of the SCA® system whereby the number of pink-stained (non-viable) spermatozoa and those unstained (viable) were counted in various randomly selected fields. Results were expressed as a percentage of viable spermatozoa.

3.2.5. Storage of samples

Spermatozoa were isolated from seminal plasma immediately after basic semen analysis, by centrifugation where-after the seminal plasma and remaining spermatozoa were separately cryopreserved in liquid nitrogen (LN) (-196°C) until further analysis.

3.3. Epididymal and accessory sex gland biomarkers

All parameters of samples were analyzed on a FLUOstar™ Omega micro plate reader (BMG Labtech, Offenburg, Germany) using commercially available kits. For each kit, a Greiner 96 well flat bottom plate was used.

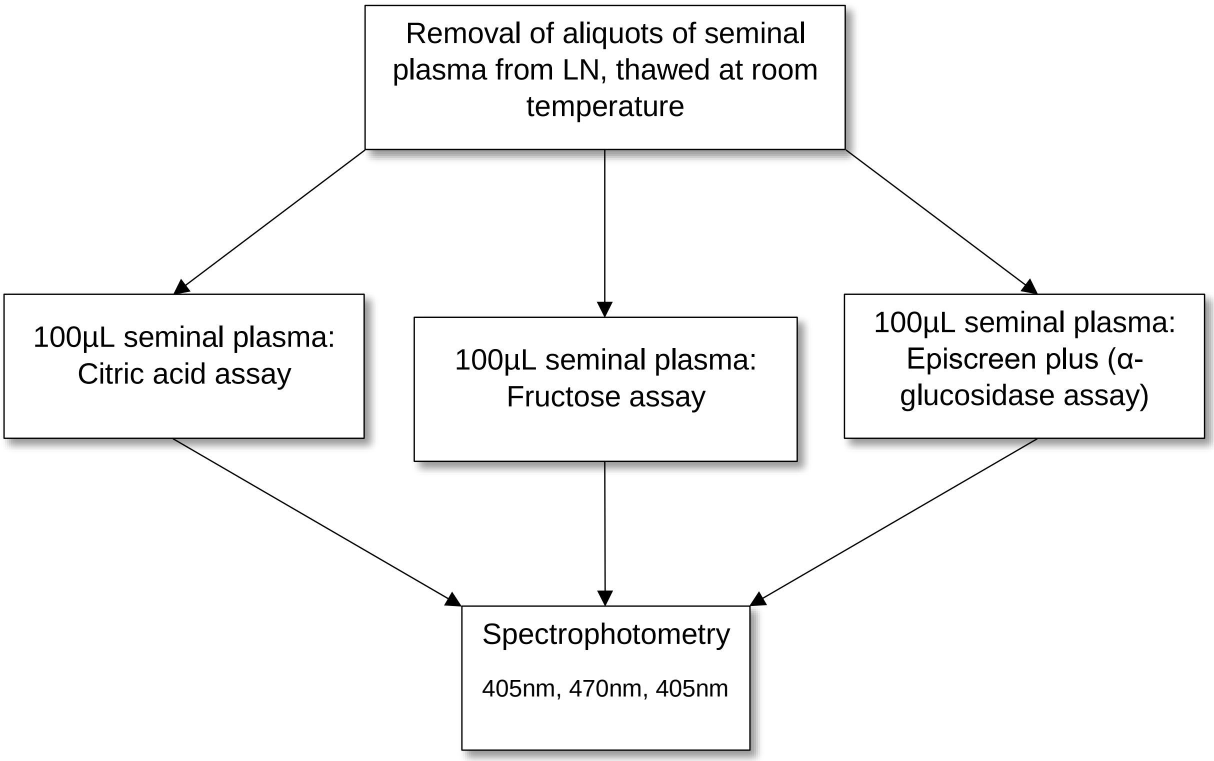


Figure 3.1. Summarized procedure for analysis of key epididymal and accessory sex gland biomarkers in the seminal plasma.

3.3.1. Citric acid assay:

Seminal plasma citric acid was measured using a commercially available Citric Acid Assay Kit (FertiPro, N.V., Belgium). A standard was prepared by mixing 100µL of citric acid standard with 100µL of isopropanol. 100µL of isopropanol was added to 100µL of thawed seminal plasma from each sample and then centrifuged (2500*g,* 20 minutes). Following centrifugation, 25µL of supernatant from each sample pipetted into wells and 200µL of ferric chloride was gently added to each well. The Fe^{3+}-ions form a complex with citrate that turns the solution into a yellow colour. The intensity of the colour is directly related to the amount of citrate and was measured photometrically at wavelength 405nm using the microplate reader. The normal citric acid value is 10mg or more per ejaculate. The measured optical density (OD) for the sample was divided by the OD from the standard and multiplied by the concentration of the standard (4mg/ml). Citric Acid mg/ml = $\frac{\text{OD Sample}}{\text{OD Standard}}$ x 4mg/ml (see Appendix A, Table 7.1) To obtain total citric acid amounts, we multiplied the result with the total volume of the semen sample or seminal plasma. To obtain the absolute amount of citric acid per sperm, the citric acid content per ejaculate was divided by the T.S.C.

3.3.2. Fructose assay

Seminal plasma fructose was measured using a commercially available Fructose Assay Kit (FertiPro N.V., Belgium). 100µL of thawed seminal plasma from each sample was deproteinized by the addition of 500µL of a Trichloroacetic (TCA) solution and centrifuged (x1000 *g,* 10 minutes). A standard curve with a range of fructose concentrations from 0 to 5mg/mL was calculated according to the set instructions. Following centrifugation, 20µL of the resultant supernatant that formed was pipetted into an Eppendorf tube. At 37°C and low pH (addition of 200µL 32% HCl), 20µL of indole was added to the isolated seminal plasma where it formed a colorimetric complex with fructose. The samples were left in the water bath for 30 minutes when 200µL of 0.5M NaOH was added to each tube stop the colour reaction. All samples, blanks and standards were prepared in duplicate.

This complex was measured photometrically at a wavelength 470nm. All absorbance values were transferred to an excel sheet supplied by the manufacturer which converts absorbance values into fructose concentration (mg/mL) (see Appendix A, Table 7.2). Normal values according to the WHO laboratory manual (fifth edition) are 2.4mg/ejaculate or more and 13µmol/ejaculate or more.

3.3.3. Episcreen plus™- Neutral alpha-glucosidase assay:

Seminal plasma neutral α-glucosidase was quantified using the EpiScreen Plus™ (FertiPro N.V., Belgium) assay. Under specified conditions (pH = 6.8; 37°C), 1IU of alpha-glucosidase liberates 1µM Para (4)-Nitrophenol (PNP) per minute from substrate Para (4)-Nitrophenyl-alpha-D-glucopyranoside (PNPG7). For each thawed seminal plasma sample, a reaction solution and an inhibitor solution was prepared in separate Eppendorf tubes with 20µL of seminal plasma in each. The reaction solution contained 3µL of 50x substrate solution (Para (4)-Nitrophenyl-alpha-D-glucopyranoside (PNPG) in Dimethyl sulfoxide (DMSO)) in 147µL of reaction buffer (pH 6.8), supplemented with sodium dodecyl sulfate (SDS). The inhibitor solution contained 3µL of 50x substrate solution in 147µL inhibitor solution (reaction buffer containing glucose) which acted as a negative control. The reaction and inhibitor solutions for each sample were vortexed and then incubated in a warm water bath (37^{o}C, 120 min). During incubation, para (4)-nitrophenol standard dilutions were made using 5mM standard stock solution and standard dilution buffer (0.03M NaOH + 0.1% SDS) as directed in the provided instructions.

After incubation, 1mL of stopping buffer (0.02M NaOH) was added to each tube. The tubes were vortexed and 200µL of each tube (including standards) were pipetted into separate wells on the 96-well plates. The amount of yellow colour was measured spectrophotometrically at 405nm. Alpha-glucosidase activity is expressed as IU/Litre (or mIU/mL). The lower and upper detection limit for total alpha-glucosidase is 12 - 100 mIU/mL, and 2 - 15mIU/mL for NAG. All absorbance values were transferred to an excel sheet supplied by the manufacturer which converts absorbance values into alpha-glucosidase concentration (mIU/mL) and total alpha-glucosidase values (see Appendix A, Table 7.3).

Once the amounts of all 3 epididymal and accessory sex gland biomarkers per ejaculate were calculated, these values were then divided by the corresponding T.S.C. values to provide an amount per sperm.

3.4. Statistical analysis of basic semen parameters and epididymal and accessory sex gland biomarkers.

Comparisons between parameters measured after long and short EA were performed using the Students paired t-test for normally distributed data sets and Mann-Whitney U-tests for nonparametric data sets, on GraphPad Prism© version 7.00 for Windows (GraphPad Software, La Jolla California, USA). All values are presented as mean ± SE. Statistical significance was set at $p<0.05$.

3.5. Proteomic Analysis

Proteomic analysis was performed with the aid of the Central Analytics Facility Proteomics unit, following the protocol provided by an expert in the field of protein analysis and LC-MS/MS.

3.5.1. Sample preparation and SDS-PAGE

The protein concentration of each of the 16 samples was measured using the Direct Detect® Infrared Spectrometer where 2 µl of sample made up in Laemmli sample buffer were spotted on specialized strips which were inserted into the Spectrometer and values were calculated. Samples were then pooled randomly in 4 groups consisting of 4 samples each, where each sample contributed an equal amount of protein (60µg). The combined volumes of each pool were made to be 25µL by addition of 1X Phosphate-buffered saline (PBS).

Thereafter, 25 µL of each sample pool was loaded onto 12% Criterion TGX precast gels (Bio-Rad, CA, USA) and run for 45 min at 200 volts in Laemmli electrophoresis running buffer (Bio-Rad, CA, USA). After the run, gels were fixed in a fixative (40% Methanol; 7% Acetic acid) while gently shaken for 60 min at room temperature. This was followed by staining with "Brilliant Blue G –Colloidal Concentrate" (Sigma-Aldrich, MO, USA) for 30 minutes at room temperature using gentle shaking; (40 mL stain + 10 mL Methanol). The gels were then de-stained in 25% Methanol with gentle shaking at room temperature, until the protein bands became visible and the background clear (± 4 hours). Gels were stored in milli-Q water at 4°C until processed.

3.5.2. In-gel Digestion

All reagents used were analytical grade or equivalent and all H_2O was Milli-Q filtered. Each pooled protein column was excised into 7 pieces which each clearly displaying a concentrated band of proteins (see Figure1.1), with a new surgical - grade scalpel and placed into separate marked Eppendorf 1.5 mL tube. Gel slices were de-stained with 200 mM NH_4HCO_3:acetonitrile 50:50 (Sigma-Aldrich, MO, USA) until clear. Samples were dehydrated and desiccated before reduction with 2 mM triscarboxyethyl phosphine (TCEP; Fluka® Analytical, St. Gallen, Switzerland) in 25 mM NH_4HCO_3 for 15 minutes at room temperature with agitation. Excess TCEP were removed and the gel pieces again dehydrated. Cystein residues were thiomethylated with 20 mM S-Methyl methanethiosulfonate (Sigma-Aldrich, MO, USA) in 25 mM NH_4HCO_3 for 30 minutes at room temperature. After thiomethylation the gel pieces were dehydrated and washed with 25 mM NH_4HCO_3 followed by another dehydration step. Proteins were digested by rehydrating the gel pieces in trypsin (Pierce MS grade, Thermo Fisher Scientific, MS, USA) solution (20ng/µL) and incubating at 37 °C overnight. Peptides were extracted from the gel pieces once with 50µL water and once with 50% acetonitrile. The samples were dried down and re-suspended in 30µL 2% acetonitrile:milli-Q water; 0.1% formic acid (Sigma-Aldrich, MO, USA).

Residual digest reagents were removed using an in-house manufactured C18 stage tip (Empore Octadecyl C18 extraction discs placed in a pipette tip; Supelco® Analytical, MO, USA). The samples were loaded onto the stage tip after activating the C18 membrane with 30µL methanol (Sigma-Aldrich, MO, USA) and equilibration with 30µL 2% acetonitrile: milli-Q water; 0.05% TFA. The bound sample was washed with 30µL 2% acetonitrile: milli-Q water; 0.1% TFA before elution with 30 µL 50% acetonitrile: milli-Q water 0.05% TFA. The eluate was evaporated to dryness using a SpeedVac (Eppendorff, HH, Germany). The dried peptides were dissolved in 2% acetonitrile: milli-Q water; 0.1% FA for LC-MS/MS analysis.

3.5.3. Liquid chromatography

Liquid chromatography was performed on a Thermo Scientific Ultimate 3000 RSLC (Thermo Fisher Scientific, MS, USA) equipped with a 2cm x 100µm C18 trap column and a 35cm x 75µm C18 (Luna C18, 5µm; Phenomenex Inc., CA, USA) analytical column. The solvent system employed was loading: 2% acetonitrile: milli-Q water; 0.1% FA; Solvent A: 2% acetonitrile: milli-Q water; 0.1% FA and Solvent B: 100% acetonitrile: milli-Q water. The samples were loaded onto the trap column using loading solvent at a flow rate of 15µL/min from a temperature controlled auto-sampler set at 7°C. Loading was performed for 5 min before the sample was eluted onto the analytical column. Flow rate was set to 500nL/min and the gradient generated as follows: 2.0% - 10% B over 5 min; 5% - 25% B from 5 - 50 minutes using Chromeleon non-linear gradient 6, 25%-45% from 50 - 65 minutes, using Chromeleon non-linear gradient 6. Chromatography was performed at 50°C and the outflow delivered to the mass spectrometer through a stainless steel nano-bore emitter.

3.5.4. Mass spectrometry

Mass spectrometry was performed using a Thermo Scientific Orbitrap Fusion mass spectrometer (Thermo Fisher Scientific, MS, USA) equipped with a Nanospray Flex ionization source. The sample was introduced through a stainless steel emitter. Data was collected in positive mode with spray voltage set to 2kV and ion transfer capillary set to 275°C. Spectra were internally calibrated using polysiloxane ions at m/z = 445.12003 and 371.10024. MS1 scans were performed using the Orbitrap detector set at 120 000 resolution over the scan range 350-1650 with AGC target at 3 E5 and maximum injection time of 40ms. Data was acquired in profile mode.

The second mass spectrometry acquisitions were performed using monoisotopic precursor selection for ion with charges +2 - +6 with error tolerance set to +/- 0.02ppm. Precursor ions were excluded from fragmentation once for a period of 30 seconds. Precursor ions were selected for fragmentation in Higher-energy collisional dissociation (HCD) mode using the quadrupole mass analyzer with HCD energy set to 32.5%. Ion fragments were detected in the Orbitrap mass analyzer set to 15 000 resolution. The autmomatic gain control (AGC) target was set to 1E4 and the maximum injection time to 45 milliseconds. The data was acquired in centroid mode.

3.5.5. Bioinformatics

The raw files generated by the mass spectrometer were imported into Proteome Discoverer v1.4 (Thermo Fisher Scientific, MA, USA) and processed using Sequest algorithm. Database interrogation was performed against a concatenated database created using the Uniprot human database with semi-tryptic cleavage allowing for 2 missed cleavages. Precursor mass tolerance was set to 10ppm and fragment mass tolerance set to 0.02 Da. Protein N-terminal acetylation, deamidation (NQ) and oxidation (M) was allowed as dynamic modifications and thiomethyl of C as static modification. Peptide validation was performed using the peptide validator node set to search against a decoy database with strict FDR 1%. The results files were imported into Scaffold 1.4.4 and identified peptides validated using the X!Tandem search algorithm included in Scaffold. Peptide and protein validation was performed using the Peptide and Protein Prophet algorithms. Protein quantitation was done using a t-test on the paired data with the Hochberg-Benjamini correction applied. Pathway analysis was then performed using Reactome.org database and string-db.org to formulate extensive networks of intracellular and extracellular protein interactions.

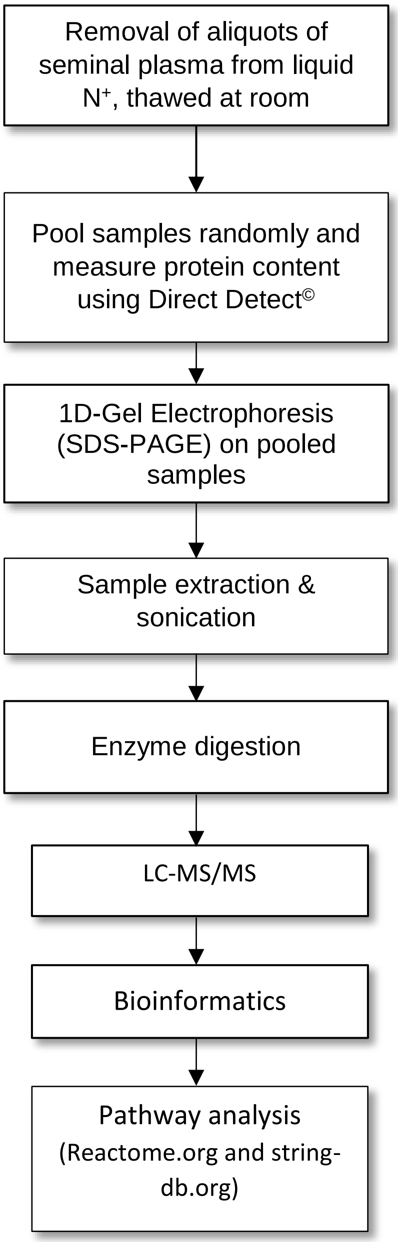


Figure 3.2. Summarized procedure for analysis of seminal plasma proteome

Chapter 4

4. Results

The results will be presented in 3 distinct stages, the first being the assessment of basic semen parameters accompanied by extensive motility and kinematic analysis of samples provided after both EA periods. Secondly, the measurement of the epididymal and accessory sex gland biomarkers in the seminal plasma and how they are influenced by T.S.C will be presented. Finally, the identification of proteins differentially expressed after each EA period and the cellular processes in which they are involved will be highlighted in great detail.

4.1. **Objective 1:** Basic semen analysis and sperm motility parameters

As displayed in Table 4.1, basic semen parameters were mostly aligned with previous literature showing significant decreases in semen volume, sperm concentration and T.S.C. after 4 hours of EA when compared with 4 days. Semen pH was slightly, yet significantly increased after 4 hours of EA, accompanied by significant improvements in both total motility and progressive motility. Viability slightly decreased after 4 hours of EA and no significant differences in morphological parameters were observed.

Table 4.1. Representative summary of the differences observed amongst the macro- and microscopic semen and spermatozoa parameters (mean ± SEM).

Parameter	Long EA (4 days)	Short EA (4 hours)	Normal distribution	Paired t-test (P-value)	Mann-Whitney test (P-value)	% change	WHO (2010) Lower limits
Semen volume (mL)	2.56 ± 0.33	1.74 ± 0.22	No	-	0.025	-32%	1.5 or more
Sperm conc. (x10^6/mL)	57.35 ± 7.2	36.83 ± 4.51	No	-	0.018	-36%	15 or more
T.S.C. (x10^6/ejaculate)	144.68 ± 22.77	58.01 ± 6.43	Yes	0.0007	-	-77%	39 or more
pH	7.68 ± 0.029	7.76 ± 0.038	No	-	0.046	1%	7.2 - 8
Viability (%)	73.06 ± 1.57	69.94 ± 1.67	Yes	0.032	-	-4%	58 or more
Total motility (%)	64.71 ± 13.94	71.84 ± 3.85	Yes	0.033	-	14%	40 or more
Progressive motility (%)	47.73 ± 14.33	58.54 ± 13.38	Yes	0.001	-	30%	32 or more

Conc. = Concentration, EA = Ejaculatory abstinence, T.S.C. = Total sperm count, WHO = World Health Organisation

Significant increases in rapid swimming sperm, curvilinear velocity, straight line velocity and average path velocity were observed in sperm after short EA when compared to long EA. The increase in the percentage of rapid swimming sperm was accompanied by a significant decrease in the percentage of slow swimming sperm (see Table 4.2). Figure 4.1 displays the relationships between each of the measured kinematic parameters after 4 days and 4 hours of EA for every sample collected.

Table 4.2. Summary of the SCA® motility parameters as measured by CASA (mean ± SEM)

CASA parameters	Long EA (4 days)	Short EA (4 hours)	Normal distribution	Paired t-test (P-value)	Mann-Whitney test (P-value)
Rapid (%)	47.09 ± 3.61	57.53 ± 3.44	Yes	0.023	-
Medium (%)	5.74 ± 0.61	5.15 ± 0.5	No	-	0.25
Slow (%)	11.69 ± 0.73	9.15 ± 0.68	Yes	0.0005	-
VCL (µm/s)	78.61 ± 4.03	91.78 ± 6.23	No	-	0.137
VSL (µm/s)	29.66 ± 1.2	34.95 ± 1.41	No	-	0.006
VAP (µm/s)	49.71 ± 2.05	57.89 ± 2.72	No	-	0.018
LIN (%)	38.28 ± 1.07	39.53 ± 1.77	Yes	0.476	-
STR (%)	60.04 ± 1.39	61.11 ± 1.81	Yes	0.318	-
WOB (%)	63.73 ± 1.0	64.27 ± 1.3	Yes	0.571	-
BCF (Hz)	13.34 ± 0.62	14.89 ± 0.64	Yes	0.068	-
ALH (µm)	2.23 ± 0.11	2.27 ± 0.15	Yes	0.865	-

CASA = Computer aided sperm analysis, EA = Ejaculatory abstinence, Rapid = Rapid swimming sperm, Medium = Medium swimming sperm, Slow = Slow swimming sperm, VCL = Curvilinear velocity, VSL = Straight line velocity, VAP = Average path velocity, LIN = Linearity index, STR = Straightness index, WOB = Oscillation index, BCF = Beat cross frequency, ALH = Amplitude of lateral head displacement, EA = Ejaculatory abstinence.

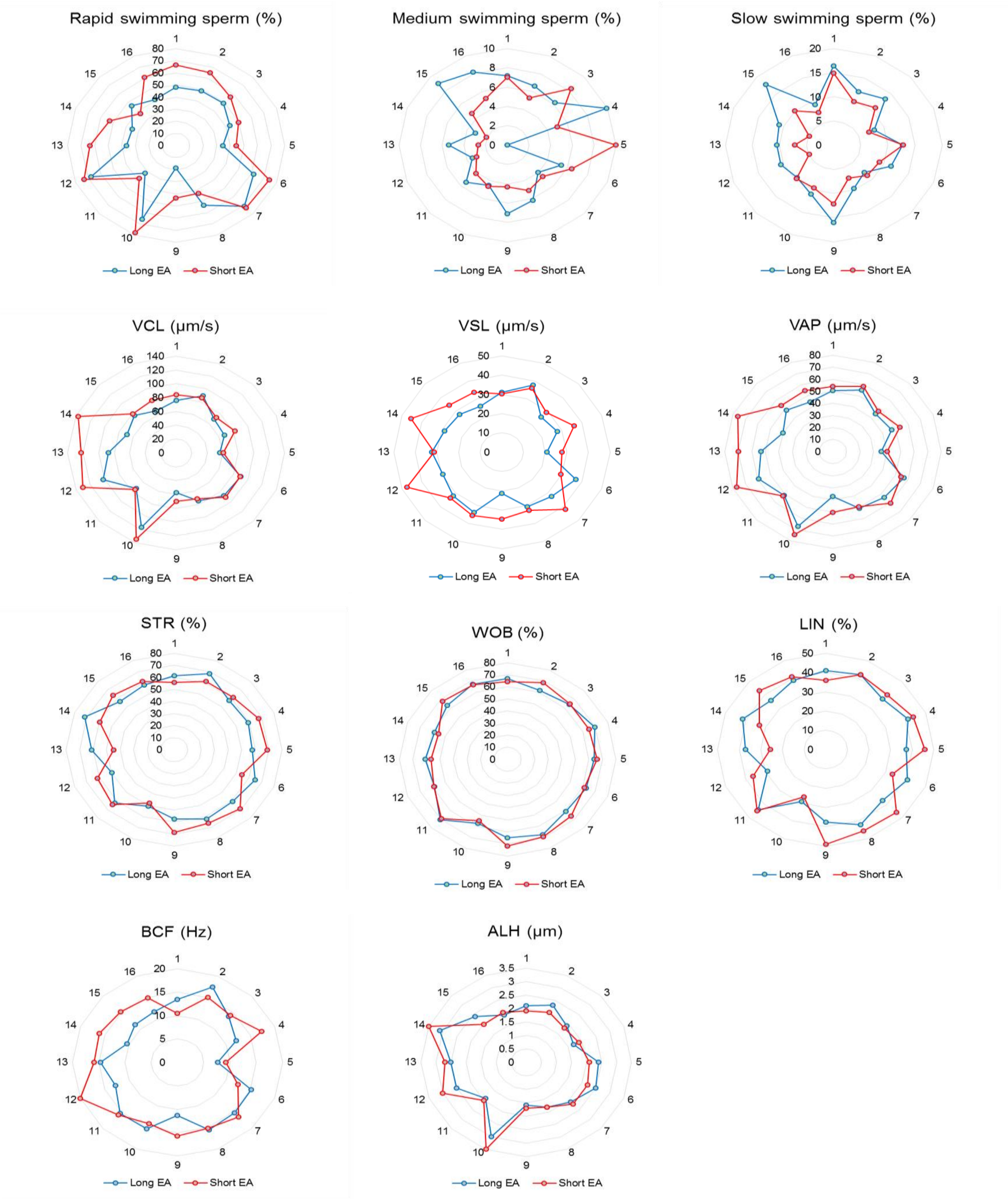


Figure 4.1: Radar plots of kinematic parameters from individual samples (N=16) for 4 days and 4 hours of EA.

Sample numbers are represented on the perimeters, and the radii demonstrate the percentage of sperm, velocity (µm/s) or displacement (µm) in the respective group. VAP = Average path velocity, VSL = Straight line velocity, VCL = Curvilinear velocity, LIN = Linearity index, WOB = Oscillation index, STR = Straightness index, BCF = Beat cross frequency, ALH = Amplitude of lateral head displacement EA = Ejaculatory abstinence.

4.2. **Objective 2:** Epididymal and accessory sex gland biomarker analysis

Citric acid, NAG and fructose concentrations were all significantly reduced after 4 hours of EA when compared to 4 days (see Table 4.3). As expected, all epididymal and accessory sex gland biomarkers significantly reduced per ejaculate after 4 hours. On the contrary, when considering T.S.C., the absolute amount of citric acid per sperm was significantly increased after 4 hours of EA and fructose per sperm significantly decreased. There was no observed change in alpha-glucosidase per sperm.

Table 4.3: Summary of accessory gland biomarkers as measured using commercially available kits (mean ± SEM)

Parameter	Long EA	Short EA	Normal distribution	Paired t-test (P-Value)	Mann-Whitney test (P-value)	% change	WHO (2010) Lower limits
Citric acid (mg/mL)	8.01 ± 1.352	5.96 ± 1.232	No	-	0.032	-25%	6.7 or more
Citric acid per sperm (ng)	0.141 ± 0.025	0.254 ± 0.056	No	-	0.034	110%	-
Total citric acid (mg/ejaculate)	14.68 ± 1.317	10.22 ± 1.042	Yes	0.005	-	-27%	-
Fructose (mg/mL)	4.07 ± 0.77	1.66 ± 0.52	No	-	0.015	-54%	1.6 or more
Fructose per sperm (ng)	0.045 ± 0.016	0.036 ± 0.011	Yes	0.037	-	-38%	-
Total fructose (mg/ejaculate)	8.478 ± 2.011	2.242 ± 0.707	No	-	0.001	-63%	-
NAG (mIU/mL)	29.32 ± 3.53	19.92 ± 3.61	Yes	0.005	-	-33%	2 – 15
NAG per sperm (nIU)	0.563 ± 0.08	0.145 ± 0.128	No	-	0.638	6%	-
Total NAG (mIU/ejaculate)	71.41 ± 13.30	28.18 ± 3.536	No	-	0.001	-53%	-

EA = Ejaculatory abstinence, NAG = Neutral alpha-glucosidase, WHO = World Health Organisation.

4.3. **Objective 3**: Proteomic analysis

LC-MS/MS analysis was successful in identifying a total of 1765 proteins expressed in the seminal plasma of all of the samples which originate from a multitude of cells, tissues and glands in the male reproductive system. A total of 19 proteins were identified to be significantly upregulated after 4 days of EA when compared to 4 hours, and 3 proteins significantly upregulated after 4 hours of EA compared to 4 days (see Tables 4.3 and 4.4).

Table 4.3: Seminal plasma proteins upregulated after 4 days of EA

Protein Name	Accession Number	Gene name	MW (kDa)	P-Value	Cellular localization (via Uniprot.org)	Description
Mammalian ependymin-related protein 1	Q9UM22	EPDR1	25.4	0.0015	Extracellular (secreted)	Possible role in calcium dependent cell adhesion (Gregorio-king *et al.*, 2002)
Transforming growth factor beta-1	P01137	TGFB1	44.3	0.0045	Extracellular (matrix)	Controls proliferation, differentiation and other functions in many cell types (Chang *et al.,* 2015)
26S proteasome non-ATPase regulatory subunit 8	P48556	PSMD8	39.6	0.0068	Cytosol, extracellular (exosome), nucleus and various proteasome complexes	ATP-dependent degradation of ubiquitinated proteins (Kanayama *et al.,* 1992)
Tandem C2 domains nuclear protein	Q8N9U0	TC2N	58.3	0.0068	Nucleus	Regulation of blood coagulation and gene expression (Antoni *et al.,* 2011)
Ras-related protein Rab-13	P51153	RAB13	22.8	0.0087	Plasma membrane, Golgi apparatus (trans-Golgi network membrane), endosome and tight junctions.	Key regulators of intracellular membrane trafficking (Marzesco *et al.,* 2002)

Ig lambda chain V-I region	P04208	IGLV1-47	12.3	0.01	Extracellular (secreted) and plasma membrane	Participates in antigen recognition (Lefranc, 2014)
Limbic system-associated membrane protein	Q13449	LSAMP	37.3	0.013	Plasma membrane	Mediates selective neuronal growth and axon targeting (Pimenta *et al.,* 1995)
Transketolase-like protein 1	P51854	TKTL1	37.4	0.015	Nucleus and cytoplasm	Catalyzes the transfer of a two-carbon ketol group from a ketose donor to an aldose acceptor (Coy *et al.,* 2005)
Phosphatidylethanolamine-binding protein 4	Q96S96	PEBP4	25.7	0.021	Lysosome	Postulated as having several roles in the male reproductive system (Frayne *et al.,* 1988)
Rho GTPase-activating protein 1	Q07960	ARHGAP1	50.4	0.029	Cytoplasm	Able to induce dynamic rearrangements of the plasma membrane-associated actin cytoskeleton (Aspenstrom et al, 2004)
Ubiquitin-conjugating enzyme E2 K	P61086	UBE2K	17.1	0.029	Cytoplasm	Accepts ubiquitin from the E1 complex and catalyzes its covalent attachment to other proteins (Kalchman *et al.,* 1996)
Heat shock-related protein A2	P54652	HSPA2	70	0.03	Cytoskeleton (spindle)	Molecular chaperone involved in a wide variety of cellular processes related to male fertility (Radons, 2016).
2,4-dienoyl-CoA reductase, mitochondrial	B7Z6B8	DECR1	35	0.031	Mitochondrion	Facilitates β-oxidation in fatty acid metabolism (Alphey et al., 2005)
Glyoxylate reductase/hydroxypyruvate reductase	Q9UBQ7	GRHPR	35.7	0.033	Cytosol, extracellular (exosome) and peroxisome (matrix)	Hydroxy-pyruvate reductase, glyoxylate reductase and D-glycerate dehydrogenase enzymatic activities (Mdluli *et al.,* 2005).
14 kDa phosphohistidine phosphatase	Q9NRX4	PHPT1	14	0.036	Cytoplasm	Phosphohistidine phosphatase activity affecting metabolic and immune system functioning (Krieglstein *et al.,* 2008; Srivastava *et al.,* 2008)

Ropporin-1B (Fragment)	D6RCR2	ROPN1B	15	0.041	Unknown	Unknown
Isoform 7 of Complement decay-accelerating factor	P08174-7	CD55	41.4	0.044	Plasma membrane	Virus receptor activity and complement activation (Ward *et al.,* 1994)
Sperm protein associated with the nucleus on the X chromosome B1	Q9NS25	SPANXB1	11.8	0.045	Nucleus and cytoplasm	Spermatid development (Westbrook *et al.,* 2000)
Transmembrane protease serine	O15393	TMPRSS2	53.8	0.050	Plasma membrane and extracellular (secreted)	Serine protease that proteolytically cleaves and activates the viral spike glycoproteins which facilitate virus-cell membrane fusions (Shulla *et al.,* 2011)
Metalloproteinase inhibitor	P01033	TIMP1	23.2	0.054	Extracellular (secreted)	May act as a growth factor to regulates cell differentiation, migration and cell death (Chesler *et al.,* 1995)

Table 4.4: Seminal plasma proteins upregulated after 4 days of EA

Protein Name	**Accession Number**	**Gene name**	**MW (kDa)**	**P-Value**	**Cellular localization (via Uniprot.org)**	**Description**
Isoform 5 of Tropomyosin alpha-3 chain	P06753-5	TPM3	29	0.04	Cytoskeleton	Central role, in association with the troponin complex, in the calcium dependent regulation of vertebrate striated muscle contraction (Janco *et al.,* 2012)
Calcium-binding protein 39	Q9Y376	CAB39	39.9	0.036	Cytoplasm	Stabilized the LKB1-STRAD-MO25 complex which has cellular signalling ramifications (Zeqiraj *et al.,* 2009)
Deoxyribonuclease-1	P24855	DNASE1	31.4	0.047	Extracellular (secreted), nucleus (envelope)	Involved in cell death by apoptosis

As illustrated in Figure 4.3 a), 60% of proteins identified are involved cellular processes and 40% and 45% are involved in metabolic processes and biological regulation respectively. Furthermore, 8% of the identified proteins play roles in both reproduction and reproductive processes. Additionally, of the 2 differentially expressed proteins between the two EA periods, a similar trend of cellular processes is displayed with 76% of proteins involved in cellular processes and 45% and 52% involved in metabolism and biological regulation respectively (see Figure 4.3 b). Interestingly, a large proportion (40%) of the differentially expressed proteins are involved in developmental processes.

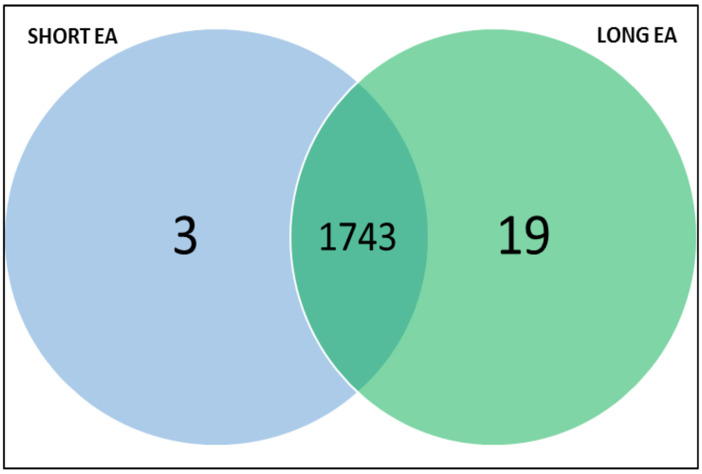


Figure 4.2: Venn diagram of proteins displaying number of differentially expressed proteins in each cohort

4 hours of ejaculatory abstinence (left); 4 days of ejaculatory abstinence (right). EA = Ejaculatory abstinence

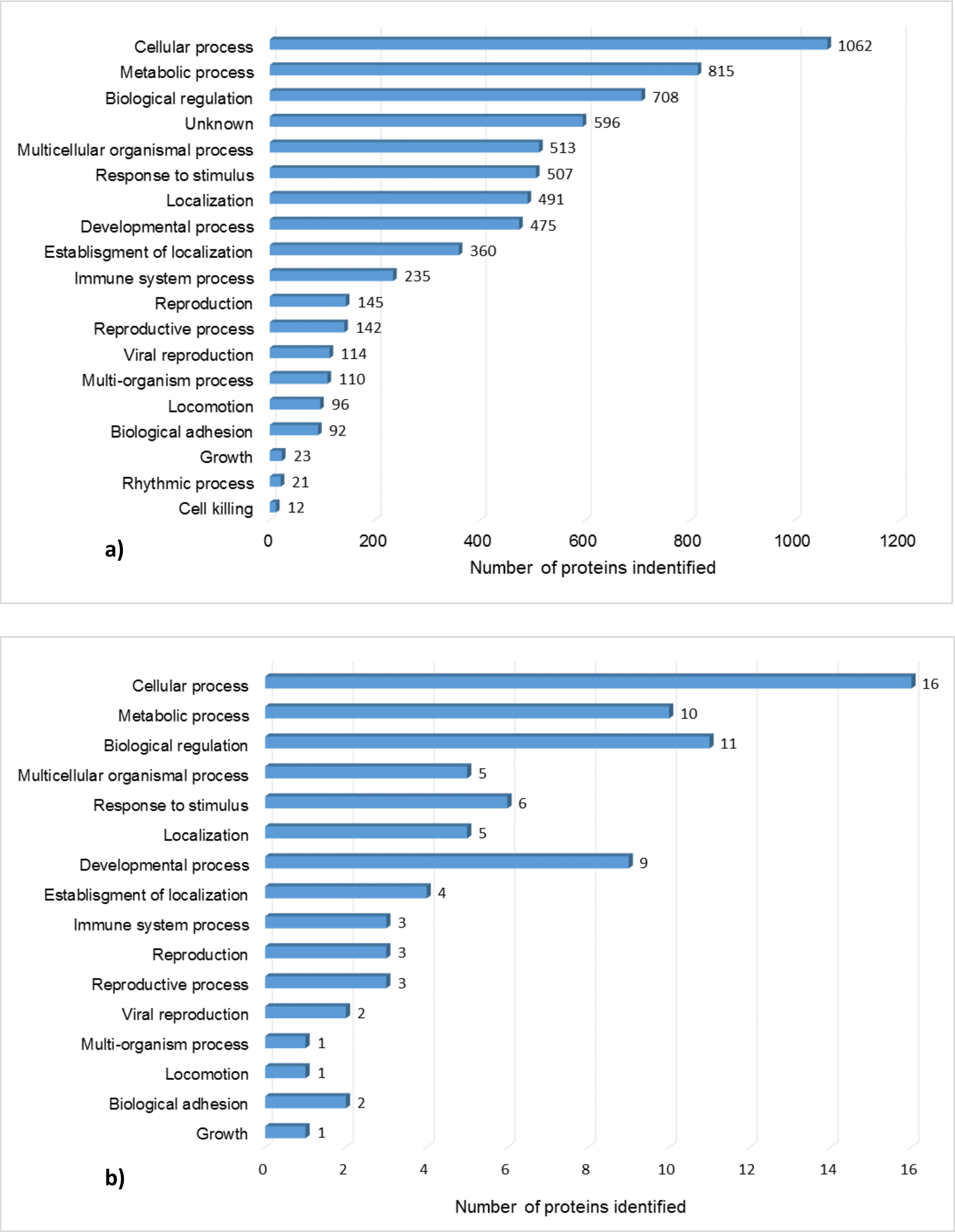


Figure 4.3: Proteomic data and significantly upregulated proteins from each cohort.

a) Total number of proteins identified in this study related to each biological process. b) Number of differentially expressed proteins identified in this study related to each biological process.

Chapter 5

5. Discussion

The discussion will be divided into three objectives as presented in the results of Chapter 4. Firstly, the evaluation of basic and functional sperm parameters measured after 4 days and 4 hours of EA, followed by the biochemical analysis of important epididymal and accessory sex gland biomarkers in seminal plasma after both EA periods covered in objective 2 will be discussed. Lastly, proteomic analysis of the seminal plasma of both cohorts as well as the results of pathway analysis of differentially expressed proteins will be explored.

5.1. Objective 1: *Evaluate the relationship between 4 days and 4 hours of EA by comparing basic semen parameters such as pH and volume, as well as sperm parameters including concentration, total sperm count (T.S.C.), motility and kinematics.*

The results of this study shows that conventional and functional semen parameters were influenced significantly by different lengths of EA. A short period of EA (4 hours) produced significant reductions in semen volume, T.S.C. sperm concentration accompanied by significant increases in both sperm motility and progressive motility. Furthermore, the percentage of viable sperm slightly yet significantly reduced after short EA and no significant morphological abnormalities were observed in either cohort.

Two substantially larger studies than indicated above and performed by Comar *et al.* (2017) and Levitas *et al.* (2005), also observed a significant positive relationship between EA period and sperm T.S.C., sperm concentration and semen volume. In the case of the shorter EA period, the sperm reserves were depleted and T.S.C. decreased (Rao et al., 2015), which may be attributed to the insufficient time for the epididymis and accessory sex glands to produce their respective secretions, resulting in reduction in semen volume associated with short abstinence (Levitas et al., 2004).

After 4 hours of EA, the release of spermatozoa may reduce exposure to the above-proposed motility-inhibiting factors which may therefore reduce the severity of the adverse effects on sperm functional parameters. Since spermatogenesis takes approximately 74 days and epididymal maturation a further 2 to 11 days, the sperm released after 4 days and 4 hours of EA are of relatively similar age which is confirmed in the morphological assessment, as no significant morphological differences were observed, thus implying similar developmental conditions. This would indicate that no major differences in spermatogenesis have occurred, which can influence sperm development and subsequent sperm function once ejaculated. Likewise, the lack of significant effects of short EA periods on sperm morphology have been widely reported (Choavaratana *et al.,* 2014; Mayorga-Torres *et al.,* 2016; Mayorga-Torres *et al.,* 2015; Sunanda *et al.,* 2014)

These effects are ascribed to the fact that sperm reserves were available and stored in the cauda epididymis or that sperm morphology is not necessarily a good reflection of sperm functionality. As mentioned above, sperm transit time through the epididymis takes between 2 and 11 days (Yanagimachi *et al.,* 1994) yet frequent ejaculations have been noted to reduce this transit time. Decreasing sperm stagnancy in the epididymis may lead to recently mature sperm to dominate the ejaculate and prevent them from being exposed for prolonged periods to harmful ROS released by immature spermatozoa, which is known to cause extensive adverse effects on sperm function and vitality (Argarwal *et al.,* 2014).

Motility reductions after prolonged EA have been attributed to increased levels of reactive oxygen species (ROS) and subsequent DNA damage in stored sperm (Comar *et al.,* 2017 and Levitas *et al*., 2005). Both damaged spermatozoa (Iwasaki *et al.,* 1992) and infiltrating leukocytes (Kessopoulou *et al.,* 1994) were suggested as sources of ROS amongst these latent sperm yet increased ROS and subsequent oxidative stress, may originate from both endogenous (pathophysiology’s and physiological events in sperm) and exogenous (chemicals, toxins and environmental factors) sources, which subsequently lead to damaging reactions in the spermatozoon including, lipid peroxidation, DNA damage and initiation of apoptosis (see Figure 5.1).

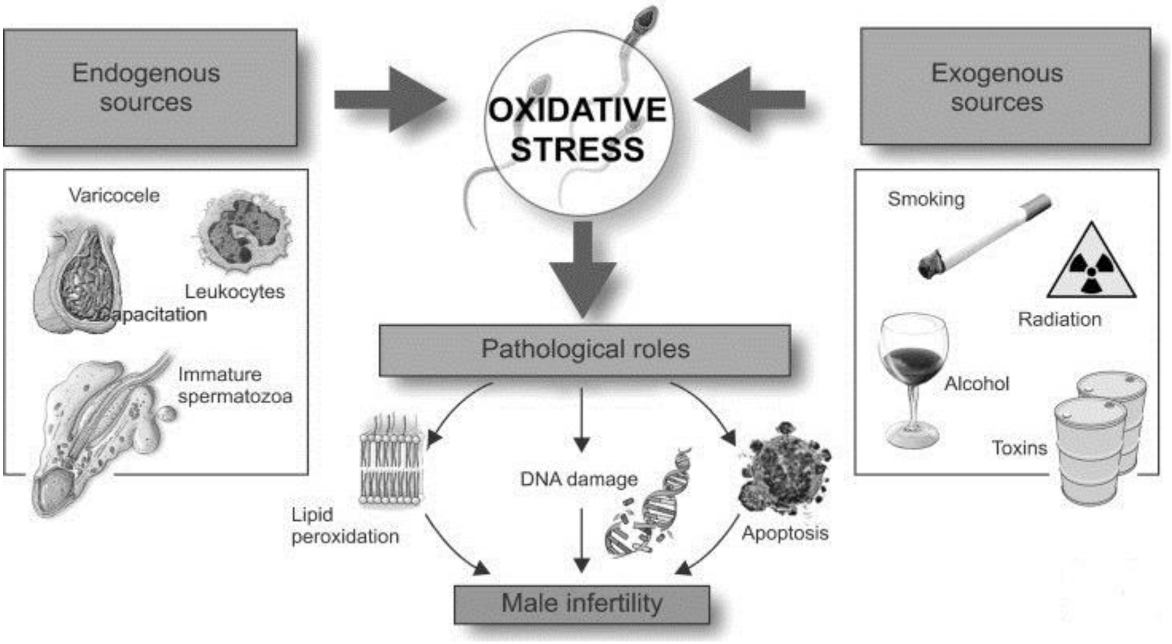


Figure 5.1: Oxidative stress in male reproduction (adapted from Kothari *et al.,* 2010).

In the current study, progressive motility increased by 30%, which is nearly double that of the increase observed in total motility. This supports the assumption that very short EA periods increase sperm functionally, thus potentially increasing fertilizing capacity (Alipour *et al.,* 2015; Ayad *et al.,* 2017; Bhahadur *et al.,* 2016). The reduced time in which the 4 hour EA sperm are exposed to epididymal fluid, along with fewer sperm and thus more energy available for motility, may be reasons for these observations. As the epididymal media surrounding sperm is regularly renewed, the constant interactions between secreted molecules by sperm and tubular epithelia have direct effects on sperm stored in the epididymis (Yanagimachi *et al.,* 1994). In the context of this study, the rate at which this epididymal media is renewed is of particular interest and will undoubtedly play a large role in how sperm are affected by epididymal transit durations and EA in general.

Furthermore, velocity and kinematic parameters provided by CASA, the percentage of rapidly swimming sperm significantly increased after 4 hours of EA, whereas the percentage of slow swimming sperm significantly decreased (see Table 4.2). Studies have shown that VCL and VSL of spermatozoa can be correlated with improved rate of fertilisation (Liu *et al.,* 2004), while ALH has previously been correlated with the efficacy of cervical mucus penetration (Aiken *et al.,* 1986). The observed increase in rapid swimming and decrease in slow swimming sperm (with no change in the percentage of medium velocity swimming sperm) equates to an improvement in sperm motility which was accompanied by significant increases in VSL and VAP. These are all highly useful parameters for assessing sperm motion (Hatef *et al.,* 2013).

Sperm hyperactivation (HA) assessment must ideally be performed using CASA and relies on reference limits explicitly stated by Mortimer *et al.* (2015). VCL must be greater than 150 µm/s; LIN must be less than 50% and ALH must be greater than 3.5 µm. The causation for these velocity results must then lie with either intrinsic activation of flagellar movement after 4 hours of EA via signalling molecules, or variations in seminal plasma conditions (e.g. pH and available energy).

5.2. **Objective 2*:*** *Investigate the role of prominent accessory sex gland biomarkers in abstinence and how they relate to sperm functional parameters.*

The WHO (2010) explicitly state normal ranges and lower reference limits of the 3 biomarkers measured in this study. Concentration measurements revealed citric acid to fall below the lower reference limit after 4 hours of EA (see Table 4.3) and both fructose and NAG remained above the lower reference limits. Interestingly, once T.S.C. was considered for each epididymal and accessory sex gland secretion, a substantial increase in citric acid available per sperm was observed accompanied by a slight decrease in the amount of available fructose.

The results of this study bring citric acid to the fore, due to the fact that per sperm, citric acid increased by 110% after short EA when compared to long EA, whereas fructose decreased by 38% after short EA.

Seminal fructose is considered to be the primary source of energy with direct effects on sperm motility (Mann, 1946), and interestingly, did not increase to account for the observed enhancement of sperm motility after 4 hours of EA. It however significantly decreased which would further reiterate the assumption that an alternative source of energy must be responsible for increased sperm motility. Patel *et al.* (1988) found direct positive correlations between seminal fructose levels and the percentage of motile sperm and this has been explained by the presence of glycolytic enzymes concentrated in the principal piece in the sperm flagellum (Eddy *et al.,* 2003; Storey & Kayne, 1975; Travis *et al.,* 1998) therefore the breakdown of fructose in glycolysis could produce ATP adjacent to the site where it is required. Furthermore, it has been suggested that glycolysis in the principal piece of the flagellum, is critical for normal sperm motility (Turner, 2003). Therefore, the observed increases in sperm motility cannot be ascribed to fructose and alternative energy sources should be responsible. This proposes citric acid as a possible source of energy due to its significant increase seen after short EA. Second to this, an alternative explanation might be related to the change observed in pH.

The fragile microenvironment created by the testes, epididymis and accessory sex glands has been found to actively manipulate the basic and functional sperm parameters including semen pH and volume, as well as sperm motility and fertilizing capacity. Studies have found EA of 2 days, to be associated with decreased prostatic secretions and increased epididymal secretions (Elzanaty, *et al.,* 2005). However, little is known about the variations in seminal accessory gland secretions after EA periods of less than 1 day.

A previous study performed by Medrano *et al.* (2006), found that citric acid acts as a substrate for energy metabolism in sperm in addition to causing slight variations in seminal plasma pH. However, its relationship with, and role in abstinence has not been elucidated.

Considering our paradoxical results, there are two possible mechanisms by which citric acid may affect sperm motility. Either the influence of sperm metabolism providing energy for flagellar movement via increased mitochondria processing utilizing the citric acid cycle, or the indirect increase of seminal pH which, according to various studies, has positive effects on sperm motility within the range of 7.2 – 8.2.

The direct mechanism mentioned above, consists of the increase in available amount of citrates per sperm, for utilization in the citric acid cycle to provide energy for sperm motility, seeing that there is more citric acid per sperm available after short EA. Sperm are capable of producing ATP by glycolysis and by oxidative phosphorylation; however, the glycolytic pathway is found to dominate ATP production (Visconti *et al.,* 2012). As mentioned previously, spermatozoa primarily utilize fructose originating from the seminal vesicles, as a source of carbohydrates however, other glycolyzable substrates including glucose, mannose and sorbitol are also effective in sustaining sperm motility through glycolysis (Visconti, 2012). Once absorbed by sperm, it is then broken down into glucose and converted to acetyl-coenzyme A (CoA), which drives the citric acid cycle ultimately leading to the production of utilizable energy in the form of Adenosine Triphosphate (ATP) produced by the electron transport chain (Figure 5.1). Furthermore, it has been shown that spermatozoa pre-incubated in citrate increase their ATP production without the addition of fructose (Medrano *et al.,* 2006). It is believed that this occurs when excess extracellular citrates are converted to malate or pyruvate by a series of enzymes, which are subsequently utilized in the citric acid cycle in sperm mitochondria (Visconti, 2012).

On the other hand, the potential role of citric acid in improving sperm motility after short EA might also be explained through a more indirect mechanism. The decrease in citric acid after 4 hours of EA was also accompanied by an overall increase in pH of the seminal plasma. As citric acid is acidic (1mM citric acid solution pH = 2.2, Silva *et al.,* 2009), the reduction in concentration in the semen may cause pH to increase, and it has been reported that this increase in alkalinity creates a more conducive environment for spermatozoa, which has been shown to enhance their motility (Zhou *et al.,* 2015). The exact mechanism by which pH alters sperm motility is not clear, yet it is well recognized (Makler *et al.,* 1981; Carr *et al.,* 1985; Ingermann *et al.,* 2002). However, it has been speculated that pH affects the activity of the alpha-4-isoform of the Na^+/K^+-ATPase, which controls the transmembrane Na^+ gradient in sperm flagella by keeping the intracellular Na^+ concentration low which is crucial to many general and cell-specific processes (Zhou *et al.,* 2015). In support of this, α4-isoform knockout mice have been reported to produce predominantly immotile sperm (Jimenez *et al.,* 2011). This may explain the observed increases in total sperm motility and progressive motility when sperm are exposed to increasing alkalinity. The ideal pH for sperm to function adequately is between 7.2 and 8.2 yet motility increases as the pH increases in this range (Zhou *et al.,* 2015).

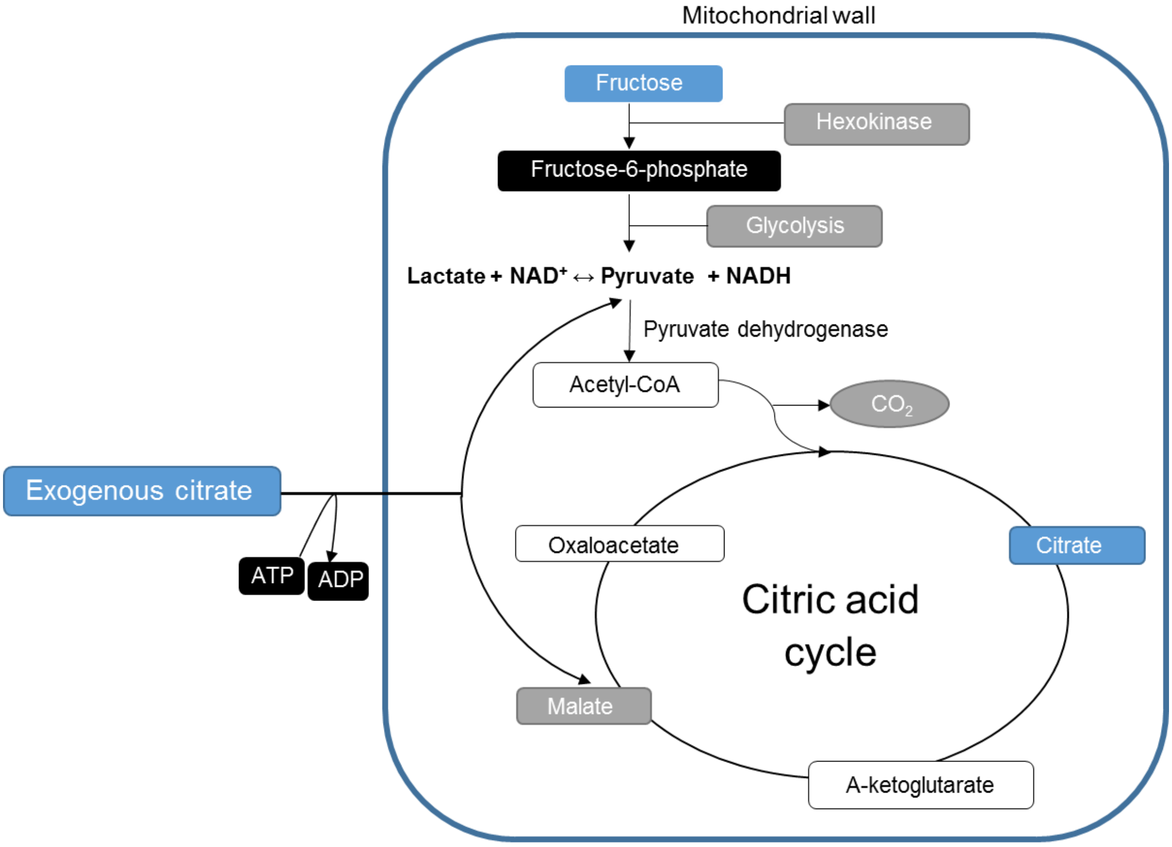


Figure 5.2: Glycolysis and Citric acid cycle in sperm mitochondria

Fructose enters the glycolytic pathway after phosphorylation by hexokinase and is subsequently converted to pyruvate via glycolysis to be used in the citric acid cycle. The entire citric acid cycle occurs within the inner mitochondrial wall. Pyruvate can enter the mitochondria through specific transporters where it can be oxidized to acetyl-coenzyme A (CoA) and CO_2*. Acetyl-CoA then enters the citric acid cycle, which generates one high-energy bond in the form of GTP and four reduced compounds (3 NADH and 1* $FADH_2$*), to be used in the oxidative phosphorylation process. Regarding citrate, when it is obtained from oxaloacetate inside the mitochondria as part of the citric acid cycle, exogenous citrate cannot permeate the inner mitochondrial membrane. Thus, before entering the cycle, it should be first converted to malate and to pyruvate by a series of enzymes with the use of ATP. Malate and pyruvate are then utilized in the citric acid cycle to produce NADH and* $FADH_2$*, which are then used to reduce oxygen in the oxidative phosphorylation process (adapted from Visconti, 2012). ADP = Adenosine diphosphate; ATP = Adenosine triphosphate.*

Alpha-glucosidase, and particularly its neutral isoenzyme, is secreted mostly in the corpus and cauda of the epididymis (Yeung, Cooper & Senge, 1990). It appears to be a sensitive indicator of epididymal function, but the subsequent effects it has on sperm functional parameters has not been thoroughly investigated. Although contradictory to this current study, Said *et al.*

(2009) and Viljoen *et al.* (1990) both observed positive correlations between seminal concentrations of NAG and percentage of motile sperm.

As mentioned above, citric acid, NAG and fructose are all effective biomarkers of the secretion and function of glands or tissues from which they originate. It may be beneficial to note variations in the secretions of these glands after the two different EA periods and how these variations may reflect on semen quality as a whole. Elzanaty *et al.* (2005) observed increases in both prostatic and epididymal secretion after longer EA periods whereas no significant differences were observed in seminal vesicle secretions. Our observations however paint a different picture. All 3 secretions were greater after 4 days of EA whereas the greatest percentage difference was observed in seminal vesicle secretion. Disproportionate reductions in epididymal and accessory sex gland secretions may be an important avenue to explore when attempting to understand the mechanisms of very short EA.

5.3. Objective 3: *Identify differentially expressed proteins as well as subsequently upregulated protein pathways in seminal plasma after 4 days and 4 hours of ejaculatory abstinence.*

In this study we used advanced techniques to extensively investigate how seminal plasma proteins differ after different EA periods. A total of 1765 proteins were identified in seminal plasma derived from pooled samples of donors. As shown in Figure 4.3, most of these proteins are involved in cellular, metabolic and regulatory processes. A total of 18 proteins were significantly upregulated after 4 days of EA and 3 proteins upregulated after 4 hours of EA. Pathway and network analysis was performed on selected proteins using the search tools Reactome (https://www.reactome.org) and String 10.5 (https://string-db.org). As illustrated in Figure 4.2, the 1765 identified proteins are involved in a multitude of cellular processes including reproduction, metabolism and cellular regulation. Many of these classifications are based on somatic cells, yet spermatozoa do share certain important cellular components and life cycle processes with somatic cells. For example, reproductive proteins identified in the seminal plasma are involved in mitotic proliferation during spermatogenesis as well as proliferation of the zygote after fertilization. As the sperm are evaluated shortly after ejaculation and the seminal plasma was isolated shortly thereafter, our ability to make observations on protein markers and their relationship with sperm functional parameters is sufficient.

When comparing levels of proteins expressed between 4 days and 4 hours of EA, 4 days of EA is essentially a control, as normal values are based on samples collected between 2 and 7 days. Thus, the upregulation of proteins after 4 days of EA may be viewed as downregulation after 4 hours of EA as they are directly compared to one another.

5.3.1. Proteins upregulated after 4 days of EA

Of the 19 proteins which were found to be upregulated after 4 days of EA, 5 proteins were specifically selected for further pathway analysis based on cellular location and involved processes. These 5 proteins are known to participate in important cellular processes including metabolism and apoptosis. All 5 proteins selected for further analysis, have been previously identified in human cells and are found in the cytoplasm or mitochondria. The identification of these proteins in the seminal plasma may be due to lysis of spermatozoa during processing (centrifugation) or due to their secretion via exosomes in the male reproductive system in response to extracellular conditions or intercellular signalling.

5.3.1.1. Heat-shock protein A2

Heat-shock proteins (HSPs), are highly conserved cellular stress proteins, present in every organism from bacteria to man (Neuer *et al.,* 2000), and are recognised for playing a critical role in the cellular defence mechanism of spermatozoa by serving two central functions. Firstly, they are involved in protein folding, translocation across membranes and the compilation of multi-protein structures (Bukau *et al.,* 2006). Secondly, HSPs maintain cellular homeostasis and function as “molecular chaperones”, subsequently regulating apoptosis and cell division (Eggert-Kruse *et al.,* 2002).

Heat-shock protein A2 (HSPA2) is a 70kDa protein identified to be located in the spindle component of the cytoskeleton in many cell types. Spindle fibre formation and centrosome integrity is critically important for successful fertilization and embryo development. In most systems, the sperm centrosome contributes the dominant nucleating seed consisting of the proximal centriole surrounded by pericentriolar components onto which the oocyte's centrosomal material is assembled (Manandhar *et al.,* 2005; Sun and Schatten, 2006, 2007). The sperm centrosome is primarily responsible for nucleating and organizing the sperm aster, which pushes the sperm head toward the oocyte centre and guides migration of the female pro-nucleus for union with the male pro-nucleus, completing the fertilization process. Reduced or abnormal centrosomal material leads to fertilization or developmental failures (Schatten *et al.*, 2009).

These proteins are synthesized in testicular seminiferous tubule cells and have been observed to be significantly downregulated in asthenozoospermic samples (Siva *et al.,* 2010;

Martínez-Heredia *et al.,* 2008). HSPA2 is a member of the 70-kDa HSPs family, and is a molecular chaperone that assists in the folding, transport and assembly of proteins in the cytoplasm, mitochondria and endoplasmic reticulum (Georgopoulos & Welch, 1993). Feng *et al.* (2001) and Dix *et al.* (1996) both observed highly detrimental effects on male fertility when the expression of heat shock proteins were disrupted. In both studies, these reductions in sperm motility and concentration were ascribed to dramatic increases in spermatocyte apoptosis and failures in proper meiosis occurring in the seminiferous epithelium.

5.3.1.2. 26S proteasome non-ATPase regulatory subunit 8 and proteasomes in protein ubiquitination.

A study on the human spermatozoon proteome identified that variable expression proteasome subunits may hold importance in sperm capacitation and motility (Kong *et al*., 2009). Proteasomes are protein complexes which degrade cytosolic and nuclear proteins that have been previously marked with ubiquitin molecules (Sutovsky, 2003). Reduced levels of proteasomes may result in increased amounts of ubiquinated proteins which has been correlated with sperm motility (Sutovsky *et al.,* 2004). Ubiquitin-conjugating enzyme E2 K (UBE2K) was also upregulated after 4 days of EA. This protein is involved in the biochemical process of ubiquinitation where it accepts ubiquitin from the E1 complex and catalyzes its covalent attachment to other proteins (Kikuchi *et al.,* 2000).

Ubiquitination of proteins serves a multitude of functions in the human cell including controlling events as diverse as cell cycle progression (Glotzer *et al.,* 1991), protein degradation and recycling (Ciechanover *et al.,* 1984), membrane receptor endocytosis (Strous & Govers, 1999), and even retroviral infection (Ott *et al*., 1998). Once the protein or peptide is marked with ubiquitin, the poly-ubiquitin chain is then removed by ubiquitin C-terminal hydrolases and the substrate is hydrolysed into smaller peptides and individual amino acids (Wilkinson & Hochstrasser, 1998). Proteasomal subunits have been identified inside or near the sperm centriole (Bialy et *al.,* 2001; Mochida *et al.,* 2000) which has been proposed as either inactive by-products of dismantled proteasomes and ubiquitinated centrosomes or important proteolytic components required for release of the centriole at fertilization (Sutovsky, 2003).

Ubiquitin has been identified in human seminal plasma (Lippert et al., 1993) as well as during epididymal passage when defective spermatozoa become ubiquitinated (Sutovsky *et al.,* 2001), thus variations in prevalence of the proteins associated with ubiquitination (i.e. proteasomes) are likely to be observed in different semen samples.

Sperm proteome studies on asthenozoospermic samples have revealed that some components of the proteasome complex are differentially expressed, suggesting an importance of the proteasome complex in sperm motility. Nevertheless, there are contradictions as to which subunits are variably expressed. For example, Martinex-Heredia *et al.* (2008) reported that 26S proteasome non-ATPase regulatory subunit 3 (PSMB3) was increased in asthenozoospermic patients, whereas Zhao *et al.* (2007) found that the 26S protease regulatory subunit 7 is significantly reduced in asthenozoospermic patients. In this study, 26S proteasome non-ATPase regulatory subunit 8 (PSMD8) was significantly upregulated after 4 days of EA when compared to 4 hours. This protein forms part of a large proteasome complex by binding to several other subunits to form the 26S proteasome (see Figure 5.2). The upregulation of this protein has been observed in samples after 4 days of EA, accompanied by lower sperm motility parameters, yet greater T.S.C., sperm concentration and volume. Reactome pathway analysis identified a multitude of protein pathways which are influenced by the 26S proteasome, primarily revolving around the ATP-dependent degradation of proteins in cytosol and nucleus, which subsequently affects numerous cellular processes including various metabolic and genetic signalling cascades (Kanyama *et al.,* 1992) (see Figure 5.3).

A balance between apoptosis and cell survival is important in multicellular organisms yet sperm also require functional apoptotic signals in order to remove unhealthy and dysfunctional sperm (Matsuzawa, 2001). In adult males, germ cell death during normal spermatogenesis plays an important role in the process of sperm production. Approximately 25%–75% of potential spermatozoa degenerate and die in the mammalian (adult) testis (Hikim & Swerdloff, 1999; Sakkas *et al.,* 1999). Defects in control of this balance may contribute to low fertility and increases in pathologies in the male reproductive system. Protein ubiquitination and degradation is one of the major mechanisms that regulate apoptotic cell death (Yang and Yu 2003). This ubiquitination thus removes proteins which inhibit the initiation of cell death. This is curiously not reflected in the basic semen analysis of the cohorts in this study, although it does raise the question that the ubiquitination of proteins in the spermatozoon, and subsequent degradation of these proteins occurs at different levels between 4 hours and 4 days of EA.

Further insight into these mechanisms of interaction between sperm the 26S proteasome is required for a comprehensive conclusion on abstinence to be made.

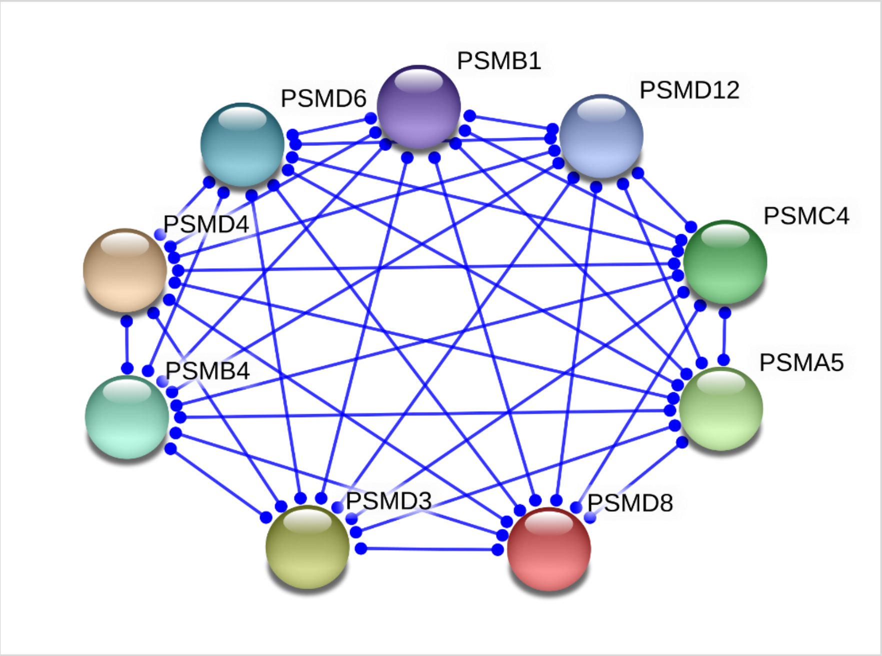


Figure 5.3: Diagram of the protein interaction network revealed by String 10.5 of the multiprotein 26S Proteasome complex.

Protein interactions consisting of the binding of a multitude of subunits to form the biologically active complex. Blue lines represent binding interactions between nodes. The highest confidence view (score 0.9) of the interaction between these proteins was prepared. SMD8 = Proteasome 26S subunit, non-ATPase, 8; PSMD4 = Proteasome 26S subunit, non-ATPase, 4; PSMD6 = Proteasome 26S subunit, non-ATPase, 6; PSMA4 = Proteasome subunit, alpha type, 4; PSMD3 = Proteasome 26S subunit, non-ATPase, 3; PSMB1 = Proteasome subunit, beta type, 1; PSMC6 = Proteasome 26S subunit, ATPase, 6; PSMA5 = Proteasome subunit, alpha type, 5; PSMC4 = Proteasome 26S subunit, ATPase, 4; PSMB4 = Proteasome subunit, beta type, 4; PSMD12 = Proteasome 26S subunit, non-ATPase.

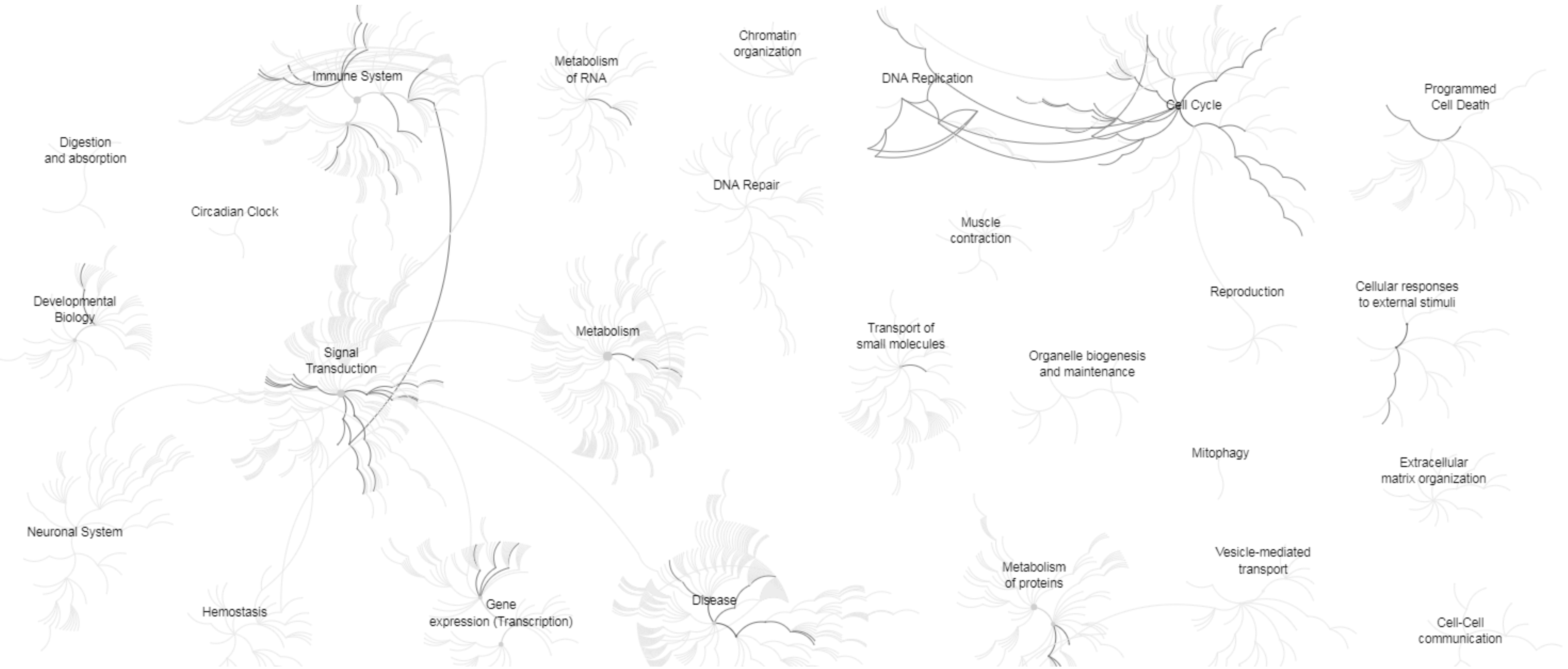


Figure 5.4. Extensive Reactome.org identification of all protein pathways influenced by the 26S Proteasome complex.

Several processes including metabolism of proteins, cell cycle, apoptosis and cellular responses to external stimuli may have direct impacts on sperm physiology thus influences observed basic and functional semen parameters.

5.3.1.3. 14 kDa phosphohistidine phosphatase and ATP-citrate synthase inhibition

Increased 14 kDa phosphohistidine phosphatase expression is associated with the inactivation of ATP-citrate synthase (ACLY) activity (Krieglstein *et al.*, 2008). ACLY is a reliable enzymatic marker of mitochondrial volume and ACLY catalyses the formation of acetyl-CoA and oxaloacetate in the cytosol from citrate and CoA with the hydrolysis of ATP to ADP and phosphate. This step is the major source of cytosolic acetyl-CoA which is used in the biosynthetic pathways of carbohydrates, fatty acids, cholesterol and acetyl-choline (Amaral *et al.,* 2013) (see Figure 5.4). The upregulation of this enzyme may have an active role in reducing available energy for sperm motility. ACLY catalyses the formation of acetyl-CoA and oxaloacetate in the cytosol from citrate and CoA with the hydrolysis of ATP to ADP and phosphate (Krieglstein *et al.,* 2008). This step is the major source of cytosolic acetyl-CoA which is used in the biosynthetic pathways of carbohydrates, fatty acids, cholesterol and acetyl choline. The inhibition of ACLY leads to reduced amounts of cytosolic acetyl-CoA and oxaloacetate available for the citric acid cycle. This may ultimately result in less glycolyzable substrates available to provide energy for sperm motility. PHPT1 is expressed at significantly lower levels after 4 hours of EA, this may result in less ACLY-facilitated reduction in glycolyzable substrates for subsequent sperm motility. Therefore, this provides further explanation for the observed increases in sperm motility after 4 hours of EA.

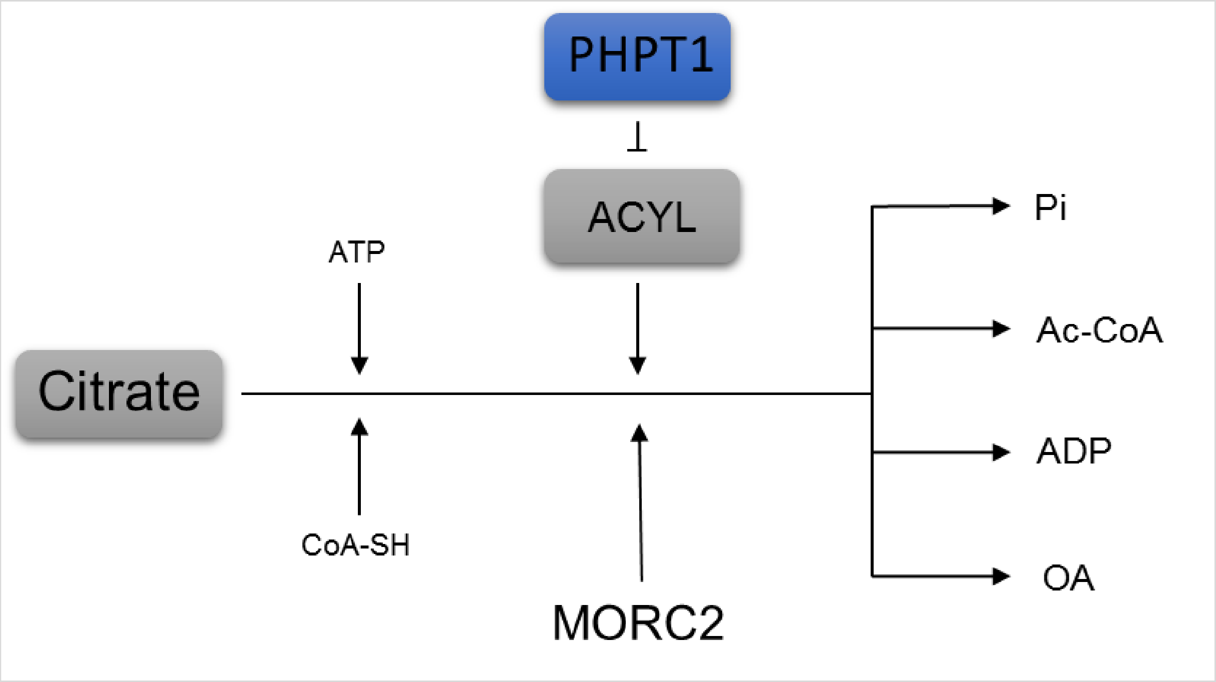


Figure 5.5: 14 kDa phosphohistidine phosphatase and subsequent ATP-citrate synthase inhibition

Mitochondrial Ac-CoA is transported to the cytosol as citrate to participate in fatty acid biosynthesis. Cytosolic ATP-citrate synthase (ACLY), in tetrameric form, catalyses the transformation of citrate to Ac-CoA and oxaloacetate (OA) (Elshourbagy et al., 1992). Cytosolic MORC family CW-type zinc finger protein 2 (MORC2) positively regulates the activity of ACLY (Sánchez-Solana et al., 2014). Phosphohistidine phosphatase (PHPT1) inactivates the ACYL thus inhibiting the conversion of citrate utilizable energy substrates.

5.3.1.4. Human Phosphatidylethanolamine-binding protein 4 and apoptosis

Although the function of human phosphatidylethanolamine-binding protein 4 (hPEBP4) is not clear in human sperm, in a study by Wang *et al.* (2004), hPEBP4 was observed to promote cellular resistance to TNF-induced apoptosis by inhibiting activation of the Raf-1/MEK/ERK pathway, c-Jun N-terminal kinases (JNKs) and phosphatidylethanolamine externalization. These same mechanisms may influence resistance to apoptotic signals in sperm during storage which may explain the higher percentage of viable cells observed in samples after 4 days of EA. As illustrated by the String network in Figure 5.5, hPEBP4 interacts with several mitochondrial ribosomal proteins which form structural constituents of those ribosomes and are thus involved in RNA binding in the mitochondria (Suzuki *et al.,* 2001).

Frayne *et al.,* (1997) found that hPEBP may be involved in the organisation of sperm membranes during spermatogenesis. The presence of hPEBP was observed in Leydig cells and testes using western blotting and immunohistochemistry. They concluded that this localization suggests diverse roles for this protein as a lipid carrier or binding constituent. Therefore further analyses is required to fully understand the possible role which human phosphatidylethanolamine-binding proteins play in the male reproductive system and in particular, variations in EA periods.

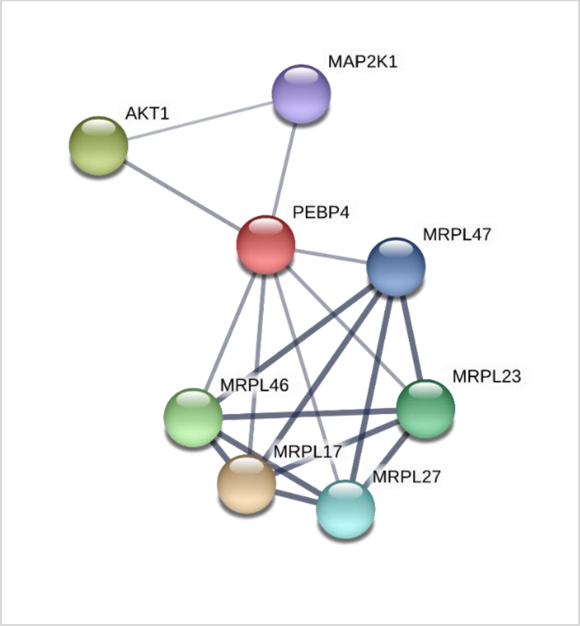


Figure 5.6. Diagram of the protein interaction network revealed by String 10.5.

Human PEBP4 interacts with several genetically important proteins involved in ribosomal function and initiation of apoptosis in cells. The thickness of the lines connecting different nodes represent the strength of the data report. A confidence view of score 0.4 was prepared for the interaction between these proteins. PEBP4 = Phosphatidylethanolamine-binding protein 4; MRPLA47 = Mitochondrial ribosomal protein L47; MRPL23 = Mitochondrial ribosomal protein L23; MRPL27 = Mitochondrial ribosomal protein L27; MRPL17 = Mitochondrial ribosomal protein L17; MRPL47 = Mitochondrial ribosomal protein L46; AKT1 = V-akt murine thymoma viral oncogene homolog 1; MAP2K11 = Mitogen-activated protein kinase kinase 1.

5.3.1.5. 2,4-dienoyl-CoA reductase, mitochondrial

Mitochondrial 2,4-dienoyl-CoA reductase (DECR1) is an auxiliary enzyme of beta-oxidation and participates in the metabolism of unsaturated fatty enoyl-CoA (Alphey *et al.,* 2005). Although human sperm are predominantly known to produce ATP from the breakdown of sugars, a study by Amaral *et al.* (2012) suggests an endogenous mechanism of mitochondrial beta-oxidation of lipids as well as several other mechanisms of lipid metabolism in sperm mitochondria. These observations were made based on the identification of various enzymes specifically involved in a host of lipid metabolic processes. This would mean that sperm may be adapted to exogenous fluctuations in primary glycolyzable energy sources. Noting that the upregulation of DECR1 after 4 days of EA equates to its downregulation after 4 hours of EA, this may indicate decreased beta-oxidation in the mitochondria-containing midpiece after 4 hours of EA, as it aids enzymes directly involved in beta-oxidation, which cannot process all the different double bond conformations occurring naturally. It does this by catalysing the NADP-dependent reduction of 2,4-dienoyl-CoA to yield trans-3-enoyl-CoA. String network analysis revealed DECR1 to interact with several important mitochondrial proteins (see Figure 5.6). DECR1 binds to Cytochrome b-245, beta polypeptide (CYBB), a vital component of a respiratory chain that transfers single electrons from cytoplasmic NADPH across the plasma membrane to molecular oxygen on the exterior and participates in the regulation of cellular pH. DECR1 interacts with several other known enzymes involved in the management of ROS, via antioxidant activation and production.

Therefore, after 4 hours of EA, decreased DECR1 may indicate that less beta-oxidation of fatty acids is occurring, thus glycolytic phosphorylation is the primary mechanism of energy production for flagellar movement.

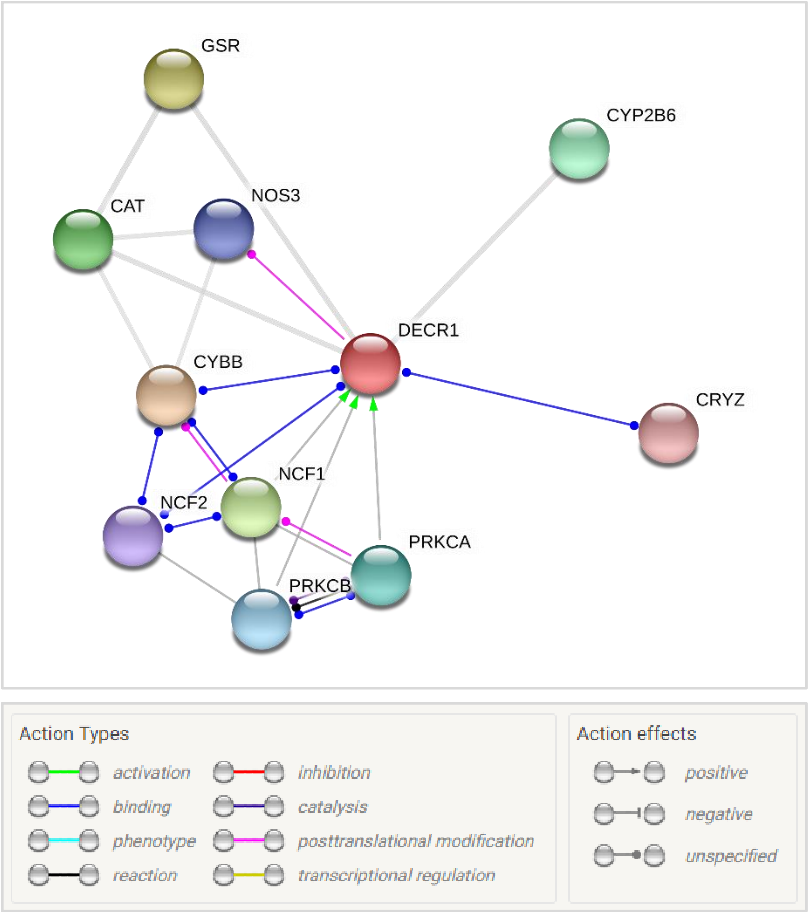


Figure 5.7. Diagram of the protein interaction network revealed using String 10.5.

Relationships are identified between DECR1 and several other proteins involved in beta oxidation of fatty acids. DECR1 is a central component of the interaction network revealed, which illustrates the activation, post-translational modification and binding of DECR1 to several other proteins. Several of the proteins identified in this network are important in immune response and apoptosis. DECR1 = 2,4-dienoyl CoA reductase 1, mitochondrial; CYP2B2 = Cytochrome P450, family 2, subfamily B; CRYZ = Crystallin, zeta (quinone reductase); PRKCA = Protein kinase C, alpha; PRKCB = Protein kinase C, beta; NCF1 = Neutrophil cytosolic factor 1; NCF2 = Neutrophil cytosolic factor 2; CYBB = Cytochrome b-245, beta polypeptide; NOS3 = Nitric oxide synthase 3 (endothelial cell); CAT = Catalase; GSR = Glutathione reductase

5.3.2. Proteins upregulated after 4 hours of EA

Only 3 proteins were observed to be upregulated after 4 hours of EA. Of these only 2 were involved in cellular metabolism and apoptosis and thus selected for further analysis. Both proteins are expressed at higher levels after 4 hours of EA due to lysis of cells during processing or release via exocytosis as they are both cytoplasmic proteins effecting cellular processes.

5.3.2.1. Calcium-binding protein 39 and energy-dependent inhibition of mTOR

Calcium-binding protein 39 (CAB39) activates protein serine/threonine kinase 11 (STK11) (Naz, 1999) by forming a complex with STK11 and enhances the formation of complexes between STE20-Related adaptor protein (STRAD) and STK11 (see Figure 5.7). These complexes have increased catalytic activity, where CAB39 acts as a scaffolding protein in addition to being a component of cellular localization. Furthermore, once the trimeric STK11:STRAD:CAB39 complex is formed, STK11 phosphorylates 5' AMP-activated protein kinase (AMPK), activating it (Hardie, 2007). This phosphorylation is immediately removed in basal conditions by protein phosphatase 2c (PP2C), but if the cellular AMP:ATP ratio rises, this activation is maintained and AMPK binding to AMP inhibits the dephosphorylation. As shown in table 4.5, fructose, the primary source of energy for spermatozoa, decreased in concentration which may be a marker for a lower amount of available energy thus leading to a higher AMP:ATP ratio.

At a molecular level, once energy abundance reduces (ie. high AMP:ATP ratio), excess AMP directly binds to tandem repeats of cystathionine-beta-synthase (CBS) domains in the AMPK gamma subunit. Binding of AMP is thought to prevent dephosphorylation of the critical activation loop-threonine in the alpha subunit (Hardie, 2007). The phosphorylation of the activation loop-threonine is unequivocally required for AMPK activation.

Biochemical and genetic analyses in worms, flies, and mice have revealed that the serine/threonine kinase STK11 (LKB1) represents the major kinase in the phosphorylation of the AMPK activation loop under conditions of energy stress across metazoans (Sakamoto et al. 2005, Lee et al. 2007). LKB1 phosphorylates AMPK on Thr174 of the alpha 1 subunit (or Thr172 on the alpha 2 subunit) leading to activation of AMPK if the cellular AMP/ATP ratio is sufficiently high.

This will allow AMPK to activate the STK11:STRAD:CAB39 complex during the build-up of AMP, which activates the intrinsic GTPase activity of Ras homolog enriched in brain (Rheb), thus resulting in GDP-loaded Rheb and the inhibition of the mammalian target of rapamycin (mTOR) pathway. The mTOR signalling pathway integrates both intracellular and extracellular signals, and serves as a central regulator of cell metabolism, growth, proliferation and survival.

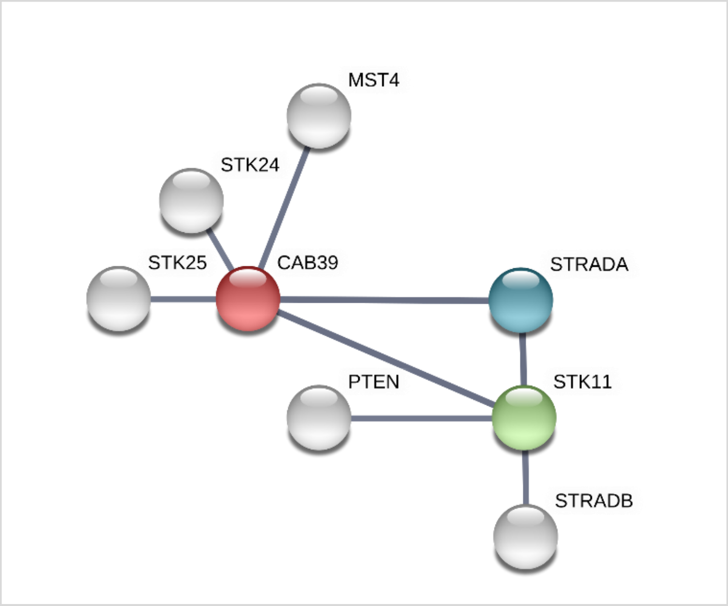


Figure 5.8: Diagram of the protein interaction network revealed by String 10.5 considering CAB39 (MO25) and the formation of the trimeric STK11:STRAD:CAB39 complex

The diagram includes the interaction between CAB39 and two other upstream proteins, STK11 (LKB1) and STRADA, which leads to the formation of the trimeric STK11:STRAD:CAB39 complex and the subsequent AMPK phosphorylation of various kinases and other protein interactions. The highest confidence view (score 0.9) of the interaction between these proteins was prepared. CAB39 = Calcium binding protein 39, STRADB = STE20-related kinase adaptor beta, MST4 = mammalian STE20-like protein kinase 4, STK11 = Serine/threonine kinase 11, STK24 = Serine/threonine kinase 24, STK25 = Serine/threonine kinase 25, STRADA = STE20 - related kinase adaptor alpha, STRADB = STE20 - related kinase adaptor beta, PTEN = Phosphatase and tensin homolog.

MTOR is a highly conserved multifunctional serine/threonine protein kinase that coordinates and integrates signals that manipulate essential processes of cellular physiology, including protein synthesis, cellular growth, proliferation, motility, survival, and autophagy. It responds to multiple signals to control processes stemming from the direct or indirect regulation of the phosphorylation of hundreds of proteins (Laplante, 2009). It associates with different proteins such as Regulatory-associated protein of mTOR (RPTOR) and Rapamycin-insensitive companion of mammalian target of rapamycin (RICTOR), to form two distinct complexes, mTORC1 and mTORC2, respectively. These two complexes display different sensitivity to the inhibitor rapamycin; with mTORC1 being acutely inhibited by rapamycin, whereas mTORC2 inhibition requires prolonged treatment and is cell/tissue dependent.

Activated mTORC1 up-regulates protein synthesis, by phosphorylating key regulators of mRNA translation and ribosome synthesis. While mTORC2, regulates cytoskeletal function and insulin signalling (Laplante & Sabatini, 2009). Despite the extensive work already done on mTOR signalling, particularly in somatic cells, its functions and activity in germ cells remain mostly unknown.

A study by Silva *et al*. found a negative correlation between the amount of activated mTOR and sperm motility yet the exact mechanism by which this occurs is not clear (Silva *et al.,* 2015). Rapamycin induced inhibition of mTOR have been found to have negative effects on male fertility (Zuber *et al.,* 2008). Conditional deletion of RPTOR in mouse skeletal muscle has been shown to reduce the expression of genes involved in mitochondrial biogenesis (Bentzinger *et al.,* 2008). Another study by Cunningham *et al.* discovered that mTORC1 controls the transcriptional activity of PPARγ coactivator 1 (PGC1-α), a nuclear cofactor that plays an important role in mitochondrial biogenesis and oxidative metabolism, by altering its physical interaction with another transcription factor, yin-yang 1 (YY1) (Cunningham *et al.,* 2007). This would mean that the proposed effects of mTOR after 4 hours of EA must occur during transit of sperm through the epididymis and not during spermatogenesis.

This aligns with the results of this current study, where sperm motility was observed to be significantly higher in samples which contain proteins known for the inhibition of mTOR. CAB39s ability to indirectly impact sperm capacitation and metabolism is of particular interest. This may serve as a possible mechanism for the observed impact of short EA on semen quality. It can be postulated that an upregulation of the CAB39 protein may elicit improved motility in conditions of reduced seminal glycolyzable molecules, and may be used as a biomarker for this particular sperm parameter.

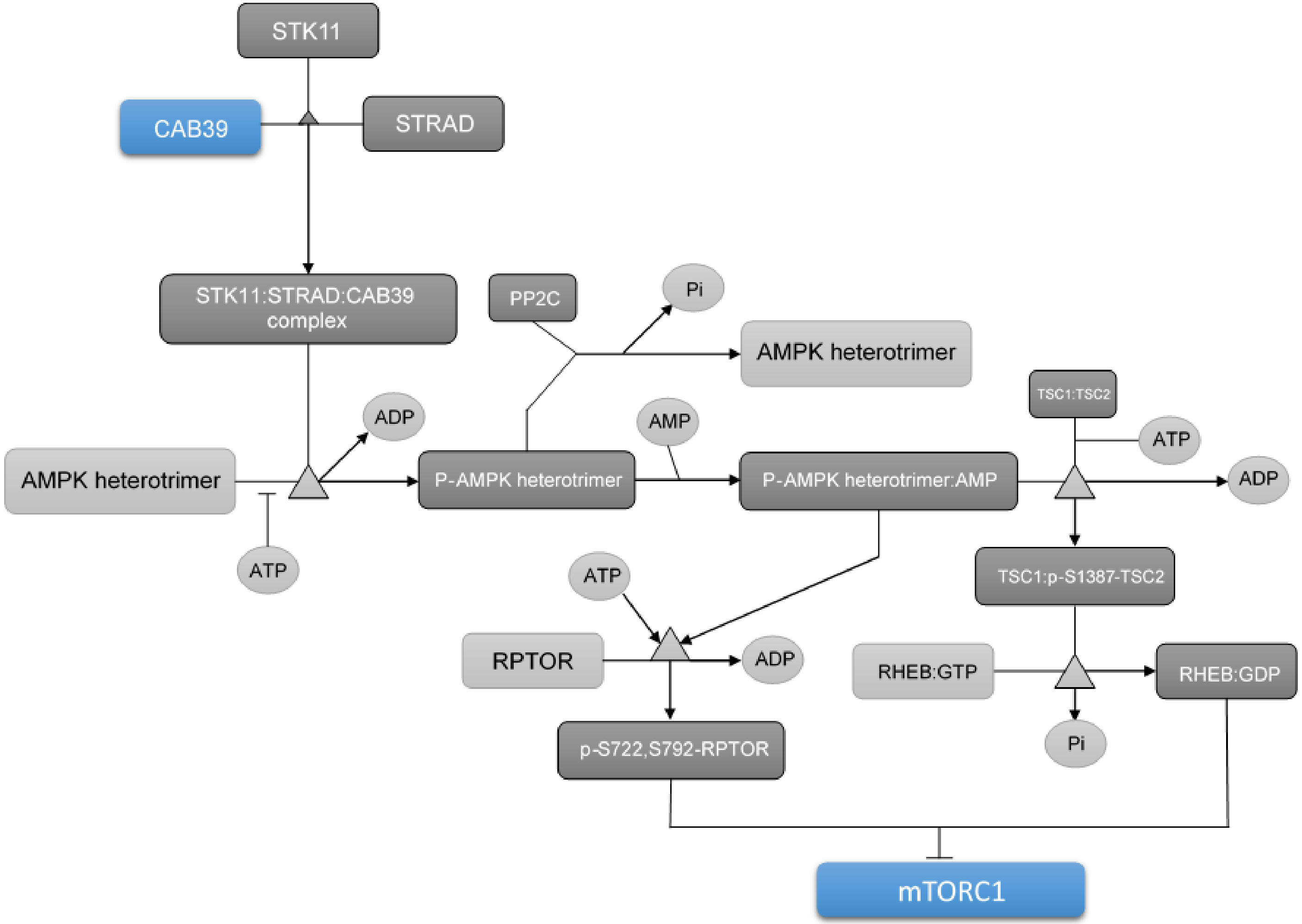


Figure 5.9. Energy dependent inhibition of mTOR

Formation of the trimeric STK11:STRAD:CAB39 complex leads to further kinase activity subsequently phosphorylating the AMP-activated protein kinase (AMPK) activation loop. The AMPK is a highly conserved heterotrimeric kinase complex consisting of a catalytic (alpha) subunit and two regulatory (beta and gamma) subunits. Once the AMP:ATP ratio elevates (ie. Energy stress conditions), AMP bind to the AMPK gamma subunit. This binding is thought to prevent the dephosphorylation of AMPK at the critical activation loop threonine by PP2C which occurs under normal conditions (Hardie, 2007). The activation loop threonine is essential in its phosphorylated state for AMPK activation (Sakamoto et al., 2005; Lee et al., 2007). Activated AMPK (phosphorylated on Thr172 or Thr174 and AMP bound) phosphorylates RPTOR on Ser722 and Ser792. This step is pivotal in the energy-dependent inhibition of mTORC1 (Gwinn et al., 2008). Furthermore, activated AMPK phosphorylates TSC2 on Ser-1387 which subsequently activates GTPase activating protein (GAP) activity in the Tuberous Sclerosis Complex (TSC). TSC is a critical upstream inhibitor of mTORC1 and does this by stimulating the intrinsic GTPase activity of the small G-protein Rheb. This then inactivates Rheb which subsequently leads to the inability of the GDP-bound form of Rheb to activate mTORC1 (Sancak et al., 2007).

5.3.2.2. Deoxyribonuclease I and sperm apoptosis:

Deoxyribonuclease-1 (DNase I) is an enzyme predominantly found in the liver, kidneys and pancreas (Kishi *et al.,* 1990), and is primarily involved in cell apoptosis (Peitsch *et al.,* 1992). However, previous studies had found DNase I activity in seminal plasma and semen (Zamenhof *et al*., 1957; Quinn, 1968). Peitsch *et al. (*1992) speculated that DNase I may be a role-player in the continuous apoptosis of differentiating spermatogonia in the testes. DNAse I may interact selectively and non-covalently with monomeric or multimeric forms of actin, including actin filaments, and can possibly prevent damage of genetic material, yet the function is unclear.

This initiation of apoptosis may be responsible for decreases in the output of viable sperm in the ejaculate. The early study by Quinn (1968) also suggested that increased activity of DNase I was linked to significant decreases in sperm motility parameters, yet the exact mechanisms are not yet clear. Shen and Ong (2000) utilized DNase I to initiate apoptosis in human sperm and used this as a positive control when comparing DNA damage amongst cohorts. Therefore, considering the significant reduction in the percentage of viable sperm after 4 hours of EA when compared to 4 days, an upregulation of DNase I may be a sign of increased apoptosis. This apoptosis may be linked to the proposed mechanism of shorter EA by Ayad *et al.* (2018) whereby it is speculated that increased sperm motility parameters were at the cost of weaker and improper functioning sperm.

This would support the possibility that an intrinsic mechanism of improving observed sperm motility was occurring after 4 hours of EA, allowing for damaged sperm to be destroyed and highly motile sperm to be prevalent as observed in the reduction of viable sperm accompanied by improved motility after shot EA. In order to substantiate this theory, a study which further analysed levels of leukocytes and DNA damage at a highly accurate level would be beneficial.

5.4. Limitations of the study/recommendations

By and large this study attained its objectives, but several shortcomings and limitations were inevitable from the beginning of the study. As mentioned, the entire cohort of donors were healthy normozoospermic and potentially fertile males between the ages of 19 and 25. For further comprehensive analysis, subjects with sub-fertile conditions such as oligozoospermia, teratozoospermia and asthenozoospermia should be included in the study. Secondly, the cohort size was relatively small (N=16) due to the huge costs of different analyses. If financially possible, future studies on shorter EA periods should incorporate larger cohorts for further research into differentialy expressed proteins and signalling pathways, to provide a deeper insight into the mechanisms by which EA may improve sperm functional characteristics. Two-dimensional gel electrophoresis for more accurate separation of proteins should be utilized if financially feasible in order to further reduce any sensitivity issues when LC-MS/MS is performed as larger abundance proteins may reduce the chances of identifying much smaller abundance proteins.

Furthermore, metabolomic analysis would prove highly useful in the context of mitochondrial metabolism and energy availability for sperm motility. Nuclear magnetic resonance spectroscopy (NMR) has been utilized as an effective identifier of metabolites and would provide a more comprehensive analysis of the seminal plasma constituents released by the accessory sex glands.

As with all biological samples, results may be influenced by donor-specific factors which could sway our results. Larger cohorts are required and further investigation into how differing epididymal transit times may alter the mechanisms which are known to influence sperm motility.

The results of this study emphasize the general consensus that male reproduction requires a multi-factoral approach to understanding how EA may manipulate sperm functional parameters. There are clearly a multitude of contributing factors to observable sperm functional characteristics, and as many as possible should be considered.

Chapter 6

6. Conclusion

Several recent publications have contradicted the official WHO guidelines for ejaculatory abstinence and this raises doubts about the true importance of EA period and how this influences sperm function. This study was performed on a relatively small cohort yet significantly better sperm motility based on total motility, progressive motility and several kinematic parameters including rapid swimming sperm, VSL and VAP was observed after 4 hours of EA when compared to 4 days, yet the reasoning for these changes are relatively ambiguous. Short EA has repeatedly been associated with reductions in T.S.C., sperm concentration and semen volume, however the controversial results of increased motility remain. Significant reductions in observed viability after 4 hours of EA may be part of the reason for the observed increases in motility as favourable sperm were observed at the cost of weaker, abnormal sperm that may have impaired membrane integrity after being marked for apoptosis.

Most previous studies have not systematically assessed the contributory role of accessory sex gland secretions and citric acid in particular. This includes citric acids ability to influence sperm functional characteristics directly or indirectly in relation to EA. This study found that citric acid may be a viable candidate in the justification of the observed improvements in sperm motility after an EA period of 4 hours, through acting as a possible alternative source of energy in the citric acid cycle. An additive effect via the increased availability of citric acid per sperm might occur which furthermore compensates for the reduction in fructose per sperm. This highlights a possible oversight of the metabolic significance of citric acid as well as being partially responsible for an increase in semen pH. Further comprehensive biochemical pathway analysis is required to better understand the role that epididymal and accessory sex glands play in the improvement of sperm motility after very short EA. Another avenue of research may be the ratios of secretions from these glands and tissues, plus the subsequent effects on basic and functional sperm parameters.

Despite the considerable advances in proteomics, there remains a lack of research into spermatozoa and seminal proteins isolated from ejaculates after very short EA periods. The utilisation of a high-output approach such as LC-MS/MS, as adopted in this study, allows for a considerable majority of the seminal plasma proteome to be identified. With 21 differentially expressed proteins between 4 hours and 4 days of EA. Changes in protein expression and the corresponding impact on the spermatozoa's functional capacity were discussed. With only 3 significantly upregulated proteins identified after 4 hours of EA, several proteins upregulated after 4 days of EA seem to influence sperm functional parameters negatively besides for the positive impact of sperm viability.

Amongst the proteins upregulated after 4 days of EA, various proteins were selected for relevant influence in metabolism, apoptosis and cellular stress management. All having proposed direct and indirect effects on sperm motility according to available literature. The upregulation of the 26S proteasome requires further attention as the ubiquitination of proteins plays an important role in every mammalian cell.

Calcium binding protein 39 may have an indirect mechanism of sperm motility improvement by the energy-dependent inhibition of mTOR in seminal conditions of reduced available energy. Deoxyribonuclease I is involved induction of apoptosis of many somatic cells, and similar effects have been observed in male germ cells (Shen & Ong, 2000), which may elucidate the reduced percentages of viable cells after 4 hours of EA. It has been speculated that apoptosis may increase motility and kinematic parameters at the cost of dysfunctional sperm.

It can be stated with reasonable certainty, that this is the first study into the proteomic profile and key epididymal and accessory sex gland secretions of seminal plasma from semen samples obtained after 4 hours of EA in order to explain improved sperm function. Further understanding of the influence of proteins, metabolites and intrinsic anatomical components on sperm characteristics after very short EA, might serve as an important tool for increasing the success rates of ART and natural conception, thus reducing cost as well as enriching sperm research in general.

Bibliography

Agarwal, A., Virk, G., Ong, C. and du Plessis, S.S., 2014. Effect of oxidative stress on male reproduction. The world journal of men's health, 32(1), pp.1-17.

Agarwal, A., Gupta, S., Du Plessis, S., Sharma, R., Esteves, S.C., Cirenza, C., Eliwa, J., Al-Najjar, W., Kumaresan, D. & Haroun, N. 2016, "Abstinence time and its impact on basic and advanced semen parameters", Urology, vol. 94, pp. 102-110.

Alavi, S.H., Rodina, M., Viveiros, A.T., Cosson, J., Gela, D., Boryshpolets, S. and Linhart, O., 2009. Effects of osmolality on sperm morphology, motility and flagellar wave parameters in Northern pike (Esox lucius L.). Theriogenology, 72(1), pp.32-43.

Alipour, H., Dardmeh, F., Van Der Horst, G., Manoharan, G., Askeland, A. & Nielsena, H. 2015, "Effect of short abstinence time on sperm motility parameters", Final Programme, 18th World Congress of in Vitro Ferilization, Isivf 2015, 27-30 September 2015, Copenhagen, DenmarkInternational Society of In Vitro Fertilization, in press.

Alphey, M.S., Yu, W., Byres, E., Li, D. and Hunter, W.N., 2005. Structure and Reactivity of Human Mitochondrial 2, 4-Dienoyl-CoA Reductase Enzyme-ligand interactions in a distinctive short-chain reductase active site. Journal of Biological Chemistry, 280(4), pp.3068-3077.

Amann, R. 1981, "A critical review of methods for evaluation of spermatogenesis from seminal characteristics", Journal of andrology, vol. 2, no. 1, pp. 37-58.

Amaral, A., Lourenco, B., Marques, M. & Ramalho-Santos, J. 2013, "Mitochondria functionality and sperm quality", Reproduction (Cambridge, England), vol. 146, no. 5, pp. R163-74.

Amaral, A., Castillo, J., Estanyol, J.M., Ballescà, J.L., Ramalho-Santos, J. and Oliva, R., 2013. Human sperm tail proteome suggests new endogenous metabolic pathways. Molecular & Cellular Proteomics, 12(2), pp.330-342.

Antoni, G., Oudot-Mellakh, T., Dimitromanolakis, A., Germain, M., Cohen, W., Wells, P., Lathrop, M., Gagnon, F., Morange, P.E. and Tregouet, D.A., 2011. Combined analysis of three genome-wide association studies on vWF and FVIII plasma levels. BMC medical genetics, 12(1), p.102.

Arienti, G., Carlini, E., Nicolucci, A., Cosmi, E.V., Santi, F. & Palmerini, C.A. 1999, "The motility of human spermatozoa as influenced by prostasomes at various pH levels", Biology of the Cell, vol. 91, no. 1, pp. 51-54.

Aumüller, G. & Riva, A. 1992, "Morphology and functions of the human seminal vesicle", Andrologia, vol. 24, no. 4, pp. 183-196.

Ayad, B.M., Horst, G.V. and Plessis, S.S.D., 2018. Revisiting the relationship between the ejaculatory abstinence period and semen characteristics. International journal of fertility & sterility, 11(4), p.238.

Ayad, B., Van der Horst, G. & du Plessis, S.S. 2017, "Short abstinence: A potential strategy for the improvement of sperm quality", Middle East Fertility Society Journal, in press.

Baccetti, B., 1984. The human spermatozoon. Ultrastructure of Reproduction: Gametogenesis, Fertilization, and Embryogenesis, 2, p.110.

Bahadur, G., Almossawi, O., Zaid, R.Z., Ilahibuccus, A., Al-Habib, A., Muneer, A. & Okolo, S. 2016, "Semen characteristics in consecutive ejaculates with short abstinence in subfertile males", Reproductive biomedicine online, vol. 32, no. 3, pp. 323-328.

Balk, S.P., Ko, Y.J. and Bubley, G.J., 2003. Biology of prostate-specific antigen. Journal of Clinical Oncology, 21(2), pp.383-391.

Barbonetti, A., Vassallo, M., Di Rosa, A., Leombruni, Y., Felzani, G., Gandini, L., Lenzi, A., Necozione, S., Francavilla, S. & Francavilla, F. 2013, "Involvement of mitochondrial dysfunction in the adverse effect exerted by seminal plasma from men with spinal cord injury on sperm motility", Andrology, vol. 1, no. 3, pp. 456-463.

Bar-Hava, I., Perri, T., Ashkenazi, J., Shelef, M., Ben-Rafael, Z. & Orvieto, R. 2000, "The rationale for requesting a second consecutive sperm ejaculate for assisted reproductive technology", Gynecological endocrinology, vol. 14, no. 6, pp. 433-436.

Batruch, I., Lecker, I., Kagedan, D., Smith, C.R., Mullen, B.J., Grober, E., Lo, K.C., Diamandis, E.P. & Jarvi, K.A. 2011, "Proteomic analysis of seminal plasma from normal volunteers and post-vasectomy patients identifies over 2000 proteins and candidate biomarkers of the urogenital system", Journal of proteome research, vol. 10, no. 3, pp. 941-953.

Bedford, J.M. 1994, "The status and the state of the human epididymis", Human reproduction (Oxford, England), vol. 9, no. 11, pp. 2187-2199.

Bencic, D., Cloud, J. & Ingermann, R. 2000, "Carbon dioxide reversibly inhibits sperm motility and fertilizing ability in steelhead (Oncorhynchus mykiss)", Fish Physiology and Biochemistry, vol. 23, no. 4, pp. 275-281.

Bentzinger, C.F., Romanino, K., Cloëtta, D., Lin, S., Mascarenhas, J.B., Oliveri, F., Xia, J., Casanova, E., Costa, C.F. & Brink, M. 2008, "Skeletal muscle-specific ablation of raptor, but not of rictor, causes metabolic changes and results in muscle dystrophy", Cell metabolism, vol. 8, no. 5, pp. 411-424.

Bererhi, L., Flamant, M., Martinez, F., Karras, A., Thervet, E. & Legendre, C. 2003, "Rapamycin-induced oligospermia", Transplantation, vol. 76, no. 5, pp. 885-886.

Biały, L.P., Ziemba, H.T., Marianowski, P., Fracki, S., Bury, M. and Wójcik, C., 2001. Localization of a proteasomal antigen in human spermatozoa: immunohistochemical electron microscopic study. Folia histochemica et cytobiologica, 39(2), pp.129-130.

Birkhead, T., Møller, A. & Sutherland, W. 1993, "Why do females make it so difficult for males to fertilize their eggs?", Journal of theoretical biology, vol. 161, no. 1, pp. 51-60.

Bishop, M.W. & Walton, A. 1960, "Spermatogenesis and the structure of mammalian spermatozoa", Marshall's physiology of reproduction, vol. 1, no. Part 2, pp. 1-129.

Boivin, J., Bunting, L., Collins, J.A. and Nygren, K.G., 2007. International estimates of infertility prevalence and treatment-seeking: potential need and demand for infertility medical care. Human reproduction, 22(6), pp.1506-1512.

Bongso, T., Ng, S., Mok, H., Lim, M., Teo, H., Wong, P. & Ratnam, S. 1989, "Effect of sperm motility on human in vitro fertilization", Archives of Andrology, vol. 22, no. 3, pp. 185-190.

Bonnycastle, L.L., Yu, C.E., Hunt, C.R., Trask, B.J., Clancy, K.P., Weber, J.L., Patterson, D. and Schellenberg, G.D., 1994. Cloning, sequencing, and mapping of the human chromosome 14 heat shock protein gene (HSPA2). Genomics, 23(1), pp.85-93.

Brackett, N.L., Davi, R.C., Padron, O.F. & Lynne, C.M. 1996, "Seminal plasma of spinal cord injured men inhibits sperm motility of normal men", The Journal of urology, vol. 155, no. 5, pp. 1632-1635.

Buckett, W. & Lewis-Jones, D. 2002, "Fructose concentrations in seminal plasma from men with nonobstructive azoospermia", Archives of Andrology, vol. 48, no. 1, pp. 23-27.

Bukau, B., Weissman, J. and Horwich, A., 2006. Molecular chaperones and protein quality control. Cell, 125(3), pp.443-451

Burnett, G. & Kennedy, E.P. 1954, "The enzymatic phosphorylation of proteins", The Journal of biological chemistry, vol. 211, no. 2, pp. 969-980.

Calvete, J., Nessau, S., Mann, K., Sanz, L., Sieme, H., Klug, E. & Töpfer-Petersen, E. 1994, "Isolation and Biochemical Characterization of Stallion Seminal-plasma Proteins", Reproduction in Domestic Animals, vol. 29, no. 5, pp. 411-426.

Camiña, J.P., Lage, M., Menendez, C., Graña, M., García-Devesa, J., Dieguez, C. & Casanueva, F.F. 2002, "Evidence of free leptin in human seminal plasma", Endocrine, vol. 17, no. 3, pp. 169-174.

Canale, D., Bartelloni, M., Negroni, A., Meschini, P., Izzo, P.L., Bianchi, B. and Menchini-Fabris, G.F., 1986. Zinc in human semen. International journal of andrology, 9(6), pp.477-480.

Carr, D.W., Usselman, M.C. & Acott, T.S. 1985, "Effects of pH, lactate, and viscoelastic drag on sperm motility: a species comparison", Biology of reproduction, vol. 33, no. 3, pp. 588-595.

Chang, H.H., Chang, M.C., Wu, I.H., Huang, G.F., Huang, W.L., Wang, Y.L., Lee, S.Y., Yeh, C.Y., Guo, M.K., Chan, C.P. and Hsien, H.C., 2015. Role of ALK5/Smad2/3 and MEK1/ERK signaling in transforming growth factor beta 1–modulated growth, collagen turnover, and differentiation of stem cells from apical papilla of human tooth. Journal of endodontics, 41(8), pp.1272-1280.

Charlesworth, B. & Charlesworth, D. 1999, "The genetic basis of inbreeding depression", Genetical research, vol. 74, no. 03, pp. 329-340.

Chesler, L., Golde, D.W., Bersch, N. and Johnson, M.D., 1995. Metalloproteinase inhibition and erythroid potentiation are independent activities of tissue inhibitor of metalloproteinases-1. Blood, 86(12), pp.4506-4515.

Ciechanover, A., Finley, D. and Varshavsky, A., 1984. Ubiquitin dependence of selective protein degradation demonstrated in the mammalian cell cycle mutant ts85. Cell, 37(1), pp.57-66.

Comar, V.A., Petersen, C.G., Mauri, A.L., Mattila, M., Vagnini, L.D., Renzi, A., Petersen, B., Nicoletti, A., Dieamant, F., Oliveira, J.B.A., Baruffi, R.L.R. & Franco, J.G.,Jr 2017, "Influence of the abstinence period on human sperm quality: analysis of 2,458 semen samples", JBRA assisted reproduction, .

Cooper, T. 1996, "Physiology and evaluation of epididymal function", Comhaire F, Male Infertility.Clinical Investigation, Cause Evaluation and Treatment.Chapman and Hall Oxford, .

Cooper, T., Weidner, W. & Nieschlag, E. 1990, "The influence of inflammation of the human male genital tract on secretion of the seminal markers α-glucosidase, glycerophosphocholine, carnitine, fructose and citric acid", International journal of andrology, vol. 13, no. 5, pp. 329-336.

Cooper, T., Keck, C., Oberdieck, U. & Nieschlag, E. 1993, "Effects of multiple ejaculations after extended periods of sexual abstinence on total, motile and normal sperm numbers, as well as accessory gland secretions, from healthy normal and oligozoospermic men", Human reproduction (Oxford, England), vol. 8, no. 8, pp. 1251-1258.

Coy, J.F., Dressler, D., Wilde, J. and Schubert, P., 2005. Mutations in the transketolase-like gene TKTL1: clinical implications for neurodegenerative diseases, diabetes and cancer. Clinical laboratory, 51(5-6), pp.257-274.

Cunningham, J.T., Rodgers, J.T., Arlow, D.H., Vazquez, F., Mootha, V.K. & Puigserver, P. 2007, "mTOR controls mitochondrial oxidative function through a YY1-PGC-1 [alpha] transcriptional complex", Nature, vol. 450, no. 7170, pp. 736.

Davis, R.O., Overstreet, J.W., Asch, R.H., Ord, T. and Silber, S.J., 1991. Movement characteristics of human epididymal sperm used for fertilization of human oocytes in vitro. Fertility and sterility, 56(6), pp.1128-1135.

De Jonge, C., LaFromboise, M., Bosmans, E., Ombelet, W., Cox, A. & Nijs, M. 2004, "Influence of the abstinence period on human sperm quality", Fertility and sterility, vol. 82, no. 1, pp. 57-65.

Ding, Z., Qu, F., Guo, W., Ying, X., Wu, M. & Zhang, Y. 2007, "Identification of sperm forward motility-related proteins in human seminal plasma", Molecular reproduction and development, vol. 74, no. 9, pp. 1124-1131.

Dix, D.J., Allen, J.W., Collins, B.W., Mori, C., Nakamura, N., Poorman-Allen, P., Goulding, E.H. and Eddy, E.M., 1996. Targeted gene disruption of Hsp70-2 results in failed meiosis, germ cell apoptosis, and male infertility. Proceedings of the National Academy of Sciences, 93(8), pp.3264-3268.

Donnelly, E.T., Lewis, S.E., McNally, J.A. & Thompson, W. 1998, "In vitro fertilization and pregnancy rates: the influence of sperm motility and morphology on IVF outcome", Fertility and sterility, vol. 70, no. 2, pp. 305-314.

Drabovich, A.P., Jarvi, K. & Diamandis, E.P. 2011, "Verification of male infertility biomarkers in seminal plasma by multiplex selected reaction monitoring assay", Molecular & cellular proteomics : MCP, vol. 10, no. 12, pp. M110.004127.

Du Plessis, S.S., Kashou, A.H., Benjamin, D.J., Yadav, S.P. & Agarwal, A. 2011, "Proteomics: a subcellular look at spermatozoa", Reproductive Biology and Endocrinology, vol. 9, no. 1, pp. 36.

Eddy, E.M., Toshimori, K. and O'Brien, D.A., 2003. Fibrous sheath of mammalian spermatozoa. Microscopy research and technique, 61(1), pp.103-115.

Eggert-Kruse, W., Neuer, A., Clussmann, C., Boit, R., Geissler, W., Rohr, G. and Strowitzki, T., 2002. Seminal antibodies to human 60kd heat shock protein (HSP 60) in male partners of subfertile couples. Human Reproduction, 17(3), pp.726-735.

Elshourbagy, N.A., Near, J.C., Kmetz, P.J., Wells, T.N., Groot, P.H., Saxty, B.A., Hughes, S.A., Franklin, M. & Gloger, I.S. 1992, "Cloning and expression of a human ATP-citrate lyase cDNA", The FEBS Journal, vol. 204, no. 2, pp. 491-499.

Elzanaty, S., Malm, J. & Giwercman, A. 2005, "Duration of sexual abstinence: epididymal and accessory sex gland secretions and their relationship to sperm motility", Human reproduction (Oxford, England), vol. 20, no. 1, pp. 221-225.

Ferramosca, A., Provenzano, S.P., Coppola, L. & Zara, V. 2012, "Mitochondrial respiratory efficiency is positively correlated with human sperm motility", Urology, vol. 79, no. 4, pp. 809-814.

Feng, H.L., Sandlow, J.I. and Sparks, A.E., 2001. Decreased expression of the heat shock protein hsp70-2 is associated with the pathogenesis of male infertility. Fertility and sterility, 76(6), pp.1136-1139.

Fichtner, J., Graves, H.C., Thatcher, K., Yemoto, C. & Shortlife, L.M. 1996, "Prostate specific antigen releases a kinin-like substance on proteolysis of seminal vesicle fluid that stimulates smooth muscle contraction", The Journal of urology, vol. 155, no. 2, pp. 738-742.

Fischer, E.H. & Krebs, E.G. 1955, "Conversion of phosphorylase b to phosphorylase a in muscle extracts", The Journal of biological chemistry, vol. 216, no. 1, pp. 121-132.

Fraser, L.R., Harrison, R.A.P. and Herod, J.E., 1990. Characterization of a decapacitation factor associated with epididymal mouse spermatozoa. Journal of reproduction and fertility, 89(1), pp.135-148.

Frayne, J., McMillen, A., Love, S. and Hall, L., 1998. "Expression of phosphatidylethanolamine-binding protein in the male reproductive tract: immunolocalisation and expression in prepubertal and adult rat testes and epididymides". Molecular reproduction and development, 49(4), pp.454-460.

Frayne, J., Ingram, C., Love, S. and Hall, L., 1999. Localisation of phosphatidylethanolamine-binding protein in the brain and other tissues of the rat. Cell and tissue research, 298(3), pp.415-423.

Gadella, B.M. & Visconti, P.E. 2006, "Regulation of capacitation", The sperm cell.Cambridge University Press, Cambridge, UK, pp. 134-169.

Gangloff, Y.G., Mueller, M., Dann, S.G., Svoboda, P., Sticker, M., Spetz, J.F., Um, S.H., Brown, E.J., Cereghini, S., Thomas, G. & Kozma, S.C. 2004, "Disruption of the mouse mTOR gene leads to early postimplantation lethality and prohibits embryonic stem cell development", Molecular and cellular biology, vol. 24, no. 21, pp. 9508-9516.

Ganong, W.F., 1981. Review of Medical Physiology, Lange Med. Pub., Los Altos, Calif, pp.329-330.

Georgopoulos, C. & Welch, W. 1993, "Role of the major heat shock proteins as molecular chaperones", Annual Review of Cell Biology, vol. 9, no. 1, pp. 601-634.

Glotzer, M., Murray, A.W. and Kirschner, M.W., 1991. Cyclin is degraded by the ubiquitin pathway. Nature, 349(6305), pp.132-138.

Gonzales, G.F. and Villena, A., 2001. True corrected seminal fructose level: a better marker of the function of seminal vesicles in infertile men. International journal of andrology, 24(5), pp.255-260.

Graham, D.R., Elliott, S.T. & Van Eyk, J.E. 2005, "Broad-based proteomic strategies: a practical guide to proteomics and functional screening", The Journal of physiology, vol. 563, no. 1, pp. 1-9.

Gregorio-King, C.C., McLeod, J.L., Collier, F.M., Collier, G.R., Bolton, K.A., Van Der Meer, G.J., Apostolopoulos, J. and Kirkland, M.A., 2002. MERP1: a mammalian ependymin-related protein gene differentially expressed in hematopoietic cells. Gene, 286(2), pp.249-257.

Gwinn, D.M., Shackelford, D.B., Egan, D.F., Mihaylova, M.M., Mery, A., Vasquez, D.S., Turk, B.E. & Shaw, R.J. 2008, "AMPK phosphorylation of raptor mediates a metabolic checkpoint", Molecular cell, vol. 30, no. 2, pp. 214-226.

Hafez, E.S.E., 1977. Techniques of human andrology (Vol. 1). North-Holland.

Haidl, G. & Schill, W. 1997, "OPINION: Is research on epididymal functions still of clinical relevance?", Andrologia, vol. 29, no. 2, pp. 117-119.

Hammerstedt, R.H. 1993, "Maintenance of bioenergetic balance in sperm and prevention of lipid peroxidation: a review of the effect on design of storage preservation systems", Reproduction, fertility and development, vol. 5, no. 6, pp. 675-690.

Hardie, D.G. 2007, "AMPK and SNF1: snuffing out stress", Cell metabolism, vol. 6, no. 5, pp. 339-340.

Harvey, C., 1948. Relation between the volume and fructose content of human semen. Nature, 162(4125), pp.812-812.

Hatef, A., Alavi, S.M.H., Golshan, M. and Linhart, O., 2013. Toxicity of environmental contaminants to fish spermatozoa function in vitro—a review. Aquatic toxicology, 140, pp.134-144.

Henault, M.A. & Killian, G.J. 1996, "Effect of homologous and heterologous seminal plasma on the fertilizing ability of ejaculated bull spermatozoa assessed by penetration of zona-free bovine oocytes", Journal of reproduction and fertility, vol. 108, no. 2, pp. 199-204.

Heshmat, S.M., Mullen, J.B., Jarvi, K.A., Soosaipillai, A., Diamandis, E.P., Hamilton, R.J. & Lo, K.C. 2008, "Seminal plasma lipocalin-type prostaglandin D synthase: a potential new marker for the diagnosis of obstructive azoospermia", The Journal of urology, vol. 179, no. 3, pp. 1077-1080.

Hikim, A.S. and Swerdloff, R.S., 1999. Hormonal and genetic control of germ cell apoptosis in the testis. Reviews of reproduction, 4(1), pp.38-47.

Hirano, Y., Shibahara, H., Obara, H., Suzuki, T., Takamizawa, S., Yamaguchi, C., Tsunoda, H. & Sato, I. 2001, "Andrology: Relationships between sperm motility characteristics assessed by the computer-aided sperm analysis (CASA) and fertilization rates in vitro", Journal of assisted reproduction and genetics, vol. 18, no. 4, pp. 215-220.

Hsu, P., Hsu, C. & Guo, Y.L. 1999, "Hydrogen peroxide induces premature acrosome reaction in rat sperm and reduces their penetration of the zona pellucida", Toxicology, vol. 139, no. 1, pp. 93-101.

Ickowicz, D., Finkelstein, M. & Breitbart, H. 2012, "Mechanism of sperm capacitation and the acrosome reaction: role of protein kinases", Asian Journal of Andrology, vol. 14, no. 6, pp. 816-821.

Ingermann, R.L., Holcomb, M., Robinson, M.L. and Cloud, J.G., 2002. Carbon dioxide and pH affect sperm motility of white sturgeon (Acipenser transmontanus). Journal of Experimental Biology, 205(18), pp.2885-2890.

Intasqui, P., Camargo, M., Antoniassi, M.P., Cedenho, A.P., Carvalho, V.M., Cardozo, K.H.M., Zylbersztejn, D.S. & Bertolla, R.P. 2016, "Association between the seminal plasma proteome and sperm functional traits", Fertility and sterility, vol. 105, no. 3, pp. 617-628.

Intasqui, P., Camargo, M., Del Giudice, P.T., Spaine, D.M., Carvalho, V.M., Cardozo, K.H., Zylbersztejn, D.S. & Bertolla, R.P. 2013, "Sperm nuclear DNA fragmentation rate is associated with differential protein expression and enriched functions in human seminal plasma", BJU international, vol. 112, no. 6, pp. 835-843.

Iwasaki, A. and Gagnon, C., 1992. Formation of reactive oxygen species in spermatozoa of infertile patients. Fertility and sterility, 57(2), pp.409-416.

Janco, M., Kalyva, A., Scellini, B., Piroddi, N., Tesi, C., Poggesi, C. and Geeves, M.A., 2012. α-Tropomyosin with a D175N or E180G mutation in only one chain differs from tropomyosin with mutations in both chains. Biochemistry, 51(49), pp.9880-9890.

Jimenez, T., McDermott, J.P., Sanchez, G. & Blanco, G. 2011, "Na,K-ATPase alpha4 isoform is essential for sperm fertility", Proceedings of the National Academy of Sciences of the United States of America, vol. 108, no. 2, pp. 644-649.

Johnson, L. & Varner, D.D. 1988, "Effect of daily spermatozoan production but not age on transit time of spermatozoa through the human epididymis", Biology of reproduction, vol. 39, no. 4, pp. 812-817.

Johnston, D.S., Wooters, J., Kopf, G.S., Qiu, Y. & Roberts, K.P. 2005, "Analysis of the human sperm proteome", Annals of the New York Academy of Sciences, vol. 1061, no. 1, pp. 190-202.

Kanayama, H.O., Tamura, T., Ugai, S., Kagawa, S., Tanahashi, N., Yoshimura, T., Tanaka, K. and Ichihara, A., 1992. Demonstration that a human 26S proteolytic complex consists of a proteasome and multiple associated protein components and hydrolyzes ATP and ubiquitin-ligated proteins by closely linked mechanisms. The FEBS Journal, 206(2), pp.567-578.

Kalchman, M.A., Graham, R.K., Xia, G., Koide, H.B., Hodgson, J.G., Graham, K.C., Goldberg, Y.P., Gietz, R.D., Pickart, C.M. and Hayden, M.R., 1996. Huntingtin is ubiquitinated and interacts with a specific ubiquitin-conjugating enzyme. Journal of Biological Chemistry, 271(32), pp.19385-19394.

Kavanagh, J. 1994, "Isocitric and citric acid in human prostatic and seminal fluid: implications for prostatic metabolism and secretion", The Prostate, vol. 24, no. 3, pp. 139-142.

Kessopoulou, E., Tomlinson, M.J., Barratt, C.L.R., Bolton, A.E. and Cooke, I.D., 1992. Origin of reactive oxygen species in human semen: spermatozoa or leucocytes?. Journal of reproduction and fertility, 94(2), pp.463-470.

Khan, Z., Aitken, A., Garcia, J.R. & Smyth, D.G. 1992, "Isolation and identification of two neutral thyrotropin releasing hormone-like peptides, pyroglutamylphenylalanineproline amide and pyroglutamylglutamineproline amide, from human seminal fluid", The Journal of biological chemistry, vol. 267, no. 11, pp. 7464-7469.

Kikuchi, J., Furukawa, Y., Kubo, N., Tokura, A., Hayashi, N., Nakamura, M., Matsuda, M. and Sakurabayashi, I., 2000. Induction of ubiquitin-conjugating enzyme by aggregated low density lipoprotein in human macrophages and its implications for atherosclerosis. Arteriosclerosis, thrombosis, and vascular biology, 20(1), pp.128-134.

Kishi K, Yasuda T, Ikehara Y, Sawazaki K, Sate W, iida R. Human serum deoxyribonuclease I (DNase I) polymorphism: pattern similarities among isozymes from serum, urine, kidney, liver, and pancreas. Am J Hum Genet 1990;47:i21-126.

Kong, M., Diaz, E.S. and Morales, P., 2009. Participation of the human sperm proteasome in the capacitation process and its regulation by protein kinase A and tyrosine kinase. Biology of reproduction, 80(5), pp.1026-1035.

Kothari, S., Thompson, A., Agarwal, A. and du Plessis, S.S., 2010. Free radicals: their beneficial and detrimental effects on sperm function.

Kret, B., Milad, M. and Jeyendran, R.S., 1995. New discriminatory level for glucosidase activity to diagnose epididymal obstruction or dysfunction. Archives of andrology, 35(1), pp.29-33.

Krieglstein, J., Lehmann, M., Mäurer, A., Gudermann, T., Pinkenburg, O., Wieland, T., Litterscheid, S. & Klumpp, S. 2008, "Reduced viability of neuronal cells after overexpression of protein histidine phosphatase", Neurochemistry international, vol. 53, no. 5, pp. 132-136.

Laplante, M. & Sabatini, D.M. 2009, "mTOR signaling at a glance", Journal of cell science, vol. 122, no. Pt 20, pp. 3589-3594.

Larsen, L., Scheike, T., Jensen, T.K., Bonde, J.P., Ernst, E., Hjollund, N.H., Zhou, Y., Skakkebæk, N.E., Giwercman, A. & Danish First Pregnancy Planner Study Team 2000, "Computer-assisted semen analysis parameters as predictors for fertility of men from the general population", Human Reproduction, vol. 15, no. 7, pp. 1562-1567.

Lee, J.H., Koh, H., Kim, M., Kim, Y., Lee, S.Y., Karess, R.E., Lee, S.H., Shong, M., Kim, J.M., Kim, J. and Chung, J., 2007. Energy-dependent regulation of cell structure by AMP-activated protein kinase. Nature, 447(7147), pp.1017-1020.

Lefranc, M.P., 2014. Immunoglobulin and T-cell receptor genes: IMGT® and the birth and rise of immunoinformatics. Frontiers in immunology, 5.

Levitas, E., Lunenfeld, E., Weiss, N., Friger, M., Har-Vardi, I., Koifman, A. & Potashnik, G. 2005, "Relationship between the duration of sexual abstinence and semen quality: analysis of 9,489 semen samples", Fertility and sterility, vol. 83, no. 6, pp. 1680-1686.

Lewis, S.E. 2007, "Is sperm evaluation useful in predicting human fertility?", Reproduction (Cambridge, England), vol. 134, no. 1, pp. 31-40.

Lilja, H. 1985, "A kallikrein-like serine protease in prostatic fluid cleaves the predominant seminal vesicle protein", The Journal of clinical investigation, vol. 76, no. 5, pp. 1899-1903.

Lilja, H., Oldbring, J., Rannevik, G. & Laurell, C.B. 1987, "Seminal vesicle-secreted proteins and their reactions during gelation and liquefaction of human semen", The Journal of clinical investigation, vol. 80, no. 2, pp. 281-285.

Lilja, H., Abrahamsson, P.A. and Lundwall, A., 1989. Semenogelin, the predominant protein in human semen. Primary structure and identification of closely related proteins in the male accessory sex glands and on the spermatozoa. Journal of Biological Chemistry, 264(3), pp.1894-1900.

Lippert, T.H., Seeger, H., Schieferstein, G. and Voelter, W., 1993. Immunoreactive ubiquitin in human seminal plasma. Journal of andrology, 14(2), pp.130-131.

Loko, F., Alihonou, E., Goufodji, B., Fagla, B. & Hounton, M. 1997, "Neutral alpha-glucosidase, a specific marker for epididymal secretion in seminal pathology", Contraception, fertilite, sexualite (1992), vol. 25, no. 12, pp. 939-941.

Lu, J., Xu, H., Chen, F., Huang, Y. & Lu, N. 2006, "Standardization and quality control for the determination of alpha-glucosidase in seminal plasma", Archives of Andrology, vol. 52, no. 6, pp. 447-453.

Lu, J.C., Chen, F., Xu, H.R., Huang, Y.F. and Lu, N.Q., 2007. Standardization and quality control for determination of fructose in seminal plasma. Journal of andrology, 28(2), pp.207-213.

Magnus, Ø, Tollefsrud, A., Árbyholm, T. & Purvis, K. 1991, "Effects of varying the abstinence period in the same individuals on sperm quality", Archives of Andrology, vol. 26, no. 3, pp. 199-203.

Mahmoud, A.M., Geslevich, J., Kint, J., Depuydt, C., Huysse, L., Zalata, A. & Comhaire, F.H. 1998, "Seminal plasma alpha-glucosidase activity and male infertility", Human reproduction (Oxford, England), vol. 13, no. 3, pp. 591-595.

Makhafola, M., Umesiobi, D., Mphaphathi, M., Masenya, M. & Nedambale, T. 2012, "Characterization of sperm cell motility rate of Southern African Indigenous Cockerel semen following analysis by sperm class analyser", Journal of Animal science advances, vol. 2, no. 4, pp. 416-424.

Makler, A., David, R., Blumenfeld, Z. and Better, O.S., 1981. Factors affecting sperm motility. VII. Sperm viability as affected by change of pH and osmolarity of semen and urine specimens. Fertility and sterility, 36(4), pp.507-511.

Manandhar, G., Feng, D., Yi, Y.J., Lai, L., Letko, J., Laurincik, J., Sutovsky, M., Salisbury, J.L., Prather, R.S., Schatten, H. and Sutovsky, P., 2006. Centrosomal protein centrin is not detectable during early pre-implantation development but reappears during late blastocyst stage in porcine embryos. Reproduction, 132(3), pp.423-434.

Mann, T. 1946, "Studies on the metabolism of semen: 3. Fructose as a normal constituent of seminal plasma. Site of formation and function of fructose in semen", The Biochemical journal, vol. 40, no. 4, pp. 481-491.

Mann, T., Mann, C.L. and Dixon, R.L., 1982. Passage of chemicals into human and animal semen: mechanisms and significance. CRC Critical Reviews in Toxicology, 11(1), pp.1-14.

Mann, T., 1964. The biochemistry of semen and of the male reproductive tract. The biochemistry of semen and of the male reproductive tract.

Martínez-Heredia, J., Estanyol, J.M., Ballescà, J.L. & Oliva, R. 2006, "Proteomic identification of human sperm proteins", Proteomics, vol. 6, no. 15, pp. 4356-4369.

Martínez-Heredia, J., de Mateo, S., Vidal-Taboada, J.M., Ballescà, J.L. & Oliva, R. 2008, "Identification of proteomic differences in asthenozoospermic sperm samples", Human reproduction, vol. 23, no. 4, pp. 783-791.

Marzesco, A.M., Dunia, I., Pandjaitan, R., Recouvreur, M., Dauzonne, D., Benedetti, E.L., Louvard, D. and Zahraoui, A., 2002. The small GTPase Rab13 regulates assembly of functional tight junctions in epithelial cells. Molecular biology of the cell, 13(6), pp.1819-1831.

Medrano, A., Fernández-Novell, J.M., Ramió, L., Alvarez, J., Goldberg, E., Rivera, M., Guinovart, J.J., Rigau, T. & Rodríguez-Gil, J.E. 2006, "Utilization of citrate and lactate through a lactate dehydrogenase and ATP-regulated pathway in boar spermatozoa", Molecular reproduction and development, vol. 73, no. 3, pp. 369-378.

Milardi, D., Grande, G., Vincenzoni, F., Messana, I., Pontecorvi, A., De Marinis, L., Castagnola, M. & Marana, R. 2012, "Proteomic approach in the identification of fertility pattern in seminal plasma of fertile men", Fertility and sterility, vol. 97, no. 1, pp. 67-73. e1.

Mochida, K., Tres, L.L. and Kierszenbaum, A.L., 2000. Structural features of the 26S proteasome complex isolated from rat testis and sperm tail. Molecular reproduction and development, 57(2), pp.176-184.

Moellering, H. & Gruber, W. 1966, "Determination of citrate with citrate lyase", Analytical Biochemistry, vol. 17, no. 3, pp. 369-376.

Moore, F.L. & Reijo-Pera, R.A. 2000, "Male sperm motility dictated by mother's mtDNA", American Journal of Human Genetics, vol. 67, no. 3, pp. 543-548.

Mortimer, D. 1994, Practical laboratory andrology, Oxford University Press on Demand.

Mortimer, S.T., van der Horst, G. and Mortimer, D., 2015. The future of computer-aided sperm analysis. Asian journal of andrology, 17(4), p.545.

Muniyan, S., Chaturvedi, N.K., Dwyer, J.G., LaGrange, C.A., Chaney, W.G. & Lin, M. 2013, "Human prostatic acid phosphatase: structure, function and regulation", International journal of molecular sciences, vol. 14, no. 5, pp. 10438-10464.

Murakami, M., Ichisaka, T., Maeda, M., Oshiro, N., Hara, K., Edenhofer, F., Kiyama, H., Yonezawa, K. & Yamanaka, S. 2004, "mTOR is essential for growth and proliferation in early mouse embryos and embryonic stem cells", Molecular and cellular biology, vol. 24, no. 15, pp. 6710-6718.

Naz, R.K. 1999, "Involvement of protein serine and threonine phosphorylation in human sperm capacitation", Biology of reproduction, vol. 60, no. 6, pp. 1402-1409.

Neuer, A., Spandorfer, S., Giraldo, P., Dieterle, S., Rosenwaks, Z. & Witkin, S. 2000, "The role of heat shock proteins in reproduction", Human reproduction update, vol. 6, no. 2, pp. 149-159.

Oliva, R., de Mateo, S. & Estanyol, J.M. 2009, "Sperm cell proteomics", Proteomics, vol. 9, no. 4, pp. 1004-1017.

Oliveira, P.F., Cheng, C. & Alves, M.G. 2017, "Emerging role for mammalian target of rapamycin in male fertility", Trends in Endocrinology & Metabolism, vol. 28, no. 3, pp. 165-167.

O'Mahony, O.A., Djahanbahkch, O., Mahmood, T., Puddefoot, J.R. & Vinson, G.P. 2000, "Angiotensin II in human seminal fluid", Human reproduction (Oxford, England), vol. 15, no. 6, pp. 1345-1349.

Ott, D.E., Coren, L.V., Copeland, T.D., Kane, B.P., Johnson, D.G., Sowder, R.C., Yoshinaka, Y., Oroszlan, S., Arthur, L.O. and Henderson, L.E., 1998. Ubiquitin Is Covalently Attached to the p6GagProteins of Human Immunodeficiency Virus Type 1 and Simian Immunodeficiency Virus and to the p12Gag Protein of Moloney Murine Leukemia Virus. Journal of virology, 72(4), pp.2962-2968.

Padova, G., Tita, P., Briguglia, G. and Giuffrida, D., 1988. Influence of abstinence length on ejaculate characteristics. Acta europaea fertilitatis, 19(1), pp.29-31.

Patel, S.M., Skandhan, K.P. and Mehta, Y.B., 1988. Seminal plasma fructose and glucose in normal and pathological conditions. Acta europaea fertilitatis, 19(6), pp.329-332.

Peitsch, M.C., Hesterkamp, T., Polzar, B., Mannherz, H.G. and Tschopp, J., 1992. Functional characterisation of serum DNase I in MRL-lprlpr mice. Biochemical and biophysical research communications, 186(2), pp.739-745.

Pellestor, F., Girardet, A. & Andreo, B. 1994, "Effect of long abstinence periods on human sperm quality", International journal of fertility and menopausal studies, vol. 39, no. 5, pp. 278-282.

Pilch, B. & Mann, M. 2006, "Large-scale and high-confidence proteomic analysis of human seminal plasma", Genome biology, vol. 7, no. 5, pp. R40.

Pienta, K.J. and Esper, P.S., 1993. Risk factors for prostate cancer. Annals of internal medicine, 118(10), pp.793-803.

Pimenta, A.F., Zhukareva, V., Barbe, M.F., Reinoso, B.S., Grimley, C., Henzel, W., Fischer, I. and Levitt, P., 1995. The limbic system-associated membrane protein is an Ig superfamily member that mediates selective neuronal growth and axon targeting. Neuron, 15(2), pp.287-297.

Poiani, A. 2006, "Complexity of seminal fluid: a review", Behavioral Ecology and Sociobiology, vol. 60, no. 3, pp. 289-310.

Quinn, P.J., 1968. Deoxyribonuclease activity in semen. Journal of reproduction and fertility, 17(1), pp.35-39.

Radons, J., 2016. The human HSP70 family of chaperones: where do we stand?. Cell Stress and Chaperones, 21(3), pp.379-404.

Rao, M., Zhao, X.L., Yang, J., Hu, S.F., Lei, H., Xia, W. and Zhu, C.H., 2015. Effect of transient scrotal hyperthermia on sperm parameters, seminal plasma biochemical markers, and oxidative stress in men. Asian journal of andrology, 17(4), p.668.

Raziel, A., Friedler, S., Schachter, M., Kaufman, S., Omanski, A., Soffer, Y. and Ron-El, R., 2001. Influence of a short or long abstinence period on semen parameters in the ejaculate of patients with nonobstructive azoospermia. Fertility and sterility, 76(3), pp.485-490.

Rhemrev JP, Lens JW, McDonnell J, Schoemaker J, Vermeiden JP. The post-wash total progressively motile sperm cell count is a reliable predictor of total fertilization failure during in vitro fertilization treatment. Fertil Steril 2001; 76: 884-91.

Robaire, B., Hinton, B. & Orgebin-Crist, M. 2006, "The epididymis. Knobil and Neill's Physiology of Reproduction, ed Neill J", Elsevier, New York, vol. 3, pp. 1071-1148.

Robert, M. and Gagnon, C., 1996. Purification and characterization of the active precursor of a human sperm motility inhibitor secreted by the seminal vesicles: identity with semenogelin. Biology of Reproduction, 55(4), pp.813-821.

Rodríguez-Martínez, H., Kvist, U., Ernerudh, J., Sanz, L. & Calvete, J.J. 2011, "Seminal plasma proteins: what role do they play?", American Journal of Reproductive Immunology, vol. 66, no. s1, pp. 11-22.

Said, L., Galeraud-Denis, I., Carreau, S. & Saâd, A. 2009, "Relationship between semen quality and seminal plasma components: alpha-glucosidase, fructose and citrate in infertile men compared with a normospermic population of Tunisian men", Andrologia, vol. 41, no. 3, pp. 150-156.

Sakamoto, K., McCarthy, A., Smith, D., Green, K.A., Hardie, D.G., Ashworth, A. and Alessi, D.R., 2005. Deficiency of LKB1 in skeletal muscle prevents AMPK activation and glucose uptake during contraction. The EMBO journal, 24(10), pp.1810-1820.

Sakkas, D., Mariethoz, E., Manicardi, G., Bizzaro, D., Bianchi, P.G. and Bianchi, U., 1999. Origin of DNA damage in ejaculated human spermatozoa. Reviews of reproduction, 4(1), pp.31-37.

Sancak, Y., Thoreen, C.C., Peterson, T.R., Lindquist, R.A., Kang, S.A., Spooner, E., Carr, S.A. & Sabatini, D.M. 2007, "PRAS40 is an insulin-regulated inhibitor of the mTORC1 protein kinase", Molecular cell, vol. 25, no. 6, pp. 903-915.

Sánchez-Solana, B., Li, D. & Kumar, R. 2014, "Cytosolic functions of MORC2 in lipogenesis and adipogenesis", Biochimica et Biophysica Acta (BBA)-Molecular Cell Research, vol. 1843, no. 2, pp. 316-326.

Sasha Forbes, (2015), Male Reproductive System [ONLINE]. Available at: http://slideplayer.com/slide/4220093/ [Accessed 21 November 2017].

Sawazaki, K., Yasuda, T., Nadano, D., Tenjo, E., Iida, R., Takeshita, H. and Kishi, K., 1992. A new individualization marker of semen: deoxyribonuclease I (DNase I) polymorphism. Forensic science international, 57(1), pp.39-44.

Schatten, H. and Sun, Q.Y., 2009. The role of centrosomes in mammalian fertilization and its significance for ICSI. Molecular human reproduction, 15(9), pp.531-538.

Schoenfeld, C., Amelar, R.D., Dubin, L. & Numeroff, M. 1979, "Prolactin, fructose, and zinc levels found in human seminal plasma", Fertility and sterility, vol. 32, no. 2, pp. 206-208.

Shamsi, M., Kumar, R. & Dada, R. 2008, "Evaluation of nuclear DNA damage in human spermatozoa in men opting for assisted reproduction", Indian Journal of Medical Research, vol. 127, no. 2, pp. 115.

Shen, H.M. and Ong, C.N., 2000. Detection of oxidative DNA damage in human sperm and its association with sperm function and male infertility. Free Radical Biology and Medicine, 28(4), pp.529-536.

Shulla, A., Heald-Sargent, T., Subramanya, G., Zhao, J., Perlman, S. and Gallagher, T., 2011. A transmembrane serine protease is linked to the severe acute respiratory syndrome coronavirus receptor and activates virus entry. Journal of virology, 85(2), pp.873-882.

Silva, A.M., Kong, X. and Hider, R.C., 2009. Determination of the pKa value of the hydroxyl group in the α-hydroxycarboxylates citrate, malate and lactate by 13C NMR: implications for metal coordination in biological systems. Biometals, 22(5), pp.771-778.

Silva, J.V., Freitas, M.J., Correia, B.R., Korrodi-Gregório, L., Patrício, A., Pelech, S. & Fardilha, M. 2015, "Profiling signaling proteins in human spermatozoa: biomarker identification for sperm quality evaluation", Fertility and sterility, vol. 104, no. 4, pp. 845-856. e8.

Siva, A.B., Kameshwari, D.B., Singh, V., Pavani, K., Sundaram, C.S., Rangaraj, N., Deenadayal, M. & Shivaji, S. 2010, "Proteomics-based study on asthenozoospermia: differential expression of proteasome alpha complex", Molecular human reproduction, vol. 16, no. 7, pp. 452-462.

Song, N., Liu, J., An, S., Nishino, T., Hishikawa, Y. and Koji, T., 2011. Immunohistochemical analysis of histone H3 modifications in germ cells during mouse spermatogenesis. Acta histochemica et cytochemica, 44(4), pp.183-190.

Srivastava, S., Zhdanova, O., Di, L., Li, Z., Albaqumi, M., Wulff, H. and Skolnik, E.Y., 2008. Protein histidine phosphatase 1 negatively regulates CD4 T cells by inhibiting the K+ channel KCa3. 1. Proceedings of the National Academy of Sciences, 105(38), pp.14442-14446.

Storey, B.T. and Kayne, F.J., 1975. Energy metabolism of spermatozoa. V. The Embden-Myerhof pathway of glycolysis: activities of pathway enzymes in hypotonically treated rabbit epididymal spermatozoa. Fertility and sterility, 26(12), pp.1257-1265.

Stukenborg, J.B., Kjartansdóttir, K.R., Reda, A., Colon, E., Albersmeier, J.P. and Söder, O., 2014. Male germ cell development in humans. Hormone research in paediatrics, 81(1), pp.2-12.

Sutovsky, P., 2003. Ubiquitin‐dependent proteolysis in mammalian spermatogenesis, fertilization, and sperm quality control: Killing three birds with one stone. Microscopy research and technique, 61(1), pp.88-102.

Sutovsky, P., Manandhar, G., McCauley, T.C., Caamano, J.N., Sutovsky, M., Thompson, W.E. and Day, B.N., 2004. Proteasomal interference prevents zona pellucida penetration and fertilization in mammals. Biology of Reproduction, 71(5), pp.1625-1637.

Suzuki, T., Terasaki, M., Takemoto-Hori, C., Hanada, T., Ueda, T., Wada, A. and Watanabe, K., 2001. Structural compensation for deficit of rRNA with proteins in mammalian mitochondrial ribosome; systematic analysis of protein components of the large ribosomal subunit from mammalian mitochondria. Journal of Biological Chemistry

Takeshita, H., Yasuda, T., Nadano, D., Tenjo, E., Sawazaki, K., Iida, R. and Kishi, K., 1994. Detection of deoxyribonucleases I and II (DNases I and II) activities in reproductive organs of male rabbits. International journal of biochemistry, 26(8), pp.1025-1031.

Terriou, P., Giorgetti, C., Auquier, P., Hans, E., Spach, J.L., Salzmann, J. and Roulier, R., 1994. Comparison of optical analysis and computerized analysis of sperm movement in a program of 316 in vitro fertilizations. Contraception, fertilite, sexualite (1992), 22(6), pp.418-422.

Travis, A.J., Foster, J.A., Rosenbaum, N.A., Visconti, P.E., Gerton, G.L., Kopf, G.S. and Moss, S.B., 1998. Targeting of a germ cell-specific type 1 hexokinase lacking a porin-binding domain to the mitochondria as well as to the head and fibrous sheath of murine spermatozoa. Molecular biology of the cell, 9(2), pp.263-276.

Tremblay, R.R., Chapdelaine, P. and Mailhot, J., 1979. α, 1-4-Glucosidase activity in human semen: Variations with number and motility of spermatozoa. Fertility and sterility, 31(5), pp.592-593.

Turner, R.M., 2003. Tales from the tail: what do we really know about sperm motility?. Journal of andrology, 24(6), pp.790-803.

Turner, T.T. 2008, "De Graaf's thread: the human epididymis", Journal of andrology, vol. 29, no. 3, pp. 237-250.

Viljoen, M., Bornman, M., Merwe, M. & Plessis, D. 1990, "Alpha-glucosidase activity and sperm motility", Andrologia, vol. 22, no. 3, pp. 205-208.

Visconti, P. 2012, "Sperm bioenergetics in a nutshell", Biology of reproduction, vol. 87, no. 3, pp. 72, 1-4.

Visconti, P.E. 2009, "Understanding the molecular basis of sperm capacitation through kinase design", Proceedings of the National Academy of Sciences of the United States of America, vol. 106, no. 3, pp. 667-668.

Vitali, G., Parente, R. & Melotti, C. 1995, "Carnitine supplementation in human idiopathic asthenospermia: clinical results", Drugs under experimental and clinical research, vol. 21, no. 4, pp. 157-159.

Wallach, E.E., Alexander, N.J. & Anderson, D.J. 1987, "Immunology of semen", Fertility and sterility, vol. 47, no. 2, pp. 192-205.

Wang, J., Wang, J., Zhang, H., Shi, H., Ma, D., Zhao, H., Lin, B. & Li, R. 2009, "Proteomic analysis of seminal plasma from asthenozoospermia patients reveals proteins that affect oxidative stress responses and semen quality", Asian Journal of Andrology, vol. 11, no. 4, pp. 484.

Wang, X., Li, N., Liu, B., Sun, H., Chen, T., Li, H., Qiu, J., Zhang, L., Wan, T. and Cao, X., 2004. A novel human phosphatidylethanolamine-binding protein resists tumor necrosis factor α-induced apoptosis by inhibiting mitogen-activated protein kinase pathway activation and phosphatidylethanolamine externalization. Journal of Biological Chemistry, 279(44), pp.45855-45864.

Ward, T., Pipkin, P.A., Clarkson, N.A., Stone, D.M., Minor, P.D. and Almond, J.W., 1994. Decay-accelerating factor CD55 is identified as the receptor for echovirus 7 using CELICS, a rapid immuno-focal cloning method. The EMBO journal, 13(21), p.5070.

Wilkinson, K.D. and Hochstrasser, M., 1998. The deubiquitinating enzymes. In Ubiquitin and the Biology of the Cell (pp. 99-125). Springer US.

Wilson, F.J., 1997. Histology image review. McGraw Hill Education. .

World Health Organisation 2010, WHO laboratory manual for the examination of human semen and sperm-cervical mucus interaction, Cambridge university press.

World Medical Association Declaration of Helsinki, 2013. "Ethical principles for medical research involving human subjects", Journal of American Medical Association, 310 (20), pp. 2191-2194.

Yasuda, T., Sawazaki, K., Nadano, D., Takeshita, H., Nakanaga, M. and Kishi, K., 1993. Human seminal deoxyribonuclease I (DNase I): purification, enzymological and immunological characterization and origin. Clinica chimica acta, 218(1), pp.5-16.

Yamakawa, K., Yoshida, K., Nishikawa, H., Kato, T. & Iwamoto, T. 2007, "Comparative analysis of interindividual variations in the seminal plasma proteome of fertile men with identification of potential markers for azoospermia in infertile patients", Journal of andrology, vol. 28, no. 6, pp. 858-865.

Yanagimachi, R., 1994. Mammalians Fertilization, 2nd ed. Raven Press, New York, NY, USA.

Yeung, C., Cooper, T. & Senge, T. 1990, "Histochemical localization and quantification of α-glucosidase in the epididymis of men and laboratory animals", Biology of reproduction, vol. 42, no. 4, pp. 669-676.

Zamenhof, S., 1957. [103] Preparation and assay of deoxyribonucleic acid from animal tissue. Methods in enzymology, 3, pp.696-704.

Zeqiraj, E., Filippi, B.M., Deak, M., Alessi, D.R. and van Aalten, D.M., 2009. Structure of the LKB1-STRAD-MO25 complex reveals an allosteric mechanism of kinase activation. Science, 326(5960), pp.1707-1711.

Zhao, C., Huo, R., Wang, F.Q., Lin, M., Zhou, Z.M. and Sha, J.H., 2007. Identification of several proteins involved in regulation of sperm motility by proteomic analysis. Fertility and sterility, 87(2), pp.436-438.

Zhou, J., Chen, L., Li, J., Li, H., Hong, Z., Xie, M., Chen, S. & Yao, B. 2015, "The semen pH affects sperm motility and capacitation", PloS one, vol. 10, no. 7, pp. e0132974.

Zöpfgen, A., Priem, F., Sudhoff, F., Jung, K., Lenk, S., Loening, S. & Sinha, P. 2000, "Relationship between semen quality and the seminal plasma components carnitine, alpha-glucosidase, fructose, citrate and granulocyte elastase in infertile men compared with a normal population", Human Reproduction, vol. 15, no. 4, pp. 840-845.

Zuber, J., Anglicheau, D., Elie, C., Bererhi, L., Timsit, M., Mamzer-Bruneel, M., Ciroldi, M., Martinez, F., Snanoudj, R. & Hiesse, C. 2008, "Sirolimus may reduce fertility in male renal transplant recipients", American Journal of Transplantation, vol. 8, no. 7, pp. 1471-1479.

Zylbersztejn, D.S., Andreoni, C., Del Giudice, P.T., Spaine, D.M., Borsari, L., Souza, G.H., Bertolla, R.P. & Fraietta, R. 2013, "Proteomic analysis of seminal plasma in adolescents with and without varicocele", Fertility and sterility, vol. 99, no. 1, pp. 92-98.

7. Appendices

Appendix A: Epididymal and accessory sex gland secretion optical densities

Table 7.1. Citric acid assay results

Donor ID	Long EA	OD	Short EA	OD
Standard		0.14375		0.14375
1A	4.05	0.15	3.95	0.14
1B	7.01	0.25	3.93	0.14
1C	4.86	0.18	4.22	0.15
1D	18.89	0.68	19.91	0.72
2A	9.89	0.36	9.16	0.33
2B	11.55	0.42	14.62	0.53
2C	5.15	0.19	3.81	0.14
2D	4.61	0.17	6.48	0.23
3A	5.04	0.18	3.91	0.14
3B	4.94	0.18	10.57	0.38
3C	3.76	0.14	2.27	0.08
3D	3.34	0.12	4.02	0.15
4A	4.40	0.16	4.15	0.15
4B	8.93	0.32	6.32	0.23
4C	4.83	0.17	7.80	0.28
4D	9.00	0.32	8.40	0.30

Table 7.2. Fructose assay results

	OD (470-492nm)		Mean	Stdev	RSD	Corrected	Fructose concentration (mg/ml)
blanc	0.113	0.104	0.11	0.01	0.06	0.00	0
standard 1	0.261	0.248	0.25	0.01	0.04	0.15	1
standard 2	0.138	0.091	0.11	0.03	0.29	0.01	2.5
standard 3	0.089	0.081	0.09	0.01	0.07	-0.02	5
1A1	0.104	0.113	0.11	0.01	0.06	0.00	4.11
1A2	0.074	0.096	0.09	0.02	0.18	-0.02	5.56
1B1	0.153	0.18	0.17	0.02	0.11	0.06	0.53
1B2	0.109	0.077	0.09	0.02	0.24	-0.02	5.07
1C1	0.092	0.071	0.08	0.01	0.18	-0.03	5.78
1C2	0.121	0.12	0.12	0.00	0.01	0.01	3.37
1D1	0.096	0.097	0.10	0.00	0.01	-0.01	4.85
1D2	0.134	0.143	0.14	0.01	0.05	0.03	2.26
2A1	0.137	0.135	0.14	0.00	0.01	0.03	2.41
2A2	0.114	0.109	0.11	0.00	0.03	0.00	3.92
2B1	0.139	0.134	0.14	0.00	0.03	0.03	2.38
2B2	0.148	0.145	0.15	0.00	0.01	0.04	1.76
2C1	0.126	0.113	0.12	0.01	0.08	0.01	3.43
2C2	0.094	0.085	0.09	0.01	0.07	-0.02	5.28
2D1	0.111	0.006	0.06	0.07	1.27	-0.05	7.20
2D2	0.106	0.108	0.11	0.00	0.01	0.00	4.20
3A1	0.132	0.114	0.12	0.01	0.10	0.01	3.21
3A2	0.118	0.179	0.15	0.04	0.29	0.04	1.64
3B1	0.206	0.218	0.21	0.01	0.04	0.10	-2.29
3B2	0.104	0.087	0.10	0.01	0.13	-0.01	4.91
3C1	0.12	0.129	0.12	0.01	0.05	0.02	3.12
3C2	0.122	0.133	0.13	0.01	0.06	0.02	2.94
3D1	0.097	0.081	0.09	0.01	0.13	-0.02	5.32
3D2	0.103	0.179	0.14	0.05	0.38	0.03	2.10
4A1	0.249	0.278	0.26	0.02	0.08	0.16	-5.47
4A2	0.1	0.08	0.09	0.01	0.16	-0.02	5.25
4B1	0.144	0.158	0.15	0.01	0.07	0.04	1.48
4B2	0.176	0.193	0.18	0.01	0.07	0.08	-0.59
4C1	0.13	0.114	0.12	0.01	0.09	0.01	3.28
4C2	0.124	0.154	0.14	0.02	0.15	0.03	2.23
4D1	0.179	0.144	0.16	0.02	0.15	0.05	0.83
4D2	0.149	0.228	0.19	0.06	0.30	0.08	-0.83

Slope:	-0.016180617
Intercept:	0.066508811
Coefficient of determination (R^2):	0.208957226

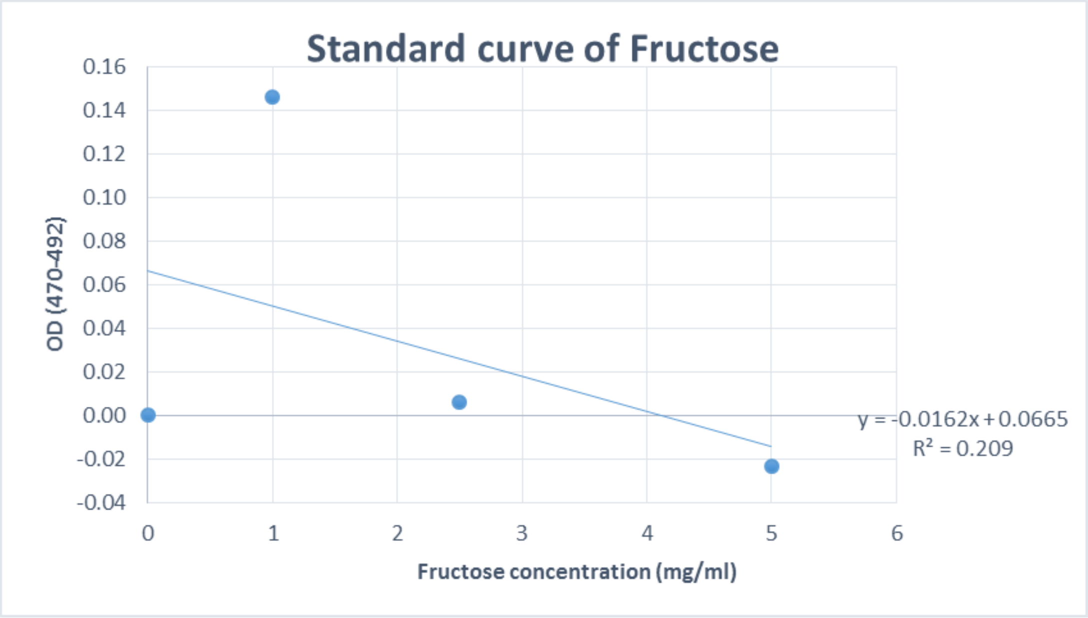


Figure 7.1. Standard curve of Fructose in seminal plasma

Table 7.3. Episcreen plus™- Neutral alpha-glucosidase assay

Sample code / Patient name	NAG activity (mIU/ml)
1A1	35.51
1A2	25.76
1B1	43.11
1B2	18.48
1C1	41.18
1C2	26.75
1D1	49.72
1D2	42.76
2A1	27.96
2A2	43.86
2B1	38.81
2B2	44.08
2C1	16.81
2C2	12.71
2D1	30.38
2D2	13.56
3A1	43.38
3A2	13.00
3B1	7.44
3B2	8.19
3C1	20.49
3C2	12.62
3D1	16.90
3D2	3.12
4A1	11.63
4A2	8.46
4B1	8.94
4B2	1.48
4C1	30.19
4C2	10.34
4D1	47.11
4D2	33.50

Slope:	0.0089
Coefficient of determination (R^2):	1.000

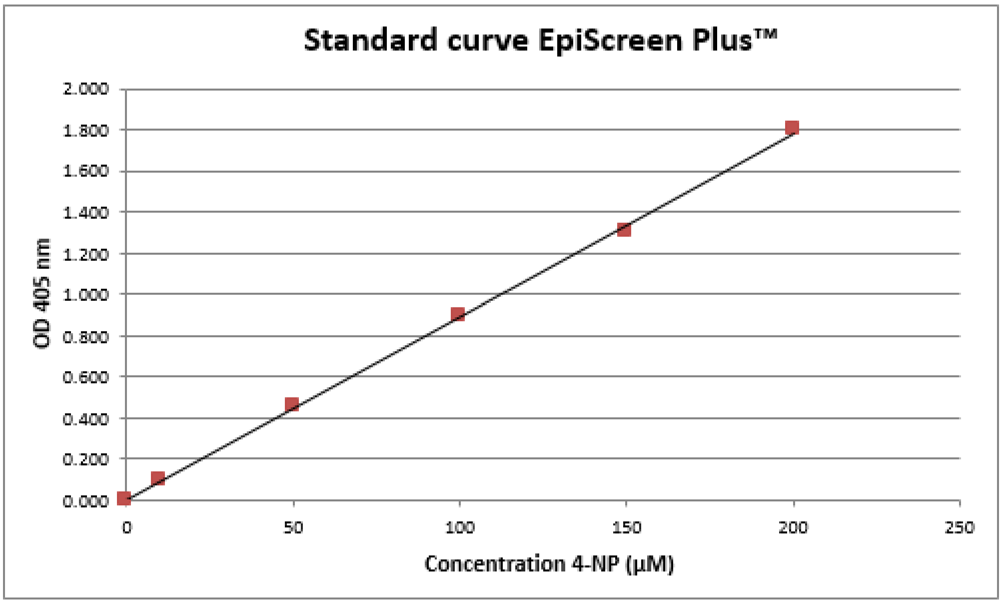


Figure 7.2. Standard curve of NAG in seminal plasma

Appendix B: Manuscript sent in to peer-reviewed journal

Appendix B contains an original article submitted for re-review in the Journal Human Fertility based on the research performed in this dissertation.

The title of this article is: **Improved sperm motility after short abstinence: The role of accessory sex gland secretions.**

Dale Goss, Bashir Ayad, Gerhard van der Horst, Bongekile Skosana, Stefan S du Plessis*.

Division of Medical Physiology, Stellenbosch University, Tygerberg, South Africa

*Corresponding author
Medical Physiology
Faculty of Medicine and Health Sciences
PO Box 19063
Tygerberg
7505
South Africa
ssdp@sun.ac.za

Improved sperm motility after short abstinence: A possible role of accessory sex gland secretions

Various studies have sought to determine the typical versus optimal abstinence period after which semen samples should be collected and many have been found to be contradictory. Several factors influence the semen microenvironment and thus sperm parameters. In this study we focused on the secretions of the prostate, seminal vesicles and the epididymis. Semen samples were obtained from normozoospermic subjects (n = 16) after long (4 days) and short (4 hours) periods of ejaculatory abstinence and standard semen analysis was performed with the assistance of computer aided sperm analysis, while the seminal plasma citric acid, neutral alpha-glucosidase and fructose concentrations were measured with commercially available assay kits. Results of this study displayed significant decreases in total sperm count ($p<0.001$), sperm concentration ($p<0.05$), semen volume ($p<0.05$) and pH ($p<0.05$) after 4 hours of ejaculatory abstinence when compared to 4 days. Furthermore, increases in total sperm motility ($p<0.05$) and sperm progressive motility ($p<0.01$) after short ejaculatory abstinence periods were observed, accompanied by a significant reduction in total citric acid ($p<0.05$), alpha-glucosidase ($P<0.01$) and fructose ($P<0.05$) concentrations. However, due to the decreased sperm number, these concentrations translated to a significant increase in citric acid ($P<0.05$) and a decrease in fructose ($P<0.05$) per spermatozoon, which, along with the effects on semen pH, could more than likely be responsible for increased metabolic function and subsequent increase in the available energy for sperm motility.

Keywords: abstinence; accessory sex glands; citric acid; motility; pH; seminal plasma; sperm.

Introduction

Basic semen parameters, including sperm concentration, motility, morphology and viability, remain the primary predictive factors for male infertility diagnosis, despite inter-individual variations in semen characteristics. Ejaculatory abstinence (EA) has been suggested to be a cost-effective approach to improve sperm quality (Levitas *et al.*, 2004).

As stated by the prescribed guidelines of the World Health Organisation (WHO), subjects must remain abstinent for a minimum period of 48 hours, but not longer than 7 days prior to collecting a sample for a standard semen analysis (WHO, 2010), yet many studies referring to these recommendations are often contradictory (Comar *et al.,* 2017; Padova *et al.,* 1988; Raziel *et al.,* 2001). Recent studies have suggested very short abstinence as a preferable measure for better quality sperm from a functional perspective. In a previous study conducted in our laboratory, we observed enhanced sperm total motility and progressive motility after only 4 hours of abstinence when compared to an EA period of 4 days (Ayad *et al.*, 2017). Similarly, Bahadur *et al.* (2016) found that only 40 minutes of EA improved sperm quality. Furthermore, Alipour *et al.* (2015) observed increases in sperm motility after only 2 hours of EA. Interestingly, none of these studies have comprehensively analysed the accessory sex gland secretions in the seminal plasma as a key attributor to these observations.

Ejaculated spermatozoa are terminally differentiated cells post-spermatogenesis, therefore the main functional changes are to be exerted by the composition and influence of the seminal plasma (Elzanaty *et al.*, 2005; *Said et al.*, 2009). The seminal plasma microenvironment is imperative as the spermatozoon is the only cell that performs its functions outside the body of the organism it originates from (Baccetti, 1984). Consequently, epididymal and accessory sex gland secretions, which constitute seminal plasma, are of particular interest in this study. The prostate gland’s main function is to produce and release large amounts of ionized derivatives of citric acid in the form of citrate into prostatic fluid (Kavanagh, 1994). Furthermore, the prostate also releases a variety of other molecules, which are of importance to the process of fertilization. Prostate specific antigen is a glycoprotein enzyme, capable of liquefying the seminal coagulum thereby allowing sperm to swim freely (Balk *et al.*, 2003). Zinc released by the prostate, aids in sperm DNA stabilization and low levels of seminal zinc are correlated with low fertility rates (Canale *et al.*, 1986). The seminal vesicles are the highest producers of fructose, which is the main source of energy for spermatozoa (Mann, 1946). Seminal vesicles also release amino acids, flavins, phosphorylcholine, prostaglandins, vitamin

C and a range of proteins and enzymes (Schoenfeld *et al.*, 1979; Mann, 1946). These molecules released by the seminal vesicles have a variety of contributory roles in sperm maturation and acquisition of fertilizing potential. The epididymis is primarily responsible for the release of neutral alpha-glucosidase (NAG) (Cooper et al., 1990) as well as proteins which prevent premature onset of capacitation during epididymal transit and storage (Fraser *et al.*, 1990).

The Percentage change in the concentrations of the selected epididymal and accessory sex gland biomarkers, have been widely utilized as clinical reflections of the global changes in the volume of secretions from each component (WHO, 2010). Many studies have attempted to formulate a specific ratio which causes variations in these secretions, but there are a multitude of variables to consider which effect secretion volumes. Therefore, minimizing subject variation by selecting samples from normozoospermic, healthy males between the ages of 19 to 25, may minimize variation in physiological conditions allowing EA to be the primary intervention.

A useful approach to further evaluating the effects of which varying concentrations of molecules in the semen, have on individual sperm, would be to analyse concentrations on a micro scale. Considering the total amount of a specific molecule in the ejaculate, and dividing that value by the total sperm count (T.S.C.), would provide a more representative view of the absolute bioavailability of these biomolecules per individual sperm.

Elzanaty *et al*. (2005) evaluated the semen from patients undergoing fertility assessment and measured motility parameters in addition to several accessory gland markers, including both fructose and NAG. However, citric acid was not measured, since prostate specific antigen (PSA) was chosen as a prostate secretion marker instead. Reductions in motility parameters were observed after shorter abstinence periods of 2 to 3 days. Additionally, all markers of epididymal and accessory gland secretions were higher after 4 to 7 days of abstinence. Although they found significant differences in the contributions of these glands, they did not focus on very short abstinence periods (1 – 4 hours) as their lowest EA period was 2-3 days.

For the purpose of this study, basic semen parameters were selected as an adequate measure of semen and sperm quality. Furthermore, citric acid, neutral alpha-glucosidase and fructose have been selected as key biomarkers of prostatic, epididymal and seminal vesicular secretion and function. Furthermore, the possible direct role related to the concentrational variations concerning sperm functional improvements were also explored.

Therefore, the aim of this study was to determine the effect of short (4 hours) and long (4 days) periods of EA on key epididymal and accessory sex gland secretions, and the subsequent relationship with semen basic and functional parameters.

Methods

Before the commencement of the study, ethical approval was obtained from the Health Research Ethics Committee of the Faculty of Medicine and Health Sciences at Stellenbosch University. Informed written consent was provided by all subjects and the study was performed in accordance with the Declaration of Helsinki (2013). Freshly ejaculated semen samples were collected from 16 consecutive healthy donors (19 to 25 years) attending the SURRG laboratories. All samples were collected according to the WHO guidelines (WHO, 2010) in a location close to the laboratory and received within 10 minutes of collection. The first sample from each donor was collected after an abstinence period of 4 days. The second sample was collected from the same donor 4 hours subsequent to the first collection. Samples were immediately placed in an incubator (37°C, 5% CO_2, 30 minutes) and allowed to fully liquefy before further processing. Information about donor identification and age, date of semen collection, time of semen collection, abstinence duration, sample volume, pH, appearance, colour, odour, liquefaction, viscosity and agglutination were reported. The sperm concentration and motility parameters were determined with Computer-

Aided Sperm Analysis (CASA) using the Sperm Class Analyser version 5.4 - SCA®, (Microptic, S.L, Barcelona, Spain).

Seminal plasma citric acid, fructose and NAG concentrations were measured with commercially available assay kits (Citric Acid, Fructose and Episcreen plus™ Assay Kits, FertiPro N.V., Belgium) respectively according to the manufacturers guidelines. Absorbance values were measured photometrically for citric acid and NAG at 405nm and for fructose at 470nm, using a FLUOstar Omega micro plate reader (BMG Labtech, Germany). Results for citric acid and fructose concentrations were expressed in mg/mL, while NAG activity was expressed as milli-international units per millilitre (mIU/mL).

Statistical analyses

Comparisons between parameters measured after long and short EA were performed using the Students paired t-test for normally distributed data sets and Mann-Whitney U-tests for nonparametric data sets, on GraphPad Prism© version 7.00 for Windows (GraphPad Software, La Jolla California, USA). All values are presented as mean ± SE. Statistical significance was set at $p<0.05$.

Results

As presented in Table 1, semen volume, sperm concentration and subsequent T.S.C. were significantly decreased after short EA when compared to long abstinence, while semen pH was slightly yet significantly increased after short EA. A significant increase in the percentage of sperm total motility and progressive motility was observed after short EA. Citric acid, NAG and fructose concentrations were all significantly reduced after short EA when compared to long EA. On the contrary, when considering T.S.C. in these cohorts, the absolute amount of citric acid per sperm was significantly higher after short EA.

Interestingly, the absolute amount of fructose per sperm was significantly decreased after short EA, while NAG per spermatozoon was not significantly affected (Table 2).

Discussion

The results of this study shows that conventional and functional semen parameters were influenced significantly by EA periods. A short period of EA (4 hours) produced significant increases in both sperm total motility and progressive motility yet highly significant reductions in T.S.C., sperm concentration and semen volume. These results are in accordance with two large studies performed by Comar *et al.* (2017) and Levitas *et al.* (2005) where the duration of EA had a significant positive relationship with sperm concentration and semen volume, yet a significant negative influence on sperm motility. These effects are ascribed to the fact that sperm reserves were available and stored in the epididymis. Motility changes were attributed to increased levels of reactive oxygen species (ROS) and subsequent DNA damage in stored sperm over longer EA periods. Damaged spermatozoa (Iwasaki et al., 1992) or infiltrating leukocytes (Kessopoulou et al., 1994) are the sources of ROS, which is correlated with decreased sperm motility. In the case of the lower EA period, the sperm reserves were depleted and T.S.C. decreased (Rao *et al.*, 2015). Significant reductions in citric acid, NAG and fructose concentrations were observed after 4 hours of EA, which may be attributed to the insufficient time for the epididymis and accessory sex glands to produce their respective secretions resulting in reduction in semen volume associated with short abstinence (Levitas *et al.*, 2004). The results of this study bring citric acid to the fore, due to the fact that per sperm, citric acid drastically increased compared to the other two accessory gland secretions, with an increase of 110% after short EA when compared to long EA. NAG slightly increased by only 6%, whereas fructose decreased by 38% after short EA. Furthermore, progressive motility increased by 30% which is nearly double that of the increase observed in total motility. This supports the assumption that very short EA periods may produce functionally favourable sperm, thus increasing fertilizing capacity (Bhahadur *et al.,* 2016; Alipour *et al.,* 2015; Ayad *et al.,* 2017).

Seminal fructose is considered to be the primary source of energy with direct effects on sperm motility (Mann, 1946). Patel *et al.* (1988) found direct positive correlations between seminal fructose levels and the percentage of motile sperm and this has been explained by the presence of glycolytic enzymes concentrated in the principal piece in the sperm flagellum (Storey and Kayne, 1975; Travis et al., 1998; Eddy et al., 2003), therefore the breakdown of fructose during glycolysis could produce ATP adjacent to the site where it is required. Furthermore, it has been suggested that glycolysis in the principal piece of the flagellum, is critical for normal sperm motility (Turner, 2003). Therefore, the observed increases in sperm motility cannot be ascribed to fructose and alternative energy sources should be responsible. This proposes citric acid as a possible source of energy due to its significant increase observed after short EA. Second to this, an alternative explanation might be related to the change observed in pH.

The fragile microenvironment created by the testes, epididymis and accessory sex glands has been found to actively manipulate the basic and functional sperm parameters including semen pH and volume, as well as sperm motility and fertilizing capacity. Studies have found short abstinence of 2 days, to be associated with decreased prostatic secretions and increased epididymal secretions (Elzanaty, *et al.,* 2005). However, little is known about the variations in seminal accessory gland secretions after EA periods of less than 1 day.

A previous study performed by Medrano *et al.* (2006), found that citric acid acts as a substrate for energy metabolism in sperm in addition to causing slight variations in seminal plasma pH. However, its relationship with, and role in abstinence has not been elucidated. Considering our paradoxical results, there are two possible mechanisms by which citric acid may affect sperm motility. The direct mechanism, which consists of the increase in available amount of citrates per sperm for utilization in the citric acid cycle to provide energy for sperm motility, seeing that there is more citric acid per sperm available after short EA. As mentioned previously, spermatozoa primarily utilize fructose originating from the seminal vesicles, as a source of carbohydrates. Once absorbed by sperm, it is then broken down into glucose and converted to acetyl-coenzyme A (CoA), which drives the citric acid cycle ultimately leading to the production of utilizable energy in the form of Adenosine Triphosphate (ATP) produced by the electron transport chain (Figure 1). Furthermore, it has been shown that spermatozoa pre-incubated in citrate increase their ATP production without the addition of fructose (Medrano *et al.*, 2006). It is believed that this occurs when citrates are converted to malate, an intermediary, which is subsequently utilized in the citric acid cycle in sperm mitochondria (Visconti, 2012).

On the other hand, the potential role of citric acid in improving sperm motility after short EA might also be explained through a more indirect mechanism. Short abstinence-related decrease in citric acid was also accompanied by an overall increase in pH of the seminal plasma. It has previously been reported that this increase in alkalinity, creates a more conducive environment for spermatozoa, which has been shown to enhance their motility (Zhou *et al.*, 2015). The exact mechanism by which pH alters sperm motility is not clear, yet it is well recognized (Makler *et al.*, 1981; Carr *et al.*, 1985; Ingermann *et al.*, 2002). However, it has been speculated that pH affects the activity of the alpha-4-isoform of the Na^+/K^+-ATPase, which controls the transmembrane Na^+ gradient in sperm flagella by keeping the intracellular Na^+ concentration low which is crucial to many general and cell-specific processes (Zhou *et al.*, 2015). In support of this, α4-isoform knockout mice have been reported to produce predominantly immotile sperm (Jimenez *et al.*, 2011). This may explain the observed increases in total sperm motility and progressive motility when sperm are exposed to increasing alkalinity. The ideal pH for sperm to function adequately is between 7.2 and 8.2, yet motility increases as the pH increases in this range (Zhou *et al.*, 2015).

Most previous studies have not systematically assessed the contributory role of citric acid in particular, and its ability to possibly influence sperm functional characteristics directly or indirectly in relation to abstinence. This study found that citric acid may be a viable candidate in the justification of the observed improvements in sperm motility after an abstinence period of 4 hours, as well as being partially responsible for an increase in semen pH. An additive effect via the increased availability of citric acid per sperm might occur which furthermore compensates for the reduction in fructose per sperm. This highlights a possible oversight of the metabolic significance of citric acid. Further comprehensive biochemical pathway analysis is required to better understand the role that accessory sex glands play in the improvement of sperm motility in the ejaculates collected after very short abstinence.

Acknowledgements

This research was supported/partially supported by The National Research Foundation. The authors wish to thank all those SURRG members who provided valuable insight when needed. No potential conflict of interest was reported by the authors.

References

Alipour, H., Dardmeh, F., Van Der Horst, G., Manoharan, G., Askeland, A. & Nielsena, H. 2015, "Effect of short abstinence time on sperm motility parameters", Final Programme, 18th World Congress of in Vitro Ferilization, Isivf 2015, 27-30 September 2015, Copenhagen, Denmark International Society of In Vitro Fertilization, in press.

Ayad, B., Van der Horst, G. & du Plessis, S.S. 2017, "Short abstinence: A potential strategy for the improvement of sperm quality", Middle East Fertility Society Journal, in press.

Ayad, B.M., Horst, G.V. and Plessis, S.S.D., 2018. Revisiting the relationship between the ejaculatory abstinence period and semen characteristics. International journal of fertility & sterility, 11(4), p.238.

Baccetti, B., 1984. The human spermatozoon. Ultrastructure of Reproduction: Gametogenesis, Fertilization, and Embryogenesis, 2, p.110.

Bahadur, G., Almossawi, O., Zaid, R.Z., Ilahibuccus, A., Al-Habib, A., Muneer, A. & Okolo, S. 2016, "Semen characteristics in consecutive ejaculates with short abstinence in subfertile males", Reproductive biomedicine online, vol. 32, no. 3, pp. 323-328.

Balk, S.P., Ko, Y.J. and Bubley, G.J., 2003. Biology of prostate-specific antigen. Journal of Clinical Oncology, 21(2), pp.383-391.

Canale, D., Bartelloni, M., Negroni, A., Meschini, P., Izzo, P.L., Bianchi, B. and Menchini-Fabris, G.F., 1986. Zinc in human semen. International journal of andrology, 9(6), pp.477-480.

Carr, D.W., Usselman, M.C. & Acott, T.S. 1985, "Effects of pH, lactate, and viscoelastic drag on sperm motility: a species comparison", Biology of reproduction, vol. 33, no. 3, pp. 588-595.

Comar, V.A., Petersen, C.G., Mauri, A.L., Mattila, M., Vagnini, L.D., Renzi, A., Petersen, B., Nicoletti, A., Dieamant, F., Oliveira, J.B.A., Baruffi, R.L.R. & Franco, J.G.,Jr 2017, "Influence of the abstinence period on human sperm quality: analysis of 2,458 semen samples", JBRA assisted reproduction, in press.

Cooper, T., Weidner, W. & Nieschlag, E. 1990, "The influence of inflammation of the human male genital tract on secretion of the seminal markers α-glucosidase, glycerophosphocholine, carnitine, fructose and citric acid", International journal of andrology, vol. 13, no. 5, pp. 329-336.

Eddy, E.M., Toshimori, K. and O'Brien, D.A., 2003. Fibrous sheath of mammalian spermatozoa. Microscopy research and technique, 61(1), pp.103-115.

Elzanaty, S., Malm, J. & Giwercman, A. 2005, "Duration of sexual abstinence: epididymal and accessory sex gland secretions and their relationship to sperm motility", Human reproduction (Oxford, England), vol. 20, no. 1, pp. 221-225.

Fraser, L.R., Harrison, R.A.P. and Herod, J.E., 1990. Characterization of a decapacitation factor associated with epididymal mouse spermatozoa. Journal of reproduction and fertility, 89(1), pp.135-148.

Ingermann, R.L., Holcomb, M., Robinson, M.L. and Cloud, J.G., 2002. Carbon dioxide and pH affect sperm motility of white sturgeon (Acipenser transmontanus). Journal of Experimental Biology, 205(18), pp.2885-2890.

Iwasaki, A. and Gagnon, C., 1992. Formation of reactive oxygen species in spermatozoa of infertile patients. Fertility and sterility, 57(2), pp.409-416.

Jimenez, T., McDermott, J.P., Sanchez, G. & Blanco, G. 2011, "Na,K-ATPase alpha4 isoform is essential for sperm fertility", Proceedings of the National Academy of Sciences of the United States of America, vol. 108, no. 2, pp. 644-649.

Kavanagh, J. 1994, "Isocitric and citric acid in human prostatic and seminal fluid: implications for prostatic metabolism and secretion", The Prostate, vol. 24, no. 3, pp. 139-142.

Kessopoulou, E., Tomlinson, M.J., Barratt, C.L.R., Bolton, A.E. and Cooke, I.D., 1992. Origin of reactive oxygen species in human semen: spermatozoa or leucocytes?. Journal of reproduction and fertility, 94(2), pp.463-470.

Levitas, E., Lunenfeld, E., Weiss, N., Friger, M., Har-Vardi, I., Koifman, A. & Potashnik, G. 2005, "Relationship between the duration of sexual abstinence and semen quality: analysis of 9,489 semen samples", Fertility and sterility, vol. 83, no. 6, pp. 1680-1686.

Makler, A., David, R., Blumenfeld, Z. and Better, O.S., 1981. Factors affecting sperm motility. VII. Sperm viability as affected by change of pH and osmolarity of semen and urine specimens. Fertility and sterility, 36(4), pp.507-511.

Mann, T. 1946, "Studies on the metabolism of semen: 3. Fructose as a normal constituent of seminal plasma. Site of formation and function of fructose in semen", The Biochemical journal, vol. 40, no. 4, pp. 481-491.

Medrano, A., Fernández-Novell, J.M., Ramió, L., Alvarez, J., Goldberg, E., Rivera, M., Guinovart, J.J., Rigau, T. & Rodríguez-Gil, J.E. 2006, "Utilization of citrate and lactate through a lactate dehydrogenase and ATP-regulated pathway in boar spermatozoa", Molecular reproduction and development, vol. 73, no. 3, pp. 369-378.

Padova, G., Tita, P., Briguglia, G. and Giuffrida, D., 1988. Influence of abstinence length on ejaculate characteristics. Acta europaea fertilitatis, 19(1), pp.29-31.

Patel, S.M., Skandhan, K.P. and Mehta, Y.B., 1988. Seminal plasma fructose and glucose in normal and pathological conditions. Acta europaea fertilitatis, 19(6), pp.329-332.

Raziel, A., Friedler, S., Schachter, M., Kaufman, S., Omanski, A., Soffer, Y. and Ron-El, R., 2001. Influence of a short or long abstinence period on semen parameters in the ejaculate of patients with non-obstructive azoospermia. Fertility and sterility, 76(3), pp.485-490.

Rao, M., Zhao, X.L., Yang, J., Hu, S.F., Lei, H., Xia, W. and Zhu, C.H., 2015. Effect of transient scrotal hyperthermia on sperm parameters, seminal plasma biochemical markers, and oxidative stress in men. Asian journal of andrology, 17(4), p.668.

Said, L., Galeraud-Denis, I., Carreau, S. & Saâd, A. 2009, "Relationship between semen quality and seminal plasma components: alpha-glucosidase, fructose and citrate in infertile men compared with a normospermic population of Tunisian men", Andrologia, vol. 41, no. 3, pp. 150-156.

Schoenfeld, C., Amelar, R.D., Dubin, L. & Numeroff, M. 1979, "Prolactin, fructose, and zinc levels found in human seminal plasma", Fertility and sterility, vol. 32, no. 2, pp. 206-208.

Storey, B.T. and Kayne, F.J., 1975. Energy metabolism of spermatozoa. V. The Embden-Myerhof pathway of glycolysis: activities of pathway enzymes in hypotonically treated rabbit epididymal spermatozoa. Fertility and sterility, 26(12), pp.1257-1265.

Travis, A.J., Foster, J.A., Rosenbaum, N.A., Visconti, P.E., Gerton, G.L., Kopf, G.S. and Moss, S.B., 1998. Targeting of a germ cell-specific type 1 hexokinase lacking a porin-binding domain to the mitochondria as well as to the head and fibrous sheath of murine spermatozoa. Molecular biology of the cell, 9(2), pp.263-276.

Turner, R.M., 2003. Tales from the tail: what do we really know about sperm motility?. Journal of andrology, 24(6), pp.790-803.

Visconti, P. 2012, "Sperm bioenergetics in a nutshell", Biology of reproduction, vol. 87, no. 3, pp. 72, 1-4.

World Health Organisation 2010, “WHO laboratory manual for the examination of human semen and sperm-cervical mucus interaction”, Cambridge university press, fifth edition.

World, M.A.G.A., 2004. World Medical Association Declaration of Helsinki: ethical principles for medical research involving human subjects. Journal international de bioéthique, International journal of bioethics, 15(1), p.124.

Zhou, J., Chen, L., Li, J., Li, H., Hong, Z., Xie, M., Chen, S. & Yao, B. 2015, "The semen pH affects sperm motility and capacitation", PloS one, vol. 10, no. 7, pp. e0132974.

Table 1: Summary of the SCA® motility parameters as measured by CASA. Values are expressed as mean ± SE

Parameter	Long EA	Short EA	Normal distribution	Paired t-test (P-value)	Mann-Whitney test (P-value)	% change	WHO (2010) Lower limits
pH	7.68 ± 0.029	7.76 ± 0.038	No	-	0.046	1%	7.2 - 8
Sperm concentration ($x10^6$/mL)	57.35 ± 7.2	36.83 ± 4.51	No	-	0.018	-36%	15 or more
Semen volume (mL)	2.56 ± 0.33	1.74 ± 0.22	No	-	0.025	-32%	1.5 or more
Total Sperm count ($x10^6$/ejaculate)	144.68 ± 22.77	58.01 ± 6.43	Yes	0.0007	-	-77%	39 or more
Total motility (%)	64.71 ± 13.94	71.84 ± 3.85	Yes	0.033	-	14%	40 or more
Progressive motility (%)	47.73 ± 14.33	58.54 ± 13.38	Yes	0.001	-	30%	32 or more

EA = Ejaculatory abstinence

Table 2: Summary of specific epididymal and accessory sex gland kits. Values are expressed as mean ± SE

Parameter	Long EA	Short EA	Normal distribution	Paired t-test (P-Value)	Mann-Whitney test (P-value)	% change	Normal range
Citric acid (mg/mL)	8.01 ± 1.352	5.96 ± 1.232	No	-	0.032	-25%	6.7 or more
Citric acid per sperm (ng)	0.141 ± 0.025	0.254 ± 0.056	No	-	0.034	110%	-
Fructose (mg/mL)	4.07 ± 0.77	1.66 ± 0.52	No	-	0.015	-54%	1.6 or more
Fructose per sperm (ng)	0.045 ± 0.016	0.036 ± 0.011	Yes	0.037	-	-38%	-
NAG (mIU/mL)	29.32 ± 3.53	19.92 ± 3.61	Yes	0.005	-	-33%	2 – 15
NAG per sperm (nIU)	0.563 ± 0.08	0.145 ± 0.128	No	-	0.638	6%	-

NAG = Neutral alpha-glucosidase, EA = Ejaculatory abstinence

Figure 1: Fructose enters the glycolytic pathway after phosphorylation by hexokinase and is subsequently converted to pyruvate via glycolysis to be used in the citric acid cycle. The entire citric acid cycle occurs within the inner mitochondrial wall. Pyruvate can enter the mitochondria through specific transporters where it can be oxidized to acetyl-coenzyme A (CoA) and CO_2. Acetyl-CoA then enters the citric acid cycle, which generates one high-energy bond in the form of GTP and four reduced compounds (3 NADH and 1 $FADH_2$), to be used in the oxidative phosphorylation process. Regarding citrate, when it is obtained from oxaloacetate inside the mitochondria as part of the citric acid cycle, exogenous citrate cannot permeate the inner mitochondrial membrane. Thus, before entering the cycle, it should be first converted to malate and to pyruvate by a series of enzymes with the use of ATP. The electrons conserved in NADH and $FADH_2$ are then used to reduce oxygen in the oxidative phosphorylation process (Visconti, 2012).

Appendix C: Proteomic results of LC-MS/MS analysis.

Identified Protein	Accession Number	T-Test (P-value):	2 (1)	1 (1)	3 (1)	4 (1)	2	4	3	1
Prostatic acid phosphatase OS=Homo sapiens GN=ACPP PE=1 SV=3	sp|P15309|PPAP_HUMAN	0.36	3610	3968	3430	3579	3579	4662	3616	4108
Prostate-specific antigen OS=Homo sapiens GN=KLK3 PE=1 SV=2	sp|P07288|KLK3_HUMAN	0.37	3040	3350	1957	3712	3712	4057	3474	3548
sp|Q02383|SEMG2_HUMAN Semenogelin-2 OS=Homo sapiens GN=SEMG2 PE=1 SV=1	sp|Q02383|SEMG2_HUMANSemenogelin-2 OS=Homo sapiens GN=SEMG2 PE=1 SV=1	0.25	3387	2945	916	3256	3256	312	3690	3498
sp|TRYP_PIG|	sp|TRYP_PIG|	0.37	2957	2832	2090	3520	3520	3346	3367	3311
Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	sp|P02768|ALBU_HUMAN	0.38	1738	2417	1777	2499	2499	2817	2301	2234
Isoform 15 of Fibronectin OS=Homo sapiens GN=FN1	sp|P02751-15|FINC_HUMAN	0.32	2005	2802	1399	2056	2056	1949	2072	2735
sp|P04279|SEMG1_HUMAN Semenogelin-1 OS=Homo sapiens GN=SEMG1 PE=1 SV=2	sp|P04279|SEMG1_HUMANSemenogelin-1 OS=Homo sapiens GN=SEMG1 PE=1 SV=2	0.18	2445	2497	554	2758	2758	38	2297	2544
Isoform DeltaLf of Lactotransferrin OS=Homo sapiens GN=LTF	sp|P02788-2|TRFL_HUMAN	0.41	1446	2212	1442	1866	1866	2237	2209	2440
Isoform 2 of Clusterin OS=Homo sapiens GN=CLU	sp|P10909-2|CLUS_HUMAN	0.32	1519	1896	1072	1553	1553	1312	1543	1883
Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1	PIP_HUMAN	0.35	1281	964	803	1112	1112	1138	1053	1148
sp|ALBU_BOVIN|	sp|ALBU_BOVIN|	0.32	1306	1359	2641	1655	1655	996	775	697
Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=2	ZA2G_HUMAN	0.36	1177	1393	1287	1311	1311	1396	1324	1475
Isoform 2 of Carboxypeptidase E OS=Homo sapiens GN=CPE	sp|P16870-2|CBPE_HUMAN (+1)	0.37	678	606	466	702	702	851	666	783
sp|P49221|TGM4_HUMAN Protein-glutamine gamma-glutamyltransferase 4 OS=Homo sapiens...	sp|P49221|TGM4_HUMAN Protein-glutamine gamma-glutamyltransferase 4 OS=Homo sapiens...	0.29	584	983	456	464	464	311	562	730
sp|P05154|IPSP_HUMAN Plasma serine protease inhibitor OS=Homo sapiens GN=SERPINA5...	sp|P05154|IPSP_HUMAN Plasma serine protease inhibitor OS=Homo sapiens GN=SERPINA5...	0.34	422	464	396	452	452	428	439	462
sp|K1C10_HUMAN|	sp|K1C10_HUMAN|	0.35	436	427	398	671	671	519	514	432

Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=2 SV=1	C9JIZ6_HUMAN	0.33	411	438	345	512	512	449	397	425
Mucin-6 OS=Homo sapiens GN=MUC6 PE=1 SV=3	MUC6_HUMAN	0.36	384	456	392	391	391	338	392	603
Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4	AMPN_HUMAN	0.37	472	420	307	408	408	541	314	605
sp|K1C9_HUMAN|	sp|K1C9_HUMAN|	0.38	495	311	310	372	372	469	556	367
Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1	ACTG_HUMAN	0.33	503	359	272	303	303	410	387	409
Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	sp|P01009|A1AT_HUMAN	0.41	287	372	310	367	367	404	450	378
Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	K2C1_HUMAN	0.41	4	6	377	575	580	2	614	7
Beta-microseminoprotein OS=Homo sapiens GN=MSMB PE=1 SV=1	sp|P08118|MSMB_HUMAN	0.33	269	317	245	253	253	206	255	249
Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1	KCRB_HUMAN	0.34	353	385	358	243	243	351	329	312
sp|TRFE_HUMAN|	sp|TRFE_HUMAN|	0.48	205	384	196	240	240	327	487	339
sp|Q08380|LG3BP_HUMAN Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	sp|Q08380|LG3BP_HUMANGalectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	0.63	287	297	138	4	319	3	357	311
Lipoprotein lipase OS=Homo sapiens GN=LPL PE=1 SV=1	LIPL_HUMAN	0.33	197	225	145	231	231	189	198	210
sp|K22E_HUMAN|	sp|K22E_HUMAN|	0.34	194	223	170	341	341	245	226	183
Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4	DHSO_HUMAN	0.33	219	292	224	224	224	234	211	247
Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	FAS_HUMAN	0.34	205	221	227	121	121	210	185	174
Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2	PPIB_HUMAN	0.37	163	147	183	207	207	194	194	221
sp|Q16610|ECM1_HUMAN Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1...	sp|Q16610|ECM1_HUMAN Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1...	0.56	143	216	122	219	219	323	263	244
Glycodelin OS=Homo sapiens GN=PAEP PE=1 SV=2	sp|P09466|PAEP_HUMAN	0.44	120	175	95	163	163	220	223	214
Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	CATD_HUMAN	0.33	192	209	160	188	188	176	224	185
Gastricsin OS=Homo sapiens GN=PGC PE=1 SV=1	sp|P20142|PEPC_HUMAN	0.32	106	70	99	47	47	46	94	58

sp|O15230|LAMA5_HUMAN Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	sp|O15230|LAMA5_HUMANLaminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	0.33	81	127	131	125	125	0	149	131
Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=1 SV=2	sp|P01011|AACT_HUMAN	0.28	138	270	105	142	142	185	112	203
Isoform 12 of Titin OS=Homo sapiens GN=TTN	sp|Q8WZ42-12|TITIN_HUMAN	0.47	3	0	0	5	5	4	0	6
sp|P80303|NUCB2_HUMAN Nucleobindin-2 OS=Homo sapiens GN=NUCB2 PE=1 SV=2	sp|P80303|NUCB2_HUMANNucleobindin-2 OS=Homo sapiens GN=NUCB2 PE=1 SV=2	0.28	167	219	127	213	213	2	243	226
sp|P30041|PRDX6_HUMAN Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	sp|P30041|PRDX6_HUMANPeroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	0.27	243	238	138	184	184	1	197	216
Neprilysin OS=Homo sapiens GN=MME PE=1 SV=2	NEP_HUMAN	0.36	176	208	100	162	162	206	179	213
Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	HORN_HUMAN	0.16	4	2	1	6	6	15	12	5
sp|O00391|QSOX1_HUMAN Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3	sp|O00391|QSOX1_HUMANSulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3	0.2	164	233	112	201	201	1	162	210
sp|P55268|LAMB2_HUMAN Laminin subunit beta-2 OS=Homo sapiens GN=LAMB2 PE=1 SV=2	sp|P55268|LAMB2_HUMANLaminin subunit beta-2 OS=Homo sapiens GN=LAMB2 PE=1 SV=2	0.31	107	133	90	126	126	0	133	173
Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	sp|P06733|ENOA_HUMAN	0.33	187	185	158	128	128	177	196	147
Cystatin-C OS=Homo sapiens GN=CST3 PE=1 SV=1	CYTC_HUMAN	0.35	129	266	120	120	120	221	164	176
sp|P01857|IGHG1_HUMAN Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	sp|P01857|IGHG1_HUMANIg gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	0.4	139	169	178	161	161	225	191	169
sp|P54107|CRIS1_HUMAN Cysteine-rich secretory protein 1 OS=Homo sapiens GN=CRISP1...	sp|P54107|CRIS1_HUMANCysteine-rich secretory protein 1 OS=Homo sapiens GN=CRISP1 PE=1 SV=1	0.25	173	255	3	3	311	3	254	381
sp|P62258|1433E_HUMAN 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	sp|P62258|1433E_HUMAN14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	0.36	157	151	104	128	128	201	134	142
sp|P07900|HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1...	sp|P07900|HS90A_HUMANHeat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	0.27	1	346	3	1	232	3	319	309
Dipeptidyl peptidase 4 OS=Homo sapiens GN=DPP4 PE=1 SV=2	DPP4_HUMAN	0.41	143	152	93	131	131	162	120	234
sp|P61916|NPC2_HUMAN Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=1...	sp|P61916|NPC2_HUMAN Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=1...	0.4	114	149	107	132	132	148	228	201

ADP-ribosyl cyclase 1 OS=Homo sapiens GN=CD38 PE=1 SV=2	sp|P28907|CD38_HUMAN	0.35	89	112	74	93	93	107	84	109
Angiotensin-converting enzyme OS=Homo sapiens GN=ACE PE=1 SV=1	ACE_HUMAN	0.3	100	123	90	103	103	0	120	152
Isoform 2 of 72 kDa type IV collagenase OS=Homo sapiens GN=MMP2	sp|P08253-2|MMP2_HUMAN	0.41	89	116	80	137	137	124	170	128
Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	IGKC_HUMAN	0.36	111	114	106	110	110	131	121	115
Carboxypeptidase M OS=Homo sapiens GN=CPM PE=1 SV=2	CBPM_HUMAN	0.47	84	93	113	130	130	229	188	111
sp|P04406-2|G3P_HUMAN Isoform 2 of Glyceraldehyde-3-phosphate dehydrogenase OS=Homo...	sp|P04406-2|G3P_HUMANIsoform 2 of Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH	0.76	205	261	53	1	137	207	175	220
Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	CO3_HUMAN	0.34	72	137	91	96	96	124	83	100
Isoform 3 of Laminin subunit alpha-3 OS=Homo sapiens GN=LAMA3	sp|Q16787-3|LAMA3_HUMAN	0.31	3	6	0	3	3	4	5	6
Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3	CATB_HUMAN	0.39	103	120	91	111	111	146	145	112
sp|P68104|EF1A1_HUMAN Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	sp|P68104|EF1A1_HUMANElongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	0.63	259	162	36	7	111	134	170	145
Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=4	LYAG_HUMAN	0.45	89	121	56	98	98	113	121	162
sp|P41222|PTGDS_HUMAN Prostaglandin-H2 D-isomerase OS=Homo sapiens GN=PTGDS PE=1...	sp|P41222|PTGDS_HUMANProstaglandin-H2 D-isomerase OS=Homo sapiens GN=PTGDS PE=1 SV=1	0.34	110	160	4	0	146	0	184	213
sp|ANXA5_HUMAN|	sp|ANXA5_HUMAN|	0.3	152	158	110	133	133	125	139	104
Isoform 2 of Protein dopey-2 OS=Homo sapiens GN=DOPEY2	sp|Q9Y3R5-2|DOP2_HUMAN	0.3	83	90	79	72	72	77	46	84
Isoform 3 of Cartilage acidic protein 1 OS=Homo sapiens GN=CRTAC1	sp|Q9NQ79-3|CRAC1_HUMAN	0.29	102	170	81	123	123	90	122	130
Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	PGK1_HUMAN	0.28	181	124	103	85	85	105	106	109
Low-density lipoprotein receptor-related protein 2 OS=Homo sapiens GN=LRP2 PE=1 SV=3	LRP2_HUMAN	0.8	0	6	0	0	0	2	0	2
sp|GSTP1_HUMAN|	sp|GSTP1_HUMAN|	0.33	145	177	166	61	61	102	111	124

sp|P11142|HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8...	sp|P11142|HSP7C_HUMANHeat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	0.15	137	159	0	0	105	172	158	116
Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2	LRP1_HUMAN	0.17	0	0	0	0	0	7	1	2
sp|P01033|TIMP1_HUMAN Metalloproteinase inhibitor 1 OS=Homo sapiens GN=TIMP1 PE=1 SV=1	sp|P01033|TIMP1_HUMANMetalloproteinase inhibitor 1 OS=Homo sapiens GN=TIMP1 PE=1 SV=1	0.054	119	145	12	0	175	135	178	176
Isoform M1 of Pyruvate kinase PKM OS=Homo sapiens GN=PKM	sp|P14618-2|KPYM_HUMAN	0.3	131	156	107	84	84	109	106	93
Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	sp|P35579|MYH9_HUMAN	0.34	89	112	120	57	57	108	83	77
Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6	PLSL_HUMAN	0.51	88	155	72	115	115	167	145	148
Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	ENPL_HUMAN	0.46	83	94	50	66	66	127	123	103
sp|Q9Y6R7|FCGBP_HUMAN IgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3	sp|Q9Y6R7|FCGBP_HUMANIgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3	0.3	58	100	59	55	55	0	81	102
Isoform 6 of Agrin OS=Homo sapiens GN=AGRN	sp|O00468-6|AGRIN_HUMAN	0.36	65	89	65	54	54	93	67	70
sp|O95716|RAB3D_HUMAN Ras-related protein Rab-3D OS=Homo sapiens GN=RAB3D PE=1 SV=1	sp|O95716|RAB3D_HUMANRas-related protein Rab-3D OS=Homo sapiens GN=RAB3D PE=1 SV=1	0.4	88	72	52	75	75	108	90	121
sp|Q6PCB0|VWA1_HUMAN von Willebrand factor A domain-containing protein 1 OS=Homo...	sp|Q6PCB0|VWA1_HUMAN von Willebrand factor A domain-containing protein 1 OS=Homo...	0.31	121	148	97	137	137	108	145	124
Ribonuclease T2 OS=Homo sapiens GN=RNASET2 PE=1 SV=2	sp|O00584|RNT2_HUMAN	0.31	100	114	64	80	80	81	90	114
sp|Q96KP4|CNDP2_HUMAN Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2 PE=1 SV=2	sp|Q96KP4|CNDP2_HUMANCytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2 PE=1 SV=2	0.11	142	155	7	1	111	174	181	158
sp|P11047|LAMC1_HUMAN Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3	sp|P11047|LAMC1_HUMANLaminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3	0.31	69	93	82	69	69	0	85	106
sp|Q13510|ASAH1_HUMAN Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=1 SV=5	sp|Q13510|ASAH1_HUMANAcid ceramidase OS=Homo sapiens GN=ASAH1 PE=1 SV=5	0.23	122	126	76	126	126	1	115	129
Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4	sp|Q04760|LGUL_HUMAN	0.34	79	80	60	70	70	64	75	77

Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1	sp|P60174-1|TPIS_HUMAN	0.34	118	121	75	84	84	106	105	117
Isoform 2 of ATP-citrate synthase OS=Homo sapiens GN=ACLY	sp|P53396-2|ACLY_HUMAN	0.25	84	81	36	28	28	67	57	36
Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2	sp|O14773|TPP1_HUMAN	0.39	66	98	72	95	95	117	119	65
sp|Q99497|PARK7_HUMAN Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2	sp|Q99497|PARK7_HUMANProtein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2	0.67	69	70	0	73	73	2	103	103
Polyubiquitin-C (Fragment) OS=Homo sapiens GN=UBC PE=2 SV=1	F5GXK7_HUMAN	0.37	68	71	69	71	71	91	64	91
sp|Q9NR99|MXRA5_HUMAN Matrix-remodeling-associated protein 5 OS=Homo sapiens GN=MXRA5 PE=2 SV=3	sp|Q9NR99|MXRA5_HUMANMatrix-remodeling-associated protein 5 OS=Homo sapiens GN=MXRA5 PE=2 SV=3	0.43	37	113	0	0	61	42	63	61
Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2	sp|P50395|GDIB_HUMAN	0.41	63	79	106	54	54	105	76	98
Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	HEMO_HUMAN	0.51	34	94	46	74	74	105	86	66
A disintegrin and metalloproteinase with thrombospondin motifs 1 OS=Homo sapiens GN=ADAMTS1 PE=1 SV=4	ATS1_HUMAN	0.49	31	65	42	59	59	118	74	47
sp|Q5JQC9|AKAP4_HUMAN A-kinase anchor protein 4 OS=Homo sapiens GN=AKAP4 PE=1 SV=1	sp|Q5JQC9|AKAP4_HUMANA-kinase anchor protein 4 OS=Homo sapiens GN=AKAP4 PE=1 SV=1	0.66	1	1	30	53	53	3	249	122
sp|P04083|ANXA1_HUMAN Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	sp|P04083|ANXA1_HUMANAnnexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	0.34	117	101	72	82	82	120	98	98
sp|P11021|GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1...	sp|P11021|GRP78_HUMAN78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	0.32	144	107	0	0	71	131	131	84
sp|Q06830|PRDX1_HUMAN Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	sp|Q06830|PRDX1_HUMANPeroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	0.49	139	114	47	0	88	110	137	114
Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=2 SV=1	F5H5D3_HUMAN	0.37	66	78	62	52	52	77	83	65
Isoform 2 of Extracellular matrix protein FRAS1 OS=Homo sapiens GN=FRAS1	sp|Q86XX4-2|FRAS1_HUMAN	0.47	0	1	1	1	1	2	1	0
Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4	EZRI_HUMAN	0.28	82	112	65	72	73	73	81	66

Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=2 SV=1	E9PBC6_HUMAN	0.74	1	10	2	4	4	4	5	11
Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3	sp|P08697|A2AP_HUMAN	0.35	72	93	67	97	97	73	93	102
sp|P01859|IGHG2_HUMAN Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2	sp|P01859|IGHG2_HUMANIg gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2	0.38	76	104	62	96	96	82	97	100
sp|Q96S96|PEBP4_HUMAN Phosphatidylethanolamine-binding protein 4 OS=Homo sapiens GN=PEBP4 PE=1 SV=3	sp|Q96S96|PEBP4_HUMANPhosphatidylethanolamine-binding protein 4 OS=Homo sapiens GN=PEBP4 PE=1 SV=3	0.021	68	80	2	0	107	70	141	129
sp|O15230|LAMA5_HUMAN Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	sp|O15230|LAMA5_HUMANLaminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8-DECOY	0.36	0	0	0	0	0	0	3	0
Pro-cathepsin H OS=Homo sapiens GN=CTSH PE=1 SV=4	CATH_HUMAN	0.36	78	66	74	63	63	66	84	76
sp|P04075|ALDOA_HUMAN Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1...	sp|P04075|ALDOA_HUMANFructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	0.96	142	172	4	2	96	4	119	125
sp|P04792|HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	sp|P04792|HSPB1_HUMANHeat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	0.21	234	82	63	58	58	0	82	96
Trypsin-1 OS=Homo sapiens GN=PRSS1 PE=2 SV=1	E7EQ64_HUMAN	0.33	39	43	21	49	49	44	36	40
sp|P68371|TBB4B_HUMAN Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	sp|P68371|TBB4B_HUMANTubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	0.23	139	103	56	86	86	0	144	112
sp|P08107|HSP71_HUMAN Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1...	sp|P08107|HSP71_HUMANHeat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	0.65	108	156	3	0	108	0	150	94
sp|P32119|PRDX2_HUMAN Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	sp|P32119|PRDX2_HUMANPeroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	0.56	78	78	3	66	66	66	74	79
Isoform 2 of Amiloride-sensitive amine oxidase [copper-containing] OS=Homo sapiens GN=AOC1	sp|P19801-2|AOC1_HUMAN	0.45	51	72	66	50	50	101	104	65
Beta-hexosaminidase OS=Homo sapiens GN=HEXA PE=2 SV=1	H3BP20_HUMAN	0.41	51	71	43	66	66	80	81	69
Complement C4-B OS=Homo sapiens GN=C4B PE=1 SV=2	CO4B_HUMAN	0.32	47	84	31	67	67	79	55	54
Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	A2MG_HUMAN	0.47	43	44	33	45	45	36	88	59

Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3	ALDR_HUMAN	0.29	55	120	37	36	36	63	81	57
sp|O43707|ACTN4_HUMAN Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	sp|O43707|ACTN4_HUMANAlpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	0.27	51	73	43	48	48	0	53	73
sp|P20337|RAB3B_HUMAN Ras-related protein Rab-3B OS=Homo sapiens GN=RAB3B PE=1 SV=2	sp|P20337|RAB3B_HUMANRas-related protein Rab-3B OS=Homo sapiens GN=RAB3B PE=1 SV=2	0.34	102	101	53	54	54	84	77	92
sp|P02647|APOA1_HUMAN Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	sp|P02647|APOA1_HUMANApolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	0.32	112	104	56	78	78	91	88	108
Maltase-glucoamylase, intestinal OS=Homo sapiens GN=MGAM PE=4 SV=2	E7ER45_HUMAN	0.57	1	2	34	77	77	3	100	1
Isoform 2 of Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1	sp|Q01518-2|CAP1_HUMAN	0.31	102	53	40	35	35	62	56	54
Kallikrein-2 OS=Homo sapiens GN=KLK2 PE=2 SV=1	sp|P20151|KLK2_HUMAN	0.41	55	52	61	63	63	85	72	80
Isoform 4 of CD109 antigen OS=Homo sapiens GN=CD109	sp|Q6YHK3-4|CD109_HUMAN	0.83	35	49	13	66	66	66	43	58
Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3	SPB6_HUMAN	0.3	57	73	37	45	45	62	52	50
Isoform 3 of Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1	sp|Q92896-3|GSLG1_HUMAN	0.31	25	27	18	22	22	14	17	34
Matrilin-2 OS=Homo sapiens GN=MATN2 PE=2 SV=1	J3KN08_HUMAN	0.32	32	68	27	46	46	39	64	38
Isoform 2 of Filamin-B OS=Homo sapiens GN=FLNB	sp|O75369-2|FLNB_HUMAN	0.35	36	64	63	12	12	55	42	31
Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4	sp|P06744|G6PI_HUMAN	0.42	56	79	58	57	57	75	102	67
Carboxypeptidase Z OS=Homo sapiens GN=CPZ PE=1 SV=2	sp|Q66K79|CBPZ_HUMAN	0.37	57	82	58	76	76	70	80	90
Proprotein convertase subtilisin/kexin type 5 (Fragment) OS=Homo sapiens GN=PCSK5 PE=2 SV=1	Q5JSG7_HUMAN	0.84	0	2	1	1	1	5	1	0
sp|Q02818|NUCB1_HUMAN Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4	sp|Q02818|NUCB1_HUMANNucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4	0.37	61	74	51	61	61	56	91	77
Kallistatin OS=Homo sapiens GN=SERPINA4 PE=1 SV=3	KAIN_HUMAN	0.32	74	106	57	97	97	85	95	88

sp|P08238|HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1...	sp|P08238|HS90B_HUMANHeat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	0.57	95	120	0	0	77	0	135	97
sp|Q9NZR2|LRP1B_HUMAN Low-density lipoprotein receptor-related protein 1B OS=Homo sapiens GN=LRP1B PE=1 SV=2	sp|Q9NZR2|LRP1B_HUMANLow-density lipoprotein receptor-related protein 1B OS=Homo sapiens GN=LRP1B PE=1 SV=2	0.8	0	4	0	1	1	0	1	2
Attractin OS=Homo sapiens GN=ATRN PE=1 SV=2	sp|O75882|ATRN_HUMAN	0.33	16	16	10	15	15	19	13	14
sp|O00560|SDCB1_HUMAN Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1	sp|O00560|SDCB1_HUMANSyntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1	0.17	62	66	15	51	51	1	59	69
Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	sp|P02751|FINC_HUMAN	0.31	80	89	65	64	64	59	64	83
Phospholipase A1 member A OS=Homo sapiens GN=PLA1A PE=2 SV=1	G5E9W0_HUMAN	0.31	45	82	35	51	51	42	54	74
Cysteine-rich secretory protein LCCL domain-containing 2 OS=Homo sapiens GN=CRISPLD2 PE=2 SV=1	H3BTI0_HUMAN	0.73	62	82	0	0	0	89	0	103
Beta-galactosidase OS=Homo sapiens GN=GLB1 PE=1 SV=2	sp|P16278|BGAL_HUMAN	0.36	54	75	30	56	56	52	70	80
sp|Q8WVQ1|CANT1_HUMAN Soluble calcium-activated nucleotidase 1 OS=Homo sapiens GN=CANT1 PE=1 SV=1	sp|Q8WVQ1|CANT1_HUMANSoluble calcium-activated nucleotidase 1 OS=Homo sapiens GN=CANT1 PE=1 SV=1	0.1	78	2	8	0	69	72	84	71
Isoform 2 of Receptor-type tyrosine-protein phosphatase S OS=Homo sapiens GN=PTPRS	sp|Q13332-6|PTPRS_HUMAN	0.36	0	0	0	0	0	0	0	2
Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	EF2_HUMAN	0.4	65	67	45	37	37	93	59	60
Isoform 2 of Cysteine-rich secretory protein 3 OS=Homo sapiens GN=CRISP3	sp|P54108-2|CRIS3_HUMAN	0.4	0	2	42	87	87	2	76	1
sp|P10586|PTPRF_HUMAN Receptor-type tyrosine-protein phosphatase F OS=Homo sapiens...	sp|P10586|PTPRF_HUMANReceptor-type tyrosine-protein phosphatase F OS=Homo sapiens GN=PTPRF PE=1 SV=2	0.67	38	58	0	1	35	1	44	44
Cystatin-S OS=Homo sapiens GN=CST4 PE=1 SV=3	CYTS_HUMAN	0.42	47	65	66	52	52	96	154	42
sp|O75874|IDHC_HUMAN Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens...	sp|O75874|IDHC_HUMAN Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens...	0.35	28	36	41	36	36	30	29	56
CD9 antigen OS=Homo sapiens GN=CD9 PE=2 SV=1	A6NNI4_HUMAN	0.35	87	60	55	82	82	84	63	80

Isoform PSMA-7 of Glutamate carboxypeptidase 2 OS=Homo sapiens GN=FOLH1	sp|Q04609-7|FOLH1_HUMAN	0.45	46	69	22	45	45	77	47	70
sp|Q9NZR2|LRP1B_HUMAN Low-density lipoprotein receptor-related protein 1B OS=Homo sapiens GN=LRP1B PE=1 SV=2	sp|Q9NZR2|LRP1B_HUMANLow-density lipoprotein receptor-related protein 1B OS=Homo sapiens GN=LRP1B PE=1 SV=2-DECOY	0.35	0	0	3	2	2	0	0	0
Isoform 3 of A-kinase anchor protein 12 OS=Homo sapiens GN=AKAP12	sp|Q02952-3|AKA12_HUMAN	0.43	2	5	4	4	4	5	6	4
Mucin-5B OS=Homo sapiens GN=MUC5B PE=2 SV=1	E9PBJ0_HUMAN	0.38	5	3	12	0	0	3	11	0
Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3	HEXB_HUMAN	0.41	0	0	92	107	107	0	111	5
Uncharacterized protein OS=Homo sapiens GN=P4HB PE=3 SV=1	F5H8J2_HUMAN	0.36	40	70	60	24	24	56	60	46
sp|P12429|ANXA3_HUMAN Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3	sp|P12429|ANXA3_HUMANAnnexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3	0.22	87	116	67	85	85	1	86	71
sp|P35556|FBN2_HUMAN Fibrillin-2 OS=Homo sapiens GN=FBN2 PE=1 SV=3	sp|P35556|FBN2_HUMAN Fibrillin-2 OS=Homo sapiens GN=FBN2 PE=1 SV=3-DECOY	0.24	0	0	0	1	1	1	5	0
Isoform APP751 of Amyloid beta A4 protein OS=Homo sapiens GN=APP	sp|P05067-8|A4_HUMAN	0.33	17	25	14	23	23	17	22	22
sp|O00462|MANBA_HUMAN Beta-mannosidase OS=Homo sapiens GN=MANBA PE=1 SV=3	sp|O00462|MANBA_HUMANBeta-mannosidase OS=Homo sapiens GN=MANBA PE=1 SV=3	0.36	40	63	25	53	53	51	48	64
Fibrillin-2 OS=Homo sapiens GN=FBN2 PE=1 SV=3	sp|P35556|FBN2_HUMAN	0.75	2	0	0	0	0	1	0	2
sp|O00194|RB27B_HUMAN Ras-related protein Rab-27B OS=Homo sapiens GN=RAB27B PE=1 SV=4	sp|O00194|RB27B_HUMANRas-related protein Rab-27B OS=Homo sapiens GN=RAB27B PE=1 SV=4	0.21	84	71	0	0	68	68	67	71
Sucrase-isomaltase, intestinal OS=Homo sapiens GN=SI PE=1 SV=6	SUIS_HUMAN	0.88	1	14	3	7	7	16	5	13
sp|P16035|TIMP2_HUMAN Metalloproteinase inhibitor 2 OS=Homo sapiens GN=TIMP2 PE=1 SV=2	sp|P16035|TIMP2_HUMANMetalloproteinase inhibitor 2 OS=Homo sapiens GN=TIMP2 PE=1 SV=2	0.25	64	53	0	0	52	36	57	57
Legumain OS=Homo sapiens GN=LGMN PE=1 SV=1	LGMN_HUMAN	0.44	29	45	27	64	64	61	57	47
Isoform 2 of Multiple epidermal growth factor-like domains protein 6 OS=Homo sapiens GN=MEGF6	MEGF6_HUMAN	0.77	2	0	0	0	0	0	1	2
Semaphorin-3C OS=Homo sapiens GN=SEMA3C PE=2 SV=1	F5H1Z7_HUMAN	0.29	48	29	18	37	37	41	22	26

Retinoid-inducible serine carboxypeptidase OS=Homo sapiens GN=SCPEP1 PE=1 SV=1	sp|Q9HB40|RISC_HUMAN	0.35	43	62	29	45	45	49	68	42
sp|P39060|COIA1_HUMAN Collagen alpha-1(XVIII) chain OS=Homo sapiens GN=COL18A1 PE=1...	sp|P39060|COIA1_HUMANCollagen alpha-1(XVIII) chain OS=Homo sapiens GN=COL18A1 PE=1 SV=5	0.34	53	51	0	0	56	0	71	64
sp|Q14204|DYHC1_HUMAN Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1...	sp|Q14204|DYHC1_HUMANCytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	0.58	29	53	0	0	27	0	45	47
sp|P30086|PEBP1_HUMAN Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3	sp|P30086|PEBP1_HUMANPhosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3	0.41	99	84	0	0	54	62	71	85
Complement factor B OS=Homo sapiens GN=CFB PE=2 SV=1	B4E1Z4_HUMAN	0.4	16	39	21	24	24	36	25	32
Tissue alpha-L-fucosidase OS=Homo sapiens GN=FUCA1 PE=1 SV=4	FUCO_HUMAN	0.41	29	34	39	35	35	55	42	34
Serum amyloid P-component OS=Homo sapiens GN=APCS PE=1 SV=2	SAMP_HUMAN	0.4	28	38	28	29	29	39	58	31
sp|P63104|1433Z_HUMAN 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	sp|P63104|1433Z_HUMAN14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	0.28	58	73	50	67	67	0	73	84
Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC	sp|Q00610-2|CLH1_HUMAN	0.48	17	42	43	24	24	70	39	47
Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1	CERU_HUMAN	0.55	17	35	18	23	23	55	28	31
Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	TSP1_HUMAN	0.38	12	22	16	29	29	26	21	19
Isoform 6 of Myoferlin OS=Homo sapiens GN=MYOF	sp|Q9NZM1-6|MYOF_HUMAN	0.28	26	27	17	11	11	14	15	27
Calsyntenin-1 (Fragment) OS=Homo sapiens GN=CLSTN1 PE=2 SV=1	Q5SR54_HUMAN	0.29	23	32	13	26	26	28	20	27
sp|P08294|SODE_HUMAN Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3...	sp|P08294|SODE_HUMAN Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3...	0.37	70	56	85	70	70	94	71	78
Sialate O-acetylesterase OS=Homo sapiens GN=SIAE PE=1 SV=1	sp|Q9HAT2|SIAE_HUMAN	0.43	32	49	33	46	46	50	49	55
sp|Q92597|NDRG1_HUMAN Protein NDRG1 OS=Homo sapiens GN=NDRG1 PE=1 SV=1	sp|Q92597|NDRG1_HUMANProtein NDRG1 OS=Homo sapiens GN=NDRG1 PE=1 SV=1	0.26	35	64	35	49	49	0	49	55
sp|P07195|LDHB_HUMAN L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1...	sp|P07195|LDHB_HUMAN L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1...	0.37	51	72	59	59	59	60	64	75

sp|Q8N6Q3|CD177_HUMAN CD177 antigen OS=Homo sapiens GN=CD177 PE=1 SV=2	sp|Q8N6Q3|CD177_HUMANCD177 antigen OS=Homo sapiens GN=CD177 PE=1 SV=2	0.43	17	44	50	51	51	33	57	58
Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2	VAT1_HUMAN	0.34	49	55	64	57	57	48	44	67
Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	TERA_HUMAN	0.9	74	83	3	0	0	97	1	60
sp|Q8WUM4|PDC6I_HUMAN Programmed cell death 6-interacting protein OS=Homo sapiens...	sp|Q8WUM4|PDC6I_HUMANProgrammed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1	0.58	80	48	0	0	67	0	54	63
sp|Q02809|PLOD1_HUMAN Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens...	sp|Q02809|PLOD1_HUMANProcollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2	0.42	42	52	0	1	43	0	64	51
Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=2 SV=1	E9PKU7_HUMAN	0.82	31	52	0	0	0	56	0	42
Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	sp|P15924|DESP_HUMAN	0.44	14	1	8	16	16	7	23	5
sp|Q5D862|FILA2_HUMAN Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	sp|Q5D862|FILA2_HUMANFilaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	0.31	0	0	0	4	4	1	3	3
Annexin OS=Homo sapiens GN=ANXA6 PE=2 SV=3	A6NN80_HUMAN	0.23	58	71	32	31	31	52	47	36
Endothelial lipase OS=Homo sapiens GN=LIPG PE=1 SV=1	sp|Q9Y5X9|LIPE_HUMAN	0.4	30	52	24	52	52	43	55	56
Biotinidase OS=Homo sapiens GN=BTD PE=1 SV=2	BTD_HUMAN	0.4	40	55	32	45	45	70	50	43
sp|PPIA_HUMAN|	sp|PPIA_HUMAN|	0.22	155	35	28	45	45	58	40	40
sp|Q13438-4|OS9_HUMAN Isoform 4 of Protein OS-9 OS=Homo sapiens GN=OS9	sp|Q13438-4|OS9_HUMANIsoform 4 of Protein OS-9 OS=Homo sapiens GN=OS9	0.28	44	51	42	45	45	0	56	50
sp|P30101|PDIA3_HUMAN Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1...	sp|P30101|PDIA3_HUMANProtein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4	0.87	1	59	54	1	51	90	98	67
Isoform 2 of Slit homolog 2 protein OS=Homo sapiens GN=SLIT2	sp|O94813-2|SLIT2_HUMAN	0.91	2	1	1	2	2	3	4	3
Nephronectin (Fragment) OS=Homo sapiens GN=NPNT PE=2 SV=1	D6RH31_HUMAN	0.33	15	21	20	16	16	22	6	11
Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=2 SV=1	D6RGG3_HUMAN	0.4	3	4	0	0	0	7	0	9

Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=2 SV=1	E9PGN7_HUMAN	0.96	89	97	0	0	0	81	0	110
Nucleotide exchange factor SIL1 OS=Homo sapiens GN=SIL1 PE=1 SV=1	SIL1_HUMAN	0.87	58	88	0	1	1	56	3	66
sp|P12830|CADH1_HUMAN Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3	sp|P12830|CADH1_HUMANCadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3	0.26	41	42	16	36	36	44	35	29
sp|P35555|FBN1_HUMAN Fibrillin-1 OS=Homo sapiens GN=FBN1 PE=1 SV=3	sp|P35555|FBN1_HUMAN Fibrillin-1 OS=Homo sapiens GN=FBN1 PE=1 SV=3-DECOY	0.38	0	2	2	0	0	0	0	3
sp|P02533|K1C14_HUMAN Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	sp|P02533|K1C14_HUMANKeratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	0.51	71	53	0	0	81	0	131	0
Nesprin-1 OS=Homo sapiens GN=SYNE1 PE=2 SV=1	E9PEL9_HUMAN	0.56	1	0	0	0	0	0	3	0
Isoform 2 of Transmembrane protease serine 2 OS=Homo sapiens GN=TMPRSS2	TMPS2_HUMAN	0.98	31	39	0	1	1	26	0	41
Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	sp|P28066|PSA5_HUMAN	0.38	18	19	25	21	21	25	29	22
Growth arrest-specific protein 6 OS=Homo sapiens GN=GAS6 PE=1 SV=2	sp|Q14393|GAS6_HUMAN	0.2	37	50	10	28	28	45	33	29
sp|P18669|PGAM1_HUMAN Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2	sp|P18669|PGAM1_HUMANPhosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2	0.86	47	58	3	47	47	2	54	70
Sortilin-related receptor OS=Homo sapiens GN=SORL1 PE=2 SV=1	E9PP43_HUMAN	0.67	4	1	0	1	1	2	3	2
Isoform 3 of Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1	sp|P40925-3|MDHC_HUMAN	0.39	36	52	29	22	22	44	52	44
Latent-transforming growth factor beta-binding protein 3 (Fragment) OS=Homo sapiens GN=LTBP3 PE=2 SV=1	E9PKW1_HUMAN	0.33	2	2	1	0	0	1	0	3
Phosphoglycerate kinase 2 OS=Homo sapiens GN=PGK2 PE=1 SV=3	PGK2_HUMAN	0.35	20	41	24	28	28	46	46	32
Isoform 2 of Vitamin D-binding protein OS=Homo sapiens GN=GC	sp|P02774-2|VTDB_HUMAN	0.33	25	31	36	37	37	35	22	26

sp|P51159|RB27A_HUMAN Ras-related protein Rab-27A OS=Homo sapiens GN=RAB27A PE=1 SV=3	sp|P51159|RB27A_HUMANRas-related protein Rab-27A OS=Homo sapiens GN=RAB27A PE=1 SV=3	0.27	90	62	0	0	75	69	42	86
Basal cell adhesion molecule OS=Homo sapiens GN=BCAM PE=1 SV=2	BCAM_HUMAN	0.41	24	19	22	31	31	33	26	26
sp|Q8IZJ3|CPMD8_HUMAN C3 and PZP-like alpha-2-macroglobulin domain-containing protein...	sp|Q8IZJ3|CPMD8_HUMANC3 and PZP-like alpha-2-macroglobulin domain-containing protein 8 OS=Homo sapiens GN=CPAMD8 PE=1 SV=2	0.85	1	23	2	2	18	2	22	28
Leucine-rich alpha-2-glycoprotein OS=Homo sapiens GN=LRG1 PE=1 SV=2	A2GL_HUMAN	0.8	49	89	0	0	0	84	0	83
Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1	CAN1_HUMAN	0.37	18	51	15	8	8	31	27	31
Carboxypeptidase D OS=Homo sapiens GN=CPD PE=1 SV=2	sp|O75976|CBPD_HUMAN	0.31	12	19	8	10	10	11	11	18
Isoform 5 of Voltage-dependent calcium channel subunit alpha-2/delta-1 OS=Homo sapiens GN=CACNA2D1	sp|P54289-5|CA2D1_HUMAN	0.96	9	17	2	1	1	29	2	21
Bifunctional epoxide hydrolase 2 OS=Homo sapiens GN=EPHX2 PE=1 SV=2	sp|P34913|HYES_HUMAN	0.36	27	31	31	15	15	31	28	26
Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1	CALR_HUMAN	0.45	38	28	24	27	27	33	48	42
Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	sp|P23526|SAHH_HUMAN	0.37	43	52	43	36	36	56	50	49
Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2	CAH2_HUMAN (+1)	0.32	64	50	41	28	28	44	34	46
sp|P07355|ANXA2_HUMAN Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	sp|P07355|ANXA2_HUMANAnnexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	0.5	68	1	63	0	70	0	77	71
CD63 antigen (Fragment) OS=Homo sapiens GN=CD63 PE=2 SV=1	F8VWK8_HUMAN	0.37	34	40	23	28	28	41	29	47
Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1	ANT3_HUMAN	0.4	26	37	49	29	29	46	33	43
Apolipoprotein D (Fragment) OS=Homo sapiens GN=APOD PE=2 SV=1	C9JF17_HUMAN	0.37	28	38	39	45	45	45	34	44
sp|Q7Z7M0|MEGF8_HUMAN Multiple epidermal growth factor-like domains protein 8 OS=Homo sapiens GN=MEGF8 PE=1 SV=2	sp|Q7Z7M0|MEGF8_HUMANMultiple epidermal growth factor-like domains protein 8 OS=Homo sapiens GN=MEGF8 PE=1 SV=2	0.75	5	9	0	1	2	0	9	8

sp|Q9Y4L1|HYOU1_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1	sp|Q9Y4L1|HYOU1_HUMANHypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1	0.51	30	37	12	0	37	0	44	29
sp|P20618|PSB1_HUMAN Proteasome subunit beta type-1 OS=Homo sapiens GN=PSMB1 PE=1...	sp|P20618|PSB1_HUMAN Proteasome subunit beta type-1 OS=Homo sapiens GN=PSMB1 PE=1...	0.36	45	48	51	41	41	55	52	45
Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3	CBR1_HUMAN	0.33	34	47	42	28	28	36	37	28
AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=2 SV=1	K7EJT8_HUMAN	0.38	15	12	16	8	8	19	12	14
sp|Q96RW7|HMCN1_HUMAN Hemicentin-1 OS=Homo sapiens GN=HMCN1 PE=1 SV=2	sp|Q96RW7|HMCN1_HUMANHemicentin-1 OS=Homo sapiens GN=HMCN1 PE=1 SV=2	0.36	9	0	0	0	0	0	0	0
sp|P58499|FAM3B_HUMAN Protein FAM3B OS=Homo sapiens GN=FAM3B PE=1 SV=2	sp|P58499|FAM3B_HUMANProtein FAM3B OS=Homo sapiens GN=FAM3B PE=1 SV=2	0.89	38	71	0	35	35	36	34	50
sp|Q7Z7M0|MEGF8_HUMAN Multiple epidermal growth factor-like domains protein 8 OS=Homo sapiens GN=MEGF8 PE=1 SV=2	sp|Q7Z7M0|MEGF8_HUMANMultiple epidermal growth factor-like domains protein 8 OS=Homo sapiens GN=MEGF8 PE=1 SV=2-DECOY	0.3	0	2	1	0	0	0	0	0
Isoform 2 of Selenium-binding protein 1 OS=Homo sapiens GN=SELENBP1	sp|Q13228-2|SBP1_HUMAN	0.34	21	49	45	31	31	28	38	32
Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	K2C5_HUMAN	0.81	52	54	0	0	0	80	0	59
sp|P21266|GSTM3_HUMAN Glutathione S-transferase Mu 3 OS=Homo sapiens GN=GSTM3 PE=1 SV=3	sp|P21266|GSTM3_HUMANGlutathione S-transferase Mu 3 OS=Homo sapiens GN=GSTM3 PE=1 SV=3	0.16	45	59	0	0	40	44	77	45
sp|Q04721|NOTC2_HUMAN Neurogenic locus notch homolog protein 2 OS=Homo sapiens GN=NOTCH2 PE=1 SV=3	sp|Q04721|NOTC2_HUMANNeurogenic locus notch homolog protein 2 OS=Homo sapiens GN=NOTCH2 PE=1 SV=3	0.058	0	0	0	0	0	2	3	1
sp|P02763|A1AG1_HUMAN Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1	sp|P02763|A1AG1_HUMANAlpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1	0.49	37	49	42	33	33	87	57	53
Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	sp|P06396|GELS_HUMAN	0.31	36	29	9	20	20	21	27	41

sp|P49913|CAMP_HUMAN Cathelicidin antimicrobial peptide OS=Homo sapiens GN=CAMP PE=1...	sp|P49913|CAMP_HUMAN Cathelicidin antimicrobial peptide OS=Homo sapiens GN=CAMP PE=1... (+1)	0.6	31	23	15	61	61	59	50	77
sp|Q86VP6|CAND1_HUMAN Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens...	sp|Q86VP6|CAND1_HUMANCullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2	0.46	14	43	0	0	28	0	48	22
sp|Q06323|PSME1_HUMAN Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1...	sp|Q06323|PSME1_HUMANProteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1	0.67	55	60	0	0	32	54	34	21
sp|P07998|RNAS1_HUMAN Ribonuclease pancreatic OS=Homo sapiens GN=RNASE1 PE=1 SV=4	sp|P07998|RNAS1_HUMANRibonuclease pancreatic OS=Homo sapiens GN=RNASE1 PE=1 SV=4	0.94	22	29	0	56	56	0	52	0
Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1	ACTS_HUMAN	0.32	35	31	14	19	19	39	32	32
Isoform 2 of Nesprin-2 OS=Homo sapiens GN=SYNE2	sp|Q8WXH0-2|SYNE2_HUMAN	0.36	0	0	0	0	0	0	5	0
sp|Q96DA0|ZG16B_HUMAN Zymogen granule protein 16 homolog B OS=Homo sapiens GN=ZG16B PE=1 SV=3	sp|Q96DA0|ZG16B_HUMANZymogen granule protein 16 homolog B OS=Homo sapiens GN=ZG16B PE=1 SV=3	0.15	0	67	0	0	64	0	109	69
sp|Q9BZQ8|NIBAN_HUMAN Protein Niban OS=Homo sapiens GN=FAM129A PE=1 SV=1	sp|Q9BZQ8|NIBAN_HUMANProtein Niban OS=Homo sapiens GN=FAM129A PE=1 SV=1	0.25	24	29	12	23	23	0	26	34
Angiotensinogen OS=Homo sapiens GN=AGT PE=1 SV=1	ANGT_HUMAN	0.35	43	37	23	50	50	58	26	40
sp|P48723|HSP13_HUMAN Heat shock 70 kDa protein 13 OS=Homo sapiens GN=HSPA13 PE=1 SV=1	sp|P48723|HSP13_HUMANHeat shock 70 kDa protein 13 OS=Homo sapiens GN=HSPA13 PE=1 SV=1	0.094	29	43	2	0	29	35	50	46
Isoform 3 of Amyloid-like protein 2 OS=Homo sapiens GN=APLP2	sp|Q06481-3|APLP2_HUMAN	0.33	6	10	8	8	8	5	4	11
Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	COF1_HUMAN	0.25	115	24	23	20	20	48	21	31
N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3	GNS_HUMAN	0.45	8	13	17	16	16	25	15	16
Fibromodulin OS=Homo sapiens GN=FMOD PE=1 SV=2	FMOD_HUMAN	0.33	42	39	42	48	48	52	23	40
Carbonic anhydrase 4 OS=Homo sapiens GN=CA4 PE=1 SV=2	CAH4_HUMAN	0.48	19	29	17	24	24	43	44	39
Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1	B2MG_HUMAN (+1)	0.35	19	42	20	34	34	28	39	30

sp|P46940|IQGA1_HUMAN Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	sp|P46940|IQGA1_HUMANRas GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	0.79	19	35	0	0	12	0	22	30
sp|P22314|UBA1_HUMAN Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens...	sp|P22314|UBA1_HUMAN Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens...	0.34	41	64	46	16	16	50	38	33
Isoform 2 of Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1	GFPT1_HUMAN	0.39	14	35	27	23	23	35	36	16
Isoform 3 of Mesothelin OS=Homo sapiens GN=MSLN	sp|Q13421-2|MSLN_HUMAN	0.34	21	33	21	39	39	31	21	33
sp|P30043|BLVRB_HUMAN Flavin reductase (NADPH) OS=Homo sapiens GN=BLVRB PE=1 SV=3	sp|P30043|BLVRB_HUMANFlavin reductase (NADPH) OS=Homo sapiens GN=BLVRB PE=1 SV=3	0.23	43	56	16	42	42	0	50	46
Dipeptidyl peptidase 2 OS=Homo sapiens GN=DPP7 PE=1 SV=3	DPP2_HUMAN	0.23	38	34	25	31	31	19	24	33
L-lactate dehydrogenase OS=Homo sapiens GN=LDHC PE=2 SV=1	F5H245_HUMAN	0.96	20	33	15	15	15	56	67	37
Neogenin OS=Homo sapiens GN=NEO1 PE=1 SV=2	sp|Q92859|NEO1_HUMAN	0.79	7	3	5	12	12	18	10	10
Isoform 2 of Cytosol aminopeptidase OS=Homo sapiens GN=LAP3	sp|P28838-2|AMPL_HUMAN	0.37	24	29	35	17	17	35	30	20
sp|Q16651|PRSS8_HUMAN Prostasin OS=Homo sapiens GN=PRSS8 PE=1 SV=1	sp|Q16651|PRSS8_HUMANProstasin OS=Homo sapiens GN=PRSS8 PE=1 SV=1	0.77	43	47	24	0	58	52	42	62
sp|Q9UHC6|CNTP2_HUMAN Contactin-associated protein-like 2 OS=Homo sapiens GN=CNTNAP2 PE=1 SV=1	sp|Q9UHC6|CNTP2_HUMANContactin-associated protein-like 2 OS=Homo sapiens GN=CNTNAP2 PE=1 SV=1	0.24	2	3	0	2	7	0	5	4
Alpha-galactosidase A OS=Homo sapiens GN=GLA PE=1 SV=1	AGAL_HUMAN	0.34	26	32	30	28	28	24	27	30
Myosin-7 OS=Homo sapiens GN=MYH7 PE=1 SV=5	MYH7_HUMAN	0.55	17	82	0	2	2	0	43	0
sp|P19652|A1AG2_HUMAN Alpha-1-acid glycoprotein 2 OS=Homo sapiens GN=ORM2 PE=1 SV=2	sp|P19652|A1AG2_HUMANAlpha-1-acid glycoprotein 2 OS=Homo sapiens GN=ORM2 PE=1 SV=2	0.53	44	40	50	0	38	73	46	50
Neutrophil gelatinase-associated lipocalin OS=Homo sapiens GN=LCN2 PE=2 SV=1	H9KV70_HUMAN (+1)	0.35	43	28	45	26	26	39	22	38
sp|Q5CZC0|FSIP2_HUMAN Fibrous sheath-interacting protein 2 OS=Homo sapiens GN=FSIP2 PE=2 SV=4	sp|Q5CZC0|FSIP2_HUMANFibrous sheath-interacting protein 2 OS=Homo sapiens GN=FSIP2 PE=2 SV=4	0.36	0	0	0	0	5	0	0	0

sp|P15291|B4GT1_HUMAN Beta-1,4-galactosyltransferase 1 OS=Homo sapiens GN=B4GALT1 PE=1 SV=5	sp|P15291|B4GT1_HUMANBeta-1,4-galactosyltransferase 1 OS=Homo sapiens GN=B4GALT1 PE=1 SV=5	0.35	55	59	0	0	40	46	36	54
Kielin/chordin-like protein OS=Homo sapiens GN=KCP PE=2 SV=2	KCP_HUMAN	0.33	4	0	1	0	0	0	3	0
sp|P19021-5|AMD_HUMAN Isoform 5 of Peptidyl-glycine alpha-amidating monooxygenase...	sp|P19021-5|AMD_HUMANIsoform 5 of Peptidyl-glycine alpha-amidating monooxygenase OS=Homo sapiens GN=PAM	0.47	9	0	3	0	8	14	15	11
sp|P98095-2|FBLN2_HUMAN Isoform 2 of Fibulin-2 OS=Homo sapiens GN=FBLN2	sp|P98095-2|FBLN2_HUMAN Isoform 2 of Fibulin-2 OS=Homo sapiens GN=FBLN2-DECOY	0.94	0	0	0	2	2	0	0	0
sp|P09467|F16P1_HUMAN Fructose-1,6-bisphosphatase 1 OS=Homo sapiens GN=FBP1 PE=1...	sp|P09467|F16P1_HUMANFructose-1,6-bisphosphatase 1 OS=Homo sapiens GN=FBP1 PE=1 SV=5	0.2	32	61	0	0	39	49	38	44
T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=2 SV=1	B7Z9L0_HUMAN	0.38	23	25	22	11	11	27	31	20
Homogentisate 1,2-dioxygenase OS=Homo sapiens GN=HGD PE=1 SV=2	HGD_HUMAN	0.24	19	34	13	19	19	19	13	28
Carboxypeptidase Q OS=Homo sapiens GN=CPQ PE=1 SV=1	CBPQ_HUMAN	0.36	25	35	20	30	30	32	33	32
Neuropilin-1 OS=Homo sapiens GN=NRP1 PE=1 SV=3	sp|O14786|NRP1_HUMAN	0.33	12	37	17	27	27	19	28	24
Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	VTNC_HUMAN	0.31	28	33	19	29	29	33	24	26
Isoform 3 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1	sp|P12814-3|ACTN1_HUMAN	0.39	20	20	8	9	9	29	11	23
Isoform 3 of Importin-5 OS=Homo sapiens GN=IPO5	sp|O00410-3|IPO5_HUMAN (+1)	0.79	1	16	3	5	5	12	13	9
sp|O43175|SERA_HUMAN D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH...	sp|O43175|SERA_HUMAN D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH...	0.34	39	46	51	24	24	34	30	42
Isoform B of Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1	sp|P63000-2|RAC1_HUMAN	0.36	32	35	17	33	33	47	38	22
Isoform 4 of Carboxylesterase 5A OS=Homo sapiens GN=CES5A	sp|Q6NT32-4|EST5A_HUMAN	0.2	7	33	4	19	19	33	33	34
sp|P29401-2|TKT_HUMAN Isoform 2 of Transketolase OS=Homo sapiens GN=TKT	sp|P29401-2|TKT_HUMANIsoform 2 of Transketolase OS=Homo sapiens GN=TKT	0.23	29	32	32	25	25	1	21	23
Synaptotagmin-7 OS=Homo sapiens GN=SYT7 PE=2 SV=1	F5H126_HUMAN	0.34	17	22	27	17	17	28	7	15

Neuroserpin OS=Homo sapiens GN=SERPINI1 PE=1 SV=1	NEUS_HUMAN	0.35	18	22	23	28	28	25	18	23
Di-N-acetylchitobiase OS=Homo sapiens GN=CTBS PE=1 SV=1	DIAC_HUMAN	0.42	17	30	26	40	40	36	28	32
Isoform 1 of Kallikrein-11 OS=Homo sapiens GN=KLK11	sp|Q9UBX7-1|KLK11_HUMAN	0.4	20	27	27	20	20	33	51	29
sp|Q9BRK5|CAB45_HUMAN 45 kDa calcium-binding protein OS=Homo sapiens GN=SDF4 PE=1...	sp|Q9BRK5|CAB45_HUMAN45 kDa calcium-binding protein OS=Homo sapiens GN=SDF4 PE=1 SV=1	0.28	24	37	7	0	25	36	55	57
Polymeric immunoglobulin receptor OS=Homo sapiens GN=PIGR PE=1 SV=4	PIGR_HUMAN	0.93	32	40	0	0	0	39	0	37
sp|P01876|IGHA1_HUMAN Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	sp|P01876|IGHA1_HUMANIg alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	0.4	22	42	47	28	28	41	46	31
ADAMTS-like protein 1 OS=Homo sapiens GN=ADAMTSL1 PE=1 SV=4	sp|Q8N6G6|ATL1_HUMAN	0.41	0	3	5	2	2	3	5	1
Antileukoproteinase OS=Homo sapiens GN=SLPI PE=1 SV=2	SLPI_HUMAN	0.24	64	89	42	20	20	7	8	24
Isoform 2 of Fibulin-2 OS=Homo sapiens GN=FBLN2	FBLN2_HUMAN	0.4	4	10	0	3	3	6	34	2
Isoform 2 of Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1	sp|P15531-2|NDKA_HUMAN	0.37	36	13	45	18	18	41	26	27
Isoform 2 of Teneurin-2 OS=Homo sapiens GN=TENM2	sp|Q9NT68-2|TEN2_HUMAN	0.57	0	5	1	1	1	1	4	3
sp|P06727|APOA4_HUMAN Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3	sp|P06727|APOA4_HUMANApolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3	0.52	28	1	19	41	41	35	25	31
sp|Q13162|PRDX4_HUMAN Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1	sp|Q13162|PRDX4_HUMANPeroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1	0.36	29	32	30	36	36	30	50	36
sp|Q99519|NEUR1_HUMAN Sialidase-1 OS=Homo sapiens GN=NEU1 PE=1 SV=1	sp|Q99519|NEUR1_HUMANSialidase-1 OS=Homo sapiens GN=NEU1 PE=1 SV=1	0.23	33	30	13	28	28	1	35	34
sp|P62820|RAB1A_HUMAN Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3	sp|P62820|RAB1A_HUMANRas-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3	0.25	28	23	13	23	23	0	30	14
sp|P07711|CATL1_HUMAN Cathepsin L1 OS=Homo sapiens GN=CTSL PE=1 SV=2	sp|P07711|CATL1_HUMANCathepsin L1 OS=Homo sapiens GN=CTSL PE=1 SV=2	0.17	23	35	15	26	26	0	14	23
Dystroglycan OS=Homo sapiens GN=DAG1 PE=1 SV=2	DAG1_HUMAN	0.37	11	24	13	11	11	15	20	20

sp|P30711|GSTT1_HUMAN Glutathione S-transferase theta-1 OS=Homo sapiens GN=GSTT1 PE=1 SV=4	sp|P30711|GSTT1_HUMANGlutathione S-transferase theta-1 OS=Homo sapiens GN=GSTT1 PE=1 SV=4	0.79	49	69	0	0	34	0	16	42
Peptidase inhibitor 15 OS=Homo sapiens GN=PI15 PE=1 SV=1	PI15_HUMAN	0.37	23	19	27	25	25	35	25	26
sp|Q8IYJ3|SYTL1_HUMAN Synaptotagmin-like protein 1 OS=Homo sapiens GN=SYTL1 PE=1...	sp|Q8IYJ3|SYTL1_HUMANSynaptotagmin-like protein 1 OS=Homo sapiens GN=SYTL1 PE=1 SV=1	0.75	37	30	0	0	26	0	37	19
Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1	KINH_HUMAN	0.43	19	18	15	5	5	26	10	29
Low-density lipoprotein receptor-related protein 8 OS=Homo sapiens GN=LRP8 PE=1 SV=4	sp|Q14114|LRP8_HUMAN	0.59	2	2	0	3	3	1	1	0
Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5	LEG3_HUMAN	0.33	43	27	29	36	36	34	25	28
Protein tyrosine phosphatase, receptor type, D, isoform CRA_f OS=Homo sapiens GN=PTPRD PE=2 SV=1	G3XAE2_HUMAN	0.4	1	1	0	0	0	5	0	6
sp|Q8NBJ4|GOLM1_HUMAN Golgi membrane protein 1 OS=Homo sapiens GN=GOLM1 PE=1 SV=1	sp|Q8NBJ4|GOLM1_HUMANGolgi membrane protein 1 OS=Homo sapiens GN=GOLM1 PE=1 SV=1	0.78	5	9	2	9	9	14	18	0
sp|P52565|GDIR1_HUMAN Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA...	sp|P52565|GDIR1_HUMANRho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=1 SV=3	0.18	47	37	0	0	34	38	43	40
Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2	SODC_HUMAN	0.36	21	11	18	25	25	19	25	15
Annexin OS=Homo sapiens GN=ANXA11 PE=2 SV=1	B4DVE7_HUMAN	0.41	21	30	43	21	21	42	24	35
T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	sp|P49368|TCPG_HUMAN	0.39	13	12	14	7	7	19	13	11
Isoform 3 of Inositol monophosphatase 1 OS=Homo sapiens GN=IMPA1	sp|P29218-3|IMPA1_HUMAN	0.62	10	29	10	19	19	42	31	31
Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2	PNPH_HUMAN	0.61	0	0	12	44	44	0	65	0
Anosmin-1 OS=Homo sapiens GN=KAL1 PE=1 SV=3	KALM_HUMAN	0.37	14	11	13	13	13	14	13	17
Cartilage oligomeric matrix protein OS=Homo sapiens GN=COMP PE=1 SV=2	COMP_HUMAN	0.36	0	0	0	0	0	4	0	0

Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2	IDHC_HUMAN	0.76	0	2	1	0	0	1	1	5
sp|Q8NHP8|PLBL2_HUMAN Putative phospholipase B-like 2 OS=Homo sapiens GN=PLBD2 PE=1...	sp|Q8NHP8|PLBL2_HUMANPutative phospholipase B-like 2 OS=Homo sapiens GN=PLBD2 PE=1 SV=2	0.69	19	13	10	0	15	12	22	22
Cathepsin F OS=Homo sapiens GN=CTSF PE=1 SV=1	CATF_HUMAN	0.33	5	14	8	25	25	7	16	6
L-xylulose reductase (Fragment) OS=Homo sapiens GN=DCXR PE=3 SV=1	J3QS36_HUMAN	0.39	1	1	38	46	46	1	55	0
Thrombospondin-4 OS=Homo sapiens GN=THBS4 PE=1 SV=2	TSP4_HUMAN	0.37	11	10	22	13	13	24	10	14
sp|P50502|F10A1_HUMAN Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2	sp|P50502|F10A1_HUMANHsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2	0.38	27	18	10	9	9	29	29	0
Transthyretin OS=Homo sapiens GN=TTR PE=1 SV=1	TTHY_HUMAN	0.37	34	21	29	33	33	37	26	37
Isoform 3 of Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5	sp|Q14008-3|CKAP5_HUMAN	0.28	0	5	2	0	0	1	1	1
Glycogen debranching enzyme OS=Homo sapiens GN=AGL PE=1 SV=3	GDE_HUMAN	0.3	1	6	8	2	2	0	2	0
sp|P27348|1433T_HUMAN 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	sp|P27348|1433T_HUMAN14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	0.33	27	35	19	24	24	39	36	25
Monocyte differentiation antigen CD14 OS=Homo sapiens GN=CD14 PE=1 SV=2	CD14_HUMAN	0.61	17	31	15	22	22	36	34	31
sp|P54802|ANAG_HUMAN Alpha-N-acetylglucosaminidase OS=Homo sapiens GN=NAGLU PE=1...	sp|P54802|ANAG_HUMAN Alpha-N-acetylglucosaminidase OS=Homo sapiens GN=NAGLU PE=1...	0.35	24	42	24	41	41	38	23	41
sp|CATA_HUMAN|	sp|CATA_HUMAN|	0.17	95	13	9	11	11	15	12	10
PRKAR2A protein OS=Homo sapiens GN=PRKAR2A PE=2 SV=1	Q9BUB1_HUMAN	0.37	32	24	36	17	17	27	31	32
sp|P49189|AL9A1_HUMAN 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens...	sp|P49189|AL9A1_HUMAN4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3	0.36	35	43	31	0	44	0	0	43
Isoform 2 of Coatomer subunit alpha OS=Homo sapiens GN=COPA	sp|P53621-2|COPA_HUMAN	0.4	3	0	5	6	6	3	5	2
Deoxyribonuclease-2-alpha OS=Homo sapiens GN=DNASE2 PE=2 SV=1	B7Z4K6_HUMAN	0.4	13	12	19	13	13	17	14	20

Lipid phosphate phosphohydrolase 1 OS=Homo sapiens GN=PPAP2A PE=1 SV=1	sp|O14494|LPP1_HUMAN	0.86	18	20	2	5	5	24	5	29
sp|P61019|RAB2A_HUMAN Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1	sp|P61019|RAB2A_HUMANRas-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1	0.78	42	38	0	2	23	35	37	0
sp|Q02790|FKBP4_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4...	sp|Q02790|FKBP4_HUMANPeptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3	0.49	14	26	15	0	4	21	25	17
sp|P51149|RAB7A_HUMAN Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1	sp|P51149|RAB7A_HUMANRas-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1	0.49	21	32	6	22	22	29	30	34
Ganglioside GM2 activator OS=Homo sapiens GN=GM2A PE=1 SV=4	SAP3_HUMAN	0.3	9	24	2	12	12	15	11	17
Peroxidasin homolog OS=Homo sapiens GN=PXDN PE=1 SV=2	sp|Q92626|PXDN_HUMAN	0.72	8	7	0	4	4	9	2	8
sp|Q13275|SEM3F_HUMAN Semaphorin-3F OS=Homo sapiens GN=SEMA3F PE=2 SV=2	sp|Q13275|SEM3F_HUMANSemaphorin-3F OS=Homo sapiens GN=SEMA3F PE=2 SV=2	0.5	11	26	7	14	14	19	23	19
Annexin OS=Homo sapiens GN=ANXA4 PE=2 SV=1	Q6P452_HUMAN	0.32	26	35	15	28	28	33	32	21
Ferritin heavy chain OS=Homo sapiens GN=FTH1 PE=1 SV=2	FRIH_HUMAN	0.33	27	26	17	12	12	19	23	19
Isoform 2 of Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1	sp|P36871-2|PGM1_HUMAN	0.48	4	14	15	17	17	20	19	10
Isoform 2 of Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1	sp|Q9P2E9-3|RRBP1_HUMAN	0.19	5	12	5	3	3	2	4	5
Metalloreductase STEAP4 OS=Homo sapiens GN=STEAP4 PE=2 SV=1	C9JS50_HUMAN	0.54	18	17	7	15	15	28	10	21
Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3	APOH_HUMAN	0.67	4	20	16	21	21	27	18	36
sp|P54652|HSP72_HUMAN Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2...	sp|P54652|HSP72_HUMANHeat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1	0.03	10	25	0	0	29	38	58	29
Isoform 2 of Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH	GLU2B_HUMAN	0.45	5	10	0	4	4	0	14	15
Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2	sp|P40121|CAPG_HUMAN	0.26	31	30	19	18	18	16	16	16
Paragranulin (Fragment) OS=Homo sapiens GN=GRN PE=4 SV=1	K7EKL3_HUMAN	0.42	8	14	14	14	14	18	16	14

sp|Q9H336|CRLD1_HUMAN Cysteine-rich secretory protein LCCL domain-containing 1 OS=Homo sapiens GN=CRISPLD1 PE=1 SV=1	sp|Q9H336|CRLD1_HUMANCysteine-rich secretory protein LCCL domain-containing 1 OS=Homo sapiens GN=CRISPLD1 PE=1 SV=1	0.18	0	28	0	0	20	39	30	0
Latent-transforming growth factor beta-binding protein 2 OS=Homo sapiens GN=LTBP2 PE=2 SV=1	G3V3X5_HUMAN	0.5	0	1	0	1	1	0	0	4
UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1	sp|O60701|UGDH_HUMAN	0.38	19	21	18	25	25	26	32	13
NAD(P)H-hydrate epimerase OS=Homo sapiens GN=APOA1BP PE=1 SV=2	sp|Q8NCW5|NNRE_HUMAN	0.33	17	23	22	16	16	12	18	17
sp|Q14515|SPRL1_HUMAN SPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2	sp|Q14515|SPRL1_HUMANSPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2	0.4	2	12	6	0	3	9	7	0
sp|P12109|CO6A1_HUMAN Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3	sp|P12109|CO6A1_HUMANCollagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3	0.34	13	0	9	17	17	0	4	14
sp|B9A064|IGLL5_HUMAN Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2	sp|B9A064|IGLL5_HUMANImmunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2	0.45	32	39	2	0	45	45	35	0
Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1	CATZ_HUMAN	0.37	20	16	26	16	16	15	16	33
Alkaline phosphodiesterase I OS=Homo sapiens GN=ENPP3 PE=2 SV=1	F8W6H5_HUMAN	0.52	7	13	1	0	0	9	0	8
sp|Q13449|LSAMP_HUMAN Limbic system-associated membrane protein OS=Homo sapiens GN=LSAMP PE=1 SV=2	sp|Q13449|LSAMP_HUMANLimbic system-associated membrane protein OS=Homo sapiens GN=LSAMP PE=1 SV=2	0.013	0	31	0	0	44	38	27	37
sp|O00299|CLIC1_HUMAN Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4	sp|O00299|CLIC1_HUMANChloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4	0.69	77	58	0	0	51	0	0	38
T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	TCPQ_HUMAN	0.32	39	34	26	12	12	35	25	19
Integrin beta-like protein 1 OS=Homo sapiens GN=ITGBL1 PE=2 SV=1	B4DQ02_HUMAN	0.55	0	2	0	0	0	3	0	1
Ig lambda-3 chain C regions OS=Homo sapiens GN=IGLC3 PE=1 SV=1	LAC3_HUMAN	0.36	20	15	19	21	21	28	25	18

Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3	sp|P28074|PSB5_HUMAN	0.41	17	16	25	23	23	29	43	25
Probable serine carboxypeptidase CPVL OS=Homo sapiens GN=CPVL PE=1 SV=2	CPVL_HUMAN	0.69	13	27	10	30	30	35	13	33
Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=2 SV=1	F5H4R7_HUMAN	0.48	4	5	5	5	5	7	5	10
sp|Q14508|WFDC2_HUMAN WAP four-disulfide core domain protein 2 OS=Homo sapiens GN=WFDC2 PE=1 SV=2	sp|Q14508|WFDC2_HUMANWAP four-disulfide core domain protein 2 OS=Homo sapiens GN=WFDC2 PE=1 SV=2	0.27	22	39	0	0	31	0	83	37
sp|Q9H4B8|DPEP3_HUMAN Dipeptidase 3 OS=Homo sapiens GN=DPEP3 PE=2 SV=2	sp|Q9H4B8|DPEP3_HUMANDipeptidase 3 OS=Homo sapiens GN=DPEP3 PE=2 SV=2	0.55	22	0	8	22	22	32	38	34
sp|P49721|PSB2_HUMAN Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1...	sp|P49721|PSB2_HUMAN Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1...	0.42	13	25	11	15	15	35	28	16
Atrial natriuretic peptide-converting enzyme, 180 kDa soluble fragment OS=Homo sapiens GN=CORIN PE=2 SV=1	J3KR90_HUMAN	0.36	0	0	0	0	0	2	0	0
Dipeptidyl peptidase 3 OS=Homo sapiens GN=DPP3 PE=2 SV=1	G3V1D3_HUMAN	0.27	8	22	6	10	10	11	16	8
Protein-L-isoaspartate O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=2 SV=1	J3KP72_HUMAN	0.59	16	22	6	17	17	34	34	10
Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	H4_HUMAN	0.12	126	38	12	21	21	32	23	20
Isoform Long of Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1	sp|P25786-2|PSA1_HUMAN	0.73	47	30	0	0	0	27	2	27
Protein NAMPTL (Fragment) OS=Homo sapiens GN=NAMPTL PE=2 SV=1	Q5SYT8_HUMAN	0.33	21	12	17	5	5	10	18	12
sp|Q12841|FSTL1_HUMAN Follistatin-related protein 1 OS=Homo sapiens GN=FSTL1 PE=1...	sp|Q12841|FSTL1_HUMANFollistatin-related protein 1 OS=Homo sapiens GN=FSTL1 PE=1 SV=1	0.63	0	51	1	0	31	31	18	0
6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=2 SV=1	F5H7U0_HUMAN	0.37	20	26	20	9	9	26	32	9
Valine--tRNA ligase OS=Homo sapiens GN=VARS PE=1 SV=4	SYVC_HUMAN	0.91	2	5	4	2	2	10	12	10

Ras-related protein Ral-B OS=Homo sapiens GN=RALB PE=2 SV=1	B4E040_HUMAN	0.39	20	30	25	40	40	29	34	43
sp|P01769|HV308_HUMAN Ig heavy chain V-III region GA OS=Homo sapiens PE=1 SV=1	sp|P01769|HV308_HUMANIg heavy chain V-III region GA OS=Homo sapiens PE=1 SV=1-DECOY	0.63	2	1	0	2	2	2	3	0
sp|Q13217|DNJC3_HUMAN DnaJ homolog subfamily C member 3 OS=Homo sapiens GN=DNAJC3...	sp|Q13217|DNJC3_HUMANDnaJ homolog subfamily C member 3 OS=Homo sapiens GN=DNAJC3 PE=1 SV=1	0.88	35	23	6	0	18	0	41	26
Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=2 SV=1	B7Z463_HUMAN	0.52	17	22	0	0	0	42	0	29
sp|P48668|K2C6C_HUMAN Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1...	sp|P48668|K2C6C_HUMANKeratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3	0.37	0	12	7	1	29	1	37	32
Mannose-6-phosphate isomerase OS=Homo sapiens GN=MPI PE=1 SV=2	MPI_HUMAN	0.12	12	21	6	12	12	0	12	9
sp|P80723|BASP1_HUMAN Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2	sp|P80723|BASP1_HUMANBrain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2	0.81	50	24	0	0	27	30	28	0
Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=2 SV=1	B4DWL3_HUMAN	0.4	0	1	23	14	14	0	22	0
6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2	sp|Q01813|K6PP_HUMAN	0.89	1	18	5	2	2	14	23	14
sp|O14818|PSA7_HUMAN Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1...	sp|O14818|PSA7_HUMAN Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1...	0.4	13	27	22	27	27	32	31	24
Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=2 SV=1	C9JV77_HUMAN	0.46	10	19	21	19	19	20	17	32
Isoform 1 of Vinculin OS=Homo sapiens GN=VCL	sp|P18206-2|VINC_HUMAN (+1)	0.32	16	7	17	3	3	11	3	8
Bile salt-activated lipase OS=Homo sapiens GN=CEL PE=1 SV=3	CEL_HUMAN	0.82	6	24	6	9	9	23	41	0
Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4	sp|P04217|A1BG_HUMAN	0.45	13	30	20	9	9	28	25	23
Isoform CNPI of 2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens GN=CNP	sp|P09543-2|CN37_HUMAN	0.39	0	0	23	25	25	0	22	0
Isoform 2 of Neural cell adhesion molecule L1-like protein OS=Homo sapiens GN=CHL1	sp|O00533-2|CHL1_HUMAN	0.55	0	4	0	11	11	8	3	4

Isoform 2 of Melanophilin OS=Homo sapiens GN=MLPH	sp|Q9BV36-2|MELPH_HUMAN	0.28	30	13	12	17	17	16	17	18
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=2 SV=1	B7Z6Z4_HUMAN	0.27	31	23	14	15	15	16	11	13
Thymosin beta-4 OS=Homo sapiens GN=TMSB4X PE=1 SV=2	TYB4_HUMAN	0.36	230	0	0	0	0	0	0	0
Secretogranin-1 OS=Homo sapiens GN=CHGB PE=1 SV=2	SCG1_HUMAN	0.36	13	17	7	14	14	12	13	22
sp|Q9NZ08|ERAP1_HUMAN Endoplasmic reticulum aminopeptidase 1 OS=Homo sapiens GN=ERAP1 PE=1 SV=3	sp|Q9NZ08|ERAP1_HUMANEndoplasmic reticulum aminopeptidase 1 OS=Homo sapiens GN=ERAP1 PE=1 SV=3	0.76	12	13	5	0	17	0	20	12
sp|P14550|AK1A1_HUMAN Alcohol dehydrogenase [NADP(+)] OS=Homo sapiens GN=AKR1A1 PE=1...	sp|P14550|AK1A1_HUMANAlcohol dehydrogenase [NADP(+)] OS=Homo sapiens GN=AKR1A1 PE=1 SV=3	0.13	42	0	0	0	27	32	34	54
Nidogen-1 OS=Homo sapiens GN=NID1 PE=1 SV=3	sp|P14543|NID1_HUMAN	0.068	2	6	0	7	7	6	12	14
Zinc finger MYM-type protein 4 (Fragment) OS=Homo sapiens GN=ZMYM4 PE=4 SV=1	H7C1I7_HUMAN	0.94	0	0	0	5	5	0	0	0
sp|P07737|PROF1_HUMAN Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	sp|P07737|PROF1_HUMANProfilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	0.86	69	38	0	0	19	30	20	23
Isoform 8 of Fibronectin OS=Homo sapiens GN=FN1	sp|P02751-8|FINC_HUMAN	0.31	25	29	11	36	36	23	23	25
sp|Q15907|RB11B_HUMAN Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1...	sp|Q15907|RB11B_HUMANRas-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4	0.13	44	28	0	0	35	46	34	35
Isoform 17 of CD44 antigen OS=Homo sapiens GN=CD44	sp|P16070-17|CD44_HUMAN	0.87	5	10	1	3	3	5	9	8
Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	FIBB_HUMAN	0.34	8	7	16	4	4	6	2	10
G-protein-coupled receptor family C group 5 member C (Fragment) OS=Homo sapiens GN=GPRC5C PE=4 SV=2	A8MXZ4_HUMAN	0.83	15	15	4	15	15	26	13	25
sp|Q13200|PSMD2_HUMAN 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	sp|Q13200|PSMD2_HUMAN26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	0.52	16	0	19	0	7	18	19	21
Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=2 SV=1	F5H6E2_HUMAN (+1)	0.24	8	13	5	8	8	6	4	12
Isoform 1 of Unconventional myosin-VI OS=Homo sapiens GN=MYO6	sp|Q9UM54-1|MYO6_HUMAN	0.51	2	2	4	6	6	6	4	6

sp|P00352|AL1A1_HUMAN Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2	sp|P00352|AL1A1_HUMANRetinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2	0.24	16	40	18	7	7	0	19	26
Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	SYEP_HUMAN	0.79	6	2	0	0	0	4	0	2
Spermine synthase OS=Homo sapiens GN=SMS PE=1 SV=2	sp|P52788|SPSY_HUMAN	0.35	15	31	16	23	23	28	16	25
Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=2 SV=1	K7ELJ7_HUMAN	0.19	25	11	2	10	10	11	17	8
Isoform 2 of 14-3-3 protein sigma OS=Homo sapiens GN=SFN	1433S_HUMAN	0.21	19	33	0	0	33	52	30	30
Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6	sp|P02788|TRFL_HUMAN	0.42	3	19	25	22	22	37	26	16
sp|O14497|ARI1A_HUMAN AT-rich interactive domain-containing protein 1A OS=Homo sapiens GN=ARID1A PE=1 SV=3	sp|O14497|ARI1A_HUMANAT-rich interactive domain-containing protein 1A OS=Homo sapiens GN=ARID1A PE=1 SV=3	0.36	2	0	0	0	0	0	0	0
Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3	NSF_HUMAN	0.3	13	14	8	6	6	12	11	8
Histone H2A type 1 OS=Homo sapiens GN=HIST1H2AG PE=1 SV=2	H2A1_HUMAN	0.23	107	9	2	11	11	11	6	7
Brevican core protein OS=Homo sapiens GN=BCAN PE=1 SV=2	sp|Q96GW7|PGCB_HUMAN	0.43	9	28	1	13	13	15	17	33
Glypican-1 OS=Homo sapiens GN=GPC1 PE=1 SV=2	GPC1_HUMAN	0.91	12	6	5	10	10	38	13	9
Beta-glucuronidase OS=Homo sapiens GN=GUSB PE=1 SV=2	sp|P08236|BGLR_HUMAN	0.45	10	26	11	15	15	21	20	25
sp|Q14914|PTGR1_HUMAN Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2	sp|Q14914|PTGR1_HUMANProstaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2	0.37	10	47	16	0	16	22	13	17
5'-nucleotidase OS=Homo sapiens GN=NT5E PE=1 SV=1	sp|P21589|5NTD_HUMAN	0.96	6	5	3	15	15	11	7	11
sp|Q96BH3|ESPB1_HUMAN Epididymal sperm-binding protein 1 OS=Homo sapiens GN=ELSPBP1 PE=1 SV=2	sp|Q96BH3|ESPB1_HUMANEpididymal sperm-binding protein 1 OS=Homo sapiens GN=ELSPBP1 PE=1 SV=2	0.18	7	23	2	3	20	16	38	22
sp|P06702|S10A9_HUMAN Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	sp|P06702|S10A9_HUMANProtein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	0.49	23	29	2	0	28	23	13	17
sp|O75969|AKAP3_HUMAN A-kinase anchor protein 3 OS=Homo sapiens GN=AKAP3 PE=1 SV=2	sp|O75969|AKAP3_HUMANA-kinase anchor protein 3 OS=Homo sapiens GN=AKAP3 PE=1 SV=2	0.13	0	11	0	7	7	6	25	16

sp|P42785-2|PCP_HUMAN Isoform 2 of Lysosomal Pro-X carboxypeptidase OS=Homo sapiens...	sp|P42785-2|PCP_HUMANIsoform 2 of Lysosomal Pro-X carboxypeptidase OS=Homo sapiens GN=PRCP	0.53	11	29	18	0	19	0	30	27
Galactoside 3(4)-L-fucosyltransferase OS=Homo sapiens GN=FUT3 PE=2 SV=1	FUT3_HUMAN	0.37	17	24	9	21	21	20	25	22
Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5	PYGB_HUMAN	0.43	0	0	18	16	16	0	25	0
Glutathione synthetase OS=Homo sapiens GN=GSS PE=1 SV=1	sp|P48637|GSHB_HUMAN	0.37	8	23	21	13	13	18	13	19
sp|P31948|STIP1_HUMAN Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1	sp|P31948|STIP1_HUMANStress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1	0.42	17	13	0	0	13	0	24	15
Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1	HPT_HUMAN	0.3	33	27	33	22	22	4	29	23
Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA	sp|P00338-3|LDHA_HUMAN	0.51	0	0	20	40	40	0	49	0
sp|Q15435|PP1R7_HUMAN Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens...	sp|Q15435|PP1R7_HUMANProtein phosphatase 1 regulatory subunit 7 OS=Homo sapiens GN=PPP1R7 PE=1 SV=1	0.37	13	22	13	0	9	0	22	13
Isoform 2 of Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C	RAB5C_HUMAN	0.42	17	25	0	19	19	25	16	24
Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	EF1G_HUMAN	0.63	1	17	13	3	3	26	30	19
sp|P01617|KV204_HUMAN Ig kappa chain V-II region TEW OS=Homo sapiens PE=1 SV=1	sp|P01617|KV204_HUMANIg kappa chain V-II region TEW OS=Homo sapiens PE=1 SV=1	0.22	4	3	0	0	1	6	4	4
T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=2 SV=1	F8VQ14_HUMAN	0.98	32	21	0	0	0	29	0	22
Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1	RHOA_HUMAN	0.31	25	20	7	12	12	16	16	22
T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=2 SV=1	B4DPJ8_HUMAN	0.3	11	20	11	5	5	10	12	10
ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2	ARF3_HUMAN	0.38	25	11	24	17	17	33	25	18
Lipase member I OS=Homo sapiens GN=LIPI PE=1 SV=2	sp|Q6XZB0|LIPI_HUMAN	0.44	7	9	1	3	3	15	6	10
Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2	AMPB_HUMAN	0.35	17	26	18	11	11	21	19	20

sp|O60568|PLOD3_HUMAN Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1	sp|O60568|PLOD3_HUMANProcollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1	0.51	19	30	5	0	29	0	22	0
Isoform 3 of Interleukin-6 receptor subunit beta OS=Homo sapiens GN=IL6ST	sp|P40189-3|IL6RB_HUMAN	0.44	0	0	10	5	5	0	13	0
Isoform 2 of Niban-like protein 1 OS=Homo sapiens GN=FAM129B	NIBL1_HUMAN	0.83	3	5	1	4	4	3	7	5
sp|P20336|RAB3A_HUMAN Ras-related protein Rab-3A OS=Homo sapiens GN=RAB3A PE=1 SV=1	sp|P20336|RAB3A_HUMANRas-related protein Rab-3A OS=Homo sapiens GN=RAB3A PE=1 SV=1	0.38	22	21	18	24	24	24	22	28
sp|P11717|MPRI_HUMAN Cation-independent mannose-6-phosphate receptor OS=Homo sapiens...	sp|P11717|MPRI_HUMAN Cation-independent mannose-6-phosphate receptor OS=Homo sapiens...	0.4	16	15	17	34	34	27	13	38
sp|P34932|HSP74_HUMAN Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4	sp|P34932|HSP74_HUMANHeat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4	0.22	11	26	14	9	9	0	17	0
sp|P17987|TCPA_HUMAN T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1...	sp|P17987|TCPA_HUMAN T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1...	0.26	37	30	21	22	22	37	23	15
4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=2 SV=1	J3KPF3_HUMAN	0.97	9	14	0	0	0	12	0	11
Isoform PTPS-MEA of Receptor-type tyrosine-protein phosphatase S OS=Homo sapiens GN=PTPRS	sp|Q13332-2|PTPRS_HUMAN	0.4	11	22	13	15	15	21	28	17
sp|Q9UNW1|MINP1_HUMAN Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens...	sp|Q9UNW1|MINP1_HUMANMultiple inositol polyphosphate phosphatase 1 OS=Homo sapiens GN=MINPP1 PE=1 SV=1	0.74	11	13	13	0	30	20	18	0
6-phosphogluconolactonase OS=Homo sapiens GN=PGLS PE=1 SV=2	6PGL_HUMAN	0.34	26	19	26	19	19	22	15	21
Alanine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2	SYAC_HUMAN	0.35	3	20	14	1	1	10	3	13
sp|Q9NQX4|MYO5C_HUMAN Unconventional myosin-Vc OS=Homo sapiens GN=MYO5C PE=1 SV=2	sp|Q9NQX4|MYO5C_HUMANUnconventional myosin-Vc OS=Homo sapiens GN=MYO5C PE=1 SV=2	0.62	0	0	2	1	1	0	1	6
sp|P52907|CAZA1_HUMAN F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	sp|P52907|CAZA1_HUMANF-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	0.67	56	28	0	0	28	0	25	0

Isoform 4 of Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H	sp|P09960-4|LKHA4_HUMAN	0.44	12	15	16	13	13	21	19	15
Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3	sp|P22234|PUR6_HUMAN	0.35	22	10	9	7	7	14	18	12
sp|O94760|DDAH1_HUMAN N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Homo...	sp|O94760|DDAH1_HUMANN(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Homo sapiens GN=DDAH1 PE=1 SV=3	0.98	29	50	3	0	22	21	26	28
sp|P08779|K1C16_HUMAN Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1...	sp|P08779|K1C16_HUMANKeratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	0.37	9	6	9	0	21	0	54	47
sp|Q9BUD6|SPON2_HUMAN Spondin-2 OS=Homo sapiens GN=SPON2 PE=1 SV=3	sp|Q9BUD6|SPON2_HUMANSpondin-2 OS=Homo sapiens GN=SPON2 PE=1 SV=3	0.91	15	20	0	24	24	0	21	22
Otogelin OS=Homo sapiens GN=OTOG PE=1 SV=3	sp|Q6ZRI0|OTOG_HUMAN	0.94	0	0	0	3	3	0	0	0
sp|Q9GZX9|TWSG1_HUMAN Twisted gastrulation protein homolog 1 OS=Homo sapiens GN=TWSG1 PE=2 SV=1	sp|Q9GZX9|TWSG1_HUMANTwisted gastrulation protein homolog 1 OS=Homo sapiens GN=TWSG1 PE=2 SV=1	0.43	12	8	0	0	11	9	0	13
Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2	PSB3_HUMAN	0.39	0	0	25	16	16	1	36	0
Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4	PLST_HUMAN	0.58	10	9	9	6	6	16	11	8
sp|P45877|PPIC_HUMAN Peptidyl-prolyl cis-trans isomerase C OS=Homo sapiens GN=PPIC...	sp|P45877|PPIC_HUMAN Peptidyl-prolyl cis-trans isomerase C OS=Homo sapiens GN=PPIC...	0.35	14	19	9	12	12	15	13	15
Sphingomyelin phosphodiesterase OS=Homo sapiens GN=SMPD1 PE=1 SV=4	ASM_HUMAN	0.47	0	0	12	15	15	0	21	0
Aspartate aminotransferase OS=Homo sapiens GN=GOT1 PE=2 SV=1	B7Z7E9_HUMAN	0.34	11	24	16	12	12	12	21	16
Isoform 2 of Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR	sp|P00390-3|GSHR_HUMAN	0.42	1	1	26	21	21	0	28	0
Isoform 2 of Probable phospholipid-transporting ATPase IIB OS=Homo sapiens GN=ATP9B	ATP9B_HUMAN	0.52	2	3	4	0	1	9	1	3
sp|O43278|SPIT1_HUMAN Kunitz-type protease inhibitor 1 OS=Homo sapiens GN=SPINT1...	sp|O43278|SPIT1_HUMANKunitz-type protease inhibitor 1 OS=Homo sapiens GN=SPINT1 PE=1 SV=2	0.16	9	16	0	0	17	23	23	1

sp|Q99466|NOTC4_HUMAN Neurogenic locus notch homolog protein 4 OS=Homo sapiens GN=NOTCH4 PE=1 SV=2	sp|Q99466|NOTC4_HUMANNeurogenic locus notch homolog protein 4 OS=Homo sapiens GN=NOTCH4 PE=1 SV=2-DECOY	0.75	1	0	0	1	1	0	2	0
Isoform 3 of Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B	sp|P61224-3|RAP1B_HUMAN	0.33	34	20	19	18	18	21	27	19
Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	TLN1_HUMAN	0.28	11	2	10	0	0	2	2	0
Isoform 2 of Syntaxin-binding protein 2 OS=Homo sapiens GN=STXBP2	STXB2_HUMAN	0.25	4	9	4	9	9	0	8	6
Protein unc-13 homolog B OS=Homo sapiens GN=UNC13B PE=2 SV=1	B1AM27_HUMAN	0.84	3	3	0	0	0	4	0	3
UMP-CMP kinase OS=Homo sapiens GN=CMPK1 PE=1 SV=3	KCY_HUMAN	0.73	23	25	0	8	8	21	21	16
Suppressor of tumorigenicity 14 protein OS=Homo sapiens GN=ST14 PE=1 SV=2	ST14_HUMAN	0.85	2	2	0	6	6	2	0	1
Hexokinase-1 OS=Homo sapiens GN=HK1 PE=2 SV=1	E7ENR4_HUMAN	0.88	4	10	1	10	10	8	10	6
Isoform 2 of Plectin OS=Homo sapiens GN=PLEC	sp|Q15149-2|PLEC_HUMAN	0.26	5	0	1	0	0	0	0	2
Isoform 4 of Protein MON2 homolog OS=Homo sapiens GN=MON2	sp|Q7Z3U7-4|MON2_HUMAN	0.71	1	1	2	0	0	3	3	5
sp|Q9P2K2|TXD16_HUMAN Thioredoxin domain-containing protein 16 OS=Homo sapiens GN=TXNDC16 PE=2 SV=4	sp|Q9P2K2|TXD16_HUMANThioredoxin domain-containing protein 16 OS=Homo sapiens GN=TXNDC16 PE=2 SV=4	0.54	4	13	0	0	2	0	11	15
sp|Q99832|TCPH_HUMAN T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1...	sp|Q99832|TCPH_HUMAN T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1...	0.28	45	20	14	6	6	23	23	20
Isoform 3 of DCC-interacting protein 13-beta OS=Homo sapiens GN=APPL2	sp|Q8NEU8-3|DP13B_HUMAN	0.36	0	0	7	1	1	0	1	0
sp|Q8TDW7|FAT3_HUMAN Protocadherin Fat 3 OS=Homo sapiens GN=FAT3 PE=2 SV=2	sp|Q8TDW7|FAT3_HUMAN Protocadherin Fat 3 OS=Homo sapiens GN=FAT3 PE=2 SV=2-DECOY	0.36	0	0	2	0	0	0	0	0
sp|P34096|RNAS4_HUMAN Ribonuclease 4 OS=Homo sapiens GN=RNASE4 PE=1 SV=3	sp|P34096|RNAS4_HUMANRibonuclease 4 OS=Homo sapiens GN=RNASE4 PE=1 SV=3	0.86	31	9	0	15	15	14	17	17
Zinc finger protein 469 OS=Homo sapiens GN=ZNF469 PE=2 SV=1	H3BS19_HUMAN	0.36	0	4	0	0	0	0	0	0
Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2	PLMN_HUMAN	0.44	8	13	6	4	4	16	11	7
Arylsulfatase A OS=Homo sapiens GN=ARSA PE=1 SV=3	sp|P15289|ARSA_HUMAN	0.36	21	20	18	28	28	24	24	20

Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4	ACPH_HUMAN	0.77	10	18	0	0	0	10	0	11
Plasma serine protease inhibitor OS=Homo sapiens GN=SERPINA5 PE=1 SV=3	IPSP_HUMAN	0.88	0	2	1	2	2	0	2	0
sp|P29966|MARCS_HUMAN Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4	sp|P29966|MARCS_HUMANMyristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4	0.68	24	10	5	0	14	15	18	0
EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1	EHD4_HUMAN	0.43	6	12	5	6	6	10	10	9
Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4	PSB4_HUMAN	0.73	16	30	0	0	0	31	0	30
Phosphoglucomutase-2 OS=Homo sapiens GN=PGM2 PE=1 SV=4	PGM2_HUMAN	0.36	7	16	6	21	21	9	12	12
Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2	sp|P46013|KI67_HUMAN	0.36	8	0	0	0	0	0	0	0
Translin OS=Homo sapiens GN=TSN PE=2 SV=1	E9PGT1_HUMAN	0.55	7	17	10	11	11	20	37	21
Isoform 2 of Ester hydrolase C11orf54 OS=Homo sapiens GN=C11orf54	sp|Q9H0W9-2|CK054_HUMAN	0.25	15	17	13	15	15	8	9	12
sp|P18136|KV313_HUMAN Ig kappa chain V-III region HIC OS=Homo sapiens PE=2 SV=2	sp|P18136|KV313_HUMANIg kappa chain V-III region HIC OS=Homo sapiens PE=2 SV=2	0.34	13	14	14	15	15	0	13	25
sp|P47895|AL1A3_HUMAN Aldehyde dehydrogenase family 1 member A3 OS=Homo sapiens GN=ALDH1A3 PE=1 SV=2	sp|P47895|AL1A3_HUMANAldehyde dehydrogenase family 1 member A3 OS=Homo sapiens GN=ALDH1A3 PE=1 SV=2	0.75	29	22	0	0	19	1	27	15
sp|O75503|CLN5_HUMAN Ceroid-lipofuscinosis neuronal protein 5 OS=Homo sapiens GN=CLN5...	sp|O75503|CLN5_HUMAN Ceroid-lipofuscinosis neuronal protein 5 OS=Homo sapiens GN=CLN5...	0.37	12	17	19	18	18	19	19	14
Isoform 2 of Sodium-dependent phosphate transport protein 2B OS=Homo sapiens GN=SLC34A2	NPT2B_HUMAN	0.36	0	0	0	0	0	0	0	2
sp|P05109|S10A8_HUMAN Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	sp|P05109|S10A8_HUMANProtein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	0.43	15	19	0	9	9	10	4	6
sp|P04406|G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH...	sp|P04406|G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH...	0.32	20	28	28	18	18	28	26	15

sp|P09972|ALDOC_HUMAN Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1...	sp|P09972|ALDOC_HUMANFructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2	0.86	21	27	1	0	13	0	20	13
sp|P12110|CO6A2_HUMAN Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4	sp|P12110|CO6A2_HUMANCollagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4	0.29	9	12	7	22	22	0	10	14
Alpha-soluble NSF attachment protein OS=Homo sapiens GN=NAPA PE=1 SV=3	SNAA_HUMAN	0.4	0	0	16	11	11	0	19	0
Isoform 2 of Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM	HNRPM_HUMAN	0.36	65	0	0	0	0	0	0	0
Isoform 5 of Seizure 6-like protein 2 OS=Homo sapiens GN=SEZ6L2	sp|Q6UXD5-5|SE6L2_HUMAN	0.27	6	13	6	6	6	4	7	6
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	APOE_HUMAN	0.29	10	25	15	15	15	13	9	14
Isoform C of Protein CutA OS=Homo sapiens GN=CUTA	sp|O60888-3|CUTA_HUMAN	0.35	17	10	8	8	8	10	20	8
Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4	sp|P06737|PYGL_HUMAN	0.18	18	18	11	4	4	4	2	12
sp|P60953|CDC42_HUMAN Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2	sp|P60953|CDC42_HUMANCell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2	0.25	21	20	0	0	20	23	15	15
T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=2 SV=1	E9PCA1_HUMAN	0.47	0	0	14	7	7	0	15	0
Isoform 4 of E3 ubiquitin-protein ligase UBR2 OS=Homo sapiens GN=UBR2	sp|Q8IWV8-4|UBR2_HUMAN	0.33	0	2	2	0	0	0	0	0
60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=2 SV=1	A8MUD9_HUMAN	0.39	12	9	11	4	4	20	5	14
Alpha-L-iduronidase OS=Homo sapiens GN=IDUA PE=1 SV=2	IDUA_HUMAN	0.5	3	7	11	16	16	9	15	15
sp|Q14697|GANAB_HUMAN Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3	sp|Q14697|GANAB_HUMANNeutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3	0.36	15	12	2	0	17	0	22	24
Glypican-4 OS=Homo sapiens GN=GPC4 PE=1 SV=4	GPC4_HUMAN	0.61	5	7	0	1	1	9	6	2
Isoform 2 of UPF0577 protein KIAA1324 OS=Homo sapiens GN=KIAA1324	sp|Q6UXG2-2|K1324_HUMAN	0.36	0	0	0	0	0	5	0	0

Selenoprotein P (Fragment) OS=Homo sapiens GN=SEPP1 PE=4 SV=1	D6REX5_HUMAN	0.33	19	16	12	16	16	20	14	16
Xaa-Pro aminopeptidase 1 OS=Homo sapiens GN=XPNPEP1 PE=1 SV=3	sp|Q9NQW7|XPP1_HUMAN	0.33	8	6	7	1	1	11	1	2
Calcyphosin OS=Homo sapiens GN=CAPS PE=4 SV=1	K7EL21_HUMAN	0.33	16	12	16	16	16	12	11	9
Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=2 SV=1	G3V5Z7_HUMAN	0.62	17	23	2	0	0	23	0	30
sp|Q9UQ35|SRRM2_HUMAN Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2	sp|Q9UQ35|SRRM2_HUMANSerine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2	0.36	29	0	0	0	0	0	0	0
Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4	MIF_HUMAN	0.27	29	32	15	13	13	16	16	12
Isoform 2 of Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=TARS	sp|P26639-2|SYTC_HUMAN	0.39	0	0	0	1	1	0	3	0
sp|Q9HC38|GLOD4_HUMAN Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4...	sp|Q9HC38|GLOD4_HUMANGlyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1	0.66	21	30	0	0	23	28	14	0
sp|Q9BR76|COR1B_HUMAN Coronin-1B OS=Homo sapiens GN=CORO1B PE=1 SV=1	sp|Q9BR76|COR1B_HUMANCoronin-1B OS=Homo sapiens GN=CORO1B PE=1 SV=1	0.27	11	14	13	10	10	8	10	6
Insulin-like growth factor-binding protein 4 OS=Homo sapiens GN=IGFBP4 PE=1 SV=2	IBP4_HUMAN	0.29	17	22	15	9	9	2	13	9
Cullin-3 OS=Homo sapiens GN=CUL3 PE=1 SV=2	sp|Q13618|CUL3_HUMAN	0.72	1	1	4	0	0	6	11	4
Isoform 2 of Signal peptide, CUB and EGF-like domain-containing protein 2 OS=Homo sapiens GN=SCUBE2	sp|Q9NQ36-2|SCUB2_HUMAN	0.59	0	2	0	0	0	0	0	5
sp|Q5JWF2|GNAS1_HUMAN Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens GN=GNAS PE=1 SV=2	sp|Q5JWF2|GNAS1_HUMANGuanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens GN=GNAS PE=1 SV=2	0.67	0	11	3	0	13	7	11	11
Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2	HPRT_HUMAN	0.42	13	21	10	15	15	25	21	22

sp|Q09666|AHNK_HUMAN Neuroblast differentiation-associated protein AHNAK OS=Homo...	sp|Q09666|AHNK_HUMAN Neuroblast differentiation-associated protein AHNAK OS=Homo...	0.37	100	7	0	1	1	6	2	5
Isoform 3 of Probable phospholipid-transporting ATPase IA OS=Homo sapiens GN=ATP8A1	sp|Q9Y2Q0-3|AT8A1_HUMAN	0.36	0	0	9	5	5	0	3	0
sp|P13667|PDIA4_HUMAN Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2	sp|P13667|PDIA4_HUMANProtein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2	0.69	7	12	0	0	9	0	0	15
Serpin B5 OS=Homo sapiens GN=SERPINB5 PE=1 SV=2	sp|P36952|SPB5_HUMAN	0.45	0	2	5	4	4	6	2	3
sp|Q86X29-4|LSR_HUMAN Isoform 4 of Lipolysis-stimulated lipoprotein receptor OS=Homo...	sp|Q86X29-4|LSR_HUMANIsoform 4 of Lipolysis-stimulated lipoprotein receptor OS=Homo sapiens GN=LSR	0.65	2	12	3	0	11	8	11	13
Isoform 2 of UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2	sp|Q16851-2|UGPA_HUMAN	0.44	0	0	15	16	16	0	18	0
Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2	RINI_HUMAN	0.39	10	13	12	8	8	8	18	15
N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase OS=Homo sapiens GN=AGA PE=1 SV=2	ASPG_HUMAN	0.39	1	0	8	0	0	1	7	1
Isoform 3 of SEC14-like protein 2 OS=Homo sapiens GN=SEC14L2	sp|O76054-5|S14L2_HUMAN	0.42	5	11	4	8	8	8	9	11
sp|Q92484|ASM3A_HUMAN Acid sphingomyelinase-like phosphodiesterase 3a OS=Homo sapiens GN=SMPDL3A PE=1 SV=2	sp|Q92484|ASM3A_HUMANAcid sphingomyelinase-like phosphodiesterase 3a OS=Homo sapiens GN=SMPDL3A PE=1 SV=2	0.37	9	11	1	0	12	18	11	0
Glutathione peroxidase 3 OS=Homo sapiens GN=GPX3 PE=1 SV=2	GPX3_HUMAN	0.29	18	11	6	11	11	10	7	13
Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=2 SV=1	B4DY72_HUMAN	0.33	4	2	6	0	0	1	2	3
Reticulocalbin-1 OS=Homo sapiens GN=RCN1 PE=1 SV=1	RCN1_HUMAN	0.59	4	10	8	3	3	10	12	19
sp|Q96BQ1|FAM3D_HUMAN Protein FAM3D OS=Homo sapiens GN=FAM3D PE=1 SV=1	sp|Q96BQ1|FAM3D_HUMANProtein FAM3D OS=Homo sapiens GN=FAM3D PE=1 SV=1	0.42	20	32	0	20	20	16	9	0
Protein lifeguard 3 OS=Homo sapiens GN=TMBIM1 PE=1 SV=2	LFG3_HUMAN	0.44	15	12	13	12	12	23	17	16
sp|Q96C24|SYTL4_HUMAN Synaptotagmin-like protein 4 OS=Homo sapiens GN=SYTL4 PE=1...	sp|Q96C24|SYTL4_HUMANSynaptotagmin-like protein 4 OS=Homo sapiens GN=SYTL4 PE=1 SV=2	0.82	19	0	3	0	12	0	5	18

Isoform 3 of Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L	sp|Q8WWM7-3|ATX2L_HUMAN	0.36	17	0	0	0	0	0	0	0
sp|O75326|SEM7A_HUMAN Semaphorin-7A OS=Homo sapiens GN=SEMA7A PE=1 SV=1	sp|O75326|SEM7A_HUMANSemaphorin-7A OS=Homo sapiens GN=SEMA7A PE=1 SV=1	0.25	5	7	5	4	4	4	5	3
sp|Q12913|PTPRJ_HUMAN Receptor-type tyrosine-protein phosphatase eta OS=Homo sapiens...	sp|Q12913|PTPRJ_HUMANReceptor-type tyrosine-protein phosphatase eta OS=Homo sapiens GN=PTPRJ PE=1 SV=3	0.31	5	0	0	0	3	0	3	9
Isoform 3 of G-protein coupled receptor 56 OS=Homo sapiens GN=GPR56	sp|Q9Y653-3|GPR56_HUMAN	0.97	4	15	0	0	0	7	0	12
sp|Q9BY14|TX101_HUMAN Testis-expressed sequence 101 protein OS=Homo sapiens GN=TEX101...	sp|Q9BY14|TX101_HUMANTestis-expressed sequence 101 protein OS=Homo sapiens GN=TEX101 PE=2 SV=2	0.34	8	34	0	0	23	30	27	0
sp|O60664|PLIN3_HUMAN Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3	sp|O60664|PLIN3_HUMANPerilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3	0.25	27	9	4	2	2	5	11	12
sp|Q9H3Z4|DNJC5_HUMAN DnaJ homolog subfamily C member 5 OS=Homo sapiens GN=DNAJC5...	sp|Q9H3Z4|DNJC5_HUMANDnaJ homolog subfamily C member 5 OS=Homo sapiens GN=DNAJC5 PE=1 SV=1	0.37	11	18	1	2	22	19	18	0
sp|Q7L266|ASGL1_HUMAN Isoaspartyl peptidase/L-asparaginase OS=Homo sapiens GN=ASRGL1 PE=1 SV=2	sp|Q7L266|ASGL1_HUMANIsoaspartyl peptidase/L-asparaginase OS=Homo sapiens GN=ASRGL1 PE=1 SV=2	0.13	13	18	0	0	7	36	25	16
Isoform 2 of Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1	sp|Q01082-3|SPTB2_HUMAN	0.36	0	0	3	0	0	0	0	0
Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2	sp|P25788|PSA3_HUMAN	0.97	35	26	0	0	0	27	0	36
Cathepsin S OS=Homo sapiens GN=CTSS PE=1 SV=3	sp|P25774|CATS_HUMAN	0.35	2	6	7	2	2	5	4	2
sp|Q86SF2|GALT7_HUMAN N-acetylgalactosaminyltransferase 7 OS=Homo sapiens GN=GALNT7 PE=1 SV=1	sp|Q86SF2|GALT7_HUMANN-acetylgalactosaminyltransferase 7 OS=Homo sapiens GN=GALNT7 PE=1 SV=1	0.16	5	11	0	0	17	9	5	8
Myomegalin OS=Homo sapiens GN=PDE4DIP PE=2 SV=1	F8WAP3_HUMAN	0.64	0	4	0	0	0	8	0	0
sp|P35609|ACTN2_HUMAN Alpha-actinin-2 OS=Homo sapiens GN=ACTN2 PE=1 SV=1	sp|P35609|ACTN2_HUMANAlpha-actinin-2 OS=Homo sapiens GN=ACTN2 PE=1 SV=1	0.13	0	0	0	0	0	0	6	0
DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	DDB1_HUMAN	0.41	2	3	8	2	2	5	3	6

Isoform 2 of Tryptophan--tRNA ligase, cytoplasmic OS=Homo sapiens GN=WARS	sp|P23381-2|SYWC_HUMAN	0.42	0	0	10	11	11	0	9	0
Cytoplasmic FMR1-interacting protein 2 OS=Homo sapiens GN=CYFIP2 PE=2 SV=1	F5H583_HUMAN	0.53	0	0	2	1	1	0	5	0
Isoform 7 of Protein PRRC2C OS=Homo sapiens GN=PRRC2C	sp|Q9Y520|PRC2C_HUMANProtein PRRC2C OS=Homo sapiens GN=PRRC2C PE=1 SV=4	0.39	18	0	0	1	1	0	0	2
sp|Q9UK41|VPS28_HUMAN Vacuolar protein sorting-associated protein 28 homolog OS=Homo sapiens GN=VPS28 PE=1 SV=1	sp|Q9UK41|VPS28_HUMANVacuolar protein sorting-associated protein 28 homolog OS=Homo sapiens GN=VPS28 PE=1 SV=1	0.66	18	16	0	1	28	0	21	0
Isoform 2 of Cysteine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=CARS	sp|P49589-2|SYCC_HUMAN	0.2	1	10	3	1	1	2	1	1
Afamin OS=Homo sapiens GN=AFM PE=1 SV=1	AFAM_HUMAN	0.24	16	10	5	6	6	5	7	15
Isoform B of AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1	sp|Q10567-2|AP1B1_HUMAN	0.79	8	10	0	0	0	11	0	5
sp|P01768|HV307_HUMAN Ig heavy chain V-III region CAM OS=Homo sapiens PE=1 SV=1	sp|P01768|HV307_HUMANIg heavy chain V-III region CAM OS=Homo sapiens PE=1 SV=1	0.47	2	1	4	1	1	4	5	0
sp|Q99816|TS101_HUMAN Tumor susceptibility gene 101 protein OS=Homo sapiens GN=TSG101...	sp|Q99816|TS101_HUMANTumor susceptibility gene 101 protein OS=Homo sapiens GN=TSG101 PE=1 SV=2	0.79	10	15	8	0	27	19	11	21
Isoform 5 of Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3	sp|P06753-5|TPM3_HUMAN	0.04	15	16	2	3	3	5	7	2
sp|P21399|ACOC_HUMAN Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1...	sp|P21399|ACOC_HUMAN Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1...	0.37	14	19	12	10	10	21	12	18
sp|Q9BTY2|FUCO2_HUMAN Plasma alpha-L-fucosidase OS=Homo sapiens GN=FUCA2 PE=1 SV=2	sp|Q9BTY2|FUCO2_HUMANPlasma alpha-L-fucosidase OS=Homo sapiens GN=FUCA2 PE=1 SV=2	0.38	13	15	14	10	10	9	14	23
sp|Q9Y5P6|GMPPB_HUMAN Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens...	sp|Q9Y5P6|GMPPB_HUMANMannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB PE=1 SV=2	0.21	18	22	9	0	5	11	7	0
Thrombospondin-2 OS=Homo sapiens GN=THBS2 PE=1 SV=2	TSP2_HUMAN	0.14	0	0	0	0	0	1	6	2
Leukemia inhibitory factor receptor OS=Homo sapiens GN=LIFR PE=1 SV=1	LIFR_HUMAN	0.75	11	14	0	0	0	13	1	17
Proto-oncogene tyrosine-protein kinase receptor Ret OS=Homo sapiens GN=RET PE=1 SV=3	RET_HUMAN	0.89	0	1	0	3	3	2	0	0

Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=2 SV=1	B3KW71_HUMAN	0.34	15	16	12	11	11	17	13	12
Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	PLAK_HUMAN	0.43	0	7	0	11	11	8	11	3
Isoform Short of Glucosylceramidase OS=Homo sapiens GN=GBA	sp|P04062-2|GLCM_HUMAN	0.36	12	6	4	0	0	1	17	1
sp|Q9Y5Z4|HEBP2_HUMAN Heme-binding protein 2 OS=Homo sapiens GN=HEBP2 PE=1 SV=1	sp|Q9Y5Z4|HEBP2_HUMANHeme-binding protein 2 OS=Homo sapiens GN=HEBP2 PE=1 SV=1	0.19	17	28	0	0	16	39	20	18
Isoform 2 of Histone H2B type 2-F OS=Homo sapiens GN=HIST2H2BF	H2B2F_HUMAN	0.29	74	24	0	9	9	0	12	10
sp|P15907|SIAT1_HUMAN Beta-galactoside alpha-2,6-sialyltransferase 1 OS=Homo sapiens GN=ST6GAL1 PE=1 SV=1	sp|P15907|SIAT1_HUMANBeta-galactoside alpha-2,6-sialyltransferase 1 OS=Homo sapiens GN=ST6GAL1 PE=1 SV=1	0.63	22	18	2	0	19	0	19	0
sp|O43505|B3GN1_HUMAN N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase OS=Homo sapiens GN=B3GNT1 PE=1 SV=1	sp|O43505|B3GN1_HUMANN-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase OS=Homo sapiens GN=B3GNT1 PE=1 SV=1	0.63	12	17	11	0	15	18	13	15
Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1	sp|P25789|PSA4_HUMAN	0.37	0	0	19	15	15	0	14	0
sp|P36969-2|GPX4_HUMAN Isoform Cytoplasmic of Phospholipid hydroperoxide glutathione...	sp|P36969-2|GPX4_HUMAN Isoform Cytoplasmic of Phospholipid hydroperoxide glutathione... (+1)	0.43	11	9	12	10	10	18	33	11
sp|O75629|CREG1_HUMAN Protein CREG1 OS=Homo sapiens GN=CREG1 PE=1 SV=1	sp|O75629|CREG1_HUMANProtein CREG1 OS=Homo sapiens GN=CREG1 PE=1 SV=1	0.75	12	18	3	12	12	16	14	21
sp|Q8N335|GPD1L_HUMAN Glycerol-3-phosphate dehydrogenase 1-like protein OS=Homo sapiens GN=GPD1L PE=1 SV=1	sp|Q8N335|GPD1L_HUMANGlycerol-3-phosphate dehydrogenase 1-like protein OS=Homo sapiens GN=GPD1L PE=1 SV=1	0.36	15	19	7	0	7	12	12	10
Isoform 2 of Transmembrane channel-like protein 5 OS=Homo sapiens GN=TMC5	sp|Q6UXY8-2|TMC5_HUMAN (+1)	0.61	4	1	0	3	3	2	4	2
sp|O43396|TXNL1_HUMAN Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3	sp|O43396|TXNL1_HUMANThioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3	0.39	4	4	5	3	3	5	9	0
Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1	THIL_HUMAN	0.16	0	0	0	0	0	1	2	0

Kinesin heavy chain isoform 5C OS=Homo sapiens GN=KIF5C PE=2 SV=2	E9PET8_HUMAN	0.38	0	0	7	0	0	0	4	0
sp|P26371|KRA59_HUMAN Keratin-associated protein 5-9 OS=Homo sapiens GN=KRTAP5-9 PE=1 SV=1	sp|P26371|KRA59_HUMANKeratin-associated protein 5-9 OS=Homo sapiens GN=KRTAP5-9 PE=1 SV=1-DECOY	0.42	0	2	2	1	1	3	1	0
sp|P31946|1433B_HUMAN 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3	sp|P31946|1433B_HUMAN14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3	0.32	12	12	10	7	7	18	10	13
Isoform 6 of Myosin-14 OS=Homo sapiens GN=MYH14	sp|Q7Z406-6|MYH14_HUMAN	0.39	1	5	1	0	0	2	1	0
sp|P17612|KAPCA_HUMAN cAMP-dependent protein kinase catalytic subunit alpha OS=Homo sapiens GN=PRKACA PE=1 SV=2	sp|P17612|KAPCA_HUMANcAMP-dependent protein kinase catalytic subunit alpha OS=Homo sapiens GN=PRKACA PE=1 SV=2	0.29	15	19	0	0	10	12	14	22
Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2	sp|P22626|ROA2_HUMAN	0.36	114	0	0	0	0	2	0	0
sp|P01781|HV320_HUMAN Ig heavy chain V-III region GAL OS=Homo sapiens PE=1 SV=1	sp|P01781|HV320_HUMANIg heavy chain V-III region GAL OS=Homo sapiens PE=1 SV=1	0.35	0	3	0	0	0	0	4	5
sp|P01861|IGHG4_HUMAN Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	sp|P01861|IGHG4_HUMANIg gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	0.45	2	13	5	9	9	2	6	11
sp|P60842|IF4A1_HUMAN Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	sp|P60842|IF4A1_HUMANEukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	0.47	15	3	3	0	1	8	13	0
Tyrosine-protein kinase Yes OS=Homo sapiens GN=YES1 PE=1 SV=3	YES_HUMAN	0.54	2	3	3	1	1	3	5	3
Isoform 6 of Dynactin subunit 1 OS=Homo sapiens GN=DCTN1	sp|Q14203-6|DCTN1_HUMAN	0.54	3	1	4	0	0	9	5	0
Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2	ASSY_HUMAN	0.36	5	17	20	1	1	5	12	12
sp|P55259-3|GP2_HUMAN Isoform Alpha of Pancreatic secretory granule membrane major glycoprotein GP2 OS=Homo sapiens GN=GP2	sp|P55259-3|GP2_HUMANIsoform Alpha of Pancreatic secretory granule membrane major glycoprotein GP2 OS=Homo sapiens GN=GP2	0.99	1	4	4	0	9	0	13	7
sp|Q9UL46|PSME2_HUMAN Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4	sp|Q9UL46|PSME2_HUMANProteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4	0.063	11	0	0	0	9	17	21	5

Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1	BLMH_HUMAN	0.4	2	1	3	4	4	3	3	1
Methionine aminopeptidase 2 OS=Homo sapiens GN=METAP2 PE=1 SV=1	MAP2_HUMAN	0.24	3	1	2	1	1	1	1	1
Zinc finger CCCH domain-containing protein 4 (Fragment) OS=Homo sapiens GN=ZC3H4 PE=4 SV=1	M0QY97_HUMAN	0.36	4	0	0	0	0	0	0	0
sp|Q8IZ41|RASEF_HUMAN Ras and EF-hand domain-containing protein OS=Homo sapiens GN=RASEF PE=1 SV=1	sp|Q8IZ41|RASEF_HUMANRas and EF-hand domain-containing protein OS=Homo sapiens GN=RASEF PE=1 SV=1	0.2	0	4	0	0	1	0	6	5
sp|Q00839|HNRPU_HUMAN Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	sp|Q00839|HNRPU_HUMANHeterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	0.36	88	0	0	0	0	0	0	0
Serine incorporator 5 OS=Homo sapiens GN=SERINC5 PE=2 SV=1	D6RHG7_HUMAN	0.65	3	0	1	1	1	4	0	3
sp|O14672|ADA10_HUMAN Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens GN=ADAM10 PE=1 SV=1	sp|O14672|ADA10_HUMANDisintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens GN=ADAM10 PE=1 SV=1	0.096	3	1	0	0	5	10	6	0
sp|P20073|ANXA7_HUMAN Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3	sp|P20073|ANXA7_HUMANAnnexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3	0.53	5	10	7	0	10	10	13	0
Isoform 6 of Calpastatin OS=Homo sapiens GN=CAST	sp|P20810-6|ICAL_HUMAN	0.11	23	10	1	1	1	1	3	9
Arachidonate 15-lipoxygenase B OS=Homo sapiens GN=ALOX15B PE=2 SV=1	I3L1D5_HUMAN	0.48	0	0	8	17	17	0	11	0
sp|Q9Y230|RUVB2_HUMAN RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	sp|Q9Y230|RUVB2_HUMANRuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	0.91	12	5	5	7	7	24	25	0
sp|P31150|GDIA_HUMAN Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1...	sp|P31150|GDIA_HUMAN Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1...	0.44	11	12	11	12	12	22	16	16
sp|Q16348|S15A2_HUMAN Solute carrier family 15 member 2 OS=Homo sapiens GN=SLC15A2 PE=2 SV=2	sp|Q16348|S15A2_HUMANSolute carrier family 15 member 2 OS=Homo sapiens GN=SLC15A2 PE=2 SV=2	0.67	3	0	4	0	5	10	3	0
sp|Q13263|TIF1B_HUMAN Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	sp|Q13263|TIF1B_HUMANTranscription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	0.42	15	0	0	0	0	0	2	0

sp|O75223|GGCT_HUMAN Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGCT PE=1...	sp|O75223|GGCT_HUMAN Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGCT PE=1...	0.37	16	9	14	18	18	13	21	18
sp|P49419|AL7A1_HUMAN Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5	sp|P49419|AL7A1_HUMANAlpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5	0.71	8	10	1	0	4	9	16	0
Cytochrome b561 OS=Homo sapiens GN=CYB561 PE=2 SV=1	F5H757_HUMAN	0.38	9	14	17	13	13	19	15	15
sp|Q6UX06|OLFM4_HUMAN Olfactomedin-4 OS=Homo sapiens GN=OLFM4 PE=1 SV=1	sp|Q6UX06|OLFM4_HUMANOlfactomedin-4 OS=Homo sapiens GN=OLFM4 PE=1 SV=1	0.13	20	19	5	16	16	0	20	15
Isoform 2 of Syntaxin-binding protein 1 OS=Homo sapiens GN=STXBP1	STXB1_HUMAN	0.97	2	4	0	2	2	2	0	4
Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_d OS=Homo sapiens GN=CAPZB PE=2 SV=1	B1AK88_HUMAN	0.68	20	25	0	2	2	31	0	32
Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1	sp|P05164|PERM_HUMAN	0.15	11	2	4	9	9	4	0	1
sp|P19012|K1C15_HUMAN Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1...	sp|P19012|K1C15_HUMANKeratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3	0.12	0	1	0	0	1	0	0	4
Platelet-activating factor acetylhydrolase OS=Homo sapiens GN=PLA2G7 PE=1 SV=1	PAFA_HUMAN	0.46	2	9	0	1	1	8	0	15
ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3	ARF4_HUMAN	0.36	7	9	8	8	8	8	11	8
sp|O14556|G3PT_HUMAN Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Homo...	sp|O14556|G3PT_HUMAN Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Homo...	0.16	2	6	3	14	14	16	40	22
Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2	IPYR_HUMAN	0.79	0	17	1	3	3	8	23	4
sp|Q14055|CO9A2_HUMAN Collagen alpha-2(IX) chain OS=Homo sapiens GN=COL9A2 PE=1 SV=2	sp|Q14055|CO9A2_HUMANCollagen alpha-2(IX) chain OS=Homo sapiens GN=COL9A2 PE=1 SV=2	0.14	15	2	4	0	0	0	3	0
sp|P20827|EFNA1_HUMAN Ephrin-A1 OS=Homo sapiens GN=EFNA1 PE=1 SV=2	sp|P20827|EFNA1_HUMANEphrin-A1 OS=Homo sapiens GN=EFNA1 PE=1 SV=2	0.11	11	21	0	0	17	21	10	24
Ketimine reductase mu-crystallin OS=Homo sapiens GN=CRYM PE=2 SV=1	H9KVC2_HUMAN	0.44	11	18	12	8	8	19	21	17

Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3	sp|P10599|THIO_HUMAN (+1)	0.33	10	17	15	13	13	9	15	6
sp|TRY1_BOVIN|	sp|TRY1_BOVIN|	0.69	2	0	0	1	1	3	7	3
Sortilin OS=Homo sapiens GN=SORT1 PE=1 SV=3	sp|Q99523|SORT_HUMAN	0.97	3	9	0	5	5	5	3	4
Isoform 2 of Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC	sp|P31939-2|PUR9_HUMAN	0.19	9	18	1	0	0	6	0	3
Transcobalamin-2 OS=Homo sapiens GN=TCN2 PE=1 SV=3	sp|P20062|TCO2_HUMAN	0.33	1	9	3	1	1	1	1	8
Alpha-amylase 1 OS=Homo sapiens GN=AMY1A PE=1 SV=2	AMY1_HUMAN	0.93	1	21	0	13	13	0	4	17
Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	sp|P02671|FIBA_HUMAN	0.35	7	0	6	1	1	8	0	1
Isoform C of Fibulin-1 OS=Homo sapiens GN=FBLN1	sp|P23142-4|FBLN1_HUMAN	0.59	0	2	1	2	2	5	3	6
Isoform 8 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1	sp|Q04637-8|IF4G1_HUMAN	0.44	0	0	1	5	5	0	0	0
sp|Q6P9A2|GLT18_HUMAN Polypeptide N-acetylgalactosaminyltransferase 18 OS=Homo sapiens GN=GALNT18 PE=2 SV=2	sp|Q6P9A2|GLT18_HUMANPolypeptide N-acetylgalactosaminyltransferase 18 OS=Homo sapiens GN=GALNT18 PE=2 SV=2	0.21	0	1	0	0	7	2	1	0
Anion exchange protein 2 OS=Homo sapiens GN=SLC4A2 PE=1 SV=4	sp|P04920|B3A2_HUMAN	0.36	2	0	0	0	0	0	0	0
sp|P61106|RAB14_HUMAN Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4	sp|P61106|RAB14_HUMANRas-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4	0.31	20	15	9	5	5	17	19	10
Adenosylhomocysteinase OS=Homo sapiens GN=AHCYL2 PE=2 SV=1	D7UEQ7_HUMAN	0.54	5	3	2	2	2	4	4	6
Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1	TCTP_HUMAN	0.7	29	18	0	0	0	14	0	19
Isoform 4 of Myosin-10 OS=Homo sapiens GN=MYH10	sp|P35580-4|MYH10_HUMAN	0.35	0	3	1	0	0	2	3	0
Lysosomal protective protein OS=Homo sapiens GN=CTSA PE=1 SV=2	PPGB_HUMAN	0.38	3	7	3	2	2	7	5	4
sp|P56851|EP3B_HUMAN Epididymal secretory protein E3-beta OS=Homo sapiens GN=EDDM3B...	sp|P56851|EP3B_HUMAN Epididymal secretory protein E3-beta OS=Homo sapiens GN=EDDM3B...	0.35	13	15	6	12	12	17	17	7

N-acetyl-D-glucosamine kinase OS=Homo sapiens GN=NAGK PE=1 SV=4	sp|Q9UJ70|NAGK_HUMAN	0.4	4	2	5	4	4	6	4	3
5'-3' exoribonuclease 2 OS=Homo sapiens GN=XRN2 PE=2 SV=1	B4DZC3_HUMAN	0.36	10	0	0	0	0	0	0	0
Sialic acid synthase OS=Homo sapiens GN=NANS PE=1 SV=2	SIAS_HUMAN	0.35	13	5	17	3	3	8	10	4
Isoform 2 of Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens GN=EML2	sp|O95834-2|EMAL2_HUMAN	0.55	4	7	0	0	0	3	0	3
Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2	PGS1_HUMAN	0.27	2	6	0	5	5	4	4	12
sp|P09210|GSTA2_HUMAN Glutathione S-transferase A2 OS=Homo sapiens GN=GSTA2 PE=1 SV=4	sp|P09210|GSTA2_HUMANGlutathione S-transferase A2 OS=Homo sapiens GN=GSTA2 PE=1 SV=4	0.44	27	55	0	0	10	0	24	0
Matrilysin OS=Homo sapiens GN=MMP7 PE=1 SV=1	MMP7_HUMAN	0.51	7	3	6	8	8	11	8	18
sp|Q15286|RAB35_HUMAN Ras-related protein Rab-35 OS=Homo sapiens GN=RAB35 PE=1 SV=1	sp|Q15286|RAB35_HUMANRas-related protein Rab-35 OS=Homo sapiens GN=RAB35 PE=1 SV=1	0.21	20	19	3	5	5	10	3	23
sp|P01771|HV310_HUMAN Ig heavy chain V-III region HIL OS=Homo sapiens PE=1 SV=1	sp|P01771|HV310_HUMANIg heavy chain V-III region HIL OS=Homo sapiens PE=1 SV=1-DECOY	0.26	0	0	0	0	0	5	0	1
sp|P21281|VATB2_HUMAN V-type proton ATPase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3	sp|P21281|VATB2_HUMANV-type proton ATPase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3	0.064	0	13	0	0	11	15	9	10
Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4	sp|P14618|KPYM_HUMAN	0.29	6	20	10	17	17	12	16	9
sp|Q9Y678|COPG1_HUMAN Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1	sp|Q9Y678|COPG1_HUMANCoatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1	0.44	0	3	6	2	2	4	3	5
sp|P61026|RAB10_HUMAN Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1	sp|P61026|RAB10_HUMANRas-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1	0.28	9	22	2	12	12	6	10	9
sp|Q7Z304|MAMC2_HUMAN MAM domain-containing protein 2 OS=Homo sapiens GN=MAMDC2 PE=2 SV=3	sp|Q7Z304|MAMC2_HUMANMAM domain-containing protein 2 OS=Homo sapiens GN=MAMDC2 PE=2 SV=3	0.69	2	9	0	0	2	0	6	0
Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3	ARP3_HUMAN	0.14	12	16	9	4	4	5	0	5

sp|O14950|ML12B_HUMAN Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2	sp|O14950|ML12B_HUMANMyosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2	0.64	10	5	0	0	3	8	4	5
sp|Q5BJF6|ODFP2_HUMAN Outer dense fiber protein 2 OS=Homo sapiens GN=ODF2 PE=1 SV=1	sp|Q5BJF6|ODFP2_HUMANOuter dense fiber protein 2 OS=Homo sapiens GN=ODF2 PE=1 SV=1	0.29	0	2	0	0	0	4	23	0
sp|P11908|PRPS2_HUMAN Ribose-phosphate pyrophosphokinase 2 OS=Homo sapiens GN=PRPS2...	sp|P11908|PRPS2_HUMANRibose-phosphate pyrophosphokinase 2 OS=Homo sapiens GN=PRPS2 PE=1 SV=2	0.86	6	26	0	0	8	0	17	0
Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2	PSA2_HUMAN	0.99	11	28	0	0	0	18	0	20
sp|P54578|UBP14_HUMAN Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=USP14...	sp|P54578|UBP14_HUMANUbiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=USP14 PE=1 SV=3	0.39	10	0	17	0	7	0	12	0
Isoform 2 of Partitioning defective 3 homolog OS=Homo sapiens GN=PARD3	sp|Q8TEW0-2|PARD3_HUMAN	0.38	0	1	2	0	0	0	2	0
Nicastrin OS=Homo sapiens GN=NCSTN PE=1 SV=2	sp|Q92542|NICA_HUMAN	0.43	3	4	8	2	2	8	3	7
Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=2 SV=1	B4DX49_HUMAN	0.46	0	0	0	1	1	0	2	0
sp|O75131|CPNE3_HUMAN Copine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1	sp|O75131|CPNE3_HUMANCopine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1	0.34	8	7	6	4	4	5	10	6
sp|P98160|PGBM_HUMAN Basement membrane-specific heparan sulfate proteoglycan core...	sp|P98160|PGBM_HUMAN Basement membrane-specific heparan sulfate proteoglycan core...	0.68	3	13	5	4	4	25	4	5
sp|P08754|GNAI3_HUMAN Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo...	sp|P08754|GNAI3_HUMANGuanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3	0.56	3	4	5	0	6	0	8	4
Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4	PSB6_HUMAN	0.37	5	8	9	9	9	8	8	10
Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	sp|Q08554|DSC1_HUMAN	0.58	2	0	1	2	2	0	3	2
sp|O00204|ST2B1_HUMAN Sulfotransferase family cytosolic 2B member 1 OS=Homo sapiens...	sp|O00204|ST2B1_HUMANSulfotransferase family cytosolic 2B member 1 OS=Homo sapiens GN=SULT2B1 PE=1 SV=2	0.88	0	14	7	0	13	14	15	15
sp|Q15084|PDIA6_HUMAN Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1...	sp|Q15084|PDIA6_HUMANProtein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1	0.58	13	0	4	0	8	12	13	15

sp|Q6UWU2|GLB1L_HUMAN Beta-galactosidase-1-like protein OS=Homo sapiens GN=GLB1L PE=2 SV=1	sp|Q6UWU2|GLB1L_HUMANBeta-galactosidase-1-like protein OS=Homo sapiens GN=GLB1L PE=2 SV=1	0.34	4	2	0	0	0	5	7	0
sp|P20933|ASPG_HUMAN N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase OS=Homo sapiens...	sp|P20933|ASPG_HUMAN N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase OS=Homo sapiens...	0.38	11	7	7	26	26	20	13	26
Mucin-15 OS=Homo sapiens GN=MUC15 PE=2 SV=1	E9PII6_HUMAN	0.38	8	7	6	6	6	11	3	10
sp|P49773|HINT1_HUMAN Histidine triad nucleotide-binding protein 1 OS=Homo sapiens GN=HINT1 PE=1 SV=2	sp|P49773|HINT1_HUMANHistidine triad nucleotide-binding protein 1 OS=Homo sapiens GN=HINT1 PE=1 SV=2	0.9	46	0	0	0	17	18	17	0
Angiogenin OS=Homo sapiens GN=ANG PE=1 SV=1	ANGI_HUMAN	0.36	16	4	14	18	18	20	6	10
Isoform 2 of Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A	sp|P20340-2|RAB6A_HUMAN	0.3	13	9	8	2	2	10	6	6
Junction plakoglobin OS=Homo sapiens GN=JUP PE=2 SV=1	F5GWP8_HUMAN	1	1	0	3	8	8	5	5	2
Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	DSG1_HUMAN	0.25	7	6	4	4	4	1	8	3
C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=2 SV=1	F5H2F4_HUMAN	0.12	15	5	3	0	0	1	2	2
Farnesyl pyrophosphate synthase OS=Homo sapiens GN=FDPS PE=1 SV=4	sp|P14324|FPPS_HUMAN	0.31	12	9	6	5	5	8	9	7
Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2	sp|Q15366-3|PCBP2_HUMAN	0.35	7	4	2	2	2	7	4	3
sp|P09488|GSTM1_HUMAN Glutathione S-transferase Mu 1 OS=Homo sapiens GN=GSTM1 PE=1 SV=3	sp|P09488|GSTM1_HUMANGlutathione S-transferase Mu 1 OS=Homo sapiens GN=GSTM1 PE=1 SV=3	0.28	6	10	0	0	8	9	19	0
sp|P78417|GSTO1_HUMAN Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1...	sp|P78417|GSTO1_HUMANGlutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2	0.5	1	40	0	0	28	23	17	0
Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	MOES_HUMAN	0.54	21	0	0	0	0	0	0	2
Carboxymethylenebutenolidase homolog OS=Homo sapiens GN=CMBL PE=1 SV=1	CMBL_HUMAN	0.38	8	5	4	2	2	1	7	12
Isoform 4 of Protein sidekick-2 OS=Homo sapiens GN=SDK2	sp|Q58EX2-4|SDK2_HUMAN	0.15	2	2	1	1	1	1	0	1

Epididymis-specific alpha-mannosidase OS=Homo sapiens GN=MAN2B2 PE=2 SV=1	E9PCD7_HUMAN	0.66	0	1	1	2	2	0	4	0
Solute carrier family 2, facilitated glucose transporter member 14 OS=Homo sapiens GN=SLC2A14 PE=2 SV=1	B7ZAC3_HUMAN	0.39	0	0	9	6	6	1	6	0
Specifically androgen-regulated gene protein OS=Homo sapiens GN=SARG PE=1 SV=2	sp|Q9BW04|SARG_HUMAN	0.3	0	2	0	0	0	4	0	3
sp|Q16706|MA2A1_HUMAN Alpha-mannosidase 2 OS=Homo sapiens GN=MAN2A1 PE=1 SV=2	sp|Q16706|MA2A1_HUMANAlpha-mannosidase 2 OS=Homo sapiens GN=MAN2A1 PE=1 SV=2	0.19	0	5	1	1	1	0	0	2
Isoform 2 of Sodium/hydrogen exchanger 10 OS=Homo sapiens GN=SLC9C1	SL9C1_HUMAN	0.49	4	0	0	0	0	0	1	0
Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=2 SV=1	E9PRY8_HUMAN (+1)	0.24	14	3	5	0	0	6	3	1
sp|Q12907|LMAN2_HUMAN Vesicular integral-membrane protein VIP36 OS=Homo sapiens GN=LMAN2...	sp|Q12907|LMAN2_HUMANVesicular integral-membrane protein VIP36 OS=Homo sapiens GN=LMAN2 PE=1 SV=1	0.66	5	5	3	0	7	12	25	0
sp|P51854|TKTL1_HUMAN Transketolase-like protein 1 OS=Homo sapiens GN=TKTL1 PE=1 SV=2	sp|P51854|TKTL1_HUMANTransketolase-like protein 1 OS=Homo sapiens GN=TKTL1 PE=1 SV=2	0.015	2	7	0	0	6	9	7	9
Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD PE=1 SV=3	sp|P12955|PEPD_HUMAN	0.88	5	2	1	0	0	4	8	2
V-type proton ATPase subunit S1 OS=Homo sapiens GN=ATP6AP1 PE=1 SV=2	VAS1_HUMAN	0.46	0	0	0	2	2	0	4	0
sp|P15374|UCHL3_HUMAN Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1	sp|P15374|UCHL3_HUMANUbiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1	0.43	17	8	0	0	8	16	21	0
sp|P01137|TGFB1_HUMAN Transforming growth factor beta-1 OS=Homo sapiens GN=TGFB1 PE=1 SV=2	sp|P01137|TGFB1_HUMANTransforming growth factor beta-1 OS=Homo sapiens GN=TGFB1 PE=1 SV=2	0.0045	0	0	0	0	6	5	12	15
E3 UFM1-protein ligase 1 OS=Homo sapiens GN=UFL1 PE=1 SV=2	sp|O94874|UFL1_HUMAN	0.48	15	7	0	0	0	0	2	8
Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3	sp|P28062|PSB8_HUMAN	0.3	12	9	3	5	5	10	7	8

T-cell immunomodulatory protein OS=Homo sapiens GN=ITFG1 PE=1 SV=1	TIP_HUMAN	0.46	4	5	6	5	5	10	8	4
sp|Q92743|HTRA1_HUMAN Serine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1	sp|Q92743|HTRA1_HUMANSerine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1	0.69	0	9	3	1	1	0	12	6
ATP synthase subunit beta OS=Homo sapiens GN=ATP5B PE=2 SV=1	F8VPV9_HUMAN	0.64	3	7	5	0	0	12	5	7
Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2	CO7_HUMAN	0.8	0	3	0	3	3	0	0	2
Trypsin-3 OS=Homo sapiens GN=PRSS3 PE=1 SV=2	sp|P35030|TRY3_HUMAN	0.71	0	0	0	12	12	0	1	2
Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 PE=1 SV=1	sp|O95394|AGM1_HUMAN	0.95	7	16	0	0	0	10	0	9
NADP-dependent malic enzyme OS=Homo sapiens GN=ME1 PE=1 SV=1	MAOX_HUMAN	0.75	0	16	2	1	1	11	9	0
sp|Q13277|STX3_HUMAN Syntaxin-3 OS=Homo sapiens GN=STX3 PE=1 SV=3	sp|Q13277|STX3_HUMAN Syntaxin-3 OS=Homo sapiens GN=STX3 PE=1 SV=3-DECOY	0.14	0	0	0	0	0	0	4	3
Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens GN=ACAT2 PE=2 SV=1	B7Z233_HUMAN	0.65	20	21	0	0	0	12	0	15
sp|P16949|STMN1_HUMAN Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3	sp|P16949|STMN1_HUMANStathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3	0.36	122	0	0	0	0	0	0	0
sp|Q9BXJ1|C1QT1_HUMAN Complement C1q tumor necrosis factor-related protein 1 OS=Homo...	sp|Q9BXJ1|C1QT1_HUMANComplement C1q tumor necrosis factor-related protein 1 OS=Homo sapiens GN=C1QTNF1 PE=1 SV=1	0.6	9	14	8	2	22	1	25	2
Alpha-crystallin B chain (Fragment) OS=Homo sapiens GN=CRYAB PE=2 SV=1	E9PR44_HUMAN	0.32	17	25	13	10	10	13	14	16
sp|P61981|1433G_HUMAN 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	sp|P61981|1433G_HUMAN14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	0.39	13	10	8	0	9	8	15	11
Processed exostosin-like 2 OS=Homo sapiens GN=EXTL2 PE=2 SV=1	F5GZK1_HUMAN	0.89	0	2	0	3	3	1	2	0
sp|Q96EU7|C1GLC_HUMAN C1GALT1-specific chaperone 1 OS=Homo sapiens GN=C1GALT1C1 PE=1 SV=1	sp|Q96EU7|C1GLC_HUMANC1GALT1-specific chaperone 1 OS=Homo sapiens GN=C1GALT1C1 PE=1 SV=1	0.62	13	1	0	0	2	0	4	0
N-sulphoglucosamine sulphohydrolase OS=Homo sapiens GN=SGSH PE=2 SV=1	F5H6A3_HUMAN	0.65	2	5	7	6	6	17	7	5

sp|O43488|ARK72_HUMAN Aflatoxin B1 aldehyde reductase member 2 OS=Homo sapiens GN=AKR7A2...	sp|O43488|ARK72_HUMANAflatoxin B1 aldehyde reductase member 2 OS=Homo sapiens GN=AKR7A2 PE=1 SV=3	0.079	5	6	0	0	14	14	16	0
sp|P61604|CH10_HUMAN 10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1...	sp|P61604|CH10_HUMAN 10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1...	0.36	130	0	0	0	0	0	0	0
Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1	ACTZ_HUMAN	0.35	3	11	9	8	8	4	9	9
Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2	LEG1_HUMAN	0.36	95	0	0	0	0	1	0	0
40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	RS12_HUMAN	0.16	69	4	4	1	1	7	9	1
Acrosin OS=Homo sapiens GN=ACR PE=2 SV=4	ACRO_HUMAN	0.43	0	5	2	2	2	4	20	8
sp|P17050|NAGAB_HUMAN Alpha-N-acetylgalactosaminidase OS=Homo sapiens GN=NAGA PE=1 SV=2	sp|P17050|NAGAB_HUMANAlpha-N-acetylgalactosaminidase OS=Homo sapiens GN=NAGA PE=1 SV=2	0.16	0	9	0	0	9	11	9	0
Isoform SNAP-23b of Synaptosomal-associated protein 23 OS=Homo sapiens GN=SNAP23	SNP23_HUMAN	0.95	14	5	0	8	8	11	8	0
Isoform 5 of Radixin OS=Homo sapiens GN=RDX	sp|P35241-5|RADI_HUMAN	0.092	1	4	5	0	0	3	4	1
Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=2 SV=1	F5GYN4_HUMAN	0.53	8	14	1	0	0	15	1	9
Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment) OS=Homo sapiens GN=GNB2L1 PE=2 SV=1	D6R9L0_HUMAN	0.27	0	1	0	0	0	2	0	2
Isoform 4 of Protein tweety homolog 3 OS=Homo sapiens GN=TTYH3	sp|Q9C0H2-4|TTYH3_HUMAN	0.089	0	0	0	1	1	2	5	1
sp|Q29RF7|PDS5A_HUMAN Sister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens GN=PDS5A PE=1 SV=1	sp|Q29RF7|PDS5A_HUMANSister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens GN=PDS5A PE=1 SV=1	0.36	2	0	0	0	0	0	0	0
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=2 SV=1	B3KQV6_HUMAN	0.5	2	0	9	5	5	0	24	0
Isoform 2B of Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2	sp|Q13409-2|DC1I2_HUMAN	0.37	0	0	6	1	1	0	2	0
Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=2 SV=1	Q5VZU9_HUMAN (+1)	0.43	0	6	9	3	3	6	4	9

sp|Q9UJJ9|GNPTG_HUMAN N-acetylglucosamine-1-phosphotransferase subunit gamma OS=Homo...	sp|Q9UJJ9|GNPTG_HUMANN-acetylglucosamine-1-phosphotransferase subunit gamma OS=Homo sapiens GN=GNPTG PE=1 SV=1	0.2	6	16	0	0	15	5	14	11
Glutathione peroxidase 1 OS=Homo sapiens GN=GPX1 PE=1 SV=4	sp|P07203|GPX1_HUMAN	0.37	8	6	11	6	6	14	4	8
sp|Q9Y265|RUVB1_HUMAN RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	sp|Q9Y265|RUVB1_HUMANRuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	0.29	9	5	9	4	4	0	8	6
Lipoma-preferred partner OS=Homo sapiens GN=LPP PE=1 SV=1	LPP_HUMAN	0.32	4	5	4	0	0	0	5	0
sp|Q8WXA2|PATE1_HUMAN Prostate and testis expressed protein 1 OS=Homo sapiens GN=PATE1 PE=2 SV=1	sp|Q8WXA2|PATE1_HUMANProstate and testis expressed protein 1 OS=Homo sapiens GN=PATE1 PE=2 SV=1	0.95	37	14	0	0	21	21	9	0
sp|P61978|HNRPK_HUMAN Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK...	sp|P61978|HNRPK_HUMANHeterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	0.36	51	0	0	0	0	0	1	0
Desmocollin-2 OS=Homo sapiens GN=DSC2 PE=1 SV=1	sp|Q02487|DSC2_HUMAN	0.42	7	1	2	4	4	7	2	7
sp|Q7Z794|K2C1B_HUMAN Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2...	sp|Q7Z794|K2C1B_HUMANKeratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3	0.96	0	0	1	3	6	0	0	0
sp|Q6BCY4|NB5R2_HUMAN NADH-cytochrome b5 reductase 2 OS=Homo sapiens GN=CYB5R2 PE=1...	sp|Q6BCY4|NB5R2_HUMANNADH-cytochrome b5 reductase 2 OS=Homo sapiens GN=CYB5R2 PE=1 SV=1	0.74	0	20	0	0	10	0	17	0
sp|Q9NZV1|CRIM1_HUMAN Cysteine-rich motor neuron 1 protein OS=Homo sapiens GN=CRIM1 PE=1 SV=1	sp|Q9NZV1|CRIM1_HUMANCysteine-rich motor neuron 1 protein OS=Homo sapiens GN=CRIM1 PE=1 SV=1	0.36	2	0	0	0	0	0	0	0
sp|P27037|AVR2A_HUMAN Activin receptor type-2A OS=Homo sapiens GN=ACVR2A PE=1 SV=1	sp|P27037|AVR2A_HUMANActivin receptor type-2A OS=Homo sapiens GN=ACVR2A PE=1 SV=1	0.56	0	3	0	0	0	0	1	0
sp|Q6UWW0|LCN15_HUMAN Lipocalin-15 OS=Homo sapiens GN=LCN15 PE=1 SV=1	sp|Q6UWW0|LCN15_HUMANLipocalin-15 OS=Homo sapiens GN=LCN15 PE=1 SV=1	0.26	6	4	0	8	8	5	12	7
Twinfilin-1 OS=Homo sapiens GN=TWF1 PE=1 SV=3	sp|Q12792|TWF1_HUMAN	0.39	2	15	12	3	3	13	7	11
AGR2 OS=Homo sapiens GN=AGR2 PE=2 SV=1	Q4JM47_HUMAN	0.36	9	16	16	6	6	15	12	11
sp|Q8NFZ8|CADM4_HUMAN Cell adhesion molecule 4 OS=Homo sapiens GN=CADM4 PE=1 SV=1	sp|Q8NFZ8|CADM4_HUMANCell adhesion molecule 4 OS=Homo sapiens GN=CADM4 PE=1 SV=1	0.14	6	9	4	11	11	3	4	0

Isoform 2 of Transmembrane protein 2 OS=Homo sapiens GN=TMEM2	TMEM2_HUMAN	0.22	6	3	2	1	1	0	0	4
sp|Q8N436|CPXM2_HUMAN Inactive carboxypeptidase-like protein X2 OS=Homo sapiens GN=CPXM2 PE=2 SV=3	sp|Q8N436|CPXM2_HUMANInactive carboxypeptidase-like protein X2 OS=Homo sapiens GN=CPXM2 PE=2 SV=3	0.57	1	5	0	0	1	0	6	3
Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2	sp|Q16775|GLO2_HUMAN	0.44	0	0	0	8	8	1	14	0
sp|Q8N4F0|BPIB2_HUMAN BPI fold-containing family B member 2 OS=Homo sapiens GN=BPIFB2 PE=1 SV=2	sp|Q8N4F0|BPIB2_HUMANBPI fold-containing family B member 2 OS=Homo sapiens GN=BPIFB2 PE=1 SV=2	0.18	10	29	16	0	6	0	0	0
GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3	RAN_HUMAN	0.37	9	14	12	5	5	13	20	5
S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2	ESTD_HUMAN	0.29	7	16	10	8	8	6	13	4
Delta-aminolevulinic acid dehydratase OS=Homo sapiens GN=ALAD PE=1 SV=1	sp|P13716|HEM2_HUMAN	0.41	0	0	19	11	11	0	20	0
Isoform 3 of Protein phosphatase 1A OS=Homo sapiens GN=PPM1A	sp|P35813-3|PPM1A_HUMAN	0.42	1	4	2	1	1	4	3	1
Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1	VASN_HUMAN	0.44	2	6	5	3	3	5	6	7
Calmodulin (Fragment) OS=Homo sapiens GN=CALM2 PE=2 SV=1	H0Y7A7_HUMAN	0.4	12	2	11	5	5	17	10	8
Asparagine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1	SYNC_HUMAN	0.5	7	2	3	1	1	2	3	6
Isoform 2 of Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18	sp|Q9NP72-2|RAB18_HUMAN	0.38	7	7	8	7	7	8	9	14
sp|P06889|LV405_HUMAN Ig lambda chain V-IV region MOL OS=Homo sapiens PE=1 SV=1	sp|P06889|LV405_HUMANIg lambda chain V-IV region MOL OS=Homo sapiens PE=1 SV=1-DECOY	0.65	0	2	0	3	3	0	0	0
Ecto-ADP-ribosyltransferase 3 OS=Homo sapiens GN=ART3 PE=1 SV=2	sp|Q13508|NAR3_HUMAN	0.091	0	6	0	0	0	8	9	12
sp|P38606|VATA_HUMAN V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A...	sp|P38606|VATA_HUMAN V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A... (+1)	0.45	10	6	18	4	4	19	14	7
sp|Q5KU26|COL12_HUMAN Collectin-12 OS=Homo sapiens GN=COLEC12 PE=1 SV=3	sp|Q5KU26|COL12_HUMANCollectin-12 OS=Homo sapiens GN=COLEC12 PE=1 SV=3	0.18	4	10	3	7	7	0	9	0

Isoform 2 of Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A	TBA1A_HUMAN	0.32	2	19	0	6	6	10	12	16
sp|O00754|MA2B1_HUMAN Lysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE=1 SV=3	sp|O00754|MA2B1_HUMANLysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE=1 SV=3	0.87	22	3	0	0	5	5	12	0
Isoform 2 of Mitogen-activated protein kinase 1 OS=Homo sapiens GN=MAPK1	sp|P28482-2|MK01_HUMAN	0.54	10	8	0	0	0	5	0	5
Glutaminyl-peptide cyclotransferase OS=Homo sapiens GN=QPCT PE=1 SV=1	sp|Q16769|QPCT_HUMAN	0.45	6	9	4	6	6	7	11	9
Synaptotagmin-1 OS=Homo sapiens GN=SYT1 PE=1 SV=1	SYT1_HUMAN	0.85	1	3	2	3	3	7	6	2
D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=2 SV=2	B5MC82_HUMAN	0.27	22	8	7	6	6	8	7	7
Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3	RET4_HUMAN	0.38	10	10	4	16	16	17	7	12
sp|O15144|ARPC2_HUMAN Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens...	sp|O15144|ARPC2_HUMANActin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1	0.82	9	8	0	0	4	9	4	2
sp|P29992|GNA11_HUMAN Guanine nucleotide-binding protein subunit alpha-11 OS=Homo sapiens GN=GNA11 PE=1 SV=2	sp|P29992|GNA11_HUMANGuanine nucleotide-binding protein subunit alpha-11 OS=Homo sapiens GN=GNA11 PE=1 SV=2	0.27	1	8	0	0	3	2	6	9
Protein NDRG2 (Fragment) OS=Homo sapiens GN=NDRG2 PE=4 SV=1	H0YJT9_HUMAN	0.64	1	4	3	1	1	11	1	4
sp|Q9Y376|CAB39_HUMAN Calcium-binding protein 39 OS=Homo sapiens GN=CAB39 PE=1 SV=1	sp|Q9Y376|CAB39_HUMANCalcium-binding protein 39 OS=Homo sapiens GN=CAB39 PE=1 SV=1	0.036	11	14	2	5	5	0	6	6
sp|Q9C0J8|WDR33_HUMAN pre-mRNA 3' end processing protein WDR33 OS=Homo sapiens GN=WDR33 PE=1 SV=2	sp|Q9C0J8|WDR33_HUMANpre-mRNA 3' end processing protein WDR33 OS=Homo sapiens GN=WDR33 PE=1 SV=2	0.36	2	0	0	0	0	0	0	0
Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3	sp|P60981|DEST_HUMAN	0.34	6	3	6	2	2	4	5	1
sp|Q7Z4H3|HDDC2_HUMAN HD domain-containing protein 2 OS=Homo sapiens GN=HDDC2 PE=1 SV=1	sp|Q7Z4H3|HDDC2_HUMANHD domain-containing protein 2 OS=Homo sapiens GN=HDDC2 PE=1 SV=1	0.086	1	5	0	0	7	11	17	0

Isoform Gamma-A of Fibrinogen gamma chain OS=Homo sapiens GN=FGG	sp|P02679-2|FIBG_HUMAN	0.38	0	0	17	2	2	3	0	3
sp|Q9P232|CNTN3_HUMAN Contactin-3 OS=Homo sapiens GN=CNTN3 PE=1 SV=3	sp|Q9P232|CNTN3_HUMANContactin-3 OS=Homo sapiens GN=CNTN3 PE=1 SV=3	0.49	2	2	2	2	2	4	4	0
sp|P01610|KV118_HUMAN Ig kappa chain V-I region WEA OS=Homo sapiens PE=1 SV=1	sp|P01610|KV118_HUMANIg kappa chain V-I region WEA OS=Homo sapiens PE=1 SV=1	0.35	10	15	15	8	8	12	10	12
Out at first protein homolog OS=Homo sapiens GN=OAF PE=2 SV=1	OAF_HUMAN	0.48	4	6	0	4	4	1	3	2
sp|P15259|PGAM2_HUMAN Phosphoglycerate mutase 2 OS=Homo sapiens GN=PGAM2 PE=1 SV=3	sp|P15259|PGAM2_HUMANPhosphoglycerate mutase 2 OS=Homo sapiens GN=PGAM2 PE=1 SV=3	0.84	6	15	0	7	7	0	17	11
sp|Q99988|GDF15_HUMAN Growth/differentiation factor 15 OS=Homo sapiens GN=GDF15 PE=1 SV=3	sp|Q99988|GDF15_HUMANGrowth/differentiation factor 15 OS=Homo sapiens GN=GDF15 PE=1 SV=3	0.65	19	23	0	0	9	9	10	0
sp|O75340|PDCD6_HUMAN Programmed cell death protein 6 OS=Homo sapiens GN=PDCD6 PE=1 SV=1	sp|O75340|PDCD6_HUMANProgrammed cell death protein 6 OS=Homo sapiens GN=PDCD6 PE=1 SV=1	0.34	14	0	0	0	28	0	19	0
Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3	SYG_HUMAN	0.94	1	2	1	0	0	0	8	2
sp|Q13214|SEM3B_HUMAN Semaphorin-3B OS=Homo sapiens GN=SEMA3B PE=2 SV=1	sp|Q13214|SEM3B_HUMANSemaphorin-3B OS=Homo sapiens GN=SEMA3B PE=2 SV=1	0.62	4	5	1	5	5	0	9	8
Isoform 3 of Natural resistance-associated macrophage protein 2 OS=Homo sapiens GN=SLC11A2	sp|P49281-3|NRAM2_HUMAN	0.94	0	0	0	2	2	0	0	0
sp|Q9ULD9|ZN608_HUMAN Zinc finger protein 608 OS=Homo sapiens GN=ZNF608 PE=1 SV=4	sp|Q9ULD9|ZN608_HUMANZinc finger protein 608 OS=Homo sapiens GN=ZNF608 PE=1 SV=4	0.51	4	4	0	4	4	0	4	0
sp|Q08629|TICN1_HUMAN Testican-1 OS=Homo sapiens GN=SPOCK1 PE=1 SV=1	sp|Q08629|TICN1_HUMANTestican-1 OS=Homo sapiens GN=SPOCK1 PE=1 SV=1	0.82	11	0	0	5	5	5	4	0
sp|P35625|TIMP3_HUMAN Metalloproteinase inhibitor 3 OS=Homo sapiens GN=TIMP3 PE=1 SV=2	sp|P35625|TIMP3_HUMANMetalloproteinase inhibitor 3 OS=Homo sapiens GN=TIMP3 PE=1 SV=2	0.17	5	17	0	0	15	7	17	9
Isoform 2 of Protein FAM177A1 OS=Homo sapiens GN=FAM177A1	F177A_HUMAN	0.83	5	3	0	9	9	5	7	0

sp|P01762|HV301_HUMAN Ig heavy chain V-III region TRO OS=Homo sapiens PE=1 SV=1	sp|P01762|HV301_HUMANIg heavy chain V-III region TRO OS=Homo sapiens PE=1 SV=1	0.72	6	4	2	0	2	6	3	6
Isoform 2 of Nardilysin OS=Homo sapiens GN=NRD1	sp|O43847-2|NRDC_HUMAN	0.69	1	0	1	0	0	3	2	0
sp|P18065|IBP2_HUMAN Insulin-like growth factor-binding protein 2 OS=Homo sapiens...	sp|P18065|IBP2_HUMAN Insulin-like growth factor-binding protein 2 OS=Homo sapiens...	0.31	9	14	10	16	16	10	14	16
Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1	NUDC_HUMAN	0.69	5	8	4	1	1	10	14	10
Isoform 2 of Delta-like protein 3 OS=Homo sapiens GN=DLL3	sp|Q9NYJ7-2|DLL3_HUMAN	0.65	0	0	0	4	4	0	0	4
sp|Q14990|ODFP1_HUMAN Outer dense fiber protein 1 OS=Homo sapiens GN=ODF1 PE=2 SV=2	sp|Q14990|ODFP1_HUMANOuter dense fiber protein 1 OS=Homo sapiens GN=ODF1 PE=2 SV=2	0.39	2	5	0	0	4	0	24	0
sp|Q9Y4G8|RPGF2_HUMAN Rap guanine nucleotide exchange factor 2 OS=Homo sapiens GN=RAPGEF2 PE=1 SV=1	sp|Q9Y4G8|RPGF2_HUMANRap guanine nucleotide exchange factor 2 OS=Homo sapiens GN=RAPGEF2 PE=1 SV=1	0.71	0	4	0	0	0	2	0	0
sp|Q9UQ80|PA2G4_HUMAN Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3	sp|Q9UQ80|PA2G4_HUMANProliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3	0.25	0	10	0	0	2	8	7	6
Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1	NIT2_HUMAN	0.35	6	9	11	4	4	10	5	6
sp|O95865|DDAH2_HUMAN N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Homo...	sp|O95865|DDAH2_HUMANN(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Homo sapiens GN=DDAH2 PE=1 SV=1	0.46	12	13	1	0	3	9	9	9
sp|P37802|TAGL2_HUMAN Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3	sp|P37802|TAGL2_HUMANTransgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3	0.42	49	3	0	0	3	2	5	0
Isoform 2 of Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4	sp|P67936-2|TPM4_HUMAN	0.15	1	6	3	1	1	2	3	5
Thymidine phosphorylase OS=Homo sapiens GN=TYMP PE=1 SV=2	sp|P19971|TYPH_HUMAN	0.38	3	3	3	1	1	3	4	2
Isoform 2 of Ig mu chain C region OS=Homo sapiens GN=IGHM	sp|P01871-2|IGHM_HUMAN	0.35	1	4	10	2	2	2	2	3
Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2	sp|P0C0L4|CO4A_HUMAN	0.3	7	8	2	8	8	7	6	4
Dickkopf-related protein 3 OS=Homo sapiens GN=DKK3 PE=2 SV=2	E7EUD0_HUMAN	0.68	0	2	0	0	0	0	0	1

sp|O75533|SF3B1_HUMAN Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3	sp|O75533|SF3B1_HUMANSplicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3	0.36	27	0	0	0	0	0	0	0
Ras-related protein R-Ras OS=Homo sapiens GN=RRAS PE=1 SV=1	RRAS_HUMAN	0.35	4	13	8	7	7	8	10	7
sp|Q15365|PCBP1_HUMAN Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	sp|Q15365|PCBP1_HUMANPoly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	0.46	13	4	2	0	4	6	2	3
Protein DPCD OS=Homo sapiens GN=DPCD PE=1 SV=2	DPCD_HUMAN	0.95	7	13	2	7	7	10	17	19
40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	RS8_HUMAN	0.27	22	4	9	2	2	6	6	2
Isoform 3 of Poliovirus receptor-related protein 3 OS=Homo sapiens GN=PVRL3	sp|Q9NQS3-3|PVRL3_HUMAN	0.22	0	0	0	1	1	0	1	2
Vitamin D-binding protein OS=Homo sapiens GN=GC PE=2 SV=1	D6RF35_HUMAN	0.35	5	4	5	6	6	9	7	5
Solute carrier family 2, facilitated glucose transporter member 5 OS=Homo sapiens GN=SLC2A5 PE=2 SV=1	B4DU31_HUMAN	0.53	7	6	0	0	0	12	0	11
sp|P22392-2|NDKB_HUMAN Isoform 3 of Nucleoside diphosphate kinase B OS=Homo sapiens...	sp|P22392-2|NDKB_HUMAN Isoform 3 of Nucleoside diphosphate kinase B OS=Homo sapiens... (+1)	0.37	18	4	13	15	15	15	14	9
Isoform 2 of Vigilin OS=Homo sapiens GN=HDLBP	VIGLN_HUMAN	0.49	4	0	0	0	0	5	0	4
Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=2 SV=1	B4E2S7_HUMAN	0.91	17	19	0	0	0	24	0	19
Sortilin-related receptor OS=Homo sapiens GN=SORL1 PE=1 SV=2	SORL_HUMAN	0.54	0	2	2	1	1	4	2	1
S-methyl-5'-thioadenosine phosphorylase OS=Homo sapiens GN=MTAP PE=2 SV=1	B4DUC8_HUMAN	0.64	6	10	0	0	0	6	0	4
sp|Q99828|CIB1_HUMAN Calcium and integrin-binding protein 1 OS=Homo sapiens GN=CIB1...	sp|Q99828|CIB1_HUMAN Calcium and integrin-binding protein 1 OS=Homo sapiens GN=CIB1...	0.35	17	9	5	10	10	15	10	14
Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=2 SV=1	E9PP21_HUMAN	0.22	18	4	3	4	4	9	2	0
sp|P34931|HS71L_HUMAN Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L...	sp|P34931|HS71L_HUMANHeat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2	0.11	5	2	0	0	3	11	7	3
Sepiapterin reductase OS=Homo sapiens GN=SPR PE=1 SV=1	SPRE_HUMAN	0.35	6	8	14	1	1	5	5	6

Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	IMB1_HUMAN	0.51	12	7	0	9	9	6	14	7
Tolloid-like protein 1 OS=Homo sapiens GN=TLL1 PE=1 SV=1	sp|O43897|TLL1_HUMAN	0.36	0	0	0	0	0	2	0	0
sp|P30044|PRDX5_HUMAN Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4	sp|P30044|PRDX5_HUMANPeroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4	0.53	29	0	0	0	14	17	20	0
sp|O94886|TM63A_HUMAN Transmembrane protein 63A OS=Homo sapiens GN=TMEM63A PE=2 SV=3	sp|O94886|TM63A_HUMANTransmembrane protein 63A OS=Homo sapiens GN=TMEM63A PE=2 SV=3	0.75	2	1	3	0	4	8	1	4
sp|P31153|METK2_HUMAN S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1	sp|P31153|METK2_HUMANS-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1	0.54	4	8	4	0	6	0	5	12
sp|Q92485|ASM3B_HUMAN Acid sphingomyelinase-like phosphodiesterase 3b OS=Homo sapiens GN=SMPDL3B PE=2 SV=2	sp|Q92485|ASM3B_HUMANAcid sphingomyelinase-like phosphodiesterase 3b OS=Homo sapiens GN=SMPDL3B PE=2 SV=2	0.57	0	12	8	0	13	0	14	1
Tissue-type plasminogen activator chain A OS=Homo sapiens GN=PLAT PE=2 SV=1	B4DN26_HUMAN	0.36	0	0	0	0	0	11	0	0
sp|P30040|ERP29_HUMAN Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4	sp|P30040|ERP29_HUMANEndoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4	0.59	30	7	0	0	5	7	4	4
sp|Q92945|FUBP2_HUMAN Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4	sp|Q92945|FUBP2_HUMANFar upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4	0.36	36	0	0	0	0	0	0	0
sp|O94832|MYO1D_HUMAN Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=1 SV=2	sp|O94832|MYO1D_HUMANUnconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=1 SV=2	0.62	1	1	2	1	1	7	1	1
tr|F5GWE5|F5GWE5_HUMAN Phosphatidylinositol transfer protein alpha isoform OS=Homo...	tr|F5GWE5|F5GWE5_HUMAN Phosphatidylinositol transfer protein alpha isoform OS=Homo...	0.44	4	8	8	6	6	6	12	10
sp|P24855|DNAS1_HUMAN Deoxyribonuclease-1 OS=Homo sapiens GN=DNASE1 PE=1 SV=1	sp|P24855|DNAS1_HUMANDeoxyribonuclease-1 OS=Homo sapiens GN=DNASE1 PE=1 SV=1	0.047	8	7	1	5	5	0	6	0
Isoform 3 of Calumenin OS=Homo sapiens GN=CALU	sp|O43852-3|CALU_HUMAN	0.42	6	1	7	1	1	5	5	5
sp|Q14507|EP3A_HUMAN Epididymal secretory protein E3-	sp|Q14507|EP3A_HUMAN Epididymal secretory protein E3-alpha OS=Homo sapiens GN=EDDM3A...	0.18	11	13	4	13	13	6	6	4

alpha OS=Homo sapiens GN=EDDM3A...										
Syntaxin-3 OS=Homo sapiens GN=STX3 PE=1 SV=3	sp|Q13277|STX3_HUMAN	0.16	1	6	1	2	2	2	2	1
WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4	sp|O75083|WDR1_HUMAN	0.72	0	0	5	14	14	1	19	0
26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1	PSDE_HUMAN	0.33	4	3	1	0	0	3	3	1
Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4	K2C4_HUMAN	0.72	2	2	0	5	5	1	0	0
Isoform 3 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2	sp|P04899-3|GNAI2_HUMAN	0.92	11	9	0	0	0	8	0	12
Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	DCD_HUMAN	0.065	6	2	0	0	11	11	26	3
sp|O14745|NHRF1_HUMAN Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Homo sapiens...	sp|O14745|NHRF1_HUMANNa(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Homo sapiens GN=SLC9A3R1 PE=1 SV=4	0.62	10	5	0	0	3	0	6	0
sp|O00160|MYO1F_HUMAN Unconventional myosin-If OS=Homo sapiens GN=MYO1F PE=1 SV=3	sp|O00160|MYO1F_HUMANUnconventional myosin-If OS=Homo sapiens GN=MYO1F PE=1 SV=3	0.36	6	0	0	0	0	0	0	0
Cathepsin O OS=Homo sapiens GN=CTSO PE=2 SV=1	CATO_HUMAN	0.12	5	10	2	3	3	2	3	0
Isoform 3 of Retinal dehydrogenase 2 OS=Homo sapiens GN=ALDH1A2	sp|O94788-3|AL1A2_HUMAN	0.3	0	1	2	0	0	0	0	0
sp|Q5R3I4|TTC38_HUMAN Tetratricopeptide repeat protein 38 OS=Homo sapiens GN=TTC38 PE=1 SV=1	sp|Q5R3I4|TTC38_HUMANTetratricopeptide repeat protein 38 OS=Homo sapiens GN=TTC38 PE=1 SV=1	0.7	3	5	0	1	1	0	4	2
Matrix metalloproteinase-9 OS=Homo sapiens GN=MMP9 PE=1 SV=3	MMP9_HUMAN	0.52	3	0	0	3	3	0	0	0
sp|CAS1_BOVIN|	sp|CAS1_BOVIN|	0.97	6	1	5	8	8	16	13	13
P2X purinoceptor OS=Homo sapiens GN=P2RX4 PE=2 SV=2	E7EPF7_HUMAN	0.49	0	1	1	2	2	5	2	4
Soluble interleukin-4 receptor subunit alpha OS=Homo sapiens GN=IL4R PE=2 SV=1	B4E076_HUMAN	0.36	0	2	0	0	0	0	0	0

Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=2 SV=1	B4DEK7_HUMAN	0.27	3	3	0	0	0	0	4	1
Nucleolar protein 3 OS=Homo sapiens GN=NOL3 PE=2 SV=1	B4DFL0_HUMAN	0.76	0	1	0	5	5	3	1	0
sp|O15232|MATN3_HUMAN Matrilin-3 OS=Homo sapiens GN=MATN3 PE=1 SV=2	sp|O15232|MATN3_HUMANMatrilin-3 OS=Homo sapiens GN=MATN3 PE=1 SV=2	0.13	1	1	0	0	0	2	2	2
sp|Q96N03|VTM2L_HUMAN V-set and transmembrane domain-containing protein 2-like protein...	sp|Q96N03|VTM2L_HUMANV-set and transmembrane domain-containing protein 2-like protein OS=Homo sapiens GN=VSTM2L PE=1 SV=1	0.065	9	9	0	0	9	7	14	15
Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT PE=1 SV=2	APT_HUMAN	0.92	13	12	0	0	4	12	10	0
sp|Q96QK1|VPS35_HUMAN Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2	sp|Q96QK1|VPS35_HUMANVacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2	0.88	0	6	0	0	1	0	4	0
sp|Q96IJ6|GMPPA_HUMAN Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens...	sp|Q96IJ6|GMPPA_HUMANMannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA PE=1 SV=1	0.58	6	0	7	0	10	10	7	0
Matrin-3 OS=Homo sapiens GN=MATR3 PE=2 SV=1	A8MXP9_HUMAN (+1)	0.36	12	0	0	0	0	0	0	0
40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4	RSSA_HUMAN	0.39	1	9	5	2	2	5	7	4
Isoform 2 of Actin-related protein 2 OS=Homo sapiens GN=ACTR2	sp|P61160-2|ARP2_HUMAN	0.14	5	21	5	5	5	1	2	8
Fumarylacetoacetase OS=Homo sapiens GN=FAH PE=1 SV=2	FAAA_HUMAN	0.63	0	1	2	2	2	5	2	2
Alcohol dehydrogenase class-3 OS=Homo sapiens GN=ADH5 PE=1 SV=4	ADHX_HUMAN	0.72	2	8	0	3	3	4	7	2
Tyrosine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4	SYYC_HUMAN	0.4	0	0	4	3	3	0	3	0
sp|Q9BWS9|CHID1_HUMAN Chitinase domain-containing protein 1 OS=Homo sapiens GN=CHID1...	sp|Q9BWS9|CHID1_HUMANChitinase domain-containing protein 1 OS=Homo sapiens GN=CHID1 PE=1 SV=1	0.4	11	17	4	0	10	13	0	8
Isoform 2 of Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A	IF5A1_HUMAN	0.64	3	0	0	8	8	0	12	0

sp|O95750|FGF19_HUMAN Fibroblast growth factor 19 OS=Homo sapiens GN=FGF19 PE=1 SV=1	sp|O95750|FGF19_HUMANFibroblast growth factor 19 OS=Homo sapiens GN=FGF19 PE=1 SV=1	0.12	6	11	0	3	3	0	0	0
sp|Q9H4M9|EHD1_HUMAN EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1...	sp|Q9H4M9|EHD1_HUMAN EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1...	0.43	5	6	16	6	6	7	14	7
Myoglobin (Fragment) OS=Homo sapiens GN=MB PE=2 SV=1	B0QYF8_HUMAN (+2)	0.35	1	2	7	6	6	1	4	1
sp|Q07960|RHG01_HUMAN Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1	sp|Q07960|RHG01_HUMANRho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1	0.029	1	3	0	0	3	4	2	5
Anoctamin-7 OS=Homo sapiens GN=ANO7 PE=1 SV=2	sp|Q6IWH7|ANO7_HUMAN	0.4	3	1	5	1	1	4	0	5
sp|P22059|OSBP1_HUMAN Oxysterol-binding protein 1 OS=Homo sapiens GN=OSBP PE=1 SV=1	sp|P22059|OSBP1_HUMANOxysterol-binding protein 1 OS=Homo sapiens GN=OSBP PE=1 SV=1	0.58	0	5	1	2	2	0	5	2
sp|O75110|ATP9A_HUMAN Probable phospholipid-transporting ATPase IIA OS=Homo sapiens GN=ATP9A PE=1 SV=3	sp|O75110|ATP9A_HUMANProbable phospholipid-transporting ATPase IIA OS=Homo sapiens GN=ATP9A PE=1 SV=3	0.42	2	4	5	0	1	0	8	8
Palmitoyl-protein thioesterase 1 (Fragment) OS=Homo sapiens GN=PPT1 PE=2 SV=1	E9PMG2_HUMAN	0.4	0	5	0	0	0	3	10	1
Isoform 4 of Alpha-mannosidase 2C1 OS=Homo sapiens GN=MAN2C1	sp|Q9NTJ4-4|MA2C1_HUMAN	0.18	0	0	0	0	0	2	0	1
Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3	EF1B_HUMAN	0.39	25	1	0	0	0	1	2	0
60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2	RL29_HUMAN	0.24	24	6	7	1	1	2	2	3
sp|Q8TDQ7|GNPI2_HUMAN Glucosamine-6-phosphate isomerase 2 OS=Homo sapiens GN=GNPDA2...	sp|Q8TDQ7|GNPI2_HUMANGlucosamine-6-phosphate isomerase 2 OS=Homo sapiens GN=GNPDA2 PE=1 SV=1	0.99	2	11	0	1	1	0	13	0
sp|Q9H4G4|GAPR1_HUMAN Golgi-associated plant pathogenesis-related protein 1 OS=Homo sapiens GN=GLIPR2 PE=1 SV=3	sp|Q9H4G4|GAPR1_HUMANGolgi-associated plant pathogenesis-related protein 1 OS=Homo sapiens GN=GLIPR2 PE=1 SV=3	0.52	13	4	0	0	8	8	11	0
Glycine N-methyltransferase OS=Homo sapiens GN=GNMT PE=1 SV=3	GNMT_HUMAN	0.71	0	0	5	0	0	13	5	3
Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=2 SV=1	E9PK91_HUMAN	0.36	5	0	0	0	0	0	0	0

sp|P08174-7|DAF_HUMAN Isoform 7 of Complement decay-accelerating factor OS=Homo sapiens GN=CD55	sp|P08174-7|DAF_HUMANIsoform 7 of Complement decay-accelerating factor OS=Homo sapiens GN=CD55	0.044	2	0	0	0	5	7	2	2
Isoform 2 of Transmembrane protein 132A OS=Homo sapiens GN=TMEM132A	sp|Q24JP5-2|T132A_HUMAN	0.39	0	0	0	1	1	3	0	0
sp|P68402|PA1B2_HUMAN Platelet-activating factor acetylhydrolase IB subunit beta...	sp|P68402|PA1B2_HUMANPlatelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens GN=PAFAH1B2 PE=1 SV=1	0.38	5	9	0	0	9	7	8	0
sp|Q3LXA3|DHAK_HUMAN Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase...	sp|Q3LXA3|DHAK_HUMAN Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase...	0.36	7	10	18	13	13	12	14	7
Ribosyldihydronicotinamide dehydrogenase [quinone] OS=Homo sapiens GN=NQO2 PE=1 SV=5	NQO2_HUMAN	0.32	6	6	3	6	6	7	7	2
sp|P37837|TALDO_HUMAN Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2	sp|P37837|TALDO_HUMANTransaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2	0.64	6	6	4	0	4	12	8	3
Isoform 2 of Latent-transforming growth factor beta-binding protein 3 OS=Homo sapiens GN=LTBP3	LTBP3_HUMAN	0.42	0	1	0	1	1	0	3	0
Melanotransferrin OS=Homo sapiens GN=MFI2 PE=1 SV=2	sp|P08582|TRFM_HUMAN	0.57	12	3	0	3	3	4	4	1
sp|P50591|TNF10_HUMAN Tumor necrosis factor ligand superfamily member 10 OS=Homo sapiens GN=TNFSF10 PE=1 SV=1	sp|P50591|TNF10_HUMANTumor necrosis factor ligand superfamily member 10 OS=Homo sapiens GN=TNFSF10 PE=1 SV=1	0.61	6	11	0	0	4	7	4	7
sp|P06314|KV404_HUMAN Ig kappa chain V-IV region B17 OS=Homo sapiens PE=2 SV=1	sp|P06314|KV404_HUMANIg kappa chain V-IV region B17 OS=Homo sapiens PE=2 SV=1	0.47	8	13	0	0	9	5	6	9
Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4	sp|Q99439|CNN2_HUMAN	0.36	2	0	0	0	0	0	0	0
Myosin-4 OS=Homo sapiens GN=MYH4 PE=1 SV=2	MYH4_HUMAN	0.9	0	0	0	0	0	0	2	0
Isoform 2 of Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1	sp|Q9Y617-2|SERC_HUMAN	0.46	4	7	6	11	11	13	7	7
Phospholipid transfer protein OS=Homo sapiens GN=PLTP PE=1 SV=1	sp|P55058|PLTP_HUMAN	0.52	0	1	5	2	2	3	8	3
Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2	ADO_HUMAN	0.64	0	2	2	0	0	8	0	0
Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2	H31_HUMAN	0.41	30	1	0	3	3	4	2	0

Isoform 4 of Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2	sp|P22307-4|NLTP_HUMAN	0.36	31	0	0	0	0	0	0	0
tr|D6RI10|D6RI10_HUMAN Serine protease inhibitor Kazal-type 2 OS=Homo sapiens GN=SPINK2...	tr|D6RI10|D6RI10_HUMAN Serine protease inhibitor Kazal-type 2 OS=Homo sapiens GN=SPINK2...	0.35	7	15	11	7	7	13	9	10
Pyridoxal kinase OS=Homo sapiens GN=PDXK PE=1 SV=1	sp|O00764|PDXK_HUMAN	0.24	9	4	5	6	6	6	3	2
sp|Q9UPN7|PP6R1_HUMAN Serine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens GN=PPP6R1 PE=1 SV=5	sp|Q9UPN7|PP6R1_HUMANSerine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens GN=PPP6R1 PE=1 SV=5	0.24	4	1	0	0	0	0	0	0
sp|P47755|CAZA2_HUMAN F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3	sp|P47755|CAZA2_HUMANF-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3	0.63	17	0	0	0	5	14	9	0
Ropporin-1B (Fragment) OS=Homo sapiens GN=ROPN1B PE=2 SV=1	D6RCR2_HUMAN	0.041	0	3	0	0	0	9	10	11
sp|Q9BUF7|CRUM3_HUMAN Protein crumbs homolog 3 OS=Homo sapiens GN=CRB3 PE=1 SV=3	sp|Q9BUF7|CRUM3_HUMANProtein crumbs homolog 3 OS=Homo sapiens GN=CRB3 PE=1 SV=3	0.45	0	3	4	7	7	5	5	1
sp|Q9NYU2|UGGG1_HUMAN UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3	sp|Q9NYU2|UGGG1_HUMANUDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3	0.39	0	0	6	0	0	0	3	0
Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=4	PEDF_HUMAN	0.5	0	0	8	8	8	0	15	0
Isoform 6 of Rho GTPase-activating protein 17 OS=Homo sapiens GN=ARHGAP17	sp|Q68EM7-6|RHG17_HUMAN	0.36	3	0	0	0	0	0	0	0
sp|P26572|MGAT1_HUMAN Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase OS=Homo sapiens GN=MGAT1 PE=2 SV=2	sp|P26572|MGAT1_HUMANAlpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase OS=Homo sapiens GN=MGAT1 PE=2 SV=2	0.28	8	8	0	0	8	0	11	15
Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3	KAD1_HUMAN	0.73	0	6	2	2	2	12	6	3
sp|O95460|MATN4_HUMAN Matrilin-4 OS=Homo sapiens GN=MATN4 PE=1 SV=3	sp|O95460|MATN4_HUMANMatrilin-4 OS=Homo sapiens GN=MATN4 PE=1 SV=3	0.55	4	2	0	0	0	0	6	5
Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2	sp|P01042|KNG1_HUMAN	0.38	1	7	3	0	0	6	2	2

Isoform 3 of Oxidoreductase HTATIP2 OS=Homo sapiens GN=HTATIP2	sp|Q9BUP3-3|HTAI2_HUMAN	0.097	2	3	0	3	3	5	3	5
Calsyntenin-1 OS=Homo sapiens GN=CLSTN1 PE=2 SV=1	B4E3Q1_HUMAN	0.71	5	2	0	4	4	1	1	2
Protein sidekick-1 OS=Homo sapiens GN=SDK1 PE=1 SV=3	sp|Q7Z5N4|SDK1_HUMAN	0.53	2	0	0	0	0	0	7	0
Rho GTPase-activating protein 4 OS=Homo sapiens GN=ARHGAP4 PE=2 SV=1	F5GZW3_HUMAN	0.36	3	0	0	0	0	0	0	0
Isoform 2 of Acyl-protein thioesterase 1 OS=Homo sapiens GN=LYPLA1	LYPA1_HUMAN	0.46	0	1	0	4	4	0	10	0
sp|Q9H0R4|HDHD2_HUMAN Haloacid dehalogenase-like hydrolase domain-containing protein...	sp|Q9H0R4|HDHD2_HUMANHaloacid dehalogenase-like hydrolase domain-containing protein 2 OS=Homo sapiens GN=HDHD2 PE=1 SV=1	0.68	13	11	0	0	12	11	7	0
40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	RS4X_HUMAN	0.36	14	4	9	3	3	8	13	6
Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3	PP1B_HUMAN	0.83	0	7	1	9	9	10	8	0
sp|Q9UKF5|ADA29_HUMAN Disintegrin and metalloproteinase domain-containing protein 29 OS=Homo sapiens GN=ADAM29 PE=1 SV=3	sp|Q9UKF5|ADA29_HUMANDisintegrin and metalloproteinase domain-containing protein 29 OS=Homo sapiens GN=ADAM29 PE=1 SV=3	0.94	0	0	0	2	2	0	0	0
Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2	CO9_HUMAN	0.41	0	2	4	2	2	3	2	1
sp|P49257|LMAN1_HUMAN Protein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2	sp|P49257|LMAN1_HUMANProtein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2	0.2	10	6	7	0	0	0	4	0
sp|Q9UM22|EPDR1_HUMAN Mammalian ependymin-related protein 1 OS=Homo sapiens GN=EPDR1 PE=1 SV=2	sp|Q9UM22|EPDR1_HUMANMammalian ependymin-related protein 1 OS=Homo sapiens GN=EPDR1 PE=1 SV=2	0.0015	0	2	0	0	10	9	8	5
Insulin-degrading enzyme OS=Homo sapiens GN=IDE PE=1 SV=4	IDE_HUMAN	0.48	3	0	2	0	0	4	1	2
sp|Q96AG4|LRC59_HUMAN Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1	sp|Q96AG4|LRC59_HUMANLeucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1	0.3	17	2	0	0	0	0	0	0

sp|P14317|HCLS1_HUMAN Hematopoietic lineage cell-specific protein OS=Homo sapiens...	sp|P14317|HCLS1_HUMANHematopoietic lineage cell-specific protein OS=Homo sapiens GN=HCLS1 PE=1 SV=3	0.4	46	0	0	0	0	4	0	0
Keratin-associated protein 9-1 OS=Homo sapiens GN=KRTAP9-1 PE=2 SV=1	H7BXR9_HUMAN	0.55	0	1	0	0	0	0	0	3
Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2	CYTB_HUMAN	0.31	21	7	8	3	3	9	8	9
Isoform 3 of Retinol dehydrogenase 11 OS=Homo sapiens GN=RDH11	sp|Q8TC12-3|RDH11_HUMAN	0.41	4	3	3	1	1	7	5	1
Isoform 4 of Target of Myb protein 1 OS=Homo sapiens GN=TOM1	sp|O60784-4|TOM1_HUMAN	0.16	3	4	2	1	1	2	0	2
40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	RS10_HUMAN	0.34	16	0	5	4	4	13	3	4
Lactadherin OS=Homo sapiens GN=MFGE8 PE=1 SV=2	sp|Q08431|MFGM_HUMAN	0.92	0	4	2	4	4	8	4	6
Isoform 3 of 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17	sp|P18621-3|RL17_HUMAN	0.26	20	3	4	0	0	7	4	1
sp|Q9GZN4|BSSP4_HUMAN Brain-specific serine protease 4 OS=Homo sapiens GN=PRSS22...	sp|Q9GZN4|BSSP4_HUMANBrain-specific serine protease 4 OS=Homo sapiens GN=PRSS22 PE=1 SV=1	0.77	1	3	0	0	0	3	2	0
Isoform 3 of Transmembrane emp24 domain-containing protein 4 OS=Homo sapiens GN=TMED4	sp|Q7Z7H5-3|TMED4_HUMAN	0.46	0	0	3	10	10	0	14	0
Reticulon-4 OS=Homo sapiens GN=RTN4 PE=1 SV=2	sp|Q9NQC3|RTN4_HUMAN	0.36	11	0	0	0	0	0	0	0
Maleylacetoacetate isomerase OS=Homo sapiens GN=GSTZ1 PE=1 SV=3	sp|O43708|MAAI_HUMAN	0.21	8	15	3	5	5	4	8	4
Tetraspanin-6 OS=Homo sapiens GN=TSPAN6 PE=1 SV=1	TSN6_HUMAN	0.15	3	7	1	4	4	4	3	4
Epithelial discoidin domain-containing receptor 1 OS=Homo sapiens GN=DDR1 PE=1 SV=1	sp|Q08345|DDR1_HUMAN	0.4	6	7	7	4	4	10	2	12
sp|P48556|PSMD8_HUMAN 26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens...	sp|P48556|PSMD8_HUMAN26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2	0.0068	0	0	0	0	2	7	4	4
sp|P34059|GALNS_HUMAN N-acetylgalactosamine-6-sulfatase OS=Homo sapiens GN=GALNS...	sp|P34059|GALNS_HUMANN-acetylgalactosamine-6-sulfatase OS=Homo sapiens GN=GALNS PE=1 SV=1	0.39	12	7	10	0	12	0	13	0
Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	NUCL_HUMAN	0.36	13	0	0	0	0	0	0	0
Isoform 3 of Protein scribble homolog OS=Homo sapiens GN=SCRIB	sp|Q14160-3|SCRIB_HUMAN	0.36	2	0	0	0	0	0	0	0

Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b OS=Homo sapiens GN=COPB2 PE=2 SV=1	B4DZI8_HUMAN	0.62	7	0	0	0	0	3	0	0
ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Homo sapiens GN=CARKD PE=1 SV=1	sp|Q8IW45|NNRD_HUMAN	0.75	3	6	0	0	0	9	0	3
sp|Q6P4A8|PLBL1_HUMAN Phospholipase B-like 1 OS=Homo sapiens GN=PLBD1 PE=1 SV=2	sp|Q6P4A8|PLBL1_HUMANPhospholipase B-like 1 OS=Homo sapiens GN=PLBD1 PE=1 SV=2	0.47	1	0	2	2	2	0	4	2
Phosphomannomutase 2 OS=Homo sapiens GN=PMM2 PE=1 SV=1	PMM2_HUMAN	0.36	3	11	5	3	3	6	9	4
Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2	TBB3_HUMAN	0.49	0	1	3	0	0	1	1	4
sp|Q9Y2S2|CRYL1_HUMAN Lambda-crystallin homolog OS=Homo sapiens GN=CRYL1 PE=1 SV=3	sp|Q9Y2S2|CRYL1_HUMANLambda-crystallin homolog OS=Homo sapiens GN=CRYL1 PE=1 SV=3	0.41	3	8	6	0	1	6	11	0
Isoform B of Annexin A13 OS=Homo sapiens GN=ANXA13	ANX13_HUMAN	0.35	3	4	3	0	1	4	2	1
Uncharacterized protein OS=Homo sapiens PE=2 SV=1	F8W810_HUMAN	0.49	1	2	3	1	1	4	0	4
Protocadherin-1 (Fragment) OS=Homo sapiens GN=PCDH1 PE=2 SV=1	H0Y2Z9_HUMAN	0.36	0	9	0	0	0	0	0	0
Isoform 2 of Prothymosin alpha OS=Homo sapiens GN=PTMA	sp|P06454-2|PTMA_HUMAN	0.36	62	0	0	0	0	0	0	0
Glycolipid transfer protein OS=Homo sapiens GN=GLTP PE=1 SV=3	GLTP_HUMAN	0.37	5	3	5	2	2	5	3	7
Ras-related protein Rab-5A OS=Homo sapiens GN=RAB5A PE=2 SV=1	B4DJA5_HUMAN	0.33	1	4	2	2	2	3	4	1
Kallikrein-1 OS=Homo sapiens GN=KLK1 PE=1 SV=2	sp|P06870|KLK1_HUMAN	0.15	1	7	1	5	5	1	2	1
Protein-glutamine gamma-glutamyltransferase E OS=Homo sapiens GN=TGM3 PE=1 SV=4	TGM3_HUMAN	0.39	0	2	0	1	1	1	2	1
sp|P04433|KV309_HUMAN Ig kappa chain V-III region VG (Fragment) OS=Homo sapiens PE=1 SV=1	sp|P04433|KV309_HUMANIg kappa chain V-III region VG (Fragment) OS=Homo sapiens PE=1 SV=1	0.11	9	8	0	0	8	10	8	8
Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	sp|P55060|XPO2_HUMAN	0.44	6	0	0	0	0	0	1	0
sp|P35080|PROF2_HUMAN Profilin-2 OS=Homo sapiens GN=PFN2 PE=1 SV=3	sp|P35080|PROF2_HUMANProfilin-2 OS=Homo sapiens GN=PFN2 PE=1 SV=3	0.31	7	8	0	0	3	22	14	0

Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=2 SV=1	A8MUB1_HUMAN	0.42	6	3	6	4	4	2	3	1
Alpha/beta hydrolase domain-containing protein 14B OS=Homo sapiens GN=ABHD14B PE=2 SV=1	F8W9U3_HUMAN	0.42	0	1	5	18	18	0	16	0
Protein AMBP (Fragment) OS=Homo sapiens GN=AMBP PE=4 SV=1	S4R471_HUMAN	0.12	3	9	3	6	6	1	1	1
sp|Q15389|ANGP1_HUMAN Angiopoietin-1 OS=Homo sapiens GN=ANGPT1 PE=1 SV=2	sp|Q15389|ANGP1_HUMANAngiopoietin-1 OS=Homo sapiens GN=ANGPT1 PE=1 SV=2	0.43	0	3	2	0	1	0	2	2
sp|P36543|VATE1_HUMAN V-type proton ATPase subunit E 1 OS=Homo sapiens GN=ATP6V1E1...	sp|P36543|VATE1_HUMANV-type proton ATPase subunit E 1 OS=Homo sapiens GN=ATP6V1E1 PE=1 SV=1	0.24	7	9	5	0	1	0	7	2
sp|Q9Y2W1|TR150_HUMAN Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2	sp|Q9Y2W1|TR150_HUMANThyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2	0.36	20	0	0	0	0	0	0	0
Isoform 2 of Protein HID1 OS=Homo sapiens GN=HID1	sp|Q8IV36-2|HID1_HUMAN (+1)	0.46	1	2	3	3	3	4	0	4
Tartrate-resistant acid phosphatase type 5 OS=Homo sapiens GN=ACP5 PE=1 SV=3	PPA5_HUMAN	0.51	5	5	5	2	2	11	6	6
sp|O00469|PLOD2_HUMAN Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 OS=Homo sapiens...	sp|O00469|PLOD2_HUMANProcollagen-lysine,2-oxoglutarate 5-dioxygenase 2 OS=Homo sapiens GN=PLOD2 PE=1 SV=2	0.79	5	6	8	0	17	12	13	0
40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=2 SV=1	E9PL09_HUMAN	0.5	0	9	3	1	1	7	7	1
Myosin-6 OS=Homo sapiens GN=MYH6 PE=1 SV=5	MYH6_HUMAN	0.56	4	4	0	0	0	0	3	0
sp|P05387|RLA2_HUMAN 60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1...	sp|P05387|RLA2_HUMAN 60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1...	0.38	65	0	0	0	0	0	0	4
sp|P45974-2|UBP5_HUMAN Isoform Short of Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo...	sp|P45974-2|UBP5_HUMAN Isoform Short of Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo... (+1)	0.46	5	13	4	6	6	8	13	12
Aspartyl aminopeptidase OS=Homo sapiens GN=DNPEP PE=2 SV=1	E7ETB3_HUMAN	0.48	1	1	6	1	1	3	4	4
sp|Q04917|1433F_HUMAN 14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4	sp|Q04917|1433F_HUMAN14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4	0.29	5	8	3	6	6	2	3	6
40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=2 SV=1	C9JM19_HUMAN	0.41	2	1	3	3	3	5	4	2
Isoform 2 of Kinesin light chain 2 OS=Homo sapiens GN=KLC2	sp|Q9H0B6-2|KLC2_HUMAN	0.15	4	14	1	1	1	0	0	5

COP9 signalosome complex subunit 4 OS=Homo sapiens GN=COPS4 PE=2 SV=1	D6RFN0_HUMAN	0.43	0	0	2	5	5	0	3	0
Lin-7 homolog C (C. elegans), isoform CRA_b OS=Homo sapiens GN=LIN7C PE=2 SV=1	G3V1D4_HUMAN	0.79	6	7	0	0	0	6	0	4
sp|P12931-2|SRC_HUMAN Isoform 2 of Proto-oncogene tyrosine-protein kinase Src OS=Homo sapiens GN=SRC	sp|P12931-2|SRC_HUMANIsoform 2 of Proto-oncogene tyrosine-protein kinase Src OS=Homo sapiens GN=SRC	0.15	0	1	0	0	3	2	2	0
sp|P12036-2|NFH_HUMAN Isoform 2 of Neurofilament heavy polypeptide OS=Homo sapiens GN=NEFH	sp|P12036-2|NFH_HUMANIsoform 2 of Neurofilament heavy polypeptide OS=Homo sapiens GN=NEFH	0.63	0	1	3	0	0	0	11	0
Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	sp|P08603|CFAH_HUMAN	0.31	5	0	7	0	0	1	0	0
sp|P49755|TMEDA_HUMAN Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=1 SV=2	sp|P49755|TMEDA_HUMANTransmembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=1 SV=2	0.26	8	2	0	0	2	10	9	3
sp|Q9NRV9|HEBP1_HUMAN Heme-binding protein 1 OS=Homo sapiens GN=HEBP1 PE=1 SV=1	sp|Q9NRV9|HEBP1_HUMANHeme-binding protein 1 OS=Homo sapiens GN=HEBP1 PE=1 SV=1	0.8	11	4	0	8	8	13	7	0
sp|P19022|CADH2_HUMAN Cadherin-2 OS=Homo sapiens GN=CDH2 PE=1 SV=4	sp|P19022|CADH2_HUMANCadherin-2 OS=Homo sapiens GN=CDH2 PE=1 SV=4	0.68	0	6	0	0	0	2	0	1
Protein ABHD14A-ACY1 OS=Homo sapiens GN=ABHD14A-ACY1 PE=2 SV=1	C9JMV9_HUMAN	0.94	0	0	0	5	5	0	0	0
Isoform 2 of Protein CDV3 homolog OS=Homo sapiens GN=CDV3	sp|Q9UKY7-2|CDV3_HUMAN	0.36	10	0	0	0	0	0	0	0
sp|Q4G148|GXLT1_HUMAN Glucoside xylosyltransferase 1 OS=Homo sapiens GN=GXYLT1 PE=1 SV=2	sp|Q4G148|GXLT1_HUMANGlucoside xylosyltransferase 1 OS=Homo sapiens GN=GXYLT1 PE=1 SV=2	0.23	0	2	0	0	2	1	0	3
Isoform MEF2DA'0 of Myocyte-specific enhancer factor 2D OS=Homo sapiens GN=MEF2D	sp|Q14814-5|MEF2D_HUMAN	0.36	6	0	0	0	0	0	0	0
sp|Q9ULC3|RAB23_HUMAN Ras-related protein Rab-23 OS=Homo sapiens GN=RAB23 PE=1 SV=1	sp|Q9ULC3|RAB23_HUMANRas-related protein Rab-23 OS=Homo sapiens GN=RAB23 PE=1 SV=1	0.99	5	4	0	4	4	8	1	0
Isoform 3 of V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1	sp|Q93050-3|VPP1_HUMAN	0.4	0	2	0	0	0	9	0	1
Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2	sp|P53634|CATC_HUMAN	0.23	1	2	0	0	0	2	6	2

sp|Q8IYP2|PRS58_HUMAN Serine protease 58 OS=Homo sapiens GN=PRSS58 PE=2 SV=1	sp|Q8IYP2|PRS58_HUMANSerine protease 58 OS=Homo sapiens GN=PRSS58 PE=2 SV=1	0.7	6	2	0	2	2	3	2	6
Iduronate 2-sulfatase OS=Homo sapiens GN=IDS PE=1 SV=1	IDS_HUMAN	0.85	2	8	0	4	4	10	2	0
Junctional adhesion molecule A OS=Homo sapiens GN=F11R PE=1 SV=1	JAM1_HUMAN	0.35	0	0	8	5	5	0	2	0
sp|Q7RTZ1|OVCH2_HUMAN Ovochymase-2 OS=Homo sapiens GN=OVCH2 PE=2 SV=2	sp|Q7RTZ1|OVCH2_HUMANOvochymase-2 OS=Homo sapiens GN=OVCH2 PE=2 SV=2	0.87	12	2	0	3	3	6	11	0
Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=2 SV=1	E9PLD0_HUMAN	0.38	0	6	1	10	10	9	1	6
sp|P20338|RAB4A_HUMAN Ras-related protein Rab-4A OS=Homo sapiens GN=RAB4A PE=1 SV=3	sp|P20338|RAB4A_HUMANRas-related protein Rab-4A OS=Homo sapiens GN=RAB4A PE=1 SV=3	0.26	5	1	1	0	0	3	1	2
sp|P51153|RAB13_HUMAN Ras-related protein Rab-13 OS=Homo sapiens GN=RAB13 PE=1 SV=1	sp|P51153|RAB13_HUMANRas-related protein Rab-13 OS=Homo sapiens GN=RAB13 PE=1 SV=1	0.0087	7	6	0	0	6	4	7	6
Aspartate aminotransferase OS=Homo sapiens GN=GOT2 PE=2 SV=1	E7ERW2_HUMAN	0.4	0	3	0	0	0	2	2	2
sp|Q8N9U0|TAC2N_HUMAN Tandem C2 domains nuclear protein OS=Homo sapiens GN=TC2N PE=1...	sp|Q8N9U0|TAC2N_HUMANTandem C2 domains nuclear protein OS=Homo sapiens GN=TC2N PE=1 SV=2	0.0068	0	0	0	0	1	1	2	3
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	H14_HUMAN	0.36	67	0	0	0	0	0	1	0
Cystatin-M OS=Homo sapiens GN=CST6 PE=1 SV=1	CYTM_HUMAN	0.28	5	12	6	7	7	2	4	6
Isoform 2 of Cell cycle control protein 50A OS=Homo sapiens GN=TMEM30A	sp|Q9NV96-2|CC50A_HUMAN	0.44	3	3	4	3	3	0	9	3
sp|P62906|RL10A_HUMAN 60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	sp|P62906|RL10A_HUMAN60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	0.3	10	5	0	0	3	9	6	10
sp|Q8NEB7|ACRBP_HUMAN Acrosin-binding protein OS=Homo sapiens GN=ACRBP PE=2 SV=1	sp|Q8NEB7|ACRBP_HUMANAcrosin-binding protein OS=Homo sapiens GN=ACRBP PE=2 SV=1	0.2	1	0	0	0	0	1	13	4
Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	NPM_HUMAN	0.38	39	0	0	0	0	2	0	0
Isoform 2 of Dynactin subunit 2 OS=Homo sapiens GN=DCTN2	sp|Q13561-2|DCTN2_HUMAN	0.53	2	0	8	3	3	8	4	6

sp|Q86XP3|DDX42_HUMAN ATP-dependent RNA helicase DDX42 OS=Homo sapiens GN=DDX42 PE=1 SV=1	sp|Q86XP3|DDX42_HUMANATP-dependent RNA helicase DDX42 OS=Homo sapiens GN=DDX42 PE=1 SV=1	0.36	8	0	0	0	0	0	0	0
sp|Q8TDL5|BPIB1_HUMAN BPI fold-containing family B member 1 OS=Homo sapiens GN=BPIFB1 PE=2 SV=1	sp|Q8TDL5|BPIB1_HUMANBPI fold-containing family B member 1 OS=Homo sapiens GN=BPIFB1 PE=2 SV=1	0.43	5	1	1	0	0	0	4	2
Isoform 2 of Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3	sp|P51991-2|ROA3_HUMAN	0.17	22	0	2	0	0	0	0	0
Zinc finger protein 207 OS=Homo sapiens GN=ZNF207 PE=2 SV=1	J3QRS9_HUMAN	0.36	15	0	0	0	0	0	0	0
Isoform 1B of Beta-arrestin-1 OS=Homo sapiens GN=ARRB1	ARRB1_HUMAN	0.33	4	2	4	3	3	5	1	2
Grancalcin OS=Homo sapiens GN=GCA PE=1 SV=2	GRAN_HUMAN	0.18	5	9	1	5	5	6	2	7
Vacuolar-sorting protein SNF8 OS=Homo sapiens GN=SNF8 PE=1 SV=1	sp|Q96H20|SNF8_HUMAN	0.37	2	1	1	2	2	3	2	0
sp|Q8NCC3|PAG15_HUMAN Group XV phospholipase A2 OS=Homo sapiens GN=PLA2G15 PE=1 SV=2	sp|Q8NCC3|PAG15_HUMANGroup XV phospholipase A2 OS=Homo sapiens GN=PLA2G15 PE=1 SV=2	0.23	5	1	2	3	3	4	1	0
SPARC OS=Homo sapiens GN=SPARC PE=1 SV=1	SPRC_HUMAN	0.72	0	1	1	2	2	1	4	1
Isoform 4 of EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1	sp|Q12805-4|FBLN3_HUMAN	0.87	1	3	0	0	0	1	0	2
Glypican-6 OS=Homo sapiens GN=GPC6 PE=1 SV=1	GPC6_HUMAN	0.45	0	0	0	0	0	4	0	0
Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=2 SV=1	J3KQ32_HUMAN	0.27	8	5	4	3	3	3	5	6
sp|P01766|HV305_HUMAN Ig heavy chain V-III region BRO OS=Homo sapiens PE=1 SV=1	sp|P01766|HV305_HUMANIg heavy chain V-III region BRO OS=Homo sapiens PE=1 SV=1	0.24	9	5	5	5	5	5	10	0
sp|P16150|LEUK_HUMAN Leukosialin OS=Homo sapiens GN=SPN PE=1 SV=1	sp|P16150|LEUK_HUMAN Leukosialin OS=Homo sapiens GN=SPN PE=1 SV=1-DECOY	0.97	2	0	0	0	0	0	2	0
Arrestin domain-containing protein 1 (Fragment) OS=Homo sapiens GN=ARRDC1 PE=2 SV=1	Q5T370_HUMAN	0.83	5	6	0	0	0	6	0	6
Malate dehydrogenase OS=Homo sapiens GN=MDH2 PE=2 SV=1	G3XAL0_HUMAN	0.55	3	3	4	3	3	5	10	4
40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1	RS7_HUMAN	0.24	18	1	4	1	1	1	3	0

Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 (Fragment) OS=Homo sapiens GN=GNB2 PE=2 SV=1	C9JXA5_HUMAN	0.31	1	3	0	4	4	5	3	4
sp|Q9H1M3|DB129_HUMAN Beta-defensin 129 OS=Homo sapiens GN=DEFB129 PE=2 SV=1	sp|Q9H1M3|DB129_HUMANBeta-defensin 129 OS=Homo sapiens GN=DEFB129 PE=2 SV=1	0.58	1	8	1	0	0	5	9	0
COP9 signalosome complex subunit 5 OS=Homo sapiens GN=COPS5 PE=1 SV=4	CSN5_HUMAN	0.3	0	4	0	0	0	1	8	4
60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=2 SV=1	RL18_HUMAN	0.38	2	1	12	0	0	6	7	2
sp|Q8NBS9|TXND5_HUMAN Thioredoxin domain-containing protein 5 OS=Homo sapiens GN=TXNDC5 PE=1 SV=2	sp|Q8NBS9|TXND5_HUMANThioredoxin domain-containing protein 5 OS=Homo sapiens GN=TXNDC5 PE=1 SV=2	0.31	7	0	9	0	0	3	1	0
sp|P05783|K1C18_HUMAN Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1...	sp|P05783|K1C18_HUMANKeratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2	0.87	0	8	2	0	1	0	4	2
sp|Q9UKJ8|ADA21_HUMAN Disintegrin and metalloproteinase domain-containing protein 21 OS=Homo sapiens GN=ADAM21 PE=2 SV=2	sp|Q9UKJ8|ADA21_HUMANDisintegrin and metalloproteinase domain-containing protein 21 OS=Homo sapiens GN=ADAM21 PE=2 SV=2-DECOY	0.36	0	0	0	0	0	0	2	0
sp|P61086|UBE2K_HUMAN Ubiquitin-conjugating enzyme E2 K OS=Homo sapiens GN=UBE2K...	sp|P61086|UBE2K_HUMANUbiquitin-conjugating enzyme E2 K OS=Homo sapiens GN=UBE2K PE=1 SV=3	0.029	4	4	0	0	4	6	5	7
Malectin OS=Homo sapiens GN=MLEC PE=1 SV=1	MLEC_HUMAN	0.18	0	2	0	0	0	2	6	2
Suprabasin OS=Homo sapiens GN=SBSN PE=2 SV=2	sp|Q6UWP8|SBSN_HUMAN	0.65	0	0	0	2	2	0	2	0
sp|Q13435|SF3B2_HUMAN Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2	sp|Q13435|SF3B2_HUMANSplicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2	0.36	9	0	0	0	0	0	0	0
Pumilio homolog 1 (Fragment) OS=Homo sapiens GN=PUM1 PE=4 SV=1	H0YEH2_HUMAN	0.36	2	0	0	0	0	0	0	0
sp|Q96CN7|ISOC1_HUMAN Isochorismatase domain-containing protein 1 OS=Homo sapiens GN=ISOC1 PE=1 SV=3	sp|Q96CN7|ISOC1_HUMANIsochorismatase domain-containing protein 1 OS=Homo sapiens GN=ISOC1 PE=1 SV=3	0.92	7	12	0	0	7	0	14	0
RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=2 SV=1	H3BPE7_HUMAN	0.36	10	0	0	0	0	0	0	0

sp|Q13232|NDK3_HUMAN Nucleoside diphosphate kinase 3 OS=Homo sapiens GN=NME3 PE=1...	sp|Q13232|NDK3_HUMAN Nucleoside diphosphate kinase 3 OS=Homo sapiens GN=NME3 PE=1...	0.34	12	8	12	6	6	10	8	5
Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens GN=GCLC PE=1 SV=2	GSH1_HUMAN	0.57	2	6	0	0	0	3	0	1
sp|Q9BS86|ZPBP1_HUMAN Zona pellucida-binding protein 1 OS=Homo sapiens GN=ZPBP PE=2...	sp|Q9BS86|ZPBP1_HUMANZona pellucida-binding protein 1 OS=Homo sapiens GN=ZPBP PE=2 SV=1	0.46	1	4	4	0	0	0	11	0
Isoform 3 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17	sp|Q92841-2|DDX17_HUMAN	0.36	8	0	0	0	0	0	0	0
Cystatin-SN OS=Homo sapiens GN=CST1 PE=1 SV=3	CYTN_HUMAN	0.4	1	12	6	6	6	13	8	5
60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	RL7A_HUMAN	0.16	14	1	1	0	0	2	1	1
sp|O43813|LANC1_HUMAN LanC-like protein 1 OS=Homo sapiens GN=LANCL1 PE=1 SV=1	sp|O43813|LANC1_HUMANLanC-like protein 1 OS=Homo sapiens GN=LANCL1 PE=1 SV=1	0.56	1	5	0	0	0	2	2	6
sp|P10809|CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1...	sp|P10809|CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1...	0.32	49	1	1	0	0	1	3	0
Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens GN=PPP2R4 PE=1 SV=3	sp|Q15257|PTPA_HUMAN	0.57	0	0	4	3	3	0	11	0
sp|Q13438-6|OS9_HUMAN Isoform 6 of Protein OS-9 OS=Homo sapiens GN=OS9	sp|Q13438-6|OS9_HUMANIsoform 6 of Protein OS-9 OS=Homo sapiens GN=OS9	0.23	6	6	3	3	3	0	11	6
Treacle protein OS=Homo sapiens GN=TCOF1 PE=2 SV=1	E9PHK9_HUMAN	0.36	2	0	0	0	0	0	0	0
HCG2044781 OS=Homo sapiens GN=TMEM189 PE=2 SV=1	G3V2F7_HUMAN	0.33	7	0	4	3	3	3	3	2
Early endosome antigen 1 OS=Homo sapiens GN=EEA1 PE=1 SV=2	EEA1_HUMAN	0.33	1	1	4	0	0	0	1	0
sp|Q9Y287|ITM2B_HUMAN Integral membrane protein 2B OS=Homo sapiens GN=ITM2B PE=1 SV=1	sp|Q9Y287|ITM2B_HUMANIntegral membrane protein 2B OS=Homo sapiens GN=ITM2B PE=1 SV=1	0.9	5	7	0	3	4	0	12	1
sp|Q9UNM6|PSD13_HUMAN 26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=1 SV=2	sp|Q9UNM6|PSD13_HUMAN26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=1 SV=2	0.43	1	4	5	0	1	0	10	0
Reticulon-3 OS=Homo sapiens GN=RTN3 PE=1 SV=2	sp|O95197|RTN3_HUMAN	1	7	0	0	0	0	6	1	0

Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=2 SV=1	B4DVY1_HUMAN	0.36	6	0	0	0	0	0	0	0
sp|P43487|RANG_HUMAN Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1...	sp|P43487|RANG_HUMAN Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1...	0.33	36	6	0	4	4	0	3	4
Isoform 2 of Vesicle-associated membrane protein 4 OS=Homo sapiens GN=VAMP4	VAMP4_HUMAN (+1)	0.36	0	0	0	0	0	0	0	7
Ras-related protein Ral-A OS=Homo sapiens GN=RALA PE=1 SV=1	RALA_HUMAN	0.36	2	3	3	4	4	3	6	3
Isoform 2 of Gephyrin OS=Homo sapiens GN=GPHN	sp|Q9NQX3-2|GEPH_HUMAN	0.25	3	0	2	1	1	1	0	0
Corticosteroid-binding globulin OS=Homo sapiens GN=SERPINA6 PE=1 SV=1	CBG_HUMAN	0.57	0	6	1	3	3	3	6	4
Tetraspanin-1 OS=Homo sapiens GN=TSPAN1 PE=1 SV=2	TSN1_HUMAN	0.94	0	8	1	2	2	2	3	10
sp|Q9H9H4|VP37B_HUMAN Vacuolar protein sorting-associated protein 37B OS=Homo sapiens...	sp|Q9H9H4|VP37B_HUMANVacuolar protein sorting-associated protein 37B OS=Homo sapiens GN=VPS37B PE=1 SV=1	0.47	0	7	0	0	12	1	1	2
sp|P30626|SORCN_HUMAN Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1	sp|P30626|SORCN_HUMANSorcin OS=Homo sapiens GN=SRI PE=1 SV=1	0.47	3	5	0	4	4	18	3	0
Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3 PE=1 SV=2	SODE_HUMAN	0.28	0	0	0	1	1	0	3	0
sp|Q92734-2|TFG_HUMAN Isoform 2 of Protein TFG OS=Homo sapiens GN=TFG	sp|Q92734-2|TFG_HUMANIsoform 2 of Protein TFG OS=Homo sapiens GN=TFG	0.64	6	1	0	0	0	2	0	2
Cornulin OS=Homo sapiens GN=CRNN PE=1 SV=1	CRNN_HUMAN	0.94	0	0	0	4	4	0	0	0
Zyxin (Fragment) OS=Homo sapiens GN=ZYX PE=2 SV=1	H0Y2Y8_HUMAN	0.36	31	0	0	0	0	0	0	0
sp|Q8NCL4|GALT6_HUMAN Polypeptide N-acetylgalactosaminyltransferase 6 OS=Homo sapiens GN=GALNT6 PE=2 SV=2	sp|Q8NCL4|GALT6_HUMANPolypeptide N-acetylgalactosaminyltransferase 6 OS=Homo sapiens GN=GALNT6 PE=2 SV=2	0.24	1	3	0	0	2	6	3	0
sp|P40763|STAT3_HUMAN Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2	sp|P40763|STAT3_HUMANSignal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2	0.29	1	10	7	0	1	0	3	4
Serine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=SARS PE=2 SV=1	Q5T5C7_HUMAN	0.45	0	0	4	0	0	0	4	0

sp|P07237|PDIA1_HUMAN Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3	sp|P07237|PDIA1_HUMANProtein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3	0.27	6	11	4	4	4	0	9	9
Tubulin-specific chaperone A OS=Homo sapiens GN=TBCA PE=1 SV=3	TBCA_HUMAN	0.24	21	0	6	4	4	1	1	1
BRO1 domain-containing protein BROX OS=Homo sapiens GN=BROX PE=1 SV=1	BROX_HUMAN	0.39	1	0	2	0	0	0	2	0
Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens GN=AHSA1 PE=2 SV=1	B4DUR9_HUMAN	0.98	3	4	0	0	0	3	0	4
Gastric inhibitory polypeptide receptor OS=Homo sapiens GN=GIPR PE=1 SV=1	sp|P48546|GIPR_HUMAN	0.36	0	0	0	0	0	0	5	0
sp|P61088|UBE2N_HUMAN Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1	sp|P61088|UBE2N_HUMANUbiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1	0.79	17	1	0	0	3	6	4	0
Synaptogyrin-2 OS=Homo sapiens GN=SYNGR2 PE=1 SV=1	SNG2_HUMAN	0.41	2	1	4	5	5	8	3	3
Isoform 5 of Four and a half LIM domains protein 1 OS=Homo sapiens GN=FHL1	sp|Q13642-5|FHL1_HUMAN	0.89	0	0	1	0	0	5	1	4
sp|Q9Y5K6|CD2AP_HUMAN CD2-associated protein OS=Homo sapiens GN=CD2AP PE=1 SV=1	sp|Q9Y5K6|CD2AP_HUMANCD2-associated protein OS=Homo sapiens GN=CD2AP PE=1 SV=1	0.23	2	1	1	1	1	0	2	0
sp|Q9UL25|RAB21_HUMAN Ras-related protein Rab-21 OS=Homo sapiens GN=RAB21 PE=1 SV=3	sp|Q9UL25|RAB21_HUMANRas-related protein Rab-21 OS=Homo sapiens GN=RAB21 PE=1 SV=3	0.84	0	5	1	2	2	5	5	0
sp|Q9BUL8|PDC10_HUMAN Programmed cell death protein 10 OS=Homo sapiens GN=PDCD10 PE=1 SV=1	sp|Q9BUL8|PDC10_HUMANProgrammed cell death protein 10 OS=Homo sapiens GN=PDCD10 PE=1 SV=1	0.52	0	4	0	0	0	3	5	0
sp|Q14258|TRI25_HUMAN E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2	sp|Q14258|TRI25_HUMANE3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2	0.55	3	0	0	0	0	1	0	0
Histidine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=HARS PE=2 SV=1	B3KWE1_HUMAN	0.55	0	8	6	0	0	9	5	6
sp|P09936|UCHL1_HUMAN Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Homo sapiens GN=UCHL1 PE=1 SV=2	sp|P09936|UCHL1_HUMANUbiquitin carboxyl-terminal hydrolase isozyme L1 OS=Homo sapiens GN=UCHL1 PE=1 SV=2	0.064	0	1	0	0	0	7	8	3

CapZ-interacting protein OS=Homo sapiens GN=RCSD1 PE=2 SV=1	B7ZKW8_HUMAN	0.36	8	0	0	0	0	0	0	0
sp|P31944|CASPE_HUMAN Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2	sp|P31944|CASPE_HUMANCaspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2	0.87	0	0	0	14	14	0	6	0
sp|P01860|IGHG3_HUMAN Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2	sp|P01860|IGHG3_HUMANIg gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2	0.45	1	6	1	3	3	5	5	4
Isoform 2 of Microfibril-associated glycoprotein 4 OS=Homo sapiens GN=MFAP4	MFAP4_HUMAN	0.5	0	4	0	0	0	0	0	1
sp|O95861|BPNT1_HUMAN 3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 PE=1 SV=1	sp|O95861|BPNT1_HUMAN3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 PE=1 SV=1	0.17	1	12	1	0	0	1	2	0
sp|P16562|CRIS2_HUMAN Cysteine-rich secretory protein 2 OS=Homo sapiens GN=CRISP2 PE=1 SV=1	sp|P16562|CRIS2_HUMANCysteine-rich secretory protein 2 OS=Homo sapiens GN=CRISP2 PE=1 SV=1	0.59	2	7	0	0	0	0	11	5
60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	RLA0_HUMAN	0.68	2	0	0	0	0	1	0	0
sp|Q9NZH0|GPC5B_HUMAN G-protein coupled receptor family C group 5 member B OS=Homo sapiens GN=GPRC5B PE=2 SV=2	sp|Q9NZH0|GPC5B_HUMANG-protein coupled receptor family C group 5 member B OS=Homo sapiens GN=GPRC5B PE=2 SV=2	0.16	0	0	0	0	3	0	6	0
Putative gamma-glutamyltranspeptidase 3 OS=Homo sapiens GN=GGT3P PE=5 SV=2	GGT3_HUMAN	1	13	9	0	0	0	11	0	9
Desmoglein-2 OS=Homo sapiens GN=DSG2 PE=1 SV=2	DSG2_HUMAN	0.5	1	2	1	3	3	4	2	3
sp|O00264|PGRC1_HUMAN Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3	sp|O00264|PGRC1_HUMANMembrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3	0.25	2	10	0	0	7	0	14	9
Isoform 2 of Gamma-glutamyltranspeptidase 1 OS=Homo sapiens GN=GGT1	sp|P19440-2|GGT1_HUMAN	0.42	0	0	13	10	10	0	13	0
sp|P26599|PTBP1_HUMAN Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1...	sp|P26599|PTBP1_HUMANPolypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	0.36	10	0	0	0	0	0	0	0
Cytochrome c (Fragment) OS=Homo sapiens GN=CYCS PE=2 SV=1	C9JFR7_HUMAN (+2)	0.63	2	5	2	7	7	9	10	6
Insulin-like growth factor-binding protein 5 (Fragment) OS=Homo sapiens GN=IGFBP5 PE=2 SV=1	C9JXX4_HUMAN	0.36	0	0	3	0	0	0	0	0

sp|Q96A08|H2B1A_HUMAN Histone H2B type 1-A OS=Homo sapiens GN=HIST1H2BA PE=1 SV=3	sp|Q96A08|H2B1A_HUMANHistone H2B type 1-A OS=Homo sapiens GN=HIST1H2BA PE=1 SV=3	0.33	3	1	0	9	9	0	14	0
sp|Q9Y696|CLIC4_HUMAN Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4	sp|Q9Y696|CLIC4_HUMANChloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4	0.25	0	3	0	0	1	0	7	0
sp|P59998|ARPC4_HUMAN Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3	sp|P59998|ARPC4_HUMANActin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3	0.44	14	5	0	0	10	9	14	0
sp|Q9H9S4|CB39L_HUMAN Calcium-binding protein 39-like OS=Homo sapiens GN=CAB39L PE=1...	sp|Q9H9S4|CB39L_HUMANCalcium-binding protein 39-like OS=Homo sapiens GN=CAB39L PE=1 SV=3	0.88	3	12	0	0	8	0	8	0
sp|Q9BS26|ERP44_HUMAN Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1	sp|Q9BS26|ERP44_HUMANEndoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1	0.63	1	3	0	0	1	0	6	0
Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	TFR1_HUMAN	0.66	0	1	0	0	0	0	0	2
sp|Q8IUE6|H2A2B_HUMAN Histone H2A type 2-B OS=Homo sapiens GN=HIST2H2AB PE=1 SV=3	sp|Q8IUE6|H2A2B_HUMANHistone H2A type 2-B OS=Homo sapiens GN=HIST2H2AB PE=1 SV=3	0.72	10	0	0	0	6	5	13	0
Isoform 2 of Insulin-like growth factor-binding protein 7 OS=Homo sapiens GN=IGFBP7	sp|Q16270-2|IBP7_HUMAN	0.16	0	0	0	0	0	5	0	3
sp|P01597|KV105_HUMAN Ig kappa chain V-I region DEE OS=Homo sapiens PE=1 SV=1	sp|P01597|KV105_HUMANIg kappa chain V-I region DEE OS=Homo sapiens PE=1 SV=1	0.1	9	8	2	6	6	4	5	1
Isoform 2 of GDNF family receptor alpha-2 OS=Homo sapiens GN=GFRA2	sp|O00451-2|GFRA2_HUMAN	0.38	0	0	8	6	6	4	0	0
sp|O75610|LFTY1_HUMAN Left-right determination factor 1 OS=Homo sapiens GN=LEFTY1 PE=2 SV=1	sp|O75610|LFTY1_HUMANLeft-right determination factor 1 OS=Homo sapiens GN=LEFTY1 PE=2 SV=1	0.9	0	9	0	0	1	0	5	3
Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	LUM_HUMAN	0.36	0	6	0	0	0	12	1	5
sp|Q9NS25|SPNXB_HUMAN Sperm protein associated with the nucleus on the X chromosome B/F OS=Homo sapiens GN=SPANXB1 PE=2 SV=1	sp|Q9NS25|SPNXB_HUMANSperm protein associated with the nucleus on the X chromosome B/F OS=Homo sapiens GN=SPANXB1 PE=2 SV=1	0.045	0	0	0	0	8	4	18	3

Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3	H15_HUMAN	0.36	68	0	0	0	0	0	0	0
ADP-ribosylation factor 6 OS=Homo sapiens GN=ARF6 PE=1 SV=2	ARF6_HUMAN	0.36	6	2	7	1	1	7	3	0
sp|P25705|ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1...	sp|P25705|ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1...	0.34	32	4	2	1	1	3	12	2
Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2 PE=2 SV=1	Q5VY93_HUMAN	0.36	2	0	0	0	0	0	0	0
sp|Q5GAN3|RNS13_HUMAN Probable inactive ribonuclease-like protein 13 OS=Homo sapiens GN=RNASE13 PE=2 SV=1	sp|Q5GAN3|RNS13_HUMANProbable inactive ribonuclease-like protein 13 OS=Homo sapiens GN=RNASE13 PE=2 SV=1	0.13	0	10	0	0	0	20	9	15
Pyridoxine-5'-phosphate oxidase OS=Homo sapiens GN=PNPO PE=2 SV=1	B4E152_HUMAN	0.54	1	5	0	0	0	11	0	2
sp|Q8WWA0|ITLN1_HUMAN Intelectin-1 OS=Homo sapiens GN=ITLN1 PE=1 SV=1	sp|Q8WWA0|ITLN1_HUMANIntelectin-1 OS=Homo sapiens GN=ITLN1 PE=1 SV=1	0.71	0	7	0	0	0	0	2	2
60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5	RL4_HUMAN	0.16	10	0	1	0	0	0	0	0
Isoform 2 of 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20	sp|P60866-2|RS20_HUMAN	0.19	23	0	3	3	3	3	3	2
Isoform 2 of NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3	sp|P00387-2|NB5R3_HUMAN	0.49	1	0	1	3	3	4	4	6
2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=2 SV=1	B7Z6B8_HUMAN	0.031	0	0	0	2	2	3	3	2
Muscleblind-like protein 1 OS=Homo sapiens GN=MBNL1 PE=2 SV=1	C9JP00_HUMAN	0.36	2	0	0	0	0	0	0	0
Glutamine synthetase OS=Homo sapiens GN=GLUL PE=1 SV=4	GLNA_HUMAN	0.49	0	3	1	0	0	1	2	2
sp|Q15102|PA1B3_HUMAN Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens GN=PAFAH1B3 PE=1 SV=1	sp|Q15102|PA1B3_HUMANPlatelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens GN=PAFAH1B3 PE=1 SV=1	0.99	4	14	0	0	8	0	9	0
sp|Q7Z5L9|I2BP2_HUMAN Interferon regulatory factor 2-binding protein 2 OS=Homo sapiens...	sp|Q7Z5L9|I2BP2_HUMANInterferon regulatory factor 2-binding protein 2 OS=Homo sapiens GN=IRF2BP2 PE=1 SV=2	0.36	21	0	0	0	0	0	0	0

sp|P38646|GRP75_HUMAN Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	sp|P38646|GRP75_HUMANStress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	0.44	6	0	0	0	0	0	1	0
Histidine-rich glycoprotein OS=Homo sapiens GN=HRG PE=1 SV=1	HRG_HUMAN	0.36	0	0	0	0	0	3	0	0
sp|Q9NS86|LANC2_HUMAN LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1	sp|Q9NS86|LANC2_HUMANLanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1	0.66	0	1	0	0	0	0	2	0
sp|Q8NC51|PAIRB_HUMAN Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp|Q8NC51|PAIRB_HUMANPlasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	0.36	22	0	0	0	0	0	0	0
sp|Q8WU79|SMAP2_HUMAN Stromal membrane-associated protein 2 OS=Homo sapiens GN=SMAP2 PE=1 SV=1	sp|Q8WU79|SMAP2_HUMANStromal membrane-associated protein 2 OS=Homo sapiens GN=SMAP2 PE=1 SV=1	0.36	34	0	0	0	0	0	0	0
Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2	CFAI_HUMAN	0.61	1	8	3	4	4	2	10	4
Isoform 3 of Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD	sp|P11413-3|G6PD_HUMAN	0.45	1	0	4	1	1	3	3	0
Isoform 2 of Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C	TBA3C_HUMAN	0.26	4	2	0	1	1	7	3	4
Isoform 2 of N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2	PGRP2_HUMAN	0.41	0	5	7	1	1	5	4	2
sp|P54727|RD23B_HUMAN UV excision repair protein RAD23 homolog B OS=Homo sapiens...	sp|P54727|RD23B_HUMANUV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1	0.46	10	2	0	0	1	0	3	0
sp|Q9NZP8|C1RL_HUMAN Complement C1r subcomponent-like protein OS=Homo sapiens GN=C1RL...	sp|Q9NZP8|C1RL_HUMAN Complement C1r subcomponent-like protein OS=Homo sapiens GN=C1RL...	0.53	1	12	3	2	2	11	8	6
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	TBB5_HUMAN	0.37	13	2	3	2	2	3	2	2
Protein NOV homolog OS=Homo sapiens GN=NOV PE=1 SV=1	NOV_HUMAN	0.75	0	3	0	1	1	1	1	0
sp|Q05639|EF1A2_HUMAN Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1	sp|Q05639|EF1A2_HUMANElongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1	0.83	0	1	2	0	0	0	0	0
Ras-related protein R-Ras2 OS=Homo sapiens GN=RRAS2 PE=2 SV=1	B7Z5Z2_HUMAN	0.095	0	2	0	1	1	5	3	2

Mitochondrial dicarboxylate carrier OS=Homo sapiens GN=SLC25A10 PE=2 SV=1	B4DLN1_HUMAN	0.36	7	0	0	0	0	0	0	0
sp|Q92692|PVRL2_HUMAN Poliovirus receptor-related protein 2 OS=Homo sapiens GN=PVRL2 PE=1 SV=1	sp|Q92692|PVRL2_HUMANPoliovirus receptor-related protein 2 OS=Homo sapiens GN=PVRL2 PE=1 SV=1	0.66	3	2	0	0	2	1	0	0
sp|Q9H993|CF211_HUMAN UPF0364 protein C6orf211 OS=Homo sapiens GN=C6orf211 PE=1 SV=1	sp|Q9H993|CF211_HUMANUPF0364 protein C6orf211 OS=Homo sapiens GN=C6orf211 PE=1 SV=1	0.27	1	4	1	0	0	1	1	2
Isoform 2 of Prominin-2 OS=Homo sapiens GN=PROM2	sp|Q8N271-2|PROM2_HUMAN	0.64	4	2	0	0	0	1	1	2
GDP-L-fucose synthase OS=Homo sapiens GN=TSTA3 PE=1 SV=1	FCL_HUMAN	0.22	4	3	0	1	1	0	1	1
sp|Q9NPF2|CHSTB_HUMAN Carbohydrate sulfotransferase 11 OS=Homo sapiens GN=CHST11...	sp|Q9NPF2|CHSTB_HUMANCarbohydrate sulfotransferase 11 OS=Homo sapiens GN=CHST11 PE=1 SV=1	0.93	6	4	0	0	2	4	3	0
sp|P07864|LDHC_HUMAN L-lactate dehydrogenase C chain OS=Homo sapiens GN=LDHC PE=1...	sp|P07864|LDHC_HUMAN L-lactate dehydrogenase C chain OS=Homo sapiens GN=LDHC PE=1...	0.88	1	14	1	2	2	13	6	0
Transmembrane emp24 domain-containing protein 2 (Fragment) OS=Homo sapiens GN=TMED2 PE=2 SV=2	E7EQ72_HUMAN	0.36	0	0	0	0	0	9	0	0
sp|P13645|K1C10_HUMAN Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	sp|P13645|K1C10_HUMANKeratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	0.14	0	2	0	0	6	0	7	6
Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3	ENOG_HUMAN	0.3	0	2	4	0	0	0	0	0
sp|Q15654|TRIP6_HUMAN Thyroid receptor-interacting protein 6 OS=Homo sapiens GN=TRIP6 PE=1 SV=3	sp|Q15654|TRIP6_HUMANThyroid receptor-interacting protein 6 OS=Homo sapiens GN=TRIP6 PE=1 SV=3	0.36	18	0	0	0	0	0	0	0
Calpain-5 OS=Homo sapiens GN=CAPN5 PE=2 SV=2	E7EV01_HUMAN	0.22	0	6	1	1	1	2	1	0
40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	RS3A_HUMAN	0.13	17	1	1	2	2	2	1	0
sp|O75955|FLOT1_HUMAN Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3	sp|O75955|FLOT1_HUMANFlotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3	0.92	0	1	1	0	0	1	3	2
sp|P51665|PSMD7_HUMAN 26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens...	sp|P51665|PSMD7_HUMAN26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2	0.53	0	5	2	0	1	4	2	3

sp|Q10471|GALT2_HUMAN Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens GN=GALNT2 PE=1 SV=1	sp|Q10471|GALT2_HUMANPolypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens GN=GALNT2 PE=1 SV=1	0.95	0	4	0	0	1	0	1	1
Isoform 2 of V-type proton ATPase subunit H OS=Homo sapiens GN=ATP6V1H	sp|Q9UI12-2|VATH_HUMAN	0.36	0	0	0	0	0	3	0	0
sp|Q9NRX4|PHP14_HUMAN 14 kDa phosphohistidine phosphatase OS=Homo sapiens GN=PHPT1 PE=1 SV=1	sp|Q9NRX4|PHP14_HUMAN14 kDa phosphohistidine phosphatase OS=Homo sapiens GN=PHPT1 PE=1 SV=1	0.036	3	0	0	0	11	13	6	2
tr|E7ER45|E7ER45_HUMAN Maltase-glucoamylase, intestinal OS=Homo sapiens GN=MGAM PE=4...	tr|E7ER45|E7ER45_HUMAN Maltase-glucoamylase, intestinal OS=Homo sapiens GN=MGAM PE=4...	0.7	2	10	0	0	0	17	0	5
sp|P0CG12|CTF8A_HUMAN Chromosome transmission fidelity protein 8 homolog isoform 2 OS=Homo sapiens GN=CHTF8 PE=1 SV=1	sp|P0CG12|CTF8A_HUMANChromosome transmission fidelity protein 8 homolog isoform 2 OS=Homo sapiens GN=CHTF8 PE=1 SV=1	0.36	18	0	0	0	0	0	0	0
sp|P63313|TYB10_HUMAN Thymosin beta-10 OS=Homo sapiens GN=TMSB10 PE=1 SV=2	sp|P63313|TYB10_HUMANThymosin beta-10 OS=Homo sapiens GN=TMSB10 PE=1 SV=2	0.36	61	0	0	0	0	0	0	0
sp|P07225|PROS_HUMAN Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1...	sp|P07225|PROS_HUMAN Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1...	0.57	3	3	2	8	8	3	7	10
sp|P55786|PSA_HUMAN Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS...	sp|P55786|PSA_HUMAN Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS...	0.4	4	6	14	4	4	11	7	4
Isoform 3 of Argininosuccinate lyase OS=Homo sapiens GN=ASL	sp|P04424-3|ARLY_HUMAN	0.42	2	0	6	0	0	3	2	2
sp|Q13443|ADAM9_HUMAN Disintegrin and metalloproteinase domain-containing protein...	sp|Q13443|ADAM9_HUMANDisintegrin and metalloproteinase domain-containing protein 9 OS=Homo sapiens GN=ADAM9 PE=1 SV=1	0.53	1	8	0	0	5	2	6	1
Oligoribonuclease, mitochondrial OS=Homo sapiens GN=REXO2 PE=1 SV=3	ORN_HUMAN	0.71	0	7	0	0	0	0	2	2
Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2	GGH_HUMAN	0.18	2	4	0	0	0	3	13	8
sp|Q13283|G3BP1_HUMAN Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1	sp|Q13283|G3BP1_HUMANRas GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1	0.36	17	0	0	0	0	0	0	0

sp|Q96PK6|RBM14_HUMAN RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2	sp|Q96PK6|RBM14_HUMANRNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2	0.36	15	0	0	0	0	0	0	0
Isoform 2 of Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform OS=Homo sapiens GN=PPP3CA	sp|Q08209-2|PP2BA_HUMAN	0.39	0	0	6	0	0	0	3	0
40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2	RS2_HUMAN	0.51	1	3	2	3	3	8	4	0
sp|P08727|K1C19_HUMAN Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1...	sp|P08727|K1C19_HUMANKeratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4	0.17	0	1	1	0	2	0	1	2
sp|Q5T4F7|SFRP5_HUMAN Secreted frizzled-related protein 5 OS=Homo sapiens GN=SFRP5 PE=2 SV=3	sp|Q5T4F7|SFRP5_HUMANSecreted frizzled-related protein 5 OS=Homo sapiens GN=SFRP5 PE=2 SV=3	0.13	2	0	0	0	3	4	2	0
sp|Q32P51|RA1L2_HUMAN Heterogeneous nuclear ribonucleoprotein A1-like 2 OS=Homo sapiens GN=HNRNPA1L2 PE=2 SV=2	sp|Q32P51|RA1L2_HUMANHeterogeneous nuclear ribonucleoprotein A1-like 2 OS=Homo sapiens GN=HNRNPA1L2 PE=2 SV=2	0.36	16	0	0	0	0	0	0	0
BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3	BAG3_HUMAN	0.36	4	0	0	0	0	0	0	0
sp|Q9H307|PININ_HUMAN Pinin OS=Homo sapiens GN=PNN PE=1 SV=4	sp|Q9H307|PININ_HUMANPinin OS=Homo sapiens GN=PNN PE=1 SV=4	0.36	9	0	0	0	0	0	0	0
sp|Q9UIK5|TEFF2_HUMAN Tomoregulin-2 OS=Homo sapiens GN=TMEFF2 PE=1 SV=1	sp|Q9UIK5|TEFF2_HUMANTomoregulin-2 OS=Homo sapiens GN=TMEFF2 PE=1 SV=1	0.24	0	0	0	0	0	4	0	1
sp|Q5T754|LCE1F_HUMAN Late cornified envelope protein 1F OS=Homo sapiens GN=LCE1F PE=2 SV=1	sp|Q5T754|LCE1F_HUMANLate cornified envelope protein 1F OS=Homo sapiens GN=LCE1F PE=2 SV=1	0.36	0	0	0	0	0	3	0	0
sp|Q14166|TTL12_HUMAN Tubulin--tyrosine ligase-like protein 12 OS=Homo sapiens GN=TTLL12...	sp|Q14166|TTL12_HUMANTubulin--tyrosine ligase-like protein 12 OS=Homo sapiens GN=TTLL12 PE=1 SV=2	0.46	0	3	1	0	3	0	1	0
sp|O14638|ENPP3_HUMAN Ectonucleotide pyrophosphatase/phosphodiesterase family member...	sp|O14638|ENPP3_HUMANEctonucleotide pyrophosphatase/phosphodiesterase family member 3 OS=Homo sapiens GN=ENPP3 PE=1 SV=2	0.95	2	4	0	0	2	0	2	1
sp|P30530-2|UFO_HUMAN Isoform Short of Tyrosine-protein kinase receptor UFO OS=Homo sapiens GN=AXL	sp|P30530-2|UFO_HUMANIsoform Short of Tyrosine-protein kinase receptor UFO OS=Homo sapiens GN=AXL	0.56	1	2	0	0	1	0	5	0

sp|Q53H96|P5CR3_HUMAN Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=2	sp|Q53H96|P5CR3_HUMANPyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=2	0.61	5	2	0	0	5	0	6	0
sp|O43291|SPIT2_HUMAN Kunitz-type protease inhibitor 2 OS=Homo sapiens GN=SPINT2 PE=1 SV=2	sp|O43291|SPIT2_HUMANKunitz-type protease inhibitor 2 OS=Homo sapiens GN=SPINT2 PE=1 SV=2	0.91	5	12	0	0	9	8	0	0
Isoform 6 of Splicing factor 1 OS=Homo sapiens GN=SF1	sp|Q15637-6|SF01_HUMAN	0.36	19	0	0	0	0	0	0	0
Putative hydroxypyruvate isomerase OS=Homo sapiens GN=HYI PE=1 SV=2	HYI_HUMAN	0.18	5	12	0	0	0	0	0	0
Aldose 1-epimerase OS=Homo sapiens GN=GALM PE=1 SV=1	GALM_HUMAN	0.15	5	7	3	4	4	3	1	2
60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2	sp|P62913|RL11_HUMAN	0.36	1	1	8	5	5	3	1	4
Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2	FRIL_HUMAN	0.38	1	4	5	1	1	4	2	5
Immunoglobulin J chain (Fragment) OS=Homo sapiens GN=IGJ PE=2 SV=1	D6RD17_HUMAN	0.4	0	0	6	2	2	0	8	0
ADP/ATP translocase 4 OS=Homo sapiens GN=SLC25A31 PE=2 SV=1	ADT4_HUMAN	0.36	0	0	0	0	0	0	3	0
sp|P67809|YBOX1_HUMAN Nuclease-sensitive element-binding protein 1 OS=Homo sapiens...	sp|P67809|YBOX1_HUMANNuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3	0.36	21	0	0	0	0	0	0	0
Hematological and neurological-expressed 1-like protein OS=Homo sapiens GN=HN1L PE=2 SV=1	B4DLH4_HUMAN	0.38	23	0	0	0	0	0	1	0
sp|P04207|KV308_HUMAN Ig kappa chain V-III region CLL OS=Homo sapiens PE=1 SV=2	sp|P04207|KV308_HUMANIg kappa chain V-III region CLL OS=Homo sapiens PE=1 SV=2	0.31	4	3	2	2	2	3	3	2
sp|O43915|VEGFD_HUMAN Vascular endothelial growth factor D OS=Homo sapiens GN=FIGF PE=1 SV=1	sp|O43915|VEGFD_HUMANVascular endothelial growth factor D OS=Homo sapiens GN=FIGF PE=1 SV=1	0.15	0	0	0	0	0	0	3	2
sp|Q86VR7|VS10L_HUMAN V-set and immunoglobulin domain-containing protein 10-like...	sp|Q86VR7|VS10L_HUMANV-set and immunoglobulin domain-containing protein 10-like OS=Homo sapiens GN=VSIG10L PE=2 SV=2	0.76	0	5	0	0	0	2	1	0
sp|Q5VWZ2|LYPL1_HUMAN Lysophospholipase-like protein 1 OS=Homo sapiens GN=LYPLAL1...	sp|Q5VWZ2|LYPL1_HUMANLysophospholipase-like protein 1 OS=Homo sapiens GN=LYPLAL1 PE=1 SV=3	0.91	2	4	0	0	4	2	0	0
sp|Q9Y2W2|WBP11_HUMAN WW domain-binding protein 11 OS=Homo sapiens GN=WBP11 PE=1 SV=1	sp|Q9Y2W2|WBP11_HUMANWW domain-binding protein 11 OS=Homo sapiens GN=WBP11 PE=1 SV=1	0.36	5	0	0	0	0	0	0	0

sp|P07954-2|FUMH_HUMAN Isoform Cytoplasmic of Fumarate hydratase, mitochondrial OS=Homo...	sp|P07954-2|FUMH_HUMAN Isoform Cytoplasmic of Fumarate hydratase, mitochondrial OS=Homo... (+1)	0.56	1	6	2	6	6	6	8	9
Isoform 3 of Selenium-binding protein 1 OS=Homo sapiens GN=SELENBP1	sp|Q13228-3|SBP1_HUMAN	0.36	0	2	3	6	6	2	2	3
sp|O60513|B4GT4_HUMAN Beta-1,4-galactosyltransferase 4 OS=Homo sapiens GN=B4GALT4...	sp|O60513|B4GT4_HUMANBeta-1,4-galactosyltransferase 4 OS=Homo sapiens GN=B4GALT4 PE=1 SV=1	0.45	4	4	3	0	1	0	11	0
sp|Q9UJA9|ENPP5_HUMAN Ectonucleotide pyrophosphatase/phosphodiesterase family member 5 OS=Homo sapiens GN=ENPP5 PE=1 SV=1	sp|Q9UJA9|ENPP5_HUMANEctonucleotide pyrophosphatase/phosphodiesterase family member 5 OS=Homo sapiens GN=ENPP5 PE=1 SV=1	0.68	4	2	0	0	1	2	1	0
sp|O75556|SG2A1_HUMAN Mammaglobin-B OS=Homo sapiens GN=SCGB2A1 PE=1 SV=1	sp|O75556|SG2A1_HUMANMammaglobin-B OS=Homo sapiens GN=SCGB2A1 PE=1 SV=1	0.55	4	21	0	0	5	4	2	0
sp|Q99733|NP1L4_HUMAN Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4 PE=1 SV=1	sp|Q99733|NP1L4_HUMANNucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4 PE=1 SV=1	0.31	4	1	0	0	0	1	0	0
Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=2 SV=1	G8JLB6_HUMAN	0.36	15	0	0	0	0	0	0	0
sp|Q9UQB8|BAIP2_HUMAN Brain-specific angiogenesis inhibitor 1-associated protein 2 OS=Homo sapiens GN=BAIAP2 PE=1 SV=1	sp|Q9UQB8|BAIP2_HUMANBrain-specific angiogenesis inhibitor 1-associated protein 2 OS=Homo sapiens GN=BAIAP2 PE=1 SV=1	0.31	5	10	0	0	6	0	10	6
sp|P0C7P4|UCRIL_HUMAN Putative cytochrome b-c1 complex subunit Rieske-like protein 1 OS=Homo sapiens GN=UQCRFS1P1 PE=5 SV=1	sp|P0C7P4|UCRIL_HUMANPutative cytochrome b-c1 complex subunit Rieske-like protein 1 OS=Homo sapiens GN=UQCRFS1P1 PE=5 SV=1	0.46	5	0	0	0	0	0	1	0
sp|P49223|SPIT3_HUMAN Kunitz-type protease inhibitor 3 OS=Homo sapiens GN=SPINT3 PE=2 SV=3	sp|P49223|SPIT3_HUMANKunitz-type protease inhibitor 3 OS=Homo sapiens GN=SPINT3 PE=2 SV=3	0.74	9	0	0	0	1	8	0	4
Granulins OS=Homo sapiens GN=GRN PE=1 SV=2	GRN_HUMAN	0.42	7	0	0	0	1	0	8	0
cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Homo sapiens GN=PRKAR1A PE=1 SV=1	KAP0_HUMAN	0.18	4	6	1	2	2	5	3	1
General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=2 SV=1	F5H4X1_HUMAN	0.98	1	5	0	0	0	2	0	6

sp|P45880|VDAC2_HUMAN Voltage-dependent anion-selective channel protein 2 OS=Homo...	sp|P45880|VDAC2_HUMANVoltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2	0.24	0	1	0	0	0	2	15	2
Calcyclin-binding protein OS=Homo sapiens GN=CACYBP PE=1 SV=2	sp|Q9HB71|CYBP_HUMAN	0.68	5	0	0	1	1	2	1	0
sp|Q9H2U9|ADAM7_HUMAN Disintegrin and metalloproteinase domain-containing protein 7 OS=Homo sapiens GN=ADAM7 PE=1 SV=3	sp|Q9H2U9|ADAM7_HUMANDisintegrin and metalloproteinase domain-containing protein 7 OS=Homo sapiens GN=ADAM7 PE=1 SV=3	0.46	6	6	0	0	4	0	9	6
sp|P40429|RL13A_HUMAN 60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2	sp|P40429|RL13A_HUMAN60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2	0.75	3	5	0	0	0	6	2	2
Isoform 1 of Testican-3 OS=Homo sapiens GN=SPOCK3	sp|Q9BQ16-1|TICN3_HUMAN	0.67	0	0	0	0	0	8	0	0
sp|Q9UBS3|DNJB9_HUMAN DnaJ homolog subfamily B member 9 OS=Homo sapiens GN=DNAJB9 PE=1 SV=1	sp|Q9UBS3|DNJB9_HUMANDnaJ homolog subfamily B member 9 OS=Homo sapiens GN=DNAJB9 PE=1 SV=1	0.29	0	4	0	0	0	0	7	8
sp|Q9H1E3|NUCKS_HUMAN Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 OS=Homo sapiens GN=NUCKS1 PE=1 SV=1	sp|Q9H1E3|NUCKS_HUMANNuclear ubiquitous casein and cyclin-dependent kinase substrate 1 OS=Homo sapiens GN=NUCKS1 PE=1 SV=1	0.36	22	0	0	0	0	0	0	0
Quinone oxidoreductase PIG3 OS=Homo sapiens GN=TP53I3 PE=1 SV=2	sp|Q53FA7|QORX_HUMAN	0.077	3	6	1	1	1	2	2	0
sp|OVAL_CHICK|	sp|OVAL_CHICK|	0.2	0	0	0	0	0	1	0	3
Adenylate kinase 2, mitochondrial OS=Homo sapiens GN=AK2 PE=2 SV=1	F8W1A4_HUMAN	0.36	18	0	0	0	0	0	0	0
sp|O60216|RAD21_HUMAN Double-strand-break repair protein rad21 homolog OS=Homo sapiens GN=RAD21 PE=1 SV=2	sp|O60216|RAD21_HUMANDouble-strand-break repair protein rad21 homolog OS=Homo sapiens GN=RAD21 PE=1 SV=2	0.36	3	0	0	0	0	0	0	0
Lipocalin-1 OS=Homo sapiens GN=LCN1 PE=1 SV=1	LCN1_HUMAN	0.46	2	3	2	8	8	5	2	8
40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	RS18_HUMAN	0.29	11	1	2	1	1	3	5	3
Carboxypeptidase O OS=Homo sapiens GN=CPO PE=2 SV=1	CBPO_HUMAN	0.99	0	4	0	1	1	0	1	3
Syndecan-1 OS=Homo sapiens GN=SDC1 PE=1 SV=3	SDC1_HUMAN	0.41	0	2	0	0	0	3	2	0

sp|P78371|TCPB_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1...	sp|P78371|TCPB_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1...	0.29	13	11	2	1	1	7	8	3
Salivary acidic proline-rich phosphoprotein 1/2 OS=Homo sapiens GN=PRH1 PE=1 SV=2	PRPC_HUMAN	0.25	1	7	2	1	1	2	2	0
Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1	QOR_HUMAN	0.31	6	5	3	0	0	1	7	3
sp|Q9BQT9|CSTN3_HUMAN Calsyntenin-3 OS=Homo sapiens GN=CLSTN3 PE=1 SV=1	sp|Q9BQT9|CSTN3_HUMANCalsyntenin-3 OS=Homo sapiens GN=CLSTN3 PE=1 SV=1 (+1)	0.36	0	1	0	0	1	0	2	0
60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4	RL10_HUMAN	0.42	14	1	0	0	0	2	1	0
Proline-rich protein PRCC OS=Homo sapiens GN=PRCC PE=2 SV=1	A6NG79_HUMAN	0.27	11	0	4	0	0	0	0	0
Isoform 2 of Caprin-1 OS=Homo sapiens GN=CAPRIN1	CAPR1_HUMAN (+1)	0.36	10	0	0	0	0	0	0	0
Interferon-induced transmembrane protein 1 OS=Homo sapiens GN=IFITM1 PE=1 SV=3	IFM1_HUMAN	0.83	5	3	1	3	3	5	6	10
60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	RL6_HUMAN	0.35	6	1	3	0	0	1	7	0
Isoform Short of Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H	sp|Q15056-2|IF4H_HUMAN	0.3	25	6	0	2	2	2	2	1
sp|P68400|CSK21_HUMAN Casein kinase II subunit alpha OS=Homo sapiens GN=CSNK2A1 PE=1...	sp|P68400|CSK21_HUMANCasein kinase II subunit alpha OS=Homo sapiens GN=CSNK2A1 PE=1 SV=1	0.34	0	1	0	3	3	5	2	0
sp|O95025|SEM3D_HUMAN Semaphorin-3D OS=Homo sapiens GN=SEMA3D PE=2 SV=2	sp|O95025|SEM3D_HUMANSemaphorin-3D OS=Homo sapiens GN=SEMA3D PE=2 SV=2	0.98	0	7	0	0	0	0	2	1
Calnexin OS=Homo sapiens GN=CANX PE=2 SV=1	B4DGP8_HUMAN	0.45	3	5	2	0	0	5	6	0
sp|Q8IXK2|GLT12_HUMAN Polypeptide N-acetylgalactosaminyltransferase 12 OS=Homo sapiens...	sp|Q8IXK2|GLT12_HUMANPolypeptide N-acetylgalactosaminyltransferase 12 OS=Homo sapiens GN=GALNT12 PE=1 SV=3	0.44	4	5	0	0	2	0	2	0
Isoform 3 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1	sp|Q7L1Q6-3|BZW1_HUMAN	0.79	0	6	0	0	0	1	0	3
Isoform 9 of G-protein coupled receptor 64 OS=Homo sapiens GN=GPR64	sp|Q8IZP9-9|GPR64_HUMAN	0.97	1	8	2	0	0	4	0	11
Double-stranded RNA-binding protein Staufen homolog 1	Q5JW30_HUMAN	0.36	2	0	0	0	0	0	0	0

OS=Homo sapiens GN=STAU1 PE=2 SV=1										
GDP-mannose 4,6 dehydratase OS=Homo sapiens GN=GMDS PE=1 SV=1	sp|O60547|GMDS_HUMAN	0.36	8	0	0	0	0	0	0	0
sp|Q12904|AIMP1_HUMAN Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2	sp|Q12904|AIMP1_HUMANAminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2	0.2	5	2	0	0	0	0	0	0
Biliverdin reductase A OS=Homo sapiens GN=BLVRA PE=1 SV=2	BIEA_HUMAN	0.17	1	8	2	1	1	0	0	3
sp|Q8NI22|MCFD2_HUMAN Multiple coagulation factor deficiency protein 2 OS=Homo sapiens GN=MCFD2 PE=1 SV=1	sp|Q8NI22|MCFD2_HUMANMultiple coagulation factor deficiency protein 2 OS=Homo sapiens GN=MCFD2 PE=1 SV=1	0.32	7	2	1	0	0	5	2	2
Citrate synthase (Fragment) OS=Homo sapiens GN=CS PE=2 SV=1	H0YIC4_HUMAN	0.14	0	0	0	0	0	0	7	9
sp|P39687|AN32A_HUMAN Acidic leucine-rich nuclear phosphoprotein 32 family member...	sp|P39687|AN32A_HUMANAcidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=1 SV=1	0.36	32	0	0	0	0	0	0	0
PCTP-like protein OS=Homo sapiens GN=STARD10 PE=2 SV=1	F5H8H3_HUMAN	0.66	2	2	2	2	2	4	3	6
sp|P36507|MP2K2_HUMAN Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1	sp|P36507|MP2K2_HUMANDual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1	0.32	2	3	1	0	1	1	3	0
sp|O14657|TOR1B_HUMAN Torsin-1B OS=Homo sapiens GN=TOR1B PE=1 SV=2	sp|O14657|TOR1B_HUMANTorsin-1B OS=Homo sapiens GN=TOR1B PE=1 SV=2	0.64	2	3	0	7	7	0	9	2
Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2	sp|P21964|COMT_HUMAN	0.36	0	0	0	1	1	0	5	0
Isoform 3 of Malignant T-cell-amplified sequence 1 OS=Homo sapiens GN=MCTS1	sp|Q9ULC4-3|MCTS1_HUMAN	0.81	7	2	0	0	0	4	0	3
sp|P31949|S10AB_HUMAN Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2	sp|P31949|S10AB_HUMANProtein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2	0.4	7	1	0	0	2	6	4	3
sp|P46926|GNPI1_HUMAN Glucosamine-6-phosphate isomerase 1 OS=Homo sapiens GN=GNPDA1...	sp|P46926|GNPI1_HUMANGlucosamine-6-phosphate isomerase 1 OS=Homo sapiens GN=GNPDA1 PE=1 SV=1	0.73	0	0	3	0	1	0	3	9
sp|O15145|ARPC3_HUMAN Actin-related protein 2/3 complex subunit 3 OS=Homo sapiens...	sp|O15145|ARPC3_HUMANActin-related protein 2/3 complex subunit 3 OS=Homo sapiens GN=ARPC3 PE=1 SV=3	0.88	9	3	0	0	8	4	0	1

Leucine-rich repeat-containing protein 57 (Fragment) OS=Homo sapiens GN=LRRC57 PE=2 SV=1	H3BSW0_HUMAN	0.79	2	6	0	0	0	2	0	4
sp|P36959|GMPR1_HUMAN GMP reductase 1 OS=Homo sapiens GN=GMPR PE=1 SV=1	sp|P36959|GMPR1_HUMANGMP reductase 1 OS=Homo sapiens GN=GMPR PE=1 SV=1	0.34	0	1	0	0	0	0	1	6
sp|Q04695|K1C17_HUMAN Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1...	sp|Q04695|K1C17_HUMANKeratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	0.4	1	0	0	0	3	0	0	8
sp|Q01638|ILRL1_HUMAN Interleukin-1 receptor-like 1 OS=Homo sapiens GN=IL1RL1 PE=1...	sp|Q01638|ILRL1_HUMANInterleukin-1 receptor-like 1 OS=Homo sapiens GN=IL1RL1 PE=1 SV=4	0.36	0	0	0	0	0	0	10	0
sp|P43686|PRS6B_HUMAN 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2	sp|P43686|PRS6B_HUMAN26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2	0.14	0	0	0	1	2	1	2	0
sp|P0C8F1|PATE4_HUMAN Prostate and testis expressed protein 4 OS=Homo sapiens GN=PATE4 PE=2 SV=2	sp|P0C8F1|PATE4_HUMANProstate and testis expressed protein 4 OS=Homo sapiens GN=PATE4 PE=2 SV=2	0.81	6	4	0	0	6	1	0	0
Isoform 2 of AP-2 complex subunit alpha-2 OS=Homo sapiens GN=AP2A2	sp|O94973-2|AP2A2_HUMAN	0.96	0	2	0	0	0	1	0	1
Isoform 2 of Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2	sp|P17655-2|CAN2_HUMAN	0.71	0	0	1	0	0	4	0	0
Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment) OS=Homo sapiens GN=GNB2L1 PE=2 SV=1	D6REE5_HUMAN	0.44	0	5	0	0	0	0	0	0
Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2	sp|P09493|TPM1_HUMAN	0.62	1	4	0	0	0	0	2	0
sp|Q14204|DYHC1_HUMAN Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1...	sp|Q14204|DYHC1_HUMANCytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1...	0.36	0	0	23	0	0	0	0	0
sp|P62942|FKB1A_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens GN=FKBP1A PE=1 SV=2	sp|P62942|FKB1A_HUMANPeptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens GN=FKBP1A PE=1 SV=2	0.9	4	6	0	2	2	9	0	2
Acyl-CoA-binding protein OS=Homo sapiens GN=DBI PE=1 SV=2	sp|P07108|ACBP_HUMAN	0.45	10	2	2	0	0	9	2	8
sp|Q14344|GNA13_HUMAN Guanine nucleotide-binding protein	sp|Q14344|GNA13_HUMANGuanine nucleotide-binding protein subunit alpha-13 OS=Homo sapiens GN=GNA13 PE=1 SV=2	0.29	1	3	0	0	6	0	1	4

subunit alpha-13 OS=Homo sapiens GN=GNA13 PE=1 SV=2										
sp|A5D8V6|VP37C_HUMAN Vacuolar protein sorting-associated protein 37C OS=Homo sapiens GN=VPS37C PE=1 SV=2	sp|A5D8V6|VP37C_HUMANVacuolar protein sorting-associated protein 37C OS=Homo sapiens GN=VPS37C PE=1 SV=2	0.43	0	6	0	0	8	4	1	0
sp|O75348|VATG1_HUMAN V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3	sp|O75348|VATG1_HUMANV-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3	0.56	13	4	0	0	3	0	3	3
Superoxide dismutase [Mn], mitochondrial (Fragment) OS=Homo sapiens GN=SOD2 PE=2 SV=1	F5GYZ5_HUMAN	0.31	1	1	0	0	0	3	0	3
sp|P30520|PURA2_HUMAN Adenylosuccinate synthetase isozyme 2 OS=Homo sapiens GN=ADSS PE=1 SV=3	sp|P30520|PURA2_HUMANAdenylosuccinate synthetase isozyme 2 OS=Homo sapiens GN=ADSS PE=1 SV=3	0.49	0	1	0	0	0	0	0	4
Isoform 3 of Drebrin-like protein OS=Homo sapiens GN=DBNL	sp|Q9UJU6-3|DBNL_HUMAN	0.24	4	1	0	0	0	0	0	0
sp|P01613|KV121_HUMAN Ig kappa chain V-I region Ni OS=Homo sapiens PE=1 SV=1	sp|P01613|KV121_HUMANIg kappa chain V-I region Ni OS=Homo sapiens PE=1 SV=1	0.15	0	0	0	0	0	3	5	0
sp|Q92838-3|EDA_HUMAN Isoform 3 of Ectodysplasin-A OS=Homo sapiens GN=EDA	sp|Q92838-3|EDA_HUMANIsoform 3 of Ectodysplasin-A OS=Homo sapiens GN=EDA	0.69	0	1	0	1	1	2	0	0
Suppressor of G2 allele of SKP1 homolog OS=Homo sapiens GN=SUGT1 PE=2 SV=1	F5H5A9_HUMAN	0.37	0	0	0	1	1	0	4	0
sp|P68036|UB2L3_HUMAN Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3...	sp|P68036|UB2L3_HUMANUbiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1	0.87	18	1	0	0	5	0	5	6
Isoform 2 of Signal recognition particle receptor subunit alpha OS=Homo sapiens GN=SRPR	sp|P08240-2|SRPR_HUMAN	0.36	0	0	0	0	0	0	3	0
sp|Q9H361|PABP3_HUMAN Polyadenylate-binding protein 3 OS=Homo sapiens GN=PABPC3 PE=1...	sp|Q9H361|PABP3_HUMANPolyadenylate-binding protein 3 OS=Homo sapiens GN=PABPC3 PE=1 SV=2	0.27	0	0	2	0	0	0	0	0
Alpha-endosulfine OS=Homo sapiens GN=ENSA PE=2 SV=1	Q5T5H1_HUMAN	0.36	32	0	0	0	0	0	0	0
sp|Q14894|CRYM_HUMAN Ketimine reductase mu-crystallin OS=Homo sapiens GN=CRYM PE=1...	sp|Q14894|CRYM_HUMAN Ketimine reductase mu-crystallin OS=Homo sapiens GN=CRYM PE=1...	0.41	7	5	5	4	4	4	3	7
sp|P51993-2|FUT6_HUMAN Isoform 2 of Alpha-(1,3)-fucosyltransferase 6 OS=Homo sapiens...	sp|P51993-2|FUT6_HUMAN Isoform 2 of Alpha-(1,3)-fucosyltransferase 6 OS=Homo sapiens... (+1)	0.64	0	2	4	4	4	13	4	3

40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=2 SV=1	J3KMX5_HUMAN	0.31	11	1	3	1	1	7	2	2
sp|Q9NPR2|SEM4B_HUMAN Semaphorin-4B OS=Homo sapiens GN=SEMA4B PE=1 SV=3	sp|Q9NPR2|SEM4B_HUMANSemaphorin-4B OS=Homo sapiens GN=SEMA4B PE=1 SV=3	0.79	1	2	1	0	3	0	5	0
sp|Q9UNF0|PACN2_HUMAN Protein kinase C and casein kinase substrate in neurons protein...	sp|Q9UNF0|PACN2_HUMANProtein kinase C and casein kinase substrate in neurons protein 2 OS=Homo sapiens GN=PACSIN2 PE=1 SV=2	0.51	3	4	1	0	2	0	0	6
Gamma-soluble NSF attachment protein OS=Homo sapiens GN=NAPG PE=1 SV=1	SNAG_HUMAN	0.21	0	1	0	0	0	4	0	3
sp|O15143|ARC1B_HUMAN Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3	sp|O15143|ARC1B_HUMANActin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3	0.36	4	0	0	0	0	0	0	0
sp|Q9Y3P9|RBGP1_HUMAN Rab GTPase-activating protein 1 OS=Homo sapiens GN=RABGAP1...	sp|Q9Y3P9|RBGP1_HUMANRab GTPase-activating protein 1 OS=Homo sapiens GN=RABGAP1 PE=1 SV=3	0.36	0	0	0	0	0	3	0	0
sp|P20849|CO9A1_HUMAN Collagen alpha-1(IX) chain OS=Homo sapiens GN=COL9A1 PE=1 SV=3	sp|P20849|CO9A1_HUMANCollagen alpha-1(IX) chain OS=Homo sapiens GN=COL9A1 PE=1 SV=3	0.63	0	2	4	0	0	0	7	10
sp|O43242|PSMD3_HUMAN 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2	sp|O43242|PSMD3_HUMAN26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2	0.2	2	0	0	0	0	0	8	6
Cathepsin G OS=Homo sapiens GN=CTSG PE=1 SV=2	CATG_HUMAN	0.25	17	0	2	0	0	8	0	0
sp|P49902|5NTC_HUMAN Cytosolic purine 5'-nucleotidase OS=Homo sapiens GN=NT5C2 PE=1...	sp|P49902|5NTC_HUMAN Cytosolic purine 5'-nucleotidase OS=Homo sapiens GN=NT5C2 PE=1...	0.41	2	1	6	2	2	4	4	3
sp|Q9H0E2|TOLIP_HUMAN Toll-interacting protein OS=Homo sapiens GN=TOLLIP PE=1 SV=1	sp|Q9H0E2|TOLIP_HUMANToll-interacting protein OS=Homo sapiens GN=TOLLIP PE=1 SV=1	0.3	5	0	2	2	2	4	1	0
sp|P61020|RAB5B_HUMAN Ras-related protein Rab-5B OS=Homo sapiens GN=RAB5B PE=1 SV=1	sp|P61020|RAB5B_HUMANRas-related protein Rab-5B OS=Homo sapiens GN=RAB5B PE=1 SV=1	0.4	4	4	0	0	3	3	5	3
sp|Q15008|PSMD6_HUMAN 26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1	sp|Q15008|PSMD6_HUMAN26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1	0.35	2	4	5	0	0	2	5	0
Myosin light chain 3 OS=Homo sapiens GN=MYL3 PE=1 SV=3	MYL3_HUMAN	0.68	7	8	0	0	0	0	5	1
sp|Q9UHY7|ENOPH_HUMAN Enolase-phosphatase E1 OS=Homo sapiens GN=ENOPH1 PE=1 SV=1	sp|Q9UHY7|ENOPH_HUMANEnolase-phosphatase E1 OS=Homo sapiens GN=ENOPH1 PE=1 SV=1	0.77	1	2	2	0	0	7	8	1

Myotrophin OS=Homo sapiens GN=MTPN PE=1 SV=2	MTPN_HUMAN	0.55	12	2	0	1	1	2	1	4
sp|O43854|EDIL3_HUMAN EGF-like repeat and discoidin I-like domain-containing protein 3 OS=Homo sapiens GN=EDIL3 PE=1 SV=1	sp|O43854|EDIL3_HUMANEGF-like repeat and discoidin I-like domain-containing protein 3 OS=Homo sapiens GN=EDIL3 PE=1 SV=1	0.66	1	0	4	0	5	10	5	10
26S protease regulatory subunit 10B (Fragment) OS=Homo sapiens GN=PSMC6 PE=4 SV=1	H0YJC0_HUMAN	0.39	0	0	3	0	0	0	2	0
sp|P51888|PRELP_HUMAN Prolargin OS=Homo sapiens GN=PRELP PE=1 SV=1	sp|P51888|PRELP_HUMANProlargin OS=Homo sapiens GN=PRELP PE=1 SV=1	0.41	2	0	0	1	1	8	1	0
sp|Q14151|SAFB2_HUMAN Scaffold attachment factor B2 OS=Homo sapiens GN=SAFB2 PE=1 SV=1	sp|Q14151|SAFB2_HUMANScaffold attachment factor B2 OS=Homo sapiens GN=SAFB2 PE=1 SV=1	0.12	2	0	0	1	1	0	0	0
sp|Q9BRA2|TXD17_HUMAN Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1	sp|Q9BRA2|TXD17_HUMANThioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1	0.51	6	3	0	0	6	5	3	0
sp|Q03167|TGBR3_HUMAN Transforming growth factor beta receptor type 3 OS=Homo sapiens...	sp|Q03167|TGBR3_HUMANTransforming growth factor beta receptor type 3 OS=Homo sapiens GN=TGFBR3 PE=1 SV=3	0.82	3	5	0	0	3	0	0	8
sp|Q8N1N4|K2C78_HUMAN Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=2...	sp|Q8N1N4|K2C78_HUMANKeratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=2 SV=2	0.3	1	0	0	0	8	0	2	0
Isoform 5 of Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens GN=IGF2BP2	sp|Q9Y6M1-5|IF2B2_HUMAN	0.36	7	0	0	0	0	0	0	0
Isoform 2 of WAS/WASL-interacting protein family member 1 OS=Homo sapiens GN=WIPF1	sp|O43516-2|WIPF1_HUMAN	0.36	14	0	0	0	0	0	0	0
40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=3 SV=1	Q8WVC2_HUMAN (+1)	0.36	38	0	0	0	0	0	0	0
sp|P17096|HMGA1_HUMAN High mobility group protein HMG-I/HMG-Y OS=Homo sapiens GN=HMGA1...	sp|P17096|HMGA1_HUMANHigh mobility group protein HMG-I/HMG-Y OS=Homo sapiens GN=HMGA1 PE=1 SV=3	0.36	30	0	0	0	0	0	0	0
GTPase HRas OS=Homo sapiens GN=HRAS PE=1 SV=1	sp|P01112|RASH_HUMAN	0.33	5	3	7	2	2	1	0	1
tr|H0Y8T3|H0Y8T3_HUMAN Prostatic acid phosphatase (Fragment) OS=Homo sapiens GN=ACPP...	tr|H0Y8T3|H0Y8T3_HUMAN Prostatic acid phosphatase (Fragment) OS=Homo sapiens GN=ACPP...	0.29	5	2	4	3	3	8	6	0
40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2	RS16_HUMAN	0.96	8	1	0	1	1	2	5	2

Growth arrest-specific protein 1 OS=Homo sapiens GN=GAS1 PE=1 SV=2	GAS1_HUMAN	0.17	0	0	0	0	0	0	2	1
sp|CASB_BOVIN|	sp|CASB_BOVIN|	0.088	2	0	0	2	2	4	2	7
sp|Q01469|FABP5_HUMAN Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3	sp|Q01469|FABP5_HUMANFatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3	0.52	7	8	0	0	0	3	5	0
Cochlin OS=Homo sapiens GN=COCH PE=2 SV=1	E7EN67_HUMAN	0.21	0	0	0	0	0	3	1	0
Phosphoglycolate phosphatase OS=Homo sapiens GN=PGP PE=1 SV=1	PGP_HUMAN	0.59	0	1	1	0	0	2	2	0
sp|Q96C19|EFHD2_HUMAN EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2...	sp|Q96C19|EFHD2_HUMANEF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1	0.35	9	2	0	0	1	0	0	1
Glutathione S-transferase theta-2B OS=Homo sapiens GN=GSTT2 PE=2 SV=2	B5MCL2_HUMAN	0.62	0	0	1	0	0	0	8	0
sp|Q8IYS1|P20D2_HUMAN Peptidase M20 domain-containing protein 2 OS=Homo sapiens GN=PM20D2 PE=1 SV=2	sp|Q8IYS1|P20D2_HUMANPeptidase M20 domain-containing protein 2 OS=Homo sapiens GN=PM20D2 PE=1 SV=2	0.92	8	3	0	0	4	0	8	0
Azurocidin OS=Homo sapiens GN=AZU1 PE=1 SV=3	CAP7_HUMAN	0.94	0	0	0	3	3	0	0	0
sp|Q9BY77|PDIP3_HUMAN Polymerase delta-interacting protein 3 OS=Homo sapiens GN=POLDIP3 PE=1 SV=2	sp|Q9BY77|PDIP3_HUMANPolymerase delta-interacting protein 3 OS=Homo sapiens GN=POLDIP3 PE=1 SV=2	0.36	3	0	0	0	0	0	0	0
GTP-binding protein SAR1b (Fragment) OS=Homo sapiens GN=SAR1B PE=2 SV=1	D6RD69_HUMAN	0.42	0	0	3	4	4	0	8	0
sp|Q9Y5Z0|BACE2_HUMAN Beta-secretase 2 OS=Homo sapiens GN=BACE2 PE=1 SV=1	sp|Q9Y5Z0|BACE2_HUMANBeta-secretase 2 OS=Homo sapiens GN=BACE2 PE=1 SV=1	0.29	1	2	3	0	0	1	0	0
sp|Q96FZ7|CHMP6_HUMAN Charged multivesicular body protein 6 OS=Homo sapiens GN=CHMP6...	sp|Q96FZ7|CHMP6_HUMANCharged multivesicular body protein 6 OS=Homo sapiens GN=CHMP6 PE=1 SV=3	0.43	4	0	3	0	3	1	4	0
Isoform 3 of Kinesin light chain 4 OS=Homo sapiens GN=KLC4	sp|Q9NSK0-3|KLC4_HUMAN (+1)	0.39	0	0	3	2	2	0	0	1
Nuclear transport factor 2 OS=Homo sapiens GN=NUTF2 PE=1 SV=1	NTF2_HUMAN	0.38	1	0	4	0	0	0	4	0
60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3	RL5_HUMAN	0.98	0	2	0	2	2	2	0	0

sp|O94919|ENDD1_HUMAN Endonuclease domain-containing 1 protein OS=Homo sapiens GN=ENDOD1 PE=1 SV=2	sp|O94919|ENDD1_HUMANEndonuclease domain-containing 1 protein OS=Homo sapiens GN=ENDOD1 PE=1 SV=2	0.13	3	1	1	0	0	0	0	0
sp|Q9HBR0|S38AA_HUMAN Putative sodium-coupled neutral amino acid transporter 10 OS=Homo...	sp|Q9HBR0|S38AA_HUMANPutative sodium-coupled neutral amino acid transporter 10 OS=Homo sapiens GN=SLC38A10 PE=1 SV=2	0.49	0	1	0	0	0	0	0	4
sp|O43395|PRPF3_HUMAN U4/U6 small nuclear ribonucleoprotein Prp3 OS=Homo sapiens GN=PRPF3 PE=1 SV=2	sp|O43395|PRPF3_HUMANU4/U6 small nuclear ribonucleoprotein Prp3 OS=Homo sapiens GN=PRPF3 PE=1 SV=2	0.36	4	0	0	0	0	0	0	0
sp|Q9NPC4|A4GAT_HUMAN Lactosylceramide 4-alpha-galactosyltransferase OS=Homo sapiens GN=A4GALT PE=2 SV=1	sp|Q9NPC4|A4GAT_HUMANLactosylceramide 4-alpha-galactosyltransferase OS=Homo sapiens GN=A4GALT PE=2 SV=1	0.89	0	4	0	0	2	0	0	1
sp|Q9HCN8|SDF2L_HUMAN Stromal cell-derived factor 2-like protein 1 OS=Homo sapiens GN=SDF2L1 PE=1 SV=2	sp|Q9HCN8|SDF2L_HUMANStromal cell-derived factor 2-like protein 1 OS=Homo sapiens GN=SDF2L1 PE=1 SV=2	0.36	3	0	0	0	0	0	0	0
Serpin H1 (Fragment) OS=Homo sapiens GN=SERPINH1 PE=2 SV=1	E9PMI5_HUMAN	0.36	2	0	0	0	0	0	0	0
sp|Q96E39|RMXL1_HUMAN RNA binding motif protein, X-linked-like-1 OS=Homo sapiens GN=RBMXL1 PE=1 SV=1	sp|Q96E39|RMXL1_HUMANRNA binding motif protein, X-linked-like-1 OS=Homo sapiens GN=RBMXL1 PE=1 SV=1	0.36	21	0	0	0	0	0	0	0
sp|P20700|LMNB1_HUMAN Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2	sp|P20700|LMNB1_HUMANLamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2	0.36	16	0	0	0	0	0	0	0
sp|P04208|LV106_HUMAN Ig lambda chain V-I region WAH OS=Homo sapiens PE=1 SV=1	sp|P04208|LV106_HUMANIg lambda chain V-I region WAH OS=Homo sapiens PE=1 SV=1	0.01	1	1	0	0	3	7	3	4
sp|Q96HC4|PDLI5_HUMAN PDZ and LIM domain protein 5 OS=Homo sapiens GN=PDLIM5 PE=1 SV=5	sp|Q96HC4|PDLI5_HUMANPDZ and LIM domain protein 5 OS=Homo sapiens GN=PDLIM5 PE=1 SV=5	0.52	0	9	0	0	3	4	4	2
sp|Q8N1G4|LRC47_HUMAN Leucine-rich repeat-containing protein 47 OS=Homo sapiens GN=LRRC47 PE=1 SV=1	sp|Q8N1G4|LRC47_HUMANLeucine-rich repeat-containing protein 47 OS=Homo sapiens GN=LRRC47 PE=1 SV=1	0.39	2	0	0	0	1	0	3	1
sp|Q8NBX0|SCPDL_HUMAN Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1	sp|Q8NBX0|SCPDL_HUMANSaccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1	0.21	0	1	0	0	0	1	4	1

Isoform 2 of Prostatic acid phosphatase OS=Homo sapiens GN=ACPP	sp|P15309-2|PPAP_HUMAN	0.67	1	0	4	0	0	5	1	7
sp|Q9NRF8|PYRG2_HUMAN CTP synthase 2 OS=Homo sapiens GN=CTPS2 PE=1 SV=1	sp|Q9NRF8|PYRG2_HUMANCTP synthase 2 OS=Homo sapiens GN=CTPS2 PE=1 SV=1	0.36	0	3	0	0	0	0	0	0
Galectin-7 OS=Homo sapiens GN=LGALS7 PE=1 SV=2	LEG7_HUMAN	0.23	0	0	0	2	2	0	7	2
ADP-ribosylation factor-like protein 3 OS=Homo sapiens GN=ARL3 PE=1 SV=2	ARL3_HUMAN	0.36	0	0	2	0	0	0	0	0
Isoform 2 of Basigin OS=Homo sapiens GN=BSG	sp|P35613-2|BASI_HUMAN	0.7	5	0	0	0	0	0	1	2
sp|O00151|PDLI1_HUMAN PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4	sp|O00151|PDLI1_HUMANPDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4	0.77	3	0	0	0	0	0	2	0
PITH domain-containing protein 1 OS=Homo sapiens GN=PITHD1 PE=1 SV=1	sp|Q9GZP4|PITH1_HUMAN	0.48	0	0	5	0	0	12	0	10
Serine/threonine-protein kinase PAK 2 OS=Homo sapiens GN=PAK2 PE=1 SV=3	PAK2_HUMAN	0.36	3	0	0	0	0	0	0	0
sp|Q9UK76-2|HN1_HUMAN Isoform 2 of Hematological and neurological expressed 1 protein OS=Homo sapiens GN=HN1	sp|Q9UK76-2|HN1_HUMANIsoform 2 of Hematological and neurological expressed 1 protein OS=Homo sapiens GN=HN1	0.36	7	0	0	0	0	0	0	0
sp|P30153|2AAA_HUMAN Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit...	sp|P30153|2AAA_HUMAN Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit...	0.53	5	1	3	1	1	3	6	2
sp|P57735|RAB25_HUMAN Ras-related protein Rab-25 OS=Homo sapiens GN=RAB25 PE=1 SV=2	sp|P57735|RAB25_HUMANRas-related protein Rab-25 OS=Homo sapiens GN=RAB25 PE=1 SV=2	0.49	5	7	0	0	2	2	9	3
COP9 signalosome complex subunit 6 OS=Homo sapiens GN=COPS6 PE=1 SV=1	CSN6_HUMAN	0.78	1	1	1	0	0	3	4	0
sp|Q07812-5|BAX_HUMAN Isoform Epsilon of Apoptosis regulator BAX OS=Homo sapiens GN=BAX	sp|Q07812-5|BAX_HUMANIsoform Epsilon of Apoptosis regulator BAX OS=Homo sapiens GN=BAX	0.07	0	3	0	0	5	5	0	6
sp|Q9BYZ2|LDH6B_HUMAN L-lactate dehydrogenase A-like 6B OS=Homo sapiens GN=LDHAL6B PE=1 SV=3	sp|Q9BYZ2|LDH6B_HUMANL-lactate dehydrogenase A-like 6B OS=Homo sapiens GN=LDHAL6B PE=1 SV=3	0.079	0	0	0	0	0	0	4	1

Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=2 SV=1	B4DTC3_HUMAN	0.36	4	0	0	0	0	0	0	0
sp|Q9BRG1|VPS25_HUMAN Vacuolar protein-sorting-associated protein 25 OS=Homo sapiens GN=VPS25 PE=1 SV=1	sp|Q9BRG1|VPS25_HUMANVacuolar protein-sorting-associated protein 25 OS=Homo sapiens GN=VPS25 PE=1 SV=1	0.8	0	6	0	0	1	1	2	0
Protein LYRIC OS=Homo sapiens GN=MTDH PE=2 SV=1	E5RJU9_HUMAN (+1)	0.36	16	0	0	0	0	0	0	0
Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4	VIME_HUMAN	0.36	20	0	0	0	0	0	0	0
Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=1	L7N2F9_HUMAN	0.31	4	6	2	1	1	5	3	2
sp|P49747|COMP_HUMAN Cartilage oligomeric matrix protein OS=Homo sapiens GN=COMP...	sp|P49747|COMP_HUMAN Cartilage oligomeric matrix protein OS=Homo sapiens GN=COMP... (+2)	0.41	7	10	1	1	1	6	2	4
Isoform 4 of Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR	sp|P01130-4|LDLR_HUMAN	0.71	3	4	0	0	0	2	0	2
sp|P19440|GGT1_HUMAN Gamma-glutamyltranspeptidase 1 OS=Homo sapiens GN=GGT1 PE=1...	sp|P19440|GGT1_HUMAN Gamma-glutamyltranspeptidase 1 OS=Homo sapiens GN=GGT1 PE=1...	0.93	1	9	0	2	2	4	5	0
sp|P33908|MA1A1_HUMAN Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA OS=Homo sapiens GN=MAN1A1 PE=1 SV=3	sp|P33908|MA1A1_HUMANMannosyl-oligosaccharide 1,2-alpha-mannosidase IA OS=Homo sapiens GN=MAN1A1 PE=1 SV=3	0.47	0	5	0	0	0	0	0	1
sp|Q9HCN3|TMM8A_HUMAN Transmembrane protein 8A OS=Homo sapiens GN=TMEM8A PE=1 SV=3	sp|Q9HCN3|TMM8A_HUMANTransmembrane protein 8A OS=Homo sapiens GN=TMEM8A PE=1 SV=3	0.17	4	9	0	0	0	0	0	0
sp|O76003|GLRX3_HUMAN Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2	sp|O76003|GLRX3_HUMANGlutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2	1	1	2	0	0	0	0	2	1
sp|A6NKL6|T200C_HUMAN Transmembrane protein 200C OS=Homo sapiens GN=TMEM200C PE=2 SV=2	sp|A6NKL6|T200C_HUMANTransmembrane protein 200C OS=Homo sapiens GN=TMEM200C PE=2 SV=2	0.36	0	5	0	0	0	0	0	0
Isoform 3 of Leucine zipper transcription factor-like protein 1 OS=Homo sapiens GN=LZTFL1	sp|Q9NQ48-3|LZTL1_HUMAN	0.22	0	2	0	0	0	7	0	5
sp|Q15459|SF3A1_HUMAN Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1	sp|Q15459|SF3A1_HUMANSplicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1	0.36	3	0	0	0	0	0	0	0
sp|O94766|B3GA3_HUMAN Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3	sp|O94766|B3GA3_HUMANGalactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3 OS=Homo sapiens GN=B3GAT3 PE=1 SV=2	0.58	1	1	0	0	0	0	5	0

OS=Homo sapiens GN=B3GAT3 PE=1 SV=2										
sp|P07900-2|HS90A_HUMAN Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens...	sp|P07900-2|HS90A_HUMAN Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens...	0.45	0	0	5	0	0	0	0	0
Muscarinic acetylcholine receptor M1 OS=Homo sapiens GN=CHRM1 PE=1 SV=2	ACM1_HUMAN	0.36	0	0	0	0	0	0	0	5
Erlin-2 (Fragment) OS=Homo sapiens GN=ERLIN2 PE=2 SV=1	E5RHW4_HUMAN	0.36	0	0	0	0	0	0	2	0
Prefoldin subunit 2 OS=Homo sapiens GN=PFDN2 PE=1 SV=1	PFD2_HUMAN	0.17	12	1	2	5	5	2	1	1
sp|Q9Y277|VDAC3_HUMAN Voltage-dependent anion-selective channel protein 3 OS=Homo...	sp|Q9Y277|VDAC3_HUMANVoltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1	0.34	2	0	0	1	1	0	7	2
sp|Q9BV40|VAMP8_HUMAN Vesicle-associated membrane protein 8 OS=Homo sapiens GN=VAMP8 PE=1 SV=1	sp|Q9BV40|VAMP8_HUMANVesicle-associated membrane protein 8 OS=Homo sapiens GN=VAMP8 PE=1 SV=1	0.85	11	2	0	0	4	6	5	0
sp|Q01581|HMCS1_HUMAN Hydroxymethylglutaryl-CoA synthase, cytoplasmic OS=Homo sapiens GN=HMGCS1 PE=1 SV=2	sp|Q01581|HMCS1_HUMANHydroxymethylglutaryl-CoA synthase, cytoplasmic OS=Homo sapiens GN=HMGCS1 PE=1 SV=2	0.74	2	0	0	0	1	0	0	2
sp|Q92520|FAM3C_HUMAN Protein FAM3C OS=Homo sapiens GN=FAM3C PE=1 SV=1	sp|Q92520|FAM3C_HUMANProtein FAM3C OS=Homo sapiens GN=FAM3C PE=1 SV=1	0.27	0	2	0	0	2	2	1	0
sp|P04259|K2C6B_HUMAN Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1...	sp|P04259|K2C6B_HUMANKeratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	0.093	0	2	0	0	5	0	5	3
sp|Q969X5|ERGI1_HUMAN Endoplasmic reticulum-Golgi intermediate compartment protein 1 OS=Homo sapiens GN=ERGIC1 PE=1 SV=1	sp|Q969X5|ERGI1_HUMANEndoplasmic reticulum-Golgi intermediate compartment protein 1 OS=Homo sapiens GN=ERGIC1 PE=1 SV=1	0.41	0	0	5	0	0	0	4	0
Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=1	H0YHG0_HUMAN	0.36	14	0	0	0	0	0	0	0
sp|P52566|GDIR2_HUMAN Rho GDP-dissociation inhibitor 2 OS=Homo sapiens GN=ARHGDIB PE=1 SV=3	sp|P52566|GDIR2_HUMANRho GDP-dissociation inhibitor 2 OS=Homo sapiens GN=ARHGDIB PE=1 SV=3	0.36	20	0	0	0	0	0	0	0
Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	DYHC1_HUMAN	0.36	0	0	0	0	0	11	0	0

sp|P05386|RLA1_HUMAN 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1...	sp|P05386|RLA1_HUMAN 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1...	0.2	23	0	3	1	1	3	4	1
Phosphomevalonate kinase OS=Homo sapiens GN=PMVK PE=1 SV=3	PMVK_HUMAN	0.33	1	9	7	2	2	2	2	2
Neutrophil elastase OS=Homo sapiens GN=ELANE PE=1 SV=1	ELNE_HUMAN	0.43	1	0	1	3	3	2	1	1
sp|P01619|KV301_HUMAN Ig kappa chain V-III region B6 OS=Homo sapiens PE=1 SV=1	sp|P01619|KV301_HUMANIg kappa chain V-III region B6 OS=Homo sapiens PE=1 SV=1	0.33	0	2	0	0	6	0	1	1
Corneodesmosin OS=Homo sapiens GN=CDSN PE=2 SV=1	G8JLG2_HUMAN	0.92	2	0	0	4	4	0	2	0
sp|Q11201|SIA4A_HUMAN CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase...	sp|Q11201|SIA4A_HUMANCMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase 1 OS=Homo sapiens GN=ST3GAL1 PE=2 SV=1	0.15	0	4	0	0	3	5	7	0
sp|Q9UBQ7|GRHPR_HUMAN Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens...	sp|Q9UBQ7|GRHPR_HUMANGlyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens GN=GRHPR PE=1 SV=1	0.033	0	3	0	0	3	6	6	2
60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	sp|P26373|RL13_HUMAN	0.27	10	1	5	0	0	1	1	0
Synaptobrevin homolog YKT6 OS=Homo sapiens GN=YKT6 PE=1 SV=1	YKT6_HUMAN	0.49	2	0	0	3	3	0	10	0
Isoform 7 of Tumor protein D54 OS=Homo sapiens GN=TPD52L2	sp|O43399-7|TPD54_HUMAN	0.68	2	0	0	0	0	1	0	0
sp|O43286|B4GT5_HUMAN Beta-1,4-galactosyltransferase 5 OS=Homo sapiens GN=B4GALT5 PE=2 SV=1	sp|O43286|B4GT5_HUMANBeta-1,4-galactosyltransferase 5 OS=Homo sapiens GN=B4GALT5 PE=2 SV=1	0.73	0	0	0	0	1	0	2	0
sp|Q02543|RL18A_HUMAN 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2	sp|Q02543|RL18A_HUMAN60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2	0.26	0	0	0	0	0	1	6	0
sp|O75947|ATP5H_HUMAN ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3	sp|O75947|ATP5H_HUMANATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3	0.4	11	0	0	0	0	0	1	0
Isoform 5 of Prelamin-A/C OS=Homo sapiens GN=LMNA	sp|P02545-5|LMNA_HUMAN	0.36	9	0	0	0	0	0	0	0
sp|P31146|COR1A_HUMAN Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4	sp|P31146|COR1A_HUMANCoronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4	0.36	10	0	0	0	0	0	0	0

Prefoldin subunit 1 OS=Homo sapiens GN=PFDN1 PE=1 SV=2	PFD1_HUMAN	0.36	19	0	0	0	0	0	0	0
sp|P53985|MOT1_HUMAN Monocarboxylate transporter 1 OS=Homo sapiens GN=SLC16A1 PE=1...	sp|P53985|MOT1_HUMAN Monocarboxylate transporter 1 OS=Homo sapiens GN=SLC16A1 PE=1...	0.23	0	2	1	1	1	6	6	13
sp|Q96EY5|MB12A_HUMAN Multivesicular body subunit 12A OS=Homo sapiens GN=MVB12A PE=1...	sp|Q96EY5|MB12A_HUMANMultivesicular body subunit 12A OS=Homo sapiens GN=MVB12A PE=1 SV=1	0.37	2	1	0	0	3	2	1	0
Isoform 2 of AP-1 complex subunit mu-2 OS=Homo sapiens GN=AP1M2	AP1M2_HUMAN	0.39	0	1	7	0	0	3	0	1
sp|P61421|VA0D1_HUMAN V-type proton ATPase subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=1 SV=1	sp|P61421|VA0D1_HUMANV-type proton ATPase subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=1 SV=1	0.97	0	4	0	0	0	1	2	1
Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=3	TETN_HUMAN	0.4	1	2	2	2	2	4	4	0
Isoform 1 of Retinoic acid receptor responder protein 1 OS=Homo sapiens GN=RARRES1	sp|P49788-2|TIG1_HUMAN	0.39	1	6	0	2	2	0	0	2
Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=2 SV=1	H0YK48_HUMAN	0.78	0	0	0	1	1	2	4	1
Protein MENT OS=Homo sapiens GN=MENT PE=2 SV=1	sp|Q9BUN1|MENT_HUMAN	0.17	0	0	0	0	0	0	6	3
Tryptophan--tRNA ligase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2	sp|P23381|SYWC_HUMAN	0.36	0	0	0	0	0	2	0	0
sp|Q86UN2|R4RL1_HUMAN Reticulon-4 receptor-like 1 OS=Homo sapiens GN=RTN4RL1 PE=2 SV=1	sp|Q86UN2|R4RL1_HUMANReticulon-4 receptor-like 1 OS=Homo sapiens GN=RTN4RL1 PE=2 SV=1	0.33	1	2	0	0	1	1	1	2
Prefoldin subunit 3 OS=Homo sapiens GN=VBP1 PE=1 SV=3	PFD3_HUMAN	0.29	3	10	0	0	0	1	0	1
Archain 1, isoform CRA_a OS=Homo sapiens GN=ARCN1 PE=2 SV=1	B0YIW6_HUMAN	0.54	1	0	1	0	0	1	5	0
sp|O75264|CS077_HUMAN Transmembrane protein C19orf77 OS=Homo sapiens GN=C19orf77 PE=2 SV=2	sp|O75264|CS077_HUMANTransmembrane protein C19orf77 OS=Homo sapiens GN=C19orf77 PE=2 SV=2	0.33	3	3	0	0	6	3	3	0
sp|Q6UX72|B3GN9_HUMAN UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9 OS=Homo sapiens GN=B3GNT9 PE=2 SV=1	sp|Q6UX72|B3GN9_HUMANUDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9 OS=Homo sapiens GN=B3GNT9 PE=2 SV=1	0.81	1	5	0	0	5	0	2	0

sp|Q6UW15|REG3G_HUMAN Regenerating islet-derived protein 3-gamma OS=Homo sapiens GN=REG3G PE=1 SV=1	sp|Q6UW15|REG3G_HUMANRegenerating islet-derived protein 3-gamma OS=Homo sapiens GN=REG3G PE=1 SV=1	0.26	6	0	0	0	6	5	5	0
Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3	SYK_HUMAN	0.63	1	0	2	0	0	0	6	0
Sulfatase-modifying factor 2 OS=Homo sapiens GN=SUMF2 PE=2 SV=1	F8WCW9_HUMAN	0.36	0	0	4	0	0	0	0	0
Isoform 2 of MOB kinase activator 1B OS=Homo sapiens GN=MOB1B	MOB1B_HUMAN	0.36	0	4	0	0	0	0	0	0
Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=2 SV=1	H3BVG0_HUMAN	0.36	5	0	0	0	0	0	0	0
40S ribosomal protein S30 OS=Homo sapiens GN=FAU PE=2 SV=1	E9PR30_HUMAN	0.36	24	0	0	0	0	0	0	0
sp|P09429|HMGB1_HUMAN High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1...	sp|P09429|HMGB1_HUMANHigh mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1...	0.36	31	0	0	0	0	0	0	0
sp|Q13347|EIF3I_HUMAN Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I PE=1 SV=1	sp|Q13347|EIF3I_HUMANEukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I PE=1 SV=1	0.66	1	1	0	0	0	1	2	0
Tetraspanin-8 OS=Homo sapiens GN=TSPAN8 PE=1 SV=1	TSN8_HUMAN	0.5	0	1	1	0	0	2	4	0
sp|Q99460|PSMD1_HUMAN 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2	sp|Q99460|PSMD1_HUMAN26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2	0.35	3	8	3	0	0	6	4	3
sp|Q9P1F3|ABRAL_HUMAN Costars family protein ABRACL OS=Homo sapiens GN=ABRACL PE=1 SV=1	sp|Q9P1F3|ABRAL_HUMANCostars family protein ABRACL OS=Homo sapiens GN=ABRACL PE=1 SV=1	0.31	14	0	4	0	6	2	3	0
Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=2 SV=1	E7EMK3_HUMAN	0.4	0	0	4	0	0	1	1	0
N-acylethanolamine-hydrolyzing acid amidase OS=Homo sapiens GN=NAAA PE=1 SV=3	sp|Q02083|NAAA_HUMAN	0.44	0	0	0	1	1	2	0	0
Isoform 3 of Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1	sp|Q13813-3|SPTN1_HUMAN	0.68	1	4	0	0	0	6	0	1
sp|Q9Y2E5|MA2B2_HUMAN Epididymis-specific alpha-mannosidase OS=Homo sapiens GN=MAN2B2...	sp|Q9Y2E5|MA2B2_HUMANEpididymis-specific alpha-mannosidase OS=Homo sapiens GN=MAN2B2 PE=1 SV=4	0.93	7	5	0	0	0	0	1	7

Isoform 4 of Clathrin light chain A OS=Homo sapiens GN=CLTA	sp|P09496-4|CLCA_HUMAN	0.36	9	0	0	0	0	0	0	0
Sperm histone HP2 OS=Homo sapiens GN=PRM2 PE=2 SV=1	Q6ZMM0_HUMAN	0.36	0	0	0	0	0	0	14	0
sp|P52209|6PGD_HUMAN 6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens...	sp|P52209|6PGD_HUMAN 6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens... (+1)	0.44	3	1	5	1	1	6	2	0
Claudin-3 OS=Homo sapiens GN=CLDN3 PE=1 SV=1	CLD3_HUMAN	0.3	0	3	2	4	4	0	0	1
sp|Q7Z6M3|MILR1_HUMAN Allergin-1 OS=Homo sapiens GN=MILR1 PE=1 SV=2	sp|Q7Z6M3|MILR1_HUMANAllergin-1 OS=Homo sapiens GN=MILR1 PE=1 SV=2-DECOY	0.36	0	0	0	0	0	0	0	3
sp|Q9H190|SDCB2_HUMAN Syntenin-2 OS=Homo sapiens GN=SDCBP2 PE=2 SV=2	sp|Q9H190|SDCB2_HUMANSyntenin-2 OS=Homo sapiens GN=SDCBP2 PE=2 SV=2	0.46	0	2	0	1	1	0	2	1
Interferon regulatory factor 6 OS=Homo sapiens GN=IRF6 PE=1 SV=1	sp|O14896|IRF6_HUMAN	0.34	0	0	2	1	1	0	0	0
sp|O43598|DNPH1_HUMAN 2'-deoxynucleoside 5'-phosphate N-hydrolase 1 OS=Homo sapiens GN=DNPH1 PE=1 SV=1	sp|O43598|DNPH1_HUMAN2'-deoxynucleoside 5'-phosphate N-hydrolase 1 OS=Homo sapiens GN=DNPH1 PE=1 SV=1	0.98	7	2	0	0	2	4	3	0
sp|Q8TAA3|PSA7L_HUMAN Proteasome subunit alpha type-7-like OS=Homo sapiens GN=PSMA8...	sp|Q8TAA3|PSA7L_HUMANProteasome subunit alpha type-7-like OS=Homo sapiens GN=PSMA8 PE=1 SV=3	0.24	0	3	0	0	0	1	7	1
S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=2 SV=1	E5RJR5_HUMAN	0.38	0	0	1	3	3	0	2	0
60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2	RL27_HUMAN	0.35	3	0	4	0	0	1	2	0
sp|P07686|HEXB_HUMAN Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1...	sp|P07686|HEXB_HUMAN Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1...	0.83	10	5	0	0	0	1	0	1
Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=2 SV=1	B4DP38_HUMAN	0.98	0	2	0	0	0	0	1	1
Small nuclear ribonucleoprotein-associated proteins B and B' OS=Homo sapiens GN=SNRPB PE=1 SV=2	sp|P14678|RSMB_HUMAN	0.36	9	0	0	0	0	0	0	0
Ig lambda chain V-III region LOI OS=Homo sapiens PE=1 SV=1	LV302_HUMAN	0.3	0	0	6	10	0	0	0	5
sp|Q12834|CDC20_HUMAN Cell division cycle protein 20 homolog OS=Homo sapiens GN=CDC20 PE=1 SV=2	sp|Q12834|CDC20_HUMANCell division cycle protein 20 homolog OS=Homo sapiens GN=CDC20 PE=1 SV=2	0.36	6	0	0	0	0	0	0	0

sp|Q9BX68|HINT2_HUMAN Histidine triad nucleotide-binding protein 2, mitochondrial OS=Homo sapiens GN=HINT2 PE=1 SV=1	sp|Q9BX68|HINT2_HUMANHistidine triad nucleotide-binding protein 2, mitochondrial OS=Homo sapiens GN=HINT2 PE=1 SV=1	0.36	8	0	0	0	0	0	0	0
sp|P18859|ATP5J_HUMAN ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J PE=1 SV=1	sp|P18859|ATP5J_HUMANATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J PE=1 SV=1	0.36	18	0	0	0	0	0	0	0
sp|Q07666|KHDR1_HUMAN KH domain-containing, RNA-binding, signal transduction-associated...	sp|Q07666|KHDR1_HUMANKH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1	0.36	15	0	0	0	0	0	0	0
sp|Q96PU8-3|QKI_HUMAN Isoform 2 of Protein quaking OS=Homo sapiens GN=QKI	sp|Q96PU8-3|QKI_HUMANIsoform 2 of Protein quaking OS=Homo sapiens GN=QKI	0.36	6	0	0	0	0	0	0	0
sp|P01717|LV403_HUMAN Ig lambda chain V-IV region Hil OS=Homo sapiens PE=1 SV=1	sp|P01717|LV403_HUMANIg lambda chain V-IV region Hil OS=Homo sapiens PE=1 SV=1	0.38	2	1	0	0	0	5	3	0
Isoform 2 of 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase OS=Homo sapiens GN=ADI1	sp|Q9BV57-2|MTND_HUMAN	0.32	4	0	3	1	1	2	0	0
sp|Q9NZL9|MAT2B_HUMAN Methionine adenosyltransferase 2 subunit beta OS=Homo sapiens GN=MAT2B PE=1 SV=1	sp|Q9NZL9|MAT2B_HUMANMethionine adenosyltransferase 2 subunit beta OS=Homo sapiens GN=MAT2B PE=1 SV=1	0.13	2	2	1	0	0	0	0	0
Isoform Short of Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ	sp|P23246-2|SFPQ_HUMAN	0.36	13	0	0	0	0	0	0	0
Phosphoserine phosphatase OS=Homo sapiens GN=PSPH PE=1 SV=2	SERB_HUMAN	0.55	1	1	1	1	1	3	2	2
HCG1745306, isoform CRA_a OS=Homo sapiens GN=HBA2 PE=2 SV=1	G3V1N2_HUMAN (+2)	0.85	2	6	0	0	0	4	4	1
sp|Q96I24|FUBP3_HUMAN Far upstream element-binding protein 3 OS=Homo sapiens GN=FUBP3 PE=1 SV=2	sp|Q96I24|FUBP3_HUMANFar upstream element-binding protein 3 OS=Homo sapiens GN=FUBP3 PE=1 SV=2	0.36	2	0	0	0	0	0	0	0
sp|Q9BQ61|CS043_HUMAN Uncharacterized protein C19orf43 OS=Homo sapiens GN=C19orf43...	sp|Q9BQ61|CS043_HUMANUncharacterized protein C19orf43 OS=Homo sapiens GN=C19orf43 PE=1 SV=1	0.36	14	0	0	0	0	0	0	0
sp|Q9UIQ6-2|LCAP_HUMAN Isoform 2 of Leucyl-cystinyl aminopeptidase OS=Homo sapiens...	sp|Q9UIQ6-2|LCAP_HUMAN Isoform 2 of Leucyl-cystinyl aminopeptidase OS=Homo sapiens... (+2)	0.77	0	1	1	7	7	3	2	1

sp|Q6GMV3|PTRD1_HUMAN Putative peptidyl-tRNA hydrolase PTRHD1 OS=Homo sapiens GN=PTRHD1 PE=1 SV=1	sp|Q6GMV3|PTRD1_HUMANPutative peptidyl-tRNA hydrolase PTRHD1 OS=Homo sapiens GN=PTRHD1 PE=1 SV=1	0.63	8	0	0	0	0	1	2	1
sp|P27105|STOM_HUMAN Erythrocyte band 7 integral membrane protein OS=Homo sapiens...	sp|P27105|STOM_HUMAN Erythrocyte band 7 integral membrane protein OS=Homo sapiens...	0.57	0	2	0	1	1	5	0	0
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=2 SV=1	C9J634_HUMAN	0.25	0	0	0	0	0	1	5	0
sp|P38571-2|LICH_HUMAN Isoform 2 of Lysosomal acid lipase/cholesteryl ester hydrolase...	sp|P38571-2|LICH_HUMAN Isoform 2 of Lysosomal acid lipase/cholesteryl ester hydrolase... (+1)	0.66	1	9	0	1	1	1	4	6
ETF1 protein OS=Homo sapiens GN=ETF1 PE=2 SV=1	Q96CG1_HUMAN	0.42	0	1	2	0	0	4	0	0
sp|O15511|ARPC5_HUMAN Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens GN=ARPC5 PE=1 SV=3	sp|O15511|ARPC5_HUMANActin-related protein 2/3 complex subunit 5 OS=Homo sapiens GN=ARPC5 PE=1 SV=3	0.91	7	0	0	0	2	3	1	0
sp|O60613|SEP15_HUMAN 15 kDa selenoprotein OS=Homo sapiens GN=SEP15 PE=1 SV=3	sp|O60613|SEP15_HUMAN15 kDa selenoprotein OS=Homo sapiens GN=SEP15 PE=1 SV=3	0.72	2	0	0	2	2	1	0	0
sp|Q15847|ADIRF_HUMAN Adipogenesis regulatory factor OS=Homo sapiens GN=ADIRF PE=1 SV=1	sp|Q15847|ADIRF_HUMANAdipogenesis regulatory factor OS=Homo sapiens GN=ADIRF PE=1 SV=1	0.96	0	3	0	0	0	1	1	1
tr|E9PM69|E9PM69_HUMAN 26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3...	tr|E9PM69|E9PM69_HUMAN 26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3... (+1)	0.34	5	0	5	0	0	3	2	0
Isoform 2 of Secernin-1 OS=Homo sapiens GN=SCRN1	sp|Q12765-2|SCRN1_HUMAN (+1)	0.34	2	0	2	0	0	2	0	0
sp|P07910|HNRPC_HUMAN Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=4	sp|P07910|HNRPC_HUMANHeterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=4	0.36	8	0	0	0	0	0	0	0
Isoform 9 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1	sp|Q04637-9|IF4G1_HUMAN	0.47	10	0	0	0	0	0	0	0
sp|O75368|SH3L1_HUMAN SH3 domain-binding glutamic acid-rich-like protein OS=Homo sapiens GN=SH3BGRL PE=1 SV=1	sp|O75368|SH3L1_HUMANSH3 domain-binding glutamic acid-rich-like protein OS=Homo sapiens GN=SH3BGRL PE=1 SV=1	0.81	1	4	0	1	2	1	1	1

Isoform 2 of Isopentenyl-diphosphate Delta-isomerase 1 OS=Homo sapiens GN=IDI1	sp|Q13907-2|IDI1_HUMAN	0.34	1	5	4	0	0	2	2	2
sp|P35998|PRS7_HUMAN 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1...	sp|P35998|PRS7_HUMAN 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1...	0.95	4	0	1	0	0	7	2	1
sp|P43490|NAMPT_HUMAN Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1	sp|P43490|NAMPT_HUMANNicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1	0.8	4	1	0	0	0	4	1	1
60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	sp|P30050|RL12_HUMAN	0.47	12	0	0	1	1	0	3	0
sp|Q5SRE7|PHYD1_HUMAN Phytanoyl-CoA dioxygenase domain-containing protein 1 OS=Homo sapiens GN=PHYHD1 PE=1 SV=2	sp|Q5SRE7|PHYD1_HUMANPhytanoyl-CoA dioxygenase domain-containing protein 1 OS=Homo sapiens GN=PHYHD1 PE=1 SV=2	0.68	0	2	0	0	0	0	0	1
sp|P30048|PRDX3_HUMAN Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3	sp|P30048|PRDX3_HUMANThioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3	0.68	2	0	0	0	0	1	0	0
sp|P42167|LAP2B_HUMAN Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo...	sp|P42167|LAP2B_HUMANLamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2	0.36	12	0	0	0	0	0	0	0
Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens GN=ACP1 PE=1 SV=3	sp|P24666|PPAC_HUMAN	0.36	5	0	0	0	0	0	0	0
60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	RL8_HUMAN	0.46	5	0	0	0	0	1	0	0
sp|P26447|S10A4_HUMAN Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1	sp|P26447|S10A4_HUMANProtein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1	0.36	14	0	0	0	0	0	0	0
sp|P05114|HMGN1_HUMAN Non-histone chromosomal protein HMG-14 OS=Homo sapiens GN=HMGN1...	sp|P05114|HMGN1_HUMANNon-histone chromosomal protein HMG-14 OS=Homo sapiens GN=HMGN1 PE=1 SV=3	0.36	18	0	0	0	0	0	0	0
sp|P51858|HDGF_HUMAN Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=1...	sp|P51858|HDGF_HUMAN Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=1...	0.36	21	0	0	0	0	0	0	0
Rho-related GTP-binding protein RhoG OS=Homo sapiens GN=RHOG PE=1 SV=1	RHOG_HUMAN	0.39	1	4	1	1	1	2	2	2
Keratin, type II cytoskeletal 8 (Fragment) OS=Homo sapiens GN=KRT8 PE=2 SV=1	F8VUG2_HUMAN	0.53	1	5	3	0	0	3	4	1

Isoform 4 of 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2	sp|P10155-4|RO60_HUMAN	0.12	1	1	0	1	1	2	3	1
sp|P30740|ILEU_HUMAN Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1 PE=1...	sp|P30740|ILEU_HUMAN Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1 PE=1...	0.75	2	1	0	3	3	4	0	2
sp|P60903|S10AA_HUMAN Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2	sp|P60903|S10AA_HUMANProtein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2	0.37	4	0	0	1	1	6	2	2
Vacuolar protein sorting-associated protein 29 OS=Homo sapiens GN=VPS29 PE=2 SV=1	F8VXU5_HUMAN	0.37	1	2	3	0	0	3	2	0
sp|P40189|IL6RB_HUMAN Interleukin-6 receptor subunit beta OS=Homo sapiens GN=IL6ST PE=1 SV=2	sp|P40189|IL6RB_HUMANInterleukin-6 receptor subunit beta OS=Homo sapiens GN=IL6ST PE=1 SV=2	0.49	0	4	0	0	1	0	0	2
Beta-centractin OS=Homo sapiens GN=ACTR1B PE=1 SV=1	ACTY_HUMAN	0.35	0	3	2	0	0	1	0	3
Semenogelin-2 OS=Homo sapiens GN=SEMG2 PE=1 SV=1	SEMG2_HUMAN	0.4	0	0	6	0	0	8	0	0
40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1	RS28_HUMAN	0.36	19	0	0	0	0	0	0	0
sp|Q9HAB8|PPCS_HUMAN Phosphopantothenate--cysteine ligase OS=Homo sapiens GN=PPCS...	sp|Q9HAB8|PPCS_HUMAN Phosphopantothenate--cysteine ligase OS=Homo sapiens GN=PPCS...	0.82	6	2	0	5	5	1	5	1
sp|Q16401-2|PSMD5_HUMAN Isoform 2 of 26S proteasome non-ATPase regulatory subunit...	sp|Q16401-2|PSMD5_HUMAN Isoform 2 of 26S proteasome non-ATPase regulatory subunit...	0.32	5	3	9	1	1	0	6	1
sp|Q15257-2|PTPA_HUMAN Isoform 1 of Serine/threonine-protein phosphatase 2A activator...	sp|Q15257-2|PTPA_HUMAN Isoform 1 of Serine/threonine-protein phosphatase 2A activator... (+1)	0.7	0	5	0	0	0	2	1	5
Cystatin-A OS=Homo sapiens GN=CSTA PE=1 SV=1	CYTA_HUMAN	0.26	1	0	0	0	0	2	6	0
sp|P04843|RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase...	sp|P04843|RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase...	0.35	8	0	2	0	0	4	3	0
sp|P23193|TCEA1_HUMAN Transcription elongation factor A protein 1 OS=Homo sapiens GN=TCEA1 PE=1 SV=2	sp|P23193|TCEA1_HUMANTranscription elongation factor A protein 1 OS=Homo sapiens GN=TCEA1 PE=1 SV=2	0.36	2	0	0	0	0	0	0	0
sp|P51688|SPHM_HUMAN N-sulphoglucosamine sulphohydrolase OS=Homo sapiens GN=SGSH...	sp|P51688|SPHM_HUMAN N-sulphoglucosamine sulphohydrolase OS=Homo sapiens GN=SGSH...	0.68	3	1	2	2	2	5	2	6
Isoform 2B of GTPase KRas OS=Homo sapiens GN=KRAS	sp|P01116-2|RASK_HUMAN	0.35	2	4	2	1	1	1	1	5

60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=1 SV=2	RL38_HUMAN	0.14	19	1	1	0	0	1	1	0
sp|Q8WWY7|WFD12_HUMAN WAP four-disulfide core domain protein 12 OS=Homo sapiens GN=WFDC12...	sp|Q8WWY7|WFD12_HUMANWAP four-disulfide core domain protein 12 OS=Homo sapiens GN=WFDC12 PE=2 SV=1	0.097	2	0	0	0	3	5	3	0
sp|DHE3_BOVIN|	sp|DHE3_BOVIN|	0.65	0	0	2	0	0	5	0	0
sp|P02538|K2C6A_HUMAN Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1...	sp|P02538|K2C6A_HUMANKeratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	0.025	0	0	0	0	1	0	2	3
Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=2 SV=2	E7ES43_HUMAN	0.5	0	0	0	0	0	5	0	3
sp|Q8IXA5|SACA3_HUMAN Sperm acrosome membrane-associated protein 3 OS=Homo sapiens GN=SPACA3 PE=1 SV=1	sp|Q8IXA5|SACA3_HUMANSperm acrosome membrane-associated protein 3 OS=Homo sapiens GN=SPACA3 PE=1 SV=1	0.22	1	0	0	0	0	0	3	3
Protein MAL2 OS=Homo sapiens GN=MAL2 PE=1 SV=1	MAL2_HUMAN	0.25	4	2	3	5	5	2	2	0
T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=2 SV=1	E7ENZ3_HUMAN	0.38	2	1	2	0	0	0	3	1
sp|Q15427|SF3B4_HUMAN Splicing factor 3B subunit 4 OS=Homo sapiens GN=SF3B4 PE=1 SV=1	sp|Q15427|SF3B4_HUMANSplicing factor 3B subunit 4 OS=Homo sapiens GN=SF3B4 PE=1 SV=1	0.36	5	0	0	0	0	0	0	0
sp|P51991|ROA3_HUMAN Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3...	sp|P51991|ROA3_HUMAN Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3...	0.36	16	0	0	0	0	0	0	0
sp|P00338|LDHA_HUMAN L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1...	sp|P00338|LDHA_HUMAN L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1...	0.28	4	2	7	0	0	3	0	2
40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	RS25_HUMAN	0.33	11	0	3	0	0	7	3	0
sp|Q9Y224|CN166_HUMAN UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1	sp|Q9Y224|CN166_HUMANUPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1	0.53	2	2	0	0	0	0	2	0
60S ribosomal protein L23a (Fragment) OS=Homo sapiens GN=RPL23A PE=3 SV=1	H7BY10_HUMAN	0.45	6	1	0	0	0	2	0	0
60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1	RL9_HUMAN	0.35	4	1	0	0	0	0	1	0

sp|P10153|RNAS2_HUMAN Non-secretory ribonuclease OS=Homo sapiens GN=RNASE2 PE=1 SV=2	sp|P10153|RNAS2_HUMANNon-secretory ribonuclease OS=Homo sapiens GN=RNASE2 PE=1 SV=2	0.36	7	0	0	0	0	0	0	0
THO complex subunit 4 OS=Homo sapiens GN=ALYREF PE=2 SV=1	E9PB61_HUMAN	0.36	13	0	0	0	0	0	0	0
sp|Q969E4|TCAL3_HUMAN Transcription elongation factor A protein-like 3 OS=Homo sapiens GN=TCEAL3 PE=1 SV=1	sp|Q969E4|TCAL3_HUMANTranscription elongation factor A protein-like 3 OS=Homo sapiens GN=TCEAL3 PE=1 SV=1	0.36	6	0	0	0	0	0	0	0
sp|P0CW22|RS17L_HUMAN 40S ribosomal protein S17-like OS=Homo sapiens GN=RPS17L PE=1 SV=1	sp|P0CW22|RS17L_HUMAN40S ribosomal protein S17-like OS=Homo sapiens GN=RPS17L PE=1 SV=1	0.36	10	0	0	0	0	0	0	0
sp|Q9NVJ2|ARL8B_HUMAN ADP-ribosylation factor-like protein 8B OS=Homo sapiens GN=ARL8B PE=1 SV=1	sp|Q9NVJ2|ARL8B_HUMANADP-ribosylation factor-like protein 8B OS=Homo sapiens GN=ARL8B PE=1 SV=1	0.95	0	2	0	0	0	1	1	0
sp|P13073|COX41_HUMAN Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX4I1 PE=1 SV=1	sp|P13073|COX41_HUMANCytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX4I1 PE=1 SV=1	0.37	2	0	0	0	0	2	5	0
sp|O00232|PSD12_HUMAN 26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3	sp|O00232|PSD12_HUMAN26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3	0.36	0	0	9	0	0	0	0	0
Desmin OS=Homo sapiens GN=DES PE=1 SV=3	DESM_HUMAN	0.2	1	3	0	0	0	0	0	0
sp|P10916|MLRV_HUMAN Myosin regulatory light chain 2, ventricular/cardiac muscle...	sp|P10916|MLRV_HUMAN Myosin regulatory light chain 2, ventricular/cardiac muscle...	0.45	2	11	0	0	0	0	4	0
sp|Q9GZT8|GTPC1_HUMAN Putative GTP cyclohydrolase 1 type 2 NIF3L1 OS=Homo sapiens...	sp|Q9GZT8|GTPC1_HUMANPutative GTP cyclohydrolase 1 type 2 NIF3L1 OS=Homo sapiens GN=NIF3L1 PE=1 SV=2	0.36	0	0	0	0	0	0	3	0
Syntaxin-binding protein 2 OS=Homo sapiens GN=STXBP2 PE=2 SV=1	M0R0M7_HUMAN	0.22	0	0	0	0	0	4	0	0
40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	RS6_HUMAN	0.3	6	2	2	0	0	6	0	0
Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1 SV=3	sp|P36871|PGM1_HUMAN	0.077	0	0	0	1	1	4	3	1
Sulfatase-modifying factor 2 (Fragment) OS=Homo sapiens GN=SUMF2 PE=2 SV=1	H7C3B2_HUMAN	0.82	1	3	0	0	0	2	0	1
ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7	ADT2_HUMAN	0.79	3	1	0	0	0	0	5	0

sp|P13688|CEAM1_HUMAN Carcinoembryonic antigen-related cell adhesion molecule 1 OS=Homo...	sp|P13688|CEAM1_HUMANCarcinoembryonic antigen-related cell adhesion molecule 1 OS=Homo sapiens GN=CEACAM1 PE=1 SV=2	0.46	0	2	0	0	1	0	5	0
Isoform C of Arachidonate 15-lipoxygenase B OS=Homo sapiens GN=ALOX15B	sp|O15296-3|LX15B_HUMAN	0.7	3	1	0	0	0	3	0	0
sp|P09529|INHBB_HUMAN Inhibin beta B chain OS=Homo sapiens GN=INHBB PE=1 SV=2	sp|P09529|INHBB_HUMANInhibin beta B chain OS=Homo sapiens GN=INHBB PE=1 SV=2	0.21	0	0	0	0	0	3	1	0
Dynein light chain roadblock-type 1 OS=Homo sapiens GN=DYNLRB1 PE=2 SV=1	B4DFR2_HUMAN	0.41	10	2	0	0	0	3	0	0
Isoform 4 of PDZ and LIM domain protein 7 OS=Homo sapiens GN=PDLIM7	sp|Q9NR12-4|PDLI7_HUMAN	0.36	5	0	0	0	0	0	0	0
RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=2 SV=1	B0QYK0_HUMAN (+4)	0.36	7	0	0	0	0	0	0	0
sp|P53999|TCP4_HUMAN Activated RNA polymerase II transcriptional coactivator p15...	sp|P53999|TCP4_HUMAN Activated RNA polymerase II transcriptional coactivator p15...	0.33	11	0	0	2	2	0	0	0
Isoform 2 of Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9	SRP09_HUMAN	0.36	13	0	0	0	0	0	0	0
DNA-(apurinic or apyrimidinic site) lyase (Fragment) OS=Homo sapiens GN=APEX1 PE=2 SV=1	G3V5D9_HUMAN	0.36	14	0	0	0	0	0	0	0
sp|P25325|THTM_HUMAN 3-mercaptopyruvate sulfurtransferase OS=Homo sapiens GN=MPST...	sp|P25325|THTM_HUMAN 3-mercaptopyruvate sulfurtransferase OS=Homo sapiens GN=MPST... (+1)	0.64	0	2	2	3	3	6	3	1
sp|P07360|CO8G_HUMAN Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1...	sp|P07360|CO8G_HUMAN Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1...	0.84	1	5	0	1	1	1	3	1
40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	RS11_HUMAN	0.44	6	0	0	0	0	1	0	0
sp|Q9Y5L4|TIM13_HUMAN Mitochondrial import inner membrane translocase subunit Tim13 OS=Homo sapiens GN=TIMM13 PE=1 SV=1	sp|Q9Y5L4|TIM13_HUMANMitochondrial import inner membrane translocase subunit Tim13 OS=Homo sapiens GN=TIMM13 PE=1 SV=1	0.36	7	0	0	0	0	0	0	0
Cellular retinoic acid-binding protein 2 (Fragment) OS=Homo sapiens GN=CRABP2 PE=2 SV=1	Q5SYZ4_HUMAN (+1)	0.36	0	4	0	0	0	0	0	0
Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2	H13_HUMAN	0.36	13	0	0	0	0	0	0	0

sp|P27816|MAP4_HUMAN Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1...	sp|P27816|MAP4_HUMAN Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1...	0.36	12	0	0	0	0	0	0	0
sp|Q9NZJ9|NUDT4_HUMAN Diphosphoinositol polyphosphate phosphohydrolase 2 OS=Homo sapiens GN=NUDT4 PE=1 SV=2	sp|Q9NZJ9|NUDT4_HUMANDiphosphoinositol polyphosphate phosphohydrolase 2 OS=Homo sapiens GN=NUDT4 PE=1 SV=2	0.32	0	2	0	0	1	0	1	5
sp|O15393|TMPS2_HUMAN Transmembrane protease serine 2 OS=Homo sapiens GN=TMPRSS2 PE=1 SV=3	sp|O15393|TMPS2_HUMANTransmembrane protease serine 2 OS=Homo sapiens GN=TMPRSS2 PE=1 SV=3	0.052	0	0	1	0	6	1	3	0
sp|P17405-4|ASM_HUMAN Isoform 4 of Sphingomyelin phosphodiesterase OS=Homo sapiens GN=SMPD1	sp|P17405-4|ASM_HUMANIsoform 4 of Sphingomyelin phosphodiesterase OS=Homo sapiens GN=SMPD1	0.98	2	2	0	0	0	4	0	0
sp|P24752|THIL_HUMAN Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens...	sp|P24752|THIL_HUMAN Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens...	0.41	12	0	0	0	0	0	0	2
40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	RS19_HUMAN	0.36	8	0	0	0	0	0	0	0
sp|Q9Y6H1|CHCH2_HUMAN Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial OS=Homo sapiens GN=CHCHD2 PE=1 SV=1	sp|Q9Y6H1|CHCH2_HUMANCoiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial OS=Homo sapiens GN=CHCHD2 PE=1 SV=1	0.36	10	0	0	0	0	0	0	0
Isoform 2 of U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens GN=SNRNP70	sp|P08621-2|RU17_HUMAN	0.36	4	0	0	0	0	0	0	0
sp|Q86U42|PABP2_HUMAN Polyadenylate-binding protein 2 OS=Homo sapiens GN=PABPN1 PE=1 SV=3	sp|Q86U42|PABP2_HUMANPolyadenylate-binding protein 2 OS=Homo sapiens GN=PABPN1 PE=1 SV=3	0.36	20	0	0	0	0	0	0	0
Isoform 2 of Calcium-dependent secretion activator 2 OS=Homo sapiens GN=CADPS2	sp|Q86UW7-2|CAPS2_HUMAN	0.99	3	1	0	0	0	3	0	1
sp|P13646|K1C13_HUMAN Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1...	sp|P13646|K1C13_HUMANKeratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4	0.38	1	1	0	0	6	0	2	0
sp|Q96A22|CK052_HUMAN Uncharacterized protein C11orf52 OS=Homo sapiens GN=C11orf52 PE=2 SV=2	sp|Q96A22|CK052_HUMANUncharacterized protein C11orf52 OS=Homo sapiens GN=C11orf52 PE=2 SV=2	0.4	1	0	0	0	0	1	0	2
Isoform 3 of Mitogen-activated protein kinase 3 OS=Homo sapiens GN=MAPK3	sp|P27361-3|MK03_HUMAN	0.39	0	0	2	0	0	1	0	0

sp|Q8WUJ3|K1199_HUMAN Protein KIAA1199 OS=Homo sapiens GN=KIAA1199 PE=2 SV=2	sp|Q8WUJ3|K1199_HUMANProtein KIAA1199 OS=Homo sapiens GN=KIAA1199 PE=2 SV=2	0.36	0	0	0	0	0	3	0	0
sp|Q9NP55|BPIA1_HUMAN BPI fold-containing family A member 1 OS=Homo sapiens GN=BPIFA1 PE=1 SV=1	sp|Q9NP55|BPIA1_HUMANBPI fold-containing family A member 1 OS=Homo sapiens GN=BPIFA1 PE=1 SV=1	0.36	0	0	0	0	0	0	2	0
Histone H2A type 3 OS=Homo sapiens GN=HIST3H2A PE=1 SV=3	H2A3_HUMAN	0.42	4	0	0	0	0	0	0	0
sp|Q13442|HAP28_HUMAN 28 kDa heat- and acid-stable phosphoprotein OS=Homo sapiens...	sp|Q13442|HAP28_HUMAN28 kDa heat- and acid-stable phosphoprotein OS=Homo sapiens GN=PDAP1 PE=1 SV=1	0.36	10	0	0	0	0	0	0	0
sp|O60739|EIF1B_HUMAN Eukaryotic translation initiation factor 1b OS=Homo sapiens GN=EIF1B PE=1 SV=2	sp|O60739|EIF1B_HUMANEukaryotic translation initiation factor 1b OS=Homo sapiens GN=EIF1B PE=1 SV=2	0.36	9	0	0	0	0	0	0	0
sp|O14602|IF1AY_HUMAN Eukaryotic translation initiation factor 1A, Y-chromosomal OS=Homo sapiens GN=EIF1AY PE=1 SV=4	sp|O14602|IF1AY_HUMANEukaryotic translation initiation factor 1A, Y-chromosomal OS=Homo sapiens GN=EIF1AY PE=1 SV=4	0.36	11	0	0	0	0	0	0	0
sp|Q15233-2|NONO_HUMAN Isoform 2 of Non-POU domain-containing octamer-binding protein...	sp|Q15233-2|NONO_HUMAN Isoform 2 of Non-POU domain-containing octamer-binding protein...	0.36	18	0	0	0	0	0	0	0
sp|P50148|GNAQ_HUMAN Guanine nucleotide-binding protein G(q) subunit alpha OS=Homo...	sp|P50148|GNAQ_HUMAN Guanine nucleotide-binding protein G(q) subunit alpha OS=Homo...	0.61	3	2	0	1	1	2	1	3
sp|O95166|GBRAP_HUMAN Gamma-aminobutyric acid receptor-associated protein OS=Homo sapiens GN=GABARAP PE=1 SV=1	sp|O95166|GBRAP_HUMANGamma-aminobutyric acid receptor-associated protein OS=Homo sapiens GN=GABARAP PE=1 SV=1	0.71	8	0	0	0	1	1	1	2
sp|Q7KZF4|SND1_HUMAN Staphylococcal nuclease domain-containing protein 1 OS=Homo...	sp|Q7KZF4|SND1_HUMAN Staphylococcal nuclease domain-containing protein 1 OS=Homo...	0.41	2	0	1	0	0	0	3	3
sp|P48739|PIPNB_HUMAN Phosphatidylinositol transfer protein beta isoform OS=Homo...	sp|P48739|PIPNB_HUMANPhosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB PE=1 SV=2	0.088	0	0	0	0	1	4	0	1
sp|Q96AE7|TTC17_HUMAN Tetratricopeptide repeat protein 17 OS=Homo sapiens GN=TTC17 PE=2 SV=1	sp|Q96AE7|TTC17_HUMANTetratricopeptide repeat protein 17 OS=Homo sapiens GN=TTC17 PE=2 SV=1	0.66	0	1	0	0	0	0	2	0
sp|Q8TC12|RDH11_HUMAN Retinol dehydrogenase 11 OS=Homo sapiens GN=RDH11 PE=1 SV=2	sp|Q8TC12|RDH11_HUMANRetinol dehydrogenase 11 OS=Homo sapiens GN=RDH11 PE=1 SV=2	0.13	0	0	0	0	0	2	4	0

sp|Q8WUN7|UBTD2_HUMAN Ubiquitin domain-containing protein 2 OS=Homo sapiens GN=UBTD2 PE=1 SV=2	sp|Q8WUN7|UBTD2_HUMANUbiquitin domain-containing protein 2 OS=Homo sapiens GN=UBTD2 PE=1 SV=2	0.36	0	0	0	0	4	0	0	0
sp|P10606|COX5B_HUMAN Cytochrome c oxidase subunit 5B, mitochondrial OS=Homo sapiens GN=COX5B PE=1 SV=2	sp|P10606|COX5B_HUMANCytochrome c oxidase subunit 5B, mitochondrial OS=Homo sapiens GN=COX5B PE=1 SV=2	0.36	13	0	0	0	0	0	0	0
Isoform 2 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1	sp|Q32MZ4-2|LRRF1_HUMAN	0.067	4	2	1	1	1	0	0	1
sp|P17858|K6PL_HUMAN 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1...	sp|P17858|K6PL_HUMAN 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1...	0.4	1	3	0	1	1	0	2	0
sp|P43034|LIS1_HUMAN Platelet-activating factor acetylhydrolase IB subunit alpha...	sp|P43034|LIS1_HUMAN Platelet-activating factor acetylhydrolase IB subunit alpha...	0.66	0	3	1	0	0	2	2	1
sp|P07098-3|LIPG_HUMAN Isoform 3 of Gastric triacylglycerol lipase OS=Homo sapiens...	sp|P07098-3|LIPG_HUMAN Isoform 3 of Gastric triacylglycerol lipase OS=Homo sapiens... (+1)	0.34	0	1	0	0	0	5	0	1
Isoform 3 of Dynactin subunit 3 OS=Homo sapiens GN=DCTN3	sp|O75935-3|DCTN3_HUMAN	0.46	0	0	2	0	0	7	0	0
sp|O14979|HNRDL_HUMAN Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens...	sp|O14979|HNRDL_HUMANHeterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRNPDL PE=1 SV=3	0.36	2	0	0	0	0	0	0	0
sp|Q9H3K6|BOLA2_HUMAN BolA-like protein 2 OS=Homo sapiens GN=BOLA2 PE=1 SV=1	sp|Q9H3K6|BOLA2_HUMANBolA-like protein 2 OS=Homo sapiens GN=BOLA2 PE=1 SV=1	0.36	11	0	0	0	0	0	0	0
Isoform 5 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1	sp|O60828-5|PQBP1_HUMAN	0.36	3	0	0	0	0	0	0	0
60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1	RL24_HUMAN	0.36	3	0	0	0	0	0	0	0
sp|O14737|PDCD5_HUMAN Programmed cell death protein 5 OS=Homo sapiens GN=PDCD5 PE=1 SV=3	sp|O14737|PDCD5_HUMANProgrammed cell death protein 5 OS=Homo sapiens GN=PDCD5 PE=1 SV=3	0.36	5	0	0	0	0	0	0	0
Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=2 SV=1	B4DNW0_HUMAN	0.3	0	3	1	0	0	1	1	1
60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=2 SV=1	F8VWS0_HUMAN	0.33	0	1	0	2	2	0	1	2

Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3	sp|P26639|SYTC_HUMAN	0.45	2	3	0	0	0	2	0	3
sp|P62191|PRS4_HUMAN 26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1...	sp|P62191|PRS4_HUMAN 26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1...	0.42	1	0	2	0	0	3	0	0
sp|Q9NTM9|CUTC_HUMAN Copper homeostasis protein cutC homolog OS=Homo sapiens GN=CUTC...	sp|Q9NTM9|CUTC_HUMAN Copper homeostasis protein cutC homolog OS=Homo sapiens GN=CUTC... (+1)	0.42	0	1	0	1	1	0	7	0
sp|P31151|S10A7_HUMAN Protein S100-A7 OS=Homo sapiens GN=S100A7 PE=1 SV=4	sp|P31151|S10A7_HUMANProtein S100-A7 OS=Homo sapiens GN=S100A7 PE=1 SV=4	0.14	0	0	0	0	2	0	3	0
26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3	sp|O00231|PSD11_HUMAN (+1)	0.13	0	0	0	0	0	5	0	5
sp|Q9HCU4|CELR2_HUMAN Cadherin EGF LAG seven-pass G-type receptor 2 OS=Homo sapiens...	sp|Q9HCU4|CELR2_HUMANCadherin EGF LAG seven-pass G-type receptor 2 OS=Homo sapiens...	0.47	1	0	0	0	0	0	5	0
Cell division cycle-associated protein 3 OS=Homo sapiens GN=CDCA3 PE=2 SV=1	F8WDL1_HUMAN	0.36	5	0	0	0	0	0	0	0
Prefoldin subunit 6 OS=Homo sapiens GN=PFDN6 PE=1 SV=1	PFD6_HUMAN	0.36	10	0	0	0	0	0	0	0
Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial (Fragment) OS=Homo sapiens GN=DUT PE=2 SV=1	H0YKC5_HUMAN	0.36	8	0	0	0	0	0	0	0
sp|P20674|COX5A_HUMAN Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens...	sp|P20674|COX5A_HUMANCytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=1 SV=2	0.36	10	0	0	0	0	0	0	0
Isoform 4 of Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1	sp|Q9UKV3-5|ACINU_HUMAN	0.36	2	0	0	0	0	0	0	0
sp|Q7Z6Z7-3|HUWE1_HUMAN Isoform 3 of E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens...	sp|Q7Z6Z7-3|HUWE1_HUMAN Isoform 3 of E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens... (+1)	0.36	4	0	0	0	0	0	0	0
sp|Q7Z2W4|ZCCHV_HUMAN Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3	sp|Q7Z2W4|ZCCHV_HUMANZinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3	0.82	4	1	0	0	0	1	0	3
GTP-binding protein Rheb OS=Homo sapiens GN=RHEB PE=1 SV=1	RHEB_HUMAN	0.31	2	0	1	0	0	0	1	0

sp|P05186|PPBT_HUMAN Alkaline phosphatase, tissue-nonspecific isozyme OS=Homo sapiens...	sp|P05186|PPBT_HUMAN Alkaline phosphatase, tissue-nonspecific isozyme OS=Homo sapiens...	0.54	0	5	0	0	0	7	0	3
sp|P55145|MANF_HUMAN Mesencephalic astrocyte-derived neurotrophic factor OS=Homo...	sp|P55145|MANF_HUMAN Mesencephalic astrocyte-derived neurotrophic factor OS=Homo...	0.91	6	0	0	0	0	6	0	1
Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2	H2AZ_HUMAN (+1)	0.55	11	0	0	0	0	1	0	0
sp|Q53H82|LACB2_HUMAN Beta-lactamase-like protein 2 OS=Homo sapiens GN=LACTB2 PE=1 SV=2	sp|Q53H82|LACB2_HUMANBeta-lactamase-like protein 2 OS=Homo sapiens GN=LACTB2 PE=1 SV=2	0.36	0	0	0	0	0	0	2	0
Acetyl-CoA acetyltransferase, mitochondrial (Fragment) OS=Homo sapiens GN=ACAT1 PE=3 SV=1	H0YEL7_HUMAN	0.36	11	0	0	0	0	0	0	0
sp|Q14019|COTL1_HUMAN Coactosin-like protein OS=Homo sapiens GN=COTL1 PE=1 SV=3	sp|Q14019|COTL1_HUMANCoactosin-like protein OS=Homo sapiens GN=COTL1 PE=1 SV=3	0.96	0	1	0	2	2	1	0	0
Isoform 5 of Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNRD1	sp|Q16881-5|TRXR1_HUMAN	0.51	0	0	1	4	4	0	1	0
Isoform 4 of Disintegrin and metalloproteinase domain-containing protein 15 OS=Homo sapiens GN=ADAM15	sp|Q13444-4|ADA15_HUMAN	0.37	1	0	1	0	0	0	0	5
sp|P14550|AK1A1_HUMAN Alcohol dehydrogenase [NADP(+)] OS=Homo sapiens GN=AKR1A1 PE=1...	sp|P14550|AK1A1_HUMANAlcohol dehydrogenase [NADP(+)] OS=Homo sapiens GN=AKR1A1 PE=1...	0.31	0	0	11	2	0	0	0	0
sp|Q9H299|SH3L3_HUMAN SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo...	sp|Q9H299|SH3L3_HUMANSH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGRL3 PE=1 SV=1	0.33	9	0	0	2	2	0	0	0
sp|O75340-2|PDCD6_HUMAN Isoform 2 of Programmed cell death protein 6 OS=Homo sapiens...	sp|O75340-2|PDCD6_HUMAN Isoform 2 of Programmed cell death protein 6 OS=Homo sapiens...	0.42	0	0	8	0	0	1	0	2
sp|Q12929|EPS8_HUMAN Epidermal growth factor receptor kinase substrate 8 OS=Homo...	sp|Q12929|EPS8_HUMAN Epidermal growth factor receptor kinase substrate 8 OS=Homo...	0.47	0	5	0	0	0	0	0	1
Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3	CO6A1_HUMAN	0.57	0	4	0	0	0	6	0	0
sp|P62195-2|PRS8_HUMAN Isoform 2 of 26S protease regulatory subunit 8 OS=Homo sapiens...	sp|P62195-2|PRS8_HUMAN Isoform 2 of 26S protease regulatory subunit 8 OS=Homo sapiens...	0.26	0	0	0	0	0	3	0	0
sp|Q92688|AN32B_HUMAN Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1	sp|Q92688|AN32B_HUMANAcidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1	0.36	5	0	0	0	0	0	0	0

sp|O95182|NDUA7_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7 OS=Homo sapiens GN=NDUFA7 PE=1 SV=3	sp|O95182|NDUA7_HUMANNADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7 OS=Homo sapiens GN=NDUFA7 PE=1 SV=3	0.36	3	0	0	0	0	0	0	0
sp|P78527-2|PRKDC_HUMAN Isoform 2 of DNA-dependent protein kinase catalytic subunit...	sp|P78527-2|PRKDC_HUMAN Isoform 2 of DNA-dependent protein kinase catalytic subunit... (+1)	0.36	4	0	0	0	0	0	0	0
sp|Q14847-2|LASP1_HUMAN Isoform 2 of LIM and SH3 domain protein 1 OS=Homo sapiens...	sp|Q14847-2|LASP1_HUMAN Isoform 2 of LIM and SH3 domain protein 1 OS=Homo sapiens... (+2)	0.36	12	0	0	0	0	0	0	0
tr|C9J8S2|C9J8S2_HUMAN Retinoic acid receptor responder protein 2 (Fragment) OS=Homo...	tr|C9J8S2|C9J8S2_HUMAN Retinoic acid receptor responder protein 2 (Fragment) OS=Homo...	0.8	3	1	0	1	1	1	2	2
sp|O95394|AGM1_HUMAN Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 PE=1...	sp|O95394|AGM1_HUMAN Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 PE=1...	0.66	0	0	1	3	3	0	4	0
sp|Q969H8|CS010_HUMAN UPF0556 protein C19orf10 OS=Homo sapiens GN=C19orf10 PE=1 SV=1	sp|Q969H8|CS010_HUMANUPF0556 protein C19orf10 OS=Homo sapiens GN=C19orf10 PE=1 SV=1	0.33	2	0	0	0	0	4	0	3
sp|P21283|VATC1_HUMAN V-type proton ATPase subunit C 1 OS=Homo sapiens GN=ATP6V1C1 PE=1 SV=4	sp|P21283|VATC1_HUMANV-type proton ATPase subunit C 1 OS=Homo sapiens GN=ATP6V1C1 PE=1 SV=4	0.36	0	0	0	0	0	0	0	4
Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	APOA1_HUMAN	0.36	0	0	9	0	0	0	0	0
IgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3	FCGBP_HUMAN	0.36	0	0	0	0	0	3	0	0
Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	LAMA5_HUMAN	0.36	0	0	0	0	0	9	0	0
sp|O60869-2|EDF1_HUMAN Isoform 2 of Endothelial differentiation-related factor 1...	sp|O60869-2|EDF1_HUMAN Isoform 2 of Endothelial differentiation-related factor 1... (+1)	0.36	12	0	0	0	0	0	0	0
sp|O75475-2|PSIP1_HUMAN Isoform 2 of PC4 and SFRS1-interacting protein OS=Homo sapiens...	sp|O75475-2|PSIP1_HUMAN Isoform 2 of PC4 and SFRS1-interacting protein OS=Homo sapiens... (+2)	0.36	13	0	0	0	0	0	0	0
Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=2 SV=1	H0YLE8_HUMAN	0.36	0	0	3	0	0	0	0	0
Isoform 2 of Semenogelin-1 OS=Homo sapiens GN=SEMG1	sp|P04279-2|SEMG1_HUMAN	0.36	0	0	0	0	0	7	0	0
sp|Q8WW22-2|DNJA4_HUMAN Isoform 2 of DnaJ homolog subfamily A member 4 OS=Homo sapiens...	sp|Q8WW22-2|DNJA4_HUMAN Isoform 2 of DnaJ homolog subfamily A member 4 OS=Homo sapiens... (+1)	0.94	1	0	1	0	0	4	1	1

sp|P78324|SHPS1_HUMAN Tyrosine-protein phosphatase non-receptor type substrate 1 OS=Homo sapiens GN=SIRPA PE=1 SV=2	sp|P78324|SHPS1_HUMANTyrosine-protein phosphatase non-receptor type substrate 1 OS=Homo sapiens GN=SIRPA PE=1 SV=2	0.082	0	1	0	0	2	4	2	0
Isoform 2 of Calcineurin-like phosphoesterase domain-containing protein 1 OS=Homo sapiens GN=CPPED1	CPPED_HUMAN	0.77	0	0	1	0	1	0	2	2
sp|P48047|ATPO_HUMAN ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O...	sp|P48047|ATPO_HUMAN ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O...	0.83	4	1	0	0	0	1	3	0
sp|Q9UL26|RB22A_HUMAN Ras-related protein Rab-22A OS=Homo sapiens GN=RAB22A PE=1 SV=2	sp|Q9UL26|RB22A_HUMANRas-related protein Rab-22A OS=Homo sapiens GN=RAB22A PE=1 SV=2	0.53	2	2	0	0	0	0	2	0
Isoform 3 of Neuronal cell adhesion molecule OS=Homo sapiens GN=NRCAM	sp|Q92823-3|NRCAM_HUMAN	0.55	0	3	0	0	0	0	0	1
Chromobox protein homolog 5 OS=Homo sapiens GN=CBX5 PE=1 SV=1	CBX5_HUMAN	0.36	2	0	0	0	0	0	0	0
sp|O95757|HS74L_HUMAN Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=1 SV=3	sp|O95757|HS74L_HUMANHeat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=1 SV=3	0.31	0	0	0	0	0	0	6	0
sp|P56211|ARP19_HUMAN cAMP-regulated phosphoprotein 19 OS=Homo sapiens GN=ARPP19 PE=1 SV=2	sp|P56211|ARP19_HUMANcAMP-regulated phosphoprotein 19 OS=Homo sapiens GN=ARPP19 PE=1 SV=2	0.36	8	0	0	0	0	0	0	0
sp|A6NEL2|SWAHB_HUMAN Ankyrin repeat domain-containing protein SOWAHB OS=Homo sapiens...	sp|A6NEL2|SWAHB_HUMANAnkyrin repeat domain-containing protein SOWAHB OS=Homo sapiens...	0.36	0	0	0	0	0	0	5	0
sp|P56385|ATP5I_HUMAN ATP synthase subunit e, mitochondrial OS=Homo sapiens GN=ATP5I PE=1 SV=2	sp|P56385|ATP5I_HUMANATP synthase subunit e, mitochondrial OS=Homo sapiens GN=ATP5I PE=1 SV=2	0.36	10	0	0	0	0	0	0	0
sp|Q13573|SNW1_HUMAN SNW domain-containing protein 1 OS=Homo sapiens GN=SNW1 PE=1...	sp|Q13573|SNW1_HUMAN SNW domain-containing protein 1 OS=Homo sapiens GN=SNW1 PE=1... (+1)	0.36	8	0	0	0	0	0	0	0
Small acidic protein OS=Homo sapiens GN=SMAP PE=1 SV=1	SMAP_HUMAN	0.36	6	0	0	0	0	0	0	0
Receptor-type tyrosine-protein phosphatase eta OS=Homo sapiens GN=PTPRJ PE=1 SV=3	sp|Q12913|PTPRJ_HUMAN	0.36	0	0	0	0	0	4	0	0

sp|Q8WUM4-2|PDC6I_HUMAN Isoform 2 of Programmed cell death 6-interacting protein...	sp|Q8WUM4-2|PDC6I_HUMAN Isoform 2 of Programmed cell death 6-interacting protein...	0.15	0	0	0	0	0	5	1	0
sp|P11216|PYGB_HUMAN Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1...	sp|P11216|PYGB_HUMAN Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1...	0.31	1	7	0	0	0	0	0	1
sp|O60282|KIF5C_HUMAN Kinesin heavy chain isoform 5C OS=Homo sapiens GN=KIF5C PE=1...	sp|O60282|KIF5C_HUMANKinesin heavy chain isoform 5C OS=Homo sapiens GN=KIF5C PE=1 SV=1	0.93	0	2	0	0	0	0	0	0
sp|Q9C005|DPY30_HUMAN Protein dpy-30 homolog OS=Homo sapiens GN=DPY30 PE=1 SV=1	sp|Q9C005|DPY30_HUMANProtein dpy-30 homolog OS=Homo sapiens GN=DPY30 PE=1 SV=1	0.36	2	0	0	0	0	0	0	0
60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	sp|P62899|RL31_HUMAN	0.36	8	0	0	0	0	0	0	0
sp|O43447|PPIH_HUMAN Peptidyl-prolyl cis-trans isomerase H OS=Homo sapiens GN=PPIH...	sp|O43447|PPIH_HUMAN Peptidyl-prolyl cis-trans isomerase H OS=Homo sapiens GN=PPIH...	0.36	4	0	0	0	0	0	0	0
Isoform 2 of Transcription and mRNA export factor ENY2 OS=Homo sapiens GN=ENY2	ENY2_HUMAN (+1)	0.36	10	0	0	0	0	0	0	0
sp|Q9H008|LHPP_HUMAN Phospholysine phosphohistidine inorganic pyrophosphate phosphatase...	sp|Q9H008|LHPP_HUMAN Phospholysine phosphohistidine inorganic pyrophosphate phosphatase...	0.26	1	3	1	1	1	1	2	0
5'(3')-deoxyribonucleotidase, cytosolic type OS=Homo sapiens GN=NT5C PE=2 SV=1	J3KRC4_HUMAN	0.69	1	2	0	0	0	1	0	1
sp|P14868|SYDC_HUMAN Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS...	sp|P14868|SYDC_HUMAN Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS... (+1)	0.46	0	0	3	0	0	0	2	1
V-type proton ATPase subunit D OS=Homo sapiens GN=ATP6V1D PE=2 SV=1	G3V2S6_HUMAN	0.64	0	1	0	0	0	2	0	0
sp|O75531|BAF_HUMAN Barrier-to-autointegration factor OS=Homo sapiens GN=BANF1 PE=1...	sp|O75531|BAF_HUMAN Barrier-to-autointegration factor OS=Homo sapiens GN=BANF1 PE=1...	0.42	8	0	0	0	0	0	1	0
sp|Q9BXV9|CN142_HUMAN Uncharacterized protein C14orf142 OS=Homo sapiens GN=C14orf142 PE=1 SV=2	sp|Q9BXV9|CN142_HUMANUncharacterized protein C14orf142 OS=Homo sapiens GN=C14orf142 PE=1 SV=2	0.36	4	0	0	0	0	0	0	0
sp|P23246|SFPQ_HUMAN Splicing factor, proline- and glutamine-rich OS=Homo sapiens...	sp|P23246|SFPQ_HUMAN Splicing factor, proline- and glutamine-rich OS=Homo sapiens...	0.36	6	0	0	0	0	0	0	0

sp|C9JI98|TM238_HUMAN Transmembrane protein 238 OS=Homo sapiens GN=TMEM238 PE=1 SV=1	sp|C9JI98|TM238_HUMANTransmembrane protein 238 OS=Homo sapiens GN=TMEM238 PE=1 SV=1	0.36	0	0	0	0	0	3	0	0
sp|Q96C90|PP14B_HUMAN Protein phosphatase 1 regulatory subunit 14B OS=Homo sapiens GN=PPP1R14B PE=1 SV=3	sp|Q96C90|PP14B_HUMANProtein phosphatase 1 regulatory subunit 14B OS=Homo sapiens GN=PPP1R14B PE=1 SV=3	0.36	4	0	0	0	0	0	0	0
NHP2-like protein 1 OS=Homo sapiens GN=NHP2L1 PE=2 SV=1	B1AHD1_HUMAN (+1)	0.36	7	0	0	0	0	0	0	0
sp|Q9GZT3|SLIRP_HUMAN SRA stem-loop-interacting RNA-binding protein, mitochondrial...	sp|Q9GZT3|SLIRP_HUMANSRA stem-loop-interacting RNA-binding protein, mitochondrial OS=Homo sapiens GN=SLIRP PE=1 SV=1	0.36	8	0	0	0	0	0	0	0
sp|Q8TD19|NEK9_HUMAN Serine/threonine-protein kinase Nek9 OS=Homo sapiens GN=NEK9...	sp|Q8TD19|NEK9_HUMAN Serine/threonine-protein kinase Nek9 OS=Homo sapiens GN=NEK9...	0.36	4	0	0	0	0	0	0	0
sp|Q9NPH2-2|INO1_HUMAN Isoform 2 of Inositol-3-phosphate synthase 1 OS=Homo sapiens...	sp|Q9NPH2-2|INO1_HUMAN Isoform 2 of Inositol-3-phosphate synthase 1 OS=Homo sapiens... (+5)	0.73	0	2	0	1	1	0	5	0
sp|Q9Y6E0|STK24_HUMAN Serine/threonine-protein kinase 24 OS=Homo sapiens GN=STK24 PE=1 SV=1	sp|Q9Y6E0|STK24_HUMANSerine/threonine-protein kinase 24 OS=Homo sapiens GN=STK24 PE=1 SV=1	0.64	1	1	0	0	1	0	2	0
sp|Q9Y2Q0|AT8A1_HUMAN Probable phospholipid-transporting ATPase IA OS=Homo sapiens...	sp|Q9Y2Q0|AT8A1_HUMANProbable phospholipid-transporting ATPase IA OS=Homo sapiens GN=ATP8A1 PE=1 SV=1	0.5	1	2	0	0	0	0	0	2
sp|P0C5Z0|H2AB2_HUMAN Histone H2A-Bbd type 2/3 OS=Homo sapiens GN=H2AFB2 PE=2 SV=1	sp|P0C5Z0|H2AB2_HUMANHistone H2A-Bbd type 2/3 OS=Homo sapiens GN=H2AFB2 PE=2 SV=1	0.21	0	0	0	0	0	0	3	1
Isoform 5 of Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A	sp|O15027-5|SC16A_HUMAN	0.36	6	0	0	0	0	0	0	0
sp|P62310|LSM3_HUMAN U6 snRNA-associated Sm-like protein LSm3 OS=Homo sapiens GN=LSM3...	sp|P62310|LSM3_HUMAN U6 snRNA-associated Sm-like protein LSm3 OS=Homo sapiens GN=LSM3...	0.36	3	0	0	0	0	0	0	0
sp|P38159|RBMX_HUMAN RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX...	sp|P38159|RBMX_HUMAN RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX... (+2)	0.36	6	0	0	0	0	0	0	0
sp|Q8IYB3|SRRM1_HUMAN Serine/arginine repetitive matrix protein 1 OS=Homo sapiens GN=SRRM1 PE=1 SV=2	sp|Q8IYB3|SRRM1_HUMANSerine/arginine repetitive matrix protein 1 OS=Homo sapiens GN=SRRM1 PE=1 SV=2	0.36	9	0	0	0	0	0	0	0

sp|P08238|HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1...	sp|P08238|HS90B_HUMANHeat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1...	0.36	0	0	8	0	0	0	0	0
Spondin-2 OS=Homo sapiens GN=SPON2 PE=1 SV=3	SPON2_HUMAN	0.36	0	0	0	0	0	7	0	0
sp|P05198|IF2A_HUMAN Eukaryotic translation initiation factor 2 subunit 1 OS=Homo...	sp|P05198|IF2A_HUMAN Eukaryotic translation initiation factor 2 subunit 1 OS=Homo...	0.48	2	0	1	1	1	1	2	0
sp|P63151|2ABA_HUMAN Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit...	sp|P63151|2ABA_HUMAN Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit...	0.27	1	4	1	0	0	1	0	1
Small VCP/p97-interacting protein OS=Homo sapiens GN=SVIP PE=3 SV=1	SVIP_HUMAN	0.4	0	0	1	2	2	0	2	0
sp|O95816|BAG2_HUMAN BAG family molecular chaperone regulator 2 OS=Homo sapiens GN=BAG2...	sp|O95816|BAG2_HUMAN BAG family molecular chaperone regulator 2 OS=Homo sapiens GN=BAG2...	0.44	0	1	2	0	0	4	1	0
Ethanolamine-phosphate cytidylyltransferase (Fragment) OS=Homo sapiens GN=PCYT2 PE=2 SV=1	I3L1L9_HUMAN	0.55	0	2	0	0	0	0	0	1
Immunoglobulin superfamily member 21 OS=Homo sapiens GN=IGSF21 PE=2 SV=1	IGS21_HUMAN	0.52	0	0	1	0	0	5	0	0
SAFB-like transcription modulator OS=Homo sapiens GN=SLTM PE=2 SV=1	H0YMR6_HUMAN	0.36	3	0	0	0	0	0	0	0
sp|P29762|RABP1_HUMAN Cellular retinoic acid-binding protein 1 OS=Homo sapiens GN=CRABP1 PE=2 SV=2	sp|P29762|RABP1_HUMANCellular retinoic acid-binding protein 1 OS=Homo sapiens GN=CRABP1 PE=2 SV=2	0.36	3	0	0	0	0	0	0	0
Ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=2 SV=1	J3KTE4_HUMAN (+2)	0.36	3	0	0	0	0	0	0	0
Isoform 2 of Ubiquitin-associated protein 2-like OS=Homo sapiens GN=UBAP2L	sp|Q14157-1|UBP2L_HUMAN	0.36	6	0	0	0	0	0	0	0
sp|P12956|XRCC6_HUMAN X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2	sp|P12956|XRCC6_HUMANX-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2	0.36	3	0	0	0	0	0	0	0
sp|Q8WW12|PCNP_HUMAN PEST proteolytic signal-containing nuclear protein OS=Homo sapiens...	sp|Q8WW12|PCNP_HUMAN PEST proteolytic signal-containing nuclear protein OS=Homo sapiens...	0.36	6	0	0	0	0	0	0	0

Isoform 2 of UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1	sp|Q9NYU2-2|UGGG1_HUMAN	0.36	0	0	0	0	0	2	0	0
sp|O43242|PSMD3_HUMAN 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens...	sp|O43242|PSMD3_HUMAN26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens...	0.36	0	0	4	0	0	0	0	0
Probable phospholipid-transporting ATPase IC OS=Homo sapiens GN=ATP8B1 PE=1 SV=3	AT8B1_HUMAN	0.36	0	0	0	0	0	4	0	0
sp|P13667|PDIA4_HUMAN Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1...	sp|P13667|PDIA4_HUMANProtein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1...	0.55	0	0	2	0	0	0	2	0
Keratin, type I cytoskeletal 12 OS=Homo sapiens GN=KRT12 PE=1 SV=1	K1C12_HUMAN	0.87	0	0	0	0	0	5	0	0
sp|CYB5_HUMAN|	sp|CYB5_HUMAN|	0.37	0	0	2	0	0	0	0	1
sp|P33240|CSTF2_HUMAN Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1	sp|P33240|CSTF2_HUMANCleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1	0.36	5	0	0	0	0	0	0	0
tr|G3V4I0|G3V4I0_HUMAN Ectonucleoside triphosphate diphosphohydrolase 5 OS=Homo sapiens...	tr|G3V4I0|G3V4I0_HUMAN Ectonucleoside triphosphate diphosphohydrolase 5 OS=Homo sapiens...	0.36	0	0	5	0	0	0	0	0
Isoform 2 of Protein phosphatase 1 regulatory subunit 21 OS=Homo sapiens GN=PPP1R21	sp|Q6ZMI0-2|PPR21_HUMAN	0.36	0	3	0	0	0	0	0	0
sp|Q13813-2|SPTN1_HUMAN Isoform 2 of Spectrin alpha chain, non-erythrocytic 1 OS=Homo...	sp|Q13813-2|SPTN1_HUMAN Isoform 2 of Spectrin alpha chain, non-erythrocytic 1 OS=Homo... (+1)	0.36	0	0	3	0	0	0	0	0
tr|E7ES35|E7ES35_HUMAN Tetratricopeptide repeat protein 38 OS=Homo sapiens GN=TTC38...	tr|E7ES35|E7ES35_HUMAN Tetratricopeptide repeat protein 38 OS=Homo sapiens GN=TTC38...	0.36	0	0	3	0	0	0	0	0
sp|Q9Y4Z0|LSM4_HUMAN U6 snRNA-associated Sm-like protein LSm4 OS=Homo sapiens GN=LSM4...	sp|Q9Y4Z0|LSM4_HUMAN U6 snRNA-associated Sm-like protein LSm4 OS=Homo sapiens GN=LSM4...	0.36	4	0	0	0	0	0	0	0
Transcriptional repressor p66-alpha (Fragment) OS=Homo sapiens GN=GATAD2A PE=2 SV=1	C9JHD7_HUMAN	0.36	7	0	0	0	0	0	0	0
tr|J3KNL6|J3KNL6_HUMAN Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A...	tr|J3KNL6|J3KNL6_HUMAN Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A...	0.36	7	0	0	0	0	0	0	0

Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=2 SV=1	B3KV44_HUMAN	0.35	0	0	4	1	1	0	0	0
sp|P33121|ACSL1_HUMAN Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1	sp|P33121|ACSL1_HUMANLong-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1	0.34	0	1	0	0	0	0	4	1
sp|P20042|IF2B_HUMAN Eukaryotic translation initiation factor 2 subunit 2 OS=Homo...	sp|P20042|IF2B_HUMAN Eukaryotic translation initiation factor 2 subunit 2 OS=Homo...	0.26	3	0	3	0	0	0	0	0
sp|P13647|K2C5_HUMAN Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1...	sp|P13647|K2C5_HUMAN Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1...	0.93	0	0	3	0	0	0	3	0
tr|F8W7I2|F8W7I2_HUMAN Prostaglandin-H2 D-isomerase OS=Homo sapiens GN=PTGDS PE=2...	tr|F8W7I2|F8W7I2_HUMAN Prostaglandin-H2 D-isomerase OS=Homo sapiens GN=PTGDS PE=2...	0.14	0	0	0	0	0	3	0	1
sp|P56282|DPOE2_HUMAN DNA polymerase epsilon subunit 2 OS=Homo sapiens GN=POLE2 PE=1...	sp|P56282|DPOE2_HUMANDNA polymerase epsilon subunit 2 OS=Homo sapiens GN=POLE2 PE=1 SV=2	0.36	0	3	0	0	0	0	0	0
Isoform 4 of Heterochromatin protein 1-binding protein 3 OS=Homo sapiens GN=HP1BP3	sp|Q5SSJ5-5|HP1B3_HUMAN	0.36	3	0	0	0	0	0	0	0
Alcohol dehydrogenase [NADP(+)] OS=Homo sapiens GN=AKR1A1 PE=1 SV=3	AK1A1_HUMAN	0.36	0	6	0	0	0	0	0	0
sp|P35606|COPB2_HUMAN Coatomer subunit beta' OS=Homo sapiens GN=COPB2 PE=1 SV=2	sp|P35606|COPB2_HUMANCoatomer subunit beta' OS=Homo sapiens GN=COPB2 PE=1 SV=2	0.36	0	0	0	0	0	0	2	0
SMARCA4 isoform 2 OS=Homo sapiens GN=SMARCA4 PE=2 SV=1	Q9HBD4_HUMAN (+1)	0.36	3	0	0	0	0	0	0	0
sp|Q9BUJ2|HNRL1_HUMAN Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=2	sp|Q9BUJ2|HNRL1_HUMANHeterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=2	0.36	4	0	0	0	0	0	0	0
sp|P56381|ATP5E_HUMAN ATP synthase subunit epsilon, mitochondrial OS=Homo sapiens GN=ATP5E PE=1 SV=2	sp|P56381|ATP5E_HUMANATP synthase subunit epsilon, mitochondrial OS=Homo sapiens GN=ATP5E PE=1 SV=2	0.36	5	0	0	0	0	0	0	0
sp|P55036|PSMD4_HUMAN 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1	sp|P55036|PSMD4_HUMAN26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1	0.36	5	0	0	0	0	0	0	0

Contactin-associated protein-like 2 OS=Homo sapiens GN=CNTNAP2 PE=1 SV=1	sp|Q9UHC6|CNTP2_HUMAN	0.36	0	0	0	0	0	2	0	0
tr|J3QRP6|J3QRP6_HUMAN Na(+)/H(+) exchange regulatory cofactor NHE-RF1 (Fragment)...	tr|J3QRP6|J3QRP6_HUMAN Na(+)/H(+) exchange regulatory cofactor NHE-RF1 (Fragment)...	0.36	0	0	0	0	0	2	0	0
sp|Q8TDI8|TMC1_HUMAN Transmembrane channel-like protein 1 OS=Homo sapiens GN=TMC1...	sp|Q8TDI8|TMC1_HUMAN Transmembrane channel-like protein 1 OS=Homo sapiens GN=TMC1...	0.94	0	0	0	2	2	0	0	0
sp|P21281|VATB2_HUMAN V-type proton ATPase subunit B, brain isoform OS=Homo sapiens...	sp|P21281|VATB2_HUMANV-type proton ATPase subunit B, brain isoform OS=Homo sapiens...	0.27	1	0	2	0	0	0	0	0
tr|D6REA1|D6REA1_HUMAN Nucleotide exchange factor SIL1 OS=Homo sapiens GN=SIL1 PE=2...	tr|D6REA1|D6REA1_HUMAN Nucleotide exchange factor SIL1 OS=Homo sapiens GN=SIL1 PE=2...	0.36	0	0	0	0	0	0	2	0
Isoform 2 of Eukaryotic translation initiation factor 2A OS=Homo sapiens GN=EIF2A	EIF2A_HUMAN	0.36	4	0	0	0	0	0	0	0
sp|P36543-2|VATE1_HUMAN Isoform 2 of V-type proton ATPase subunit E 1 OS=Homo sapiens...	sp|P36543-2|VATE1_HUMAN Isoform 2 of V-type proton ATPase subunit E 1 OS=Homo sapiens...	0.36	0	0	0	0	0	4	0	0
sp|Q96KP4|CNDP2_HUMAN Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2...	sp|Q96KP4|CNDP2_HUMANCytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2...	0.36	0	0	2	0	0	0	0	0
sp|O60885|BRD4_HUMAN Bromodomain-containing protein 4 OS=Homo sapiens GN=BRD4 PE=1...	sp|O60885|BRD4_HUMAN Bromodomain-containing protein 4 OS=Homo sapiens GN=BRD4 PE=1...	0.36	2	0	0	0	0	0	0	0
sp|Q03167-2|TGBR3_HUMAN Isoform 2 of Transforming growth factor beta receptor type...	sp|Q03167-2|TGBR3_HUMAN Isoform 2 of Transforming growth factor beta receptor type...	0.42	0	0	1	0	0	0	2	0
sp|P18440|ARY1_HUMAN Arylamine N-acetyltransferase 1 OS=Homo sapiens GN=NAT1 PE=1...	sp|P18440|ARY1_HUMAN Arylamine N-acetyltransferase 1 OS=Homo sapiens GN=NAT1 PE=1... (+1)	0.16	0	0	0	0	0	1	2	0
tr|E9PET8|E9PET8_HUMAN Kinesin heavy chain isoform 5C OS=Homo sapiens GN=KIF5C PE=2...	tr|E9PET8|E9PET8_HUMAN Kinesin heavy chain isoform 5C OS=Homo sapiens GN=KIF5C PE=2...	0.36	0	0	0	0	0	3	0	0
sp|P30049|ATPD_HUMAN ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D...	sp|P30049|ATPD_HUMAN ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D...	0.36	2	0	0	0	0	0	0	0
sp|O75746|CMC1_HUMAN Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo...	sp|O75746|CMC1_HUMAN Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo... (+1)	0.36	3	0	0	0	0	0	0	0

sp|P52655|TF2AA_HUMAN Transcription initiation factor IIA subunit 1 OS=Homo sapiens GN=GTF2A1 PE=1 SV=1	sp|P52655|TF2AA_HUMANTranscription initiation factor IIA subunit 1 OS=Homo sapiens GN=GTF2A1 PE=1 SV=1	0.36	2	0	0	0	0	0	0	0
MAM domain-containing protein 2 OS=Homo sapiens GN=MAMDC2 PE=2 SV=3	sp|Q7Z304|MAMC2_HUMAN	0.36	0	0	0	0	0	0	0	2
tr|E5RIU9|E5RIU9_HUMAN Charged multivesicular body protein 7 (Fragment) OS=Homo sapiens...	tr|E5RIU9|E5RIU9_HUMAN Charged multivesicular body protein 7 (Fragment) OS=Homo sapiens...	0.36	0	0	0	0	0	0	0	2